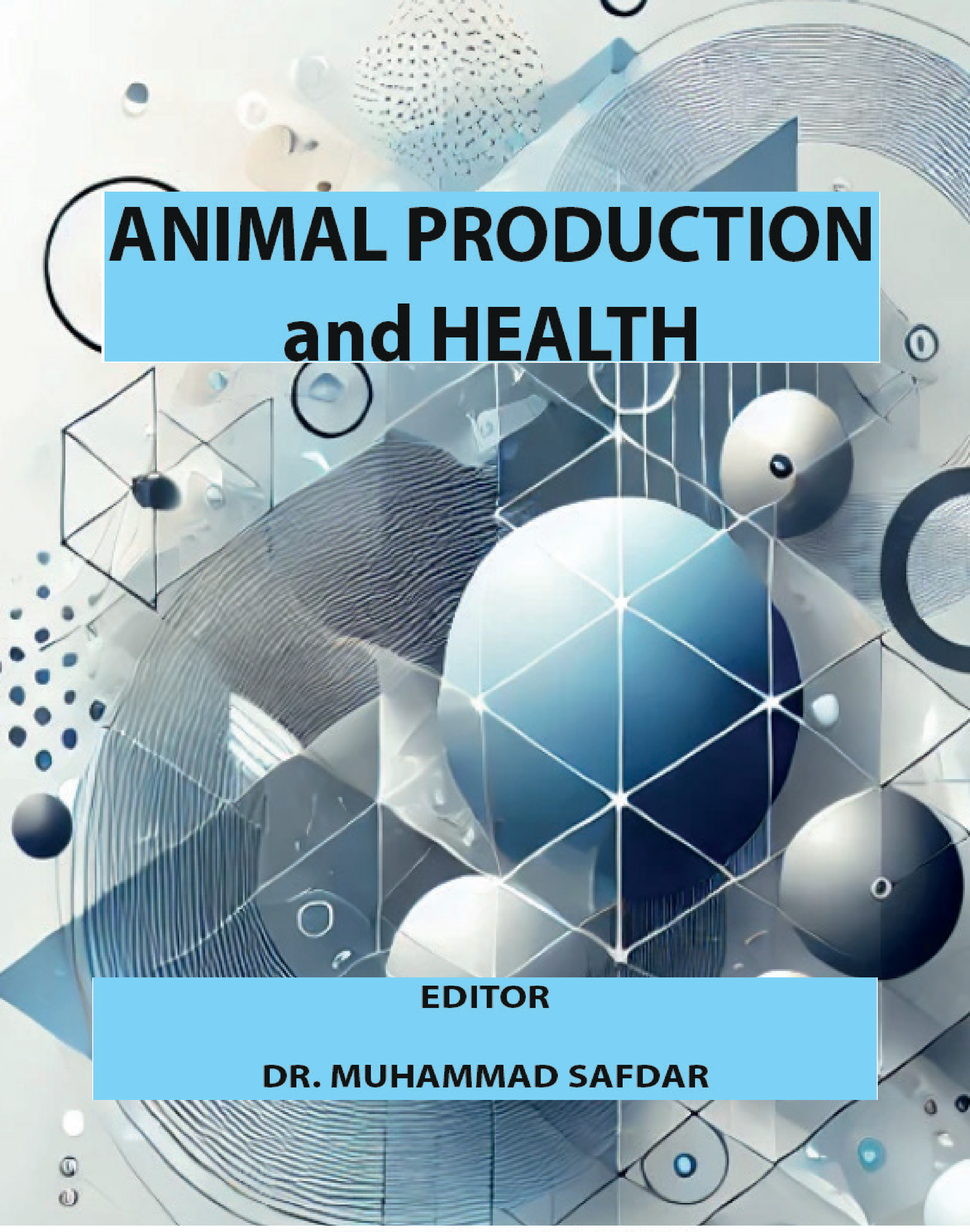

ANIMAL PRODUCTION and HEALTH

EDITOR

DR. MUHAMMAD SAFDAR

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EDITOR
Dr. Muhammed SAFDAR

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Editor
Dr. Muhammed SAFDAR

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ANIMAL PRODUCTION AND HEALTH

PREFACE

The global demand for animal products is rapidly increasing as the human population grows, necessitating more efficient, sustainable, and ethical approaches to animal production and health. This book, *Animal Production and Health*, offers a comprehensive exploration of the latest research and advancements in livestock production, genetics, and animal health. It also emphasizes the ongoing transformation in these fields, addressing the dual challenges of climate change and public health, while promoting sustainability in livestock production and management.

In Section I: Animal Production and Technology, the focus is on the historical livestock breed development, genetic improvement, and technological innovations. The chapter on the *History of Development of Livestock Breeds in the World* provides an in-depth exploration of how global breeding efforts have evolved. *Breeding Objectives: Aligning Genetics with Goals* highlights the need for setting clear genetic targets to meet industry demands. Additionally, *Genetic Diversity in Livestock Breeds: Challenges and Conservation* discusses the critical importance of conserving genetic diversity in an era of increased commercial breeding. Other key chapters include the application of *Quantitative Genetics* and the revolutionary impact of *Genomic Tools and Technologies* on livestock improvement. The role of cutting-edge methods, such as *CRISPR* Technology and Molecular Docking in feed science, is explored, along with the advent of *Precision Livestock Farming*. The environmental impact of animal production, including greenhouse gas emissions and climate change, is also thoroughly examined, along with the role of probiotics in improving poultry performance.

Section II: Animal Health shifts the focus to livestock disease prevention and control. This section covers a range of topics including the role of Probiotics in promoting animal health, prevention of major diseases like *Foot and Mouth Disease (FMD)*, and the public health implications of zoonotic diseases. The section also explores into symbiotic relationships between microorganisms and animals, highlighting potential new health interventions. Emerging technologies, such as *Green Nanoparticles* and *Nano-Emulsions*, are explored for their potential to enhance livestock health. Furthermore, discussions on the impact of diseases such as *H5N1 Influenza on Dairy Cows*, reproductive health issues, and the rising threat of *Emerging Infectious Diseases (EIDs)* emphasize the critical need for continued innovation in animal health and management.

This book is the result of a collaborative effort by leading scientists, researchers, and practitioners in the field of animal sciences. It serves as a valuable resource for researchers, veterinarians, animal breeders, and students, offering critical insights into both the challenges and opportunities in modern livestock production and health management.

October 2024

Dr. Muhammad Safdar
D.V.M (Pakistan) MS & PhD (Turkey)
Department of Breeding and Genetics, Cholistan University of Veterinary
and Animal Sciences Bahawalpur, Pakistan
Email: msafdar@cuvas.edu.pk, ORCID: 0000 0002 3720 2090

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SECTION I:

ANIMAL PRODUCTION and TECHNOLOGY

HISTORY OF DEVELOPMENT OF LIVESTOCK BREEDS IN THE WORLD

Shahzad ALI

Muhammad SAFDAR

Early Domestication (10,000–3,000 BCE)

The Neolithic Revolution, around 10,000 BCE, marked the transition from hunter-gatherer societies to agriculture and settled communities. This significant change began in the Fertile Crescent, located in modern-day Middle East. During this period, humans started the initial domestication of various animals, including sheep, goats, cattle, and pigs. These early domesticated animals were essential for providing food, clothing, and labor, which supported the growth of early human settlements. As agriculture spread across different regions, so did domesticated livestock. By 6,000 BCE, sheep and goats had reached Europe, while cattle had spread to Africa and Europe. The movement of domesticated animals was facilitated by trade routes and human migration, allowing different cultures to adopt and adapt these valuable resources.

Ancient Civilizations (3,000 BCE–500 CE)

As early civilizations developed in Mesopotamia, Egypt, the Indus Valley, and China, they began to recognize the importance of selective breeding. These civilizations started to select animals for specific traits such as docility, size, strength, and wool production. For instance, in Mesopotamia, sheep were bred for their wool, which became a crucial commodity for trade. In Egypt, cattle were valued for their milk and as draft animals. The process of specialization began during this era, with some livestock being bred for particular purposes, such as dairy production, meat, or labor. This specialization marked the beginning of more organized breeding practices, which laid the foundation for future advancements in livestock breeding.

Middle Ages (500–1500 CE)

During the Middle Ages, monasteries in Europe played a crucial role in the improvement of livestock breeds. Monks in these monasteries meticulously selected animals for desirable traits and kept detailed records of their breeding programs. This period saw the introduction of improved breeding practices, as well as the movement of people and trade routes that brought new livestock breeds to different regions. For example, the Norman conquest of England introduced new breeds of cattle and horses, which were selectively bred for better traits such as strength and endurance. These new breeds were instrumental in agricultural activities and warfare, highlighting the importance of strategic breeding during this era.

Early Modern Period (1500–1800)

The Renaissance and Enlightenment periods brought a renewed interest in scientific approaches to agriculture. This era saw the development of more systematic breeding methods, driven by the increasing knowledge of animal biology and genetics. In Britain, pioneers like Robert Bakewell applied selective breeding techniques with great succes Bakewell’s work with sheep and cattle, particularly the development of the Leicester Longwool sheep, led to significant improvements in size, wool quality, and meat production. Bakewell's systematic approach to breeding, which included inbreeding and record- keeping, laid the foundation for modern animal breeding practices and set the stage for future advancements.

Industrial Revolution (1800–1900)

The Industrial Revolution brought significant changes to livestock breeding, driven by technological advancements and the expansion of the British Empire. During this period, specialized breeds for meat, milk, and wool production emerged, catering to the growing demands of urban populations. The establishment of livestock shows and competitions, such as those organized by the Royal Agricultural Society of England, promoted breed standards and encouraged breeders to improve their stock. These events provided a platform for showcasing the best animals, fostering competition, and setting benchmarks for breeding excellence. The Industrial Revolution also facilitated the global spread of specific breeds, as improved transportation allowed for the export of livestock to colonies and other countries.

20th Century

The 20th century witnessed revolutionary advancements in livestock breeding, largely due to the development of genetics and artificial insemination. Scientists like Gregor Mendel laid the groundwork for understanding heredity and genetic traits, which became crucial for breeding programs. Improved transportation and communication led to the global dissemination of livestock breeds, allowing New World countries like the United States, Australia, and Canada to develop their own breeds, often drawing on European and African stock. For example, the Angus breed, originally from Scotland, became widely popular in the United States for its superior meat quality. Concerns about biodiversity loss also emerged during this century, leading to efforts to preserve rare and heritage breeds. Organizations like The Livestock Conservancy in the U.S. and the Rare Breeds Survival Trust in the UK were founded to protect endangered breeds and maintain genetic diversity in livestock populations.

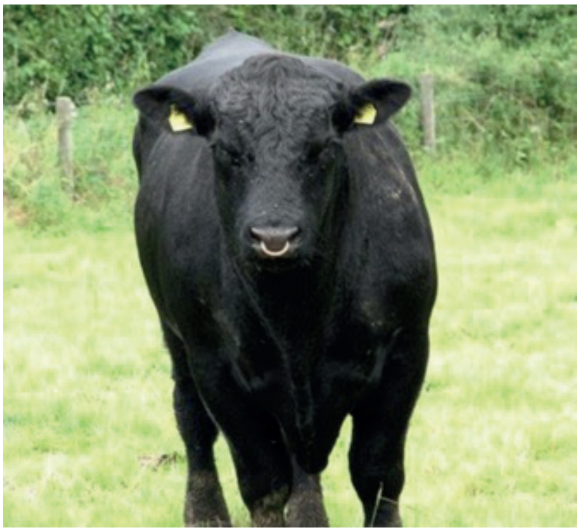
21st Century

Advances in genomic technology in the 21st century have revolutionized livestock breeding, allowing for precise selection of traits like disease resistance, growth rate, and production efficiency at the DNA level. These advancements have boosted the productivity and sustainability of livestock farming. Breeders now emphasize creating livestock that is productive, environmentally friendly, and humane, focusing on traits like improved feed efficiency and reduced methane emissions. Global communication and travel have facilitated crossbreeding, leading to new composite breeds that combine desirable traits from multiple genetic lines, enhancing livestock diversity and resilience.

CATTLE BREEDS

1. ANGUS

Angus cattle, also known as Aberdeen Angus, originate from Scotland and are renowned for their high-quality beef. Typically, solid black or red and naturally polled, they are medium-sized, hardy, and adaptable to various climates. Known for efficient feed conversion, Angus cattle are an economical choice for beef producers. Their beef is prized for its marbling, tenderness, and rich flavor, making it popular in the beef industry and sought after by high-end restaurants. Angus cattle are also key in crossbreeding programs to enhance meat quality in other breeds. They have a calm temperament, making them easy to handle, and their fertility and strong maternal instincts contribute to high calf survival rates. Overall, Angus cattle are highly valued in the beef industry for their adaptability, efficient production, and superior beef quality, with a significant global presence in cattle farming.



https://simple.m.wikipedia.org/wiki/Angus_cattle

2. AYRSHIRE

The Ayrshire cattle breed, originating from Ayrshire, Scotland, is known for its exceptional milk production and distinct red and white color patterns. Medium-sized and hardy, Ayrshires are adaptable to various climates and thrive in both pasture-based and intensive dairy systems, with excellent grazing abilities. Their milk, valued for its ideal balance of protein and butterfat, is particularly desirable for cheese production, contributing to high-quality dairy products. Ayrshires are recognized for their strong udders, longevity, and sustained milk production over multiple lactations. They have a calm temperament, making them easy to handle, and are known for their robust health and resistance to common cattle diseases. These traits make Ayrshires a reliable and favored choice among dairy farmers, contributing significantly to the global dairy industry and agricultural economy.

https://www.americandairy.com/dairy-farms/dairy-cows/ayrshire/

3. BRAHMAN

The Brahman cattle breed, originating from India, is highly valued for its adaptability and resilience in hot, humid climates. Recognizable by its distinctive hump over the shoulders, loose skin, and large, drooping ears, the Brahman is typically gray or red in color. This breed is well-known for its resistance to parasites and diseases, making it ideal for tropical environments. Brahmans are hardy animals, able to thrive on limited feed and water resources, which contributes to their popularity in various agricultural settings. They are primarily used in beef production, where their meat is appreciated for its tenderness and flavor. Additionally, Brahmans play a significant role in crossbreeding programs, enhancing the heat tolerance and disease resistance of other breeds. Their calm and intelligent nature makes them manageable in diverse farming systems. Overall, the Brahman breed is highly regarded for its adaptability, resilience, and contribution to both purebred and crossbreeding cattle operations worldwide.

https://www.farmghar.com/blogs/know-about-brahman-bull-a-complete-guide

Other breeds include Brown Swiss, Charolais, Gelbvieh, Holstein, Jersey, Limousin, Simmental and many more.

SHEEP BREEDS

1. CHEVIOT

The Cheviot sheep, originating from the Cheviot Hills on the England-Scotland border, are a hardy and distinctive breed known for their resilience, excellent wool quality, and adaptability to harsh climates. Medium-sized, with rams weighing 160 to 200 pounds and ewes 120 to 160 pounds, they have a notable appearance with white faces, upright ears, and a robust build. Their dense, fine wool, characterized by a high crimp, is highly valued for its durability and versatility in textiles like tweeds and knitwear. Cheviots produce high-quality, lean meat with a distinctive flavor and are renowned for their excellent mothering abilities, ease of lambing, and high lamb survival rates. Proper care involves a balanced diet, regular grooming, and veterinary check-ups. The breed's unique qualities are showcased in agricultural events, reflecting their rugged beauty and resilience.

http://www.rarebreedproject.com/cheviot

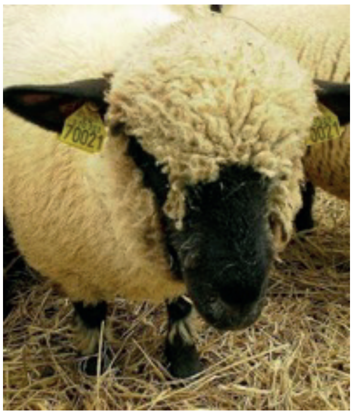
2. DORSET

The Dorset sheep, originating from the southwestern coast of England, is a versatile breed renowned for its dual-purpose capabilities, robust health, and excellent maternal instincts. Medium to large-sized, with rams weighing 225 to 275 pounds and ewes 150 to 200 pounds, Dorsets are characterized by their white faces, legs, and sturdy, muscular build, making them suitable for both meat and wool production. They are notable for their early maturity and ability to breed year-round, often having multiple births per year, which enhances their productivity. While their wool is of good quality, it is less emphasized compared to specialized wool breeds. Dorset sheep require a balanced diet of high-quality forage, grains, and minerals, with fresh water always available. They adapt well to various climates and farming systems, thriving in both extensive grazing and intensive management setups. Regular health checks, vaccinations, and grooming are essential for their well-being. Breeders actively promote and preserve the breed's qualities through shows and agricultural events, reflecting their strong maternal instincts, adaptability, and overall value in sheep farming.

https://breeds.okstate.edu/sheep/dorset-sheep.html

3. HAMPSHIRE

The Hampshire sheep, originating from Hampshire County in England, are a highly regarded breed known for their meat quality, efficiency in production, and distinctive appearance. Medium to large-sized, with rams weighing 250 to 300 pounds and ewes 200 to 250 pounds, they feature a striking black face and legs against a white woolly body. Primarily bred for meat, Hampshires are prized for their lean, flavorful lamb and mutton, offering a high muscle-to-bone ratio that results in efficient feed conversion and a high dressing percentage. They grow quickly, making them economical for commercial production, and are noted for their strong maternal instincts, ease of lambing, and high lamb survival rates. Adaptable to various farming systems, Hampshires require a balanced diet, fresh water, and regular health checks, grooming, and hoof care. Their meat production capabilities and robust health make them a valued breed in modern sheep farming.



https://www.hobbyfarms.com/hampshire/

Other breeds include Algerian Sheep, Columbia, Karakul, Polypay and many more.

GOAT BREEDS

1. ALPINE

Alpine goat, hailing from the French Alps, is highly esteemed for its exceptional milk production and versatility. Medium to large in size, Alpines display a range of colors and patterns such as black, white, tan, and gray, complemented by their upright ears and straight profiles. They are renowned for their high milk yield, which is rich in butterfat and protein, making it ideal for cheese, yogurt, and milk. Their adaptability to diverse climates—from mountainous regions to lowlands—along with their efficient foraging abilities, enhances their appeal to farmers worldwide. Known for their friendly and social nature, Alpine goats are easy to handle and interact well with both humans and other animals, making them suitable for various farming operations. Additionally, they are valued for meat and fiber in some regions, showcasing their versatility.

https://planetzoo.fandom.com/wiki/Alpine_Goat

2. ANGORA

The Angora goat, originating from the Angora region of Turkey, is renowned for its production of mohair, a luxurious fiber celebrated for its softness, sheen, and dyeing qualities. Medium-sized with a distinctive appearance, Angoras are covered in long, curly hair that gives them an elegant and fluffy look. Their mohair, which is sheared twice a year, is highly prized in the textile industry for its durability and versatility, used in products ranging from clothing to upholstery. Adaptable to various climates, Angora goats require some protection from extreme weather but are otherwise relatively easy to manage due to their docile and friendly temperament. Their gentle nature and striking appearance make them popular both as fiber producers and show animals. Overall, the Angora goat is valued for its luxurious fleece, adaptability, and calm disposition, maintaining its significance in agriculture and the textile industry.

https://blog.paradisefibers.com/mohair-a-unique-goat/

3. BOER

The Boer goat, originating from South Africa, is highly esteemed for its exceptional meat production. Recognizable by their white bodies and reddish-brown heads, Boer goats are large and muscular, contributing to their high-quality meat yield. They are renowned for their rapid growth rates and efficient feed conversion, producing lean, tender, and flavorful meat that is sought after in both local and international markets. Their adaptability to various climates and terrains, combined with their docile and friendly temperament, makes them a versatile and manageable breed. Boer goats are valued not only for their superior meat production but also for their resilience and ease of handling, solidifying their importance in sustainable farming practices and the livestock industry.

https://smartrepro.com/the-boer-goat-a-guide-to-structure-and-standards/

Other breeds include Beetal, Murciana, Savanna, Kinder, Moxoto and many more.

CHICKEN BREEDS

1. AUSTRALORP

The Australorp chicken, developed in Australia from the Black Orpington in the early 20th century, is celebrated for its exceptional egg-laying ability, friendly temperament, and adaptability. Medium to large-sized, Australorps have glossy, jet-black feathers with a greenish sheen, a broad body, and a well-rounded breast, making them dual-purpose birds ideal for both egg production and meat. Known for their prolific laying, Australorp hens can produce over 250 large brown eggs per year, with some exceeding this number. They are prized for their calm and gentle nature, making them easy to handle and well-suited for families and beginners. Adaptable to various climates, Australorps thrive in both hot and cold conditions, thanks to their robust health and well-feathered bodies. They are good foragers and enjoy free-ranging but are also content in confinement. Overall, the Australorp's blend of high productivity, hardiness, and pleasant demeanor makes it a popular choice for diverse poultry operations.

https://treatsforchickens.com/blogs/treats-for-chickens-blog/complete-guide-to-australorp-chickens-australorp-chicken-facts-treats-for-chickens

2. PLYMOUTH ROCK

The Plymouth Rock chicken, originating in the U.S. in the mid-19th century, is celebrated for its hardiness, versatility, and friendly nature. Developed as a dual-purpose breed, it excels in both egg-laying and meat production. Plymouth Rocks are medium to large chickens with a broad, deep body and distinctive barred plumage, typically featuring alternating black and white or gray and white stripes. They are prolific layers, producing around 200 to 280 large brown eggs annually, known for their strong shells and rich yolks. In addition to their egg production, they offer fine-textured, flavorful meat, making them valuable for both meat and eggs. Their calm, docile temperament makes them ideal for families and novice keepers, as they integrate well with other chickens and handle easily. Overall, the Plymouth Rock is a versatile breed that combines excellent productivity with a pleasant disposition and classic appearance, making it a favorite among poultry enthusiasts and farmers.

https://www.mypetchicken.com/products/baby-chicks-barred-plymouth-rock

3. SUSSEX

The Sussex chicken, originating from England in the early 19th century, is renowned for its dual-purpose qualities, gentle temperament, and historical significance. These medium to large birds are valued for their robust build, which includes a deep chest, moderately sized single comb, and clean legs. Sussex chickens come in various plumage colors, including white, red, and speckled, with the Speckled Sussex being particularly popular for its distinctive feather pattern. Known for their prolific egg-laying, Sussex hens produce around 250 to 300 large brown eggs annually, prized for their strong shells and rich yolks. Additionally, they are appreciated for their high-quality meat, characterized by tenderness and flavor. Sussex chickens are admired for their calm and friendly nature, making them ideal for families and novice keepers. Their docile behavior ensures they integrate well into mixed flocks. Overall, Sussex chickens offer a balanced combination of excellent egg production, quality meat, and amiable temperament, making them a favored choice among poultry enthusiasts and farmers.

https://blog.meyerhatchery.com/2021/11/breed-spotlight-the-sussex

Other breeds include Barnevelder, Brahma, Cochin, Hamburg, Aseel and many more.

HORSE BREEDS

1. APPALOOSA

Appaloosa, deeply rooted in North American history, is renowned for its distinctive spotted coat patterns and versatile abilities. Developed by the Nez Perce Native American tribe in the 18th century, this breed is celebrated for its endurance, speed, and striking appearance. Appaloosas stand between 14.2 to 16 hands high and weigh around 950 to 1,250 pounds, featuring a sturdy, muscular build with unique coat patterns like leopard, blanket, snowflake, and marble. They are known for their expressive eyes, mottled skin, and striped hooves. Intelligent and gentle, Appaloosas excel in Western riding, trail riding, show jumping, eventing, and dressage. Their resilience and agility make them ideal for various disciplines, including those requiring quick turns and bursts of speed. Proper care includes a balanced diet, regular exercise, grooming, and routine veterinary and farrier services. The Appaloosa Horse Club (ApHC) is dedicated to preserving and promoting the breed, showcasing its talents and versatility.

https://www.texarkanagazette.com/news/2020/jul/31/her-how-appaloosa-escaped-extinction/

2. FRIESIAN

The Friesian horse, originating from the Friesland region in the Netherlands and dating back to the Middle Ages, is renowned for its striking appearance and versatility. Standing between 15.2 to 17 hands high and weighing 1,200 to 1,400 pounds, Friesians are distinguished by their solid black coat, long flowing mane and tail, and feathered lower legs. Their elegant trot and powerful canter make them excel in disciplines such as dressage, driving, and show riding. Known for their calm temperament and intelligence, Friesians are highly trainable and suitable for riders of all levels. Proper care includes a balanced diet, regular exercise, grooming to maintain their coat, and routine veterinary check-ups. The Friesian Horse Association of North America (FHANA) and the Koninklijke Vereniging "Het Friesch Paarden-Stamboek" (KFPS) are key in preserving and promoting the breed, which continues to captivate with its beauty and grace.

https://horsyland.com/the-friesian-horse-because-black-is-beautiful/

3. ARABIAN

The Arabian horse, one of the world's oldest and most iconic breeds, boasts a lineage spanning over 4,500 years from the deserts of the Arabian Peninsula. Known for their beauty, endurance, and intelligence, Arabians typically stand between 14.1 to 15.1 hands high and weigh 800 to 1,000 pounds. They are easily recognized by their finely chiseled head with a concave profile, large expressive eyes, arched neck, and high-carried tail. Available in colors such as bay, gray, chestnut, black, and roan, Arabians are celebrated for their stamina and versatility, excelling in endurance riding, show jumping, dressage, and other equestrian sports. Their unique genetic makeup enhances their performance in long-distance events and endurance competitions. Known for their spirited yet gentle temperament, Arabians form strong bonds with their handlers and are highly trainable. Proper care includes a balanced diet of high-quality forage and grains, regular exercise, grooming, and routine veterinary, dental, and farrier services.

https://mynewhorse.equusmagazine.com/2024/05/30/everything-you-need-to-know-about-arabian-horses//

Other breeds include American Saddlebred, Barb, Lipizzan, Paso Fino, Fjord and many more.

CAMEL BREEDS

1. BACTRIAN CAMEL

The Bactrian Camel (Camelus bactrianus), native to the steppes of Central Asia, is distinguished by its two humps, unlike the single-humped Dromedary camel. These humps store fat, which provides energy and water during scarcity. Bactrian camels possess a thick, shaggy coat that insulates them against extreme temperatures, from hot summers to freezing winters. They are generally larger than Dromedaries, with adult males weighing between 1,300 to 2,200 pounds and females between 900 to 1,500 pounds. Adapted to desert and semi-desert environments, they have large, padded feet for navigating sandy and rocky terrain and can digest thorny vegetation. Domesticated for thousands of years, Bactrian camels are vital in Central Asia for transportation, milk, and meat. While not endangered, their wild populations face threats from habitat loss and competition with livestock. Conservation efforts are ongoing to protect them in Mongolia and China, where they continue to be a cultural and practical asset.

https://en.wikipedia.org/wiki/Bactrian_camels

2. TURKMEN CAMEL

The Turkmen Camel, also known as the Turkmenian Camel or Turkmen dromedary (Camelus dromedarius), is a breed native to Turkmenistan and surrounding Central Asian regions. This dromedary camel is distinguished by its single hump, which stores fat that can be converted into energy and water when needed. Turkmen Camels have a tall, slender build with long legs suited for traversing sandy deserts, and their short, smooth coat ranges in color from light brown to beige. Adapted to extreme desert conditions, they have large, padded feet that prevent them from sinking in sand and are capable of conserving water effectively. Domesticated for thousands of years, these camels are vital for transportation, milk, and meat production in Turkmenistan, and their wool is used in traditional textiles. They hold significant cultural value, symbolizing endurance and survival in harsh environments and playing a key role in the traditional lifestyles of nomadic tribes. Proper care involves providing adequate food, water, and shelter, along with regular veterinary check-ups to ensure their health. The Turkmen Camel remains a crucial asset in Central Asia, reflecting its enduring importance to the region's cultural and economic life.

https://en.m.wikipedia.org/wiki/File:Turkmen_man_with_camel.jpg

Other breeds include American camel, Mehsani, Syrian, Nigerian and many more

Limitations of Breeds Development

The history of livestock breed development worldwide is marked by several limitations that have affected its progress and sustainability. Geographic isolation in the early stages of domestication restricted gene flow, leading to limited genetic diversity within many breeds. Early selective breeding practices often prioritized traits like physical strength, milk, or meat production, overlooking genetic health, adaptability, and disease resistance. This focus on productivity sometimes resulted in increased susceptibility to diseases, inbreeding depression, and reduced fertility. Furthermore, the environmental conditions, such as climate, feed availability, and local diseases, played a significant role in shaping breed development, often leading to animals being well-suited to specific regions but less adaptable to other conditions. In modern times, the industrialization of agriculture and the rise of commercial breeding practices have favored a few highly productive breeds, pushing many indigenous breeds toward extinction and contributing to the loss of valuable genetic resources. The economic pressures to maximize productivity, coupled with the environmental challenges posed by climate change, make it increasingly difficult to maintain breed diversity and promote sustainable breeding practices globally.

Future Recommendations of Breeds Development

Future recommendations for livestock breed development should prioritize balancing productivity, sustainability, and genetic diversity. Conservation of rare and indigenous breeds is crucial for preserving genetic resources valuable for disease resistance, climate adaptation, and resilience. Integrating advanced genomic technologies like CRISPR and GWAS into breeding programs can accelerate the selection of desirable traits while maintaining genetic health. Promoting sustainable breeding practices, such as improving feed efficiency and reducing methane emissions, is essential for minimizing the environmental impact of livestock farming. International collaboration can bridge the technological gap between developed and developing countries, ensuring equitable access to breeding advancements and knowledge sharing. Additionally, involving local farmers and incorporating traditional knowledge will enhance breed development suited to regional conditions.

Key Points:

> **Conservation of Genetic Diversity:** Global programs to preserve rare and indigenous breeds.

> **Use of Genomic Technologies:** Application of CRISPR and GWAS to accelerate trait selection while maintaining genetic health.

> **Sustainable Breeding Practices:** Focus on feed efficiency, environmental impact reduction, and long-term sustainability.

> **Global Collaboration:** Partnerships to ensure equitable access to technologies and foster knowledge sharing.

> **Inclusion of Local Farmers**: Integrating traditional knowledge and tailoring breed development to regional needs.

In conclusion, the development of livestock breeds has been a dynamic and evolving process, influenced by historical, geographical, and technological factors. While early efforts shaped the foundation of modern breeds, ongoing challenges like genetic erosion, environmental impacts, and the need for sustainable practices remain. The integration of modern genomic tools, conservation of genetic diversity, and collaboration between global and local stakeholders are essential to address these challenges. By adopting innovative, environmentally conscious breeding strategies and leveraging traditional knowledge, the future of livestock breed development can ensure both productivity and resilience, ultimately supporting global food security and sustainability.

About The Authors

Dr. Muhammad SAFDAR earned his PhD in Molecular Biology and Genetics from Gaziantep University, Turkey. He is Lecturer in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, nutrigenomics, nano-genomics, bioinformatics, biotechnology, and their applications. He has published more than 70 research articles in national and international journals. He has also written many book chapters as well as an edited book. He is an associate editor for international journals.

E-mail: msafdar@cuvas.edu.pk ORCID: 0000 0002 3720 2090

Dr. Shahzad Ali is a Molecular Researcher specializing in animal breeding and genetics. He earned his Doctor of Veterinary Medicine (DVM) degree from the University of Veterinary and Animal Sciences, Lahore, graduating in the 2018-2023 batch. His research focuses on molecular-level aspects of animal genetics.

Email: alikhan1000sss@gmail.com ORCID: 00009-0008-7218-8563

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BREEDING OBJECTIVES: ALIGNING GENETICS WITH GOALS

Safdar IMRAN

Muhammad SAFDAR

Selection of animals for particular traits has been practiced at different levels. The preference for a single trait or set of traits depends upon multiple factors. The design, structure and implementation of breeding program focuses on achieving specific goals finalized in term of breeding objectives. The breeding objectives can be defined as preference for certain traits to maximize profit and sustainability in future generations of animals. The breeding objectives have been defined by breeders, breed associations, scientific allies, researchers, academia and industry yet the breeder's point of view has more weightage followed by consumer demands and market orientation as profit function in animal breeding gets its bases from economic weightage of traits. The breeding objectives shall include long term plans for fulfilling consumer demands in future from the animal generations bred from current population. Breeding objectives helps in selection of animals in line with the set targets that may vary among breeders, association and countries for different species or breeds. The breeding objectives may focus on conservation, maintaining biodiversity, developing new breeds, removing deleterious genes and improving genetic makeup. The socioeconomic, sociodemographic, breeder's personal, breeder associations, political and governance factors affect the finalization of breeding objectives. Selection indices and genomic techniques enriched the process of deciding breeding goals and selection of animals based on specific objectives and helped breeders to align genetics with goals to maximize genetic superiority, functionality and sustainability of animal production.

1. Breeding Objectives

Animals have long been domesticated and selectively bred by humans. Selection means preferring for breeding the best out of available population. The best may be defined by the breeder or the breed associations. The purpose (objective) of breeding differs in different species or breeds of animals. The breeding objectives brings sustainable genetic change, maximize profit function and controls the loss of genetic variation in the population. These purposes may include accumulation of superior genetics in forthcoming generations, increasing production, improving quality of products of animal origin, increasing or creating disease resistance of animals, elimination of lethal genes, decreasing frequency of undesirable genotypes in next generation and for conservation of a breed/specie. The other objectives may include improvements in type traits of animals and phenotypic beauty parameters particularly in pets and birds. Thus, the objective of selective breeding usually involves more than one trait even putting emphasis on one of the major traits and few other relatively important traits. The breeding objectives decided by farmers/breeders or at large scale by breeder associations have been implemented for development of breeds for a particular trait or set of traits. The breeding objectives include trait groups for example growth and number of traits included in that group, both vary from breeder to breeder, association to association, country to country and also for species and breed of animals under consideration.

Worldwide it is generally accepted that for initiation and implementation of any structured breeding program, defining breeding objective is the first step. The breeding objectives are one of the potential factors contributing to deciding the direction of change in a particular trait and even in deciding optimal breed size and other attributes. The selection criteria in animal breeding are defined by many factors including farmer's choice, market orientation and economic value of traits. The selection criteria and breeding objectives are only practical when these include the wishes and perception of breeders for whose animals these are designed for implementation (Dekkers & Gibson, 1998). The breeder's choice is always of prime importance in designing selection criteria. Yet sometimes, the market demand, directs the changes in the breeder's choices. It is very complex task to define a selection criterion which may be widely acceptable because of changing preferences both at producer and consumer level. The genetic changes led by the breeding objective are considered individually and the relative profit per unit change in a trait have been applied for predicting genetic merits of animals in selection index theory (Hazel, 1943) or in best linear unbiased prediction (Henderson, 1984). As traditionally, breeding objectives involves quantifications of the genetic changes associated economic benefits. The non-economic factors related to sustainability shall also be considered in defining breeding objectives for animals (Nielsen et al., 2011; Olesen et al., 2000). The cattle has long been selected for traits of economic importance currently including functional traits and more recently focusing methane emission related traits to improve sustainability and to reduce environmental impacts (Richardson et al., 2023). A methodological framework for deriving weighting the impact of genetic change on intensities of greenhouse gas emissions for inclusion in selection indices (Amer et al., 2018). The Spain dairy cattle industry incorporated in breeding objective and evaluated the genetic and economic aspects of selection index (González-Recio et al., 2020). Recently a new breeding objective with the title of beef on dairy has been observed across the globe, its acceptability and breeder's choice are yet to be determined, however it has been implemented in few countries at different level. Most of the beef originated from dairy herds, in line with it, the decisions about carcass were being made by dairy farmers (Berry, 2021), so the interest to obtain valuable calves from dairy is rising. Selection of animals and breeding objectives based on traits for feed efficiency have also been given due consideration recently. The Australian Holstein dairy cattle herds feed saved breeding values were used first in 2015 and later continued to select cows for feed saved breeding value as indicator of low energy requirement of cattle at similar production level (Bolormaa et al., 2022). Predicted nitrogen use efficiency and nitrogen losses in Holstein as proxies of nitrogen loss and use are considered traits of importance in many countries (Chen et al., 2021).

The models for derivation of economic weightage can be based on simulation, profit functions and dynamic programming. The development of model shall include as much as possible toolset variations to include all theoretically possible contexts for better quantification of trait changes. The profit function formulation is straightforward and have many useful applications (Groen, 1989). The tools may include simple profit equations and also the detailed bioeconomic models for deriving economic values (Nielsen et al., 2014b). The derived toolsets rely mostly on the methods and procedures used in the animal breeding, farm modeling and economics, even the most recently tools used for social sciences has been identified as adding aids in defining breeding objectives. The development of breeding objectives needs a multidisciplinary approach. One of these approaches, community based breeding program has been recognized as innovative and recommended approach for sustainable animal genetic resource utilization and genetic improvements (Badjibassa et al., 2024) as this approach also requires understanding of breeding objectives along with farmer's preference and production system.

2. Aspects of Conservation

The local breeds usually are preferred by farmers due to favorable traits. The indigenous knowledge about the breeds is of importance in term of deciding breeding objectives. The conservation of goat breeds is better linked with farmer's knowledge about managemental practices implemented for the breeding (Whannou et al., 2022). The breeding objectives to conserve and maintain pure populations can be achieved through participation and knowledge base of farmers that will also uplift the smallholders and improve the food of animal origin (Scholtz & Theunissen, 2010). The selective breeding favors the development of new breeds as well as preservation of genetic resources and it also favors the retention of traits adapted to local climatic conditions (Alderson, 2018; Segelbacher et al., 2022; Zhang et al., 2018).

3. Genetic Aspects

In successful implementation of breeding objectives, the genetic control of trait is of prime importance. Gene based breeding (Zhang, 2024) is an emerging concept in breeding technology both in animals and plants. Gene based breeding technique allow breeders to develop new or hybrid varieties or strains based on own breeding objectives through targeting genes controlling traits of choice. The selective breeding in cattle helps in enriching the population with higher prevalence of alleles contributing to traits of economic importance (Mei et al., 2019). The breeding objectives, finalized after due consultation with farmers/breeders and relevant stakeholders including market demand, consumer preferences, economic weightage and sustainability for future generations, bring fruitful results. The trait of economic importance has their own inheritance mechanism including underlying molecular/cellular processes. The trait's genetic control defines the responsiveness of breeding objectives. Cattle, for example, have long been intensively selected and bred for higher milk production as well as for good fat percentage in milk and milk composition. These efforts have brought in higher prevalence of traits for production as well as for higher metabolism. For all traits, genes are the primary determinants for performance. Selection for multiple traits poses difficulties as traits may have positive or negative correlation. Multi-objective optimized breeding and selection approach for multiple traits is more viable than simple multiple trait selection approaches and yield 20-30& higher gain in long term breeding simulations (Akdemir et al., 2019). The selection of Polish cattle for milk production in long run resulted in slow yet marked increase in allelic frequency of desirable alleles of casein gene, good for improving milk quality, yet decrease in frequency of allele B of betalactoglobuline gene (Kamiński et al., 2023). Intensive rapid selection for β-casein A2 allele homozygosity has resulted in increased inbreeding across genome and also on chromosome 6 in Australian A2/A2 Holstein cattle (Scott et al., 2023).

4. Selection Indices and Breeding Indices

The selection index is used to determine criteria for selection of animals for maximizing profit function of a breed in future generations. The profit function for a particular breed encompasses both the future acceptance of breed by owner in future and also the acceptability of product by consumer (Wellmann, 2023). The latest selection indices help to estimate the accuracy of selection and expected genetic gains using genomic selection and BLUP (Barwick et al., 2013; Bijma & Dekkers, 2022; Dekkers, 2007). Multiple selection indices have been introduced and used over time (Satoh, 2024). with varying range of applications. A few were with a focus on directional selection approach and few others for the stabilizing selection approach while some of these also uses restriction approach. In animal breeding, linear selection index for estimation of aggregate breeding value using phenotypic value of each trait, was first introduced by (Hazel, 1943). Next to it, restricted selection indices were introduces including Kempthorne's index (Kempthorne & Nordskog, 1959) with objectives to maximize aggregate breeding values by restricting some traits to zero, Harville's index (Harville, 1975) used the proportional changes in some traits to maximize the aggregate breeding value and Yamada's index (Yamada et al., 1975) used to achieve relative desired changes for all traits. The multistage selection implies reuse of data from earlier stages of selection (Cunningham, 1975), selection index using non-liner profit functions instead of linear profit functions (Goddard, 1983) and molecular eigen selection using first eigenvector as criteria for selection index (Cerón-Rojas et al., 2008).

The breeding indices helps the breeders in good breeding decisions for long term profitability. Irrespective of the level of management at herd level, good genetic is the sole contributor for long term profitability and sustainability of a breed. The good genetics is established through effective selection of animals based on some records of performance and also in a better way, based on the indices. Some of these indices used for cattle breeding in deciding breeding objectives include lifetime profitability index and calving index for a particular season. Along with these indices, genetic parameters for traits are also important. The market oriented or market-based milk quality or quantity related traits including milk production (quantity), fat quantity and fat percentage, protein quantity and percentage and more important persistency of production and ease of milking have also been considered in taking right breeding decisions. Breeding objectives may also consider health related traits including overall health of animal, mastitis in dairy animals, somatic cell count, fertility, life span, longevity, calf survival rates, lameness and chances of other diseases that may be potential cause of losses at farm or herd level. Relevant to these calving ease in cattle and buffalo is also considered as one of the traits during selection of animals. Management related traits particularly temperament of animals has been considered a vital trait in farm animal welfare and productivity persistency as well as feed efficiency and net merit in dollars have also been included. The breeding objectives may also include the conformation type traits in cattle including linear type traits, composite type traits and type merit. There is a long list of traits that has been included in breeding objectives and will further be modified in future as the breeding objectives are never stagnant over the years for any specie or breed. In beef few other different traits have been included in breeding objectives. So breeding animals under human care shall consider all aspects including exclusion of deleterious genes, welfare aspects, maintaining diversity, conservation of genetic resources, all covered under umbrella of precision animal breeding (Flint & Woolliams, 2008) yet based on breeding objectives. In animal breeding a new selection criterion has been introduced based on area under growth curve for cattle selection allowing farmers to identify heavier animals in production system with lower risk (Barrera-Rivera et al., 2024).

Factors influencing farmer's choice in decision-making for breeding objectives have been changing. These include social status of breeder, sociodemographic factors, regions, continents, societal or governmental laws, subsidies, market orientation, long term political decisions and sustainable environmental conditions. The breeder's viewpoints in animal breeding innovations were influenced by farm factors such as farming conditions, size and production system, socioeconomic factors including education and personal factors such as age of breeder (Läpple & Thorne, 2019; Padel et al., 2017). The cattle breeders have different choice patterns for cattle traits to be included in breeding objectives encompassing fertility, longevity, workability, resilience and animal health with dominating traits like production, reproductive and general health (Ule et al., 2024). Genomics has revolutionized the selection of animals particularly for dairy cattle helping farmers to obtain higher genetic gains. Genomic selection methods using high density genetic markers and advanced techniques are economically efficient (Demircioglu, 2024). Genomic selection created ease in selection of traits which were difficult to measure including energy balance, feed conversion ratio and methane emission in cattle (Gutierrez-Reinoso et al., 2021; Seidel et al., 2020). A reference measure was introduced to evaluate farmer's approach towards tools in animal breeding for assistance in designing effective breeding program (Martín-Collado et al., 2021). Milk production and milk composition have been considered primary goals in cattle breeding decision yet such directive selection has impacted the other traits including fertility, environmental sensitivity, health and longevity (Brito et al., 2021; Miglior et al., 2017; Nielsen et al., 2014a). although breeding for some traits out of these has been opted in breeding objectives around the world (Cole & VanRaden, 2018; Miglior et al., 2017) yet in current scenario, dairy industry need to revise the breeding objectives and selection indices and put emphasis to include the traits related to health, longevity, animal welfare, environmental efficiency and overall resilience (De Haas et al., 2021). Some breeders prefer health and fertility over yield and conformation for dairy cattle (Paakala et al., 2020). The selection of animals for fertility improves the herd performance, female animals gain more attention in term of fertility selection however contribution of bulls also remain vital in genetic improvement, so to optimized cattle production efficiency selection of bull for improved fertility is necessary (Butler et al., 2020). Genetic improvements in fertility of cattle applies to variables including calving health, longevity and changes in body condition score other than regularly used intervals and binary parameters calculated from insemination records. The genetic improvement in dairy herd for high fertility contributes to herds profitability so the inclusion of novel reproductive phenotypes in breeding objectives and selection criteria helps in improving profitability and efficiency of herd (Fleming et al., 2019).

Farmers have diverse preference for traits to be selected for breeding objectives (Ule et al., 2024). The traits are weighed according to the net economic importance in the net merit in a Nordic production environment (Kargo et al., 2014). Farmer's statement on choice of traits, in developing countries, where price and production are not widely available, has more importance in finalizing breeding objectives (Chawala et al., 2019; Kariuki et al., 2017). The breeding objectives for Brown Swiss and Fleckvieh and cattle were optimized by re-estimating the updated cost, price and parameters (Fuerst-Waltl et al., 2016). For Norwegian cattle farmer's ranked fertility at the first trait while methane emission and parasite resistance were least preferred (Skjerve et al., 2018). The update of economic in selection index criteria for Australian dairy industry were analyzed with the focus on effect of changing a trait on profit function of dairy farmers and economic implication of selective dairy breeding (Byrne et al., 2016). The selection of dairy cattle for highly heritable traits, in the past, affected functional traits yet now the breeding goals also have included functional traits in selection criteria for cattle (Miglior et al., 2017). The possible outcomes of selective breeding for organic production were evaluated (Slagboom et al., 2018). The breeding objective for Brangus cattle were evaluated for the traits including mature cow weight, warm carcass weight, pregnancy rate, tick count and fecal nematode egg count per gram, for which bioeconomic model were used for economic values estimation and it was concluded that selection indexes need to be reformulated in tropical and subtropical regions for better profitability (Simões et al., 2020). Beef cattle breeding programs offer services (evaluations and consultancy) for improving future genetic merit of herds although some breeders are having better willingness to opt best practices than others resulting in variation in genetic merit and genetic trends of various herds (Toral et al., 2023). The genetic trends of traits of economic importance in population may be considered as markers for success of animal breeding and reproductive techniques (de Oliveira Bessa et al., 2021; García-Ruiz et al., 2016). Bioeconomic profit model for Boran breed were developed and implemented for evaluation of economic variables and to characterize production system leading to conclusion that these models can be used for simulating changes in market circumstances and production (Rewe et al., 2006). Bioeconomic models were developed to explore the economic values of traits of economic importance in beef cattle to assess effects of these traits and to develop economic selection index for Angus cattle (Fernandes et al., 2018).

5. Summary

The selective breeding based on breeding objectives shall help to obtain sustainable genetic improvements, maximize profit and helps to maintain genetic variation in population. Optimization of multi-trait breeding objectives and breeding strategies are crucial for sustainable food production. Genomics, genome wide association studies and modern data analysis tools provide strong bases of gene specific selection as compared to traditional phenotypic selection. Selection indices including updated economic weight of traits and genetics of traits enhances the effectiveness of breeding objectives implementation to harness maximum profit from future generations with sustainable genetic change and fulfilling consumers need both in terms of quantity and quality of product of animal origin.

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About The Authors

Dr. Safdar Imran received his PhD in 2021 from University of Agriculture Faisalabad, Pakistan. He is Assistant Professor of Animal Breeding and Genetics at the Islamia University of Bahawalpur, Pakistan. His research interests include predictive breeding models, Genetic selection, Genomics, reproductive biotechnology and selection and judging of animals for beauty attributes. He has published ten research articles in well-reputed national and international journals. He also has written book chapters.

Email: safdar.imran@iub.edu.pk ORCID: 0000-0001-5030-2267

Dr. Muhammad SAFDAR earned his PhD in Molecular Biology and Genetics from Gaziantep University, Turkey. He is Lecturer in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, nutrigenomics, nano-genomics, bioinformatics, biotechnology, and their applications. He has published more than 70 research articles in national and international journals. He has also written many book chapters as well as an edited book. He is an associate editor for international journals.

E-mail: msafdar@cuvas.edu.pk ORCID: 0000 0002 3720 2090

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GENETIC DIVERSITY IN LIVESTOCK BREEDS: CHALLENGES AND CONSERVATION

Muhammad TARIQ

Muhammad SAFDAR

Farhad BADSHAH

Salma BIBI

Arooj FATIMA

Saba SAEED

Kiran ASHIQ

This chapter explores genetic diversity, providing insight into growing options, consumer preferences, and modern agricultural practices affecting the region. Agricultural security requires the protection of many animal species. Due to the great demand for food production, animals are generally standard and subject to breeding methods. This chapter provides an in depth look at the various risks associated with genetic diversity, focusing on the potential impact of reduced diversity on the viability of species and the ability of animals to adapt to changing environments and diseases. Changing economic and dietary patterns are affecting agriculture and have the potential to damage culture and localities by causing genetic disruption. To address these issues, this chapter examines various conservation strategies. This study explores the importance of breeding programs that seek to improve genetic diversity and highlights the importance of preserving unique traits in populations. In addition, gene banks must be established and managed correctly to preserve genetic material. They protect against known and unknown dangers while maintaining good results. Additionally, this study examines community programs that recognize the importance of local participation in traditional cattle conservation. Achieving breeding that balances economic goals with biodiversity conservation requires effective collaboration between scientists, farmers, and policymakers. The last part of the book presents an analysis of the obstacles and treatment methods for maintaining diversity in animal breeding. This approach is essentially the combination of academics with community engagement to protect and improve people's livelihoods in today's agriculture.

1. Introduction

Genetic diversity in animals is important for many reasons. Important native and rare species associated with traditional land management, which may have traits beneficial to future agriculture, should not be protected along any way (Wainwright et al., 2019). Animal diversity is important for their conservation and future generations. Fst, which evaluates genetic difference between animal breeds, has been proven to quantify their connection. Conservation of cattle breed genetic diversity is crucial for food security and animal population sustainability (KOYUN et al., 2016).

The loss of small, local breeds reduces genetic variety within and across livestock breeds, making diversity maintenance difficult. Small breeds' lower output relative to high-output international transboundary breeds causes this loss. World warming, inbreeding, and rigorous artificial selection programs endanger genetic diversity. (Biscarini et al., 2015). Exotic breeds imported without adaption in developing nations might potentially reduce genetic diversity. Poor inbreeding management and imbalanced ancestor utilization may lower genetic diversity, especially in local breeds with small populations. Conserving breeds as genetically and culturally different genetic resources and using breeding procedures that maintain genetic diversity within and between breeds might help solve these issues (KOYUN et al., 2016).

Livestock breeding and conservation need genetic diversity. DNA variations exist across species, breeds within species, and people within breeds. Diversity is needed to adjust to climate and customer demand changes and develop economically essential features genetically (Eusebi et al., 2019). Genetic difference between animal breeds is measured by the Fst statistic. Fst values vary greatly within and across species, proving that a single criteria cannot reliably quantify breed difference (Hall, 2022).

Genetic diversity is needed to satisfy production demands in different contexts, maintain genetic development, and adjust quickly to changing breeding aims. Using genomic assessments in livestock has enhanced genetic gain rates, but its consequences on genetic diversity and inbreeding have raised concerns in cow herds (Lozada-Soto et al., 2021). Livestock genetic diversity may help feed the globe in the face of climate change and hotter weather. Indiscriminate crossbreeding, the use of non-native breeds, poor regulation, the collapse of traditional production, and breed neglect continue to threaten many important breeds. (Thornton et al., 2009).

Maintaining enough breeds promotes genetic variety. Selecting within a breed must also consider species-wide diversity. Advances in genomics and bioinformatics have identified genomic similarities/differences among livestock breeds, which may explain breed phenotypic uniqueness and facilitate prioritization and genomic breeding tools to preserve these important resources (Biscarini et al., 2015).

Genetic diversity conservation in animal breeds is difficult. Many important breeds are in danger of extinction due to genetic degradation, indiscriminate crossbreeding, non-native breed usage, poor control, and the decrease of traditional production. Given climate change, new illnesses, and changing market needs, cattle genetic variety loss may have serious effects. Global food security and resilience to future challenges depend on animal genetic variety, according to the FAO (Thornton et al., 2009).

Livestock genetic diversity governance is complex and aims to compensate for the decline in genetic diversity in conventional livestock breeds and agricultural kinds. Approximately 8000 cattle breeds exist globally, with 7000 local, many of which are threatened by more productive and cosmopolitan types (Pautasso, 2012). The conservation of genetic diversity among livestock animals, including taxonomically varied breeds, is essential for addressing these problems. Harmonizing the objectives of the livestock sector, which include preserving animal genetic diversity and ensuring environmental sustainability, requires better regulation and oversight (Woolliams & Oldenbroek, 2017).

The conserving the genetic variety of cattle breeds is an international issue that need concerted international action to safeguard valuable breeds and ensure their continued sustainable use despite many challenges. Combating genetic erosion and the loss of breed traits in livestock because of insufficient management, traditional productivity decline, and crossbreeding is part of this.

2. The Significance of Genetic Diversity in Livestock

A great deal of genetic diversity in livestock is very important for several reasons. It is crucial for adaptation to environmental changes, survival in the face of stress and disease, the ability to enhance one's genes, and the maintenance of one's population (Woolliams & Oldenbroek, 2017). Livestock populations' genetic diversity is important because it provides the building blocks for evolution via natural selection and improvement programs that humans have handled. In the face of challenges like climate change, new illnesses, and feed and water shortages, it is essential to work to increase productivity while adjusting livestock numbers (Ligda & Zjalic, 2011). The presence of genetic modification promotes the development of better livestock. Increased meat and milk production, resistance to diseases and the ability to adapt to new environments are just some of the advantages of this breed. It is also important to prevent the loss of genetic diversity for livestock to have a long life. This occurs when certain genetic markers in the population change. This can lead to reduced potency and inbreeding. Therefore, preserving animal diversity is very important to maintain genetic conservation in the population and make our food edible (KOYUN et al., 2016).

The amount of genetic variation introduced during breeding can have a significant impact on meat quality. Large genetic differences within and between animals can affect the taste, texture, and overall quality of meat. Individual and environmental variables such as age, birth, weight, fat level and diet can affect this change (Sakowski et al., 2022).

Meat quality is directly affected by genetic diversity; This plays an important role in promoting the development of good traits that help animals resist diseases, change environment and work. This is due to the positive effects of genetic diversity (KOYUN et al., 2016). Another interesting finding from research on genetic diversity is that there may be a relationship between meat quality and the isolation and diversity of genes related to meat quality (Rodriguez et al., 2022). Therefore, it is important to ensure genetic diversity in animal breeding to ensure and improve meat quality.

Livestock farming practices can affect milk production through several genetic pathways. In order to meet the current needs in many fields and to ensure continuous genetic improvement, it is important to protect animals from different diseases, because the use of genetic differences is close to efficiency (Saravanan et al., 2023).

However, due to the prevalence of only a few milk types, the decrease in genetic diversity will affect milk production. Additionally, genetic diversity is important in developing traits that help cattle adapt to changing environments, disease threats, and work needs. This has a direct impact on the quantity and quality of breast milk (Kiplagat et al., 2012). Hence, the success and marketing of milk in the long run depend on genetic management in animal husbandry.

3. Factors Influencing Genetic Diversity

Animal genetic diversity is affected by several things. Natural selection, gene flow, mutation, genetic drift, and population size are all examples of such forces. A population's genetic diversity is affected by its size (Minter et al., 2022). Genetic drift and inbreeding are more likely to cause a decline in variety in smaller populations. Both the quantity and variety of a population's genes are greatly affected by environmental conditions. The fact that various bird species have evolved to adapt to varied environments exemplifies the impact of environmental variables on genetic diversity. The level of genetic variety in a population is determined by the interplay between genes and the environment. Variation in genetic makeup may result from changes in how organisms adapt, grow physiologically, and survive and reproduce. The total genetic diversity within and across populations is also influenced by other variables such as mutation, gene flow, and natural selection. Thus, the genetic diversity of animal populations is impacted by a mix of demographic, ecological, and environmental variables together (Neff et al., 2011).

3.1. Natural Selection and Evolutionary Pressures

An essential step in the development of all living things is natural selection. As a result, their traits evolve across the generations. The underlying idea behind this process is that characteristics that help people survive and reproduce in their environment are more likely to be passed down across generations. Evolution takes place when beneficial characteristics spread throughout a population and become the norm over time (Kull, 2014) .

3.1.1. Variation in Traits

Natural selection can only take place when there is genetic diversity in a population. This variation is often caused by genetic mutations, which are random traits, some of which may provide individuals with advantages in terms of survival or reproduction in specific environments (Bell, 2008).

3.1.2. Differential Reproduction

Natural selection relies on differential reproduction, meaning that not all individuals could reproduce to their full potential. In any given environment, resources such as food, space, and mates are limited. Consequently, only certain individuals will successfully reproduce. Those individuals who possess traits that give them an advantage in acquiring these resources are more likely to leave behind more offspring than those without such traits (Gregory, 2009).

3.1.3. Heredity

For natural selection to result in evolution, the advantageous traits must be heritable. This means that these traits are passed down from parents to offspring through genetic inheritance. If a trait that provides a survival or reproductive advantage has a genetic basis, it is more likely to be passed on to the next generation (Williams, 2018).

3.1.4. Selection Pressures

Selection pressures are factors that influence the survival and reproduction of individuals within a population. These pressures can include changes in the environment, human activities, and infectious diseases. For instance, a climate change may favor individuals with a particular coat color that provides better camouflage, or the emergence of a new disease may favor individuals with genetic resistance to the pathogen (Thagard & Findlay, 2010).

3.1.5. Evolutionary Change

Over time, natural selection can lead to significant evolutionary changes within a population. Traits that confer advantages in terms of survival or reproduction become more prevalent, and the population becomes better adapted to its environment. This process can eventually lead to the emergence of new species as populations diverge and adapt to different ecological niches (Nehm & Reilly, 2007).

3.2. Human Intervention: Selective Breeding and Genetic Manipulation

Selective breeding and genetic manipulation are two methods that scientists use to change the characteristics of living things. The process of selective breeding involves selecting parents with traits of interest to generate offspring that will inherit these characteristics and hopefully have even better traits. This works because of the natural differences in genes and the way traits are passed down from parents to offspring. After many generations of selective breeding, populations of organisms can have the desired traits. Nonetheless, a downside of this is that less diversity in genes could result, which may contribute to a higher chance of inheriting diseases since harmful gene variants will become more common (Milot et al., 2011).

Conversely, genetic manipulation, also referred to as genetic engineering, involves altering an organism's genes in a laboratory. With this method, scientists can make very specific modifications to certain genes to obtain desired traits in an organism. This method is faster and helps to avoid errors, but there are also doubts concerning its ethics, safety, and unintended effects. Moreover, both selective breeding and genetic manipulation have consequences in terms of genetic diversity and the welfare of the modified organisms; furthermore, ethical and social implications extend beyond them (Sabeti et al., 2006).

3.3. Environmental Factors: Climate Change and Habitat Loss

Climate change and the loss of natural homes for animals and plants are closely linked and they're both really affecting the variety of life on Earth. Climate change is all about the slow shift in weather patterns and temperatures, and it's mostly because of what people are doing. This has made Earth's average temperature go up and has caused all sorts of wild weather that's hard to predict. This is bad news for lots of different kinds of living things and is causing what some people call the sixth big wave of species dying out. The ways climate change hurts living things include making it hard for them to stay in their usual spots, ruining the places they live, and making life tough when wild weather like big storms, long dry spells, and heavy rains happen (Shivanna, 2022).

Habitats for animals and plants are being hurt in many places because people are building more factories and growing more crops. This means that the natural homes where wildlife live are being broken up and changed. Lots of areas that were once wet and full of life are going away, and different kinds of nature places are not like they used to be. For example, when people cut down a lot of trees, places like the big tropical rainforests suffer, and we end up with fewer kinds of animals and plants. Also, taking too many fish out of the ocean, hunting animals a lot, and bringing in new species from other places can make the number of different living things go down (Breitholtz et al., 2013).

The effects of climate change on habitats are quite serious and affect land and ocean ecosystems. An example of this is rising sea levels, which leads to loss of coastal habitat. Additionally, ocean acidification has a negative impact on marine ecosystems. Additionally, climate change is affecting many species and negatively impacting coral reefs, one of the most diverse species on Earth (Malhi et al., 2020).

It is important to know that climate change and habitat loss in general pose a threat to biodiversity. These challenges are closely interrelated and need to be clearly addressed to solve the current problems. A better understanding of how climate change affects ecosystems and biodiversity is necessary to develop effective strategies to reduce these impacts and ultimately preserve the diversity of life on Earth (Sebo, 2021).

4. Threats to Genetic Diversity: Modern Agricultural Practices

The spread of agriculture, the disappearance of traditional production methods, illegal animal crossbreeding and many other problems affect animal diversity. Due to this process, important traits such as immunity and the ability to adapt to harsh environments may be lost. The use of many non-native species and lack of proper care and practices have led to genetic damage. If conservation efforts focus on genetic diversity rather than genetic diversity, overall genetic diversity and variation will also decrease. To overcome these challenges and ensure the conservation and use of animal species, international management of animal genetics needs to be promoted (Nonić & Šijačić-Nikolić, 2021).

Genomic technologies and improved communication between conservation geneticists and animal breeders are essential for preserving the genetic diversity of wild and domestic animals. The use of genomic technologies, such as genome wide DNA markers and techniques to select for desired traits based on genomic information, may be beneficial in the conservation of many species. These techniques not only help preserve genetic diversity and improve traits of different species, but also make it possible to extract genomic material from affected individuals that are part of the mixture (Kristensen et al., 2015).

5. Selective Breeding: Impact on Genetic Variation

Artificial selection, sometimes called reproductive selection, has the potential to influence many genetic factors. It has the potential to reduce overall genetic diversity in the population over time. This occurs because, in the process of selecting for certain qualities, some genetic variety is eliminated. As a kind of selective breeding known as inbreeding, subsequent generations may be less equipped to withstand environmental stresses and genetic abnormalities, and the pace of genetic evolution may be slowed (Loewe & Hill, 2010).

Particularly in the cattle business, many are worried about how selective breeding would affect genes. Managing and conserving genetic alteration is fraught with difficulties, including the potential for reproductive danger and the limitation of beneficial populations. Thus, it is more intriguing to think about how we may use our knowledge of genetic conservation to regulate various species. Conservation efforts and selective breeding might both benefit from the use of genomic technology to get a deeper understanding of and command over genetic variability (Kristensen et al., 2015).

As a result of selective breeding, the genetics of the population will decrease, making it more difficult to create new varieties and make them more vulnerable to diseases and genealogy. It is becoming increasingly important to solve these problems in animal production using genetic information and genomic methods.

6. Market Forces and the Homogenization of Livestock Breeds

Due to factors such as economic pressure, the phenomenon of homogenization of animal husbandry has gained importance. Livestock farming moved from a diverse community system to one dominated by wealthy landowners, leading to the homogenization of previously diverse communities. The main driving force behind this difference is the preference for rare and high-quality animals that are commercialized and supported by government projects, extension agencies, and businesses aiming to increase sales (Kitalyi et al., 2006). Another factor contributing to the decline is the global economy of production technology; As a result, 9% of known populations have become extinct and 20% are considered endangered. Many factors, such as trade and marketing, lack of regulation of the livestock sector, inadequate protection, and inadequate capacity, have led to the extinction of many animals. Additionally, the high market for high-value animals may increase homogenization competition (Zambrano Farias et al., 2021).

The fact that the oil market has an impact on the animal breeding pattern demonstrates the need for management of animal genetics. It is important to develop traditional breeding and make regulations to protect genetic diversity. Protecting different species and using their unique characteristics to provide specialized food should be a conservation priority. This difference is important for the introduction of new genes through hybridization or migration (Fimland, 2007). Lowering the standard of animal breeding and preserving diversity for future generations are two ways to solve these problems.

7. Environmental Factors and Genetic Erosion

Environmental factors may have both short-term and long-term effects on animal breeds, deteriorating their genetic material. Livestock can be affected by natural disasters such as floods, inundation, earthquakes, or disease. Climate change and agroecological change are examples of long-term ecological events that have a significant impact on genetic degradation. Both causes and responses to the environment are greatly influenced by livestock breeding decisions. The practice of engaging livestock producers as intermediaries in the drying process while simultaneously conserving AnGR (Animals in the Country) (Cardellino et al., 2009).

The main reason for the decline in livestock farming is lack of connectivity. Loss of useful properties is the main cause of spoilage with this method. Genetic diversity in cattle is decreasing for various reasons. Some of these factors include the use of non-native varieties, lax management, loss of traditional production methods and neglect of competing varieties (Thornton et al., 2009).

There are many differences between livestock, agricultural and economic health, influencing the different ways and differences in environmental factors and animal diversity. These factors need to be understood and addressed to preserve the genetic diversity of livestock and make them more resilient to future challenges such as climate change, weather, and the emergence of new diseases (Destoumieux-Garzón et al., 2021).

8. Conservation Strategies: Selective Breeding for Diversity

One way to increase diversity in animal breeding is through the practice of selective breeding.

However, it is important that these measurements are made equally because genetic improvement is possible. Limiting the number of genetic variants and reducing the average number of ancestors and offspring are two ways that genomic selection can maximize genetic diversity while preserving diversity (Liu et al., 2020). Loss of good quality due to uncontrolled contamination is the cause of genetic diseases in animals. Climate change and agro-ecological change are two examples of environmental factors that influence genetic degradation. The genetic makeup of animals and their ability to solve future problems depends on our ability to identify and solve those problems. Protecting AnGR (pets) by related to cattle manufacturers inside the drying process (Rojas-Downing et al., 2017).

9. Gene Banks as Safeguards: Preserving Genetic Material

Another important application of biobanks, commonly referred to as gene banks, is the preservation of genetic material from species, especially cattle. To increase genetic diversity they have many methods such as DNA sequencing, gamete cryopreservation and in vitro preservation (Blackburn, 2018). The process of cryo-preservation involves the preservation of the genetic material of the organism, i. on its sperm and eggs, using specialized freezing equipment The gene pool aims to preserve agro-environmental diversity and genetic variation that can lead to new breeding methods and researchers.

The powerful management of genetic conservation in cattle depends on a higher knowledge of genetic range control, which genomics generation provides (Weise et al., 2019). Methods for figuring out the quantity of inbreeding encompass subsequent-technology DNA evaluation and homozygosity investigations. This approach offers vital insights and instruments for genetic maintenance inside the pursuit of a stability among general evolution and genetic variety. When it involves permaculture, genetic variety renovation, and helping farm animals adapt to weather trade, gene banks are vital (de Souza et al., 2024).

10. Community Engagement in Livestock Conservation

Animal conservation activities rely upon the energetic participation of the nearby inhabitants and different contributors of the network. One of the main dreams of the International Foundation for Animal Welfare (IFAW) is to ensure that everybody in society is engaged in and benefits from shielding and being concerned for animals. When it involves human-wildlife conflicts, community-primarily based applications are all about finding lengthy-time period solutions which might be proper for all of us worried. Through these projects, local groups are given the opportunity to percentage their perspectives and take part in decision-making approaches at conferences that variety from the local to the worldwide (Jackson et al., 2012).

To further have interaction rural people in animal conservation and management, the Snow Leopard Conservancy (SLC) has created a plethora of gear and tasks. Essential to these endeavors are comprehending the motives at the back of animal mortality, formulating plans to stop conflicts, and cataloging nearby resources. Building local functionality and such as the community in decision-making are two of the SLC's primary goals (Wali et al., 2017).

Improving the fine of life, imparting sources to resolve problems (including ecotourism and animal insurance) and instructing the network about monetary savings are vital steps in attractive the community in animal conservation applications. But there are still issues that need fixing. These include an absence of bottom-up decision-making in conservation leadership, an education gap that prevents conservation professionals from tapping into the enthusiasm of locals, and an absence of a system that would allow these people to reap the benefits of conservation efforts. Work related to security. Important initiatives to improve conservation in the community include developing and operating training programs, giving financial stability for inspectors and locals to travel and attend training, and establishing local schools on and surrounding dairy farms (Madden, 2004).

Animal protection can only be done effectively with the cooperation of society. As part of this effort, local communities will be empowered to build healthy communities, and community members will participate in conservation and decision-making. For conservation projects to be effective and sustainable, organizations must address challenges and limitations through community engagement (Wurzinger et al., 2021).

11. Mix of modern and contemporary techniques

The combination of traditional knowledge and modern methods can lead to a more informed and effective approach to cattle breeding and conservation. Traditional knowledge systems provide unique insights and methods that can be used to promote permaculture and environmentally friendly solutions that minimize ecological damage (Biscarini et al., 2015). By recognizing and using this knowledge, we can not only preserve culture but also promote diversity and inclusion in all areas. The integration of traditional knowledge and Aboriginal perspectives greatly advances science and technology through the field of Aboriginal science (Kristensen et al., 2015). Since it has been recognized that Indigenous and Western views of science should be equal, there have been efforts to promote cultural leadership in science and science education. However, the prerequisite for cooperation is respect, cooperation, and good communication. By combining modern understanding with historical knowledge, we can increase the success of problem solving and the long-term effectiveness of positive interventions (Fimland, 2007).

12. Policy Implications and Regulatory Frameworks

It is important that national laws and regulations work together to protect genetic material because this is a big problem that needs to be solved. The regulatory process of animal genetics has many areas. Some of these include trade in animals and animal products, animal health, nutrition, and protection. There are other considerations such as animal welfare (Ingrassia et al., 2005). The conservation of animal genetics is extremely important and requires the coordination of various national policies and management systems. The regulatory structure that controls the administration of animal genetic resources has many parts. Some of these facets include trade in animals and their products, animal welfare, food production, and conservation efforts. There are other considerations, such as animal welfare (Galal, 2006).

Government policies and strategies have a significant impact on animal breeding because they provide the groundwork for a legal framework that reflects the values of the nation. In order to protect animal genetic resources, it is essential to establish regulations that promote international and national responsibility for genetic diversity preservation (Martyniuk, 2021). In addition, the developing world must have access to a wide variety of genetic resources and efficient regulatory mechanisms so that they may breed animals that are best suited to their unique social and physical environments, as well as their production and marketing demands (Hiemstra et al., 2006).

13. Livestock Genetic Diversity Conservation

To combat problems associated with inbreeding and restricted effective population levels, as well as to guarantee sustainable agriculture, it is crucial to preserve the genetic variability in livestock breeds. Various designs and methods can be used to preserve the genetics of breeding animals. Genomic technologies, such as whole-genome DNA markers, are one method that can be used to genetically correct hybrids in endangered populations. Additionally, antibiotic use reduces depression and increases genetic diversity (Kristensen et al., 2015).

It is also important to develop national laws and regulations to protect genetics, including animals. These programs should address issues related to the loss of genetic diversity in animal agriculture, promote permaculture and ensure the survival of genetic resources (Hoffmann, 2011).

Preservation of genetic material is important because it has the potential to influence evolutionary processes such as permaculture and adaptation to climate change. Although local farming is no more profitable than commercial farming, there is an important genetic factor that makes them more adaptable, making their conservation more important. This is important for the preservation of genes and the possibility of evolution (Wainwright et al., 2019).

14. Future Opportunities and Challenges for the Livestock Conservation Industry

Agriculture will face many challenges and opportunities in the coming years. The demand for animal products is expected to increase due to factors such as increasing world population, increasing income, and expansion of large cities. However, competition for natural resources such as land and water and economic demands in a carbon-constrained economy will hinder growth (Thornton et al., 2009). This approach to cattle conservation is changing rapidly due to regulatory changes, climate change and increasing business needs. Evidence-based models are needed to support the conservation of endangered species. The challenges of the process, review process, data management and protection are explained (Rawal et al., 2019).

The livestock industry is facing growing influence from environmental and animal welfare laws, as well as social concerns. These factors may hinder the implementation of new scientific advancements and technologies aimed at delivering environmental and social advantages. Hence, the forthcoming trajectory of livestock systems on a worldwide scale is expected to exhibit disparities between industrialized and developing nations, as well as between highly concentrated production systems and small-scale farmer and agropastoral systems (Thornton et al., 2009). Managing increasing demand in a sustainable way while making optimal use of resources and taking social concerns into account is, in a nutshell, the future of cow production, which is fraught with complexity.

15. Conclusion: A Call for Sustainable Practices in Livestock Breeding

There is a strong correlation between the cattle business and improvements in food security, agricultural advancement, and poverty reduction. However, sustainable development may be jeopardized by the cattle industry's growth, which raises issues of equity, environmental impact, and public health. Hence, it is essential to internationally advocate for the sustainable management of animal genetic resources and to transition the livestock industry towards more sustainable growth (Leinonen, 2019). Actions such as formulating policies to encourage national and global accountability for preserving genetic diversity, prioritizing knowledge as a fundamental concept to enforce sustainable management principles for animal genetic resources, and implementing breed conservation measures are necessary. Livestock breeders have the potential to promote sustainable animal agriculture by ensuring a harmonious combination of safe and nutritious food, resilient and well-adapted animals, biodiversity conservation, social accountability, and a competitive and unique Europe. Pasture-based cattle play a crucial role in sustainable agricultural systems, and adopting more robust land and water management strategies may enhance the sustainability of the livestock industry (Fimland, 2007). Implementing effective animal health protocols, modifying the nutritional composition, and developing innovative products specifically designed to mitigate methane emissions are among the strategies used to enhance the sustainability of livestock production. As consumers, we possess a significant responsibility in using our purchasing influence to promote more ethical and sustainable practices in cattle production.

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About The Authors

Mr. Muhammad Tariq graduated from Cholistan University of Veterinary and Animal Sciences in Bahawalpur, Punjab, Pakistan. Now he is a PhD scholar at College of Animal Science and Technology Nanjing Agriculture University, Nanjing, Jiangsu, China. His research interests include Animal Reproduction, Genetics, Molecular Biology. He has published 12 research papers in national and International well-reputed journals. He has also reviewed some research papers.

Email: tariq@stu.njau.edu.cn ORCID: 0000-0001-5539-0454

Dr. Muhammad SAFDAR earned his PhD in Molecular Biology and Genetics from Gaziantep University, Turkey. He is Lecturer in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, nutrigenomics, nano-genomics, bioinformatics, biotechnology, and their applications. He has published more than 70 research articles in national and international journals. He has also written many book chapters as well as an edited book. He is an associate editor for international journals.

E-mail: msafdar@cuvas.edu.pk ORCID: 0000 0002 3720 2090

Mr. Farhad Badshah, currently doing PhD in Animal Genetics from Institute of Genomics Shenzhen, Chinese Academy of Agriculture Science China. His research focus on Functional Genomics. He has published more than 16 research articles in national and international well-reputed journals. He has also written many book chapters. He is a reviewer of many well-reputed national and international journals.

E-mail: farhadbadshah999@gmail.com ORCID: 0000 0001 6971 0957

Miss Saba Saeed graduated from University of the Punjab Lahore, Pakistan. Now she is a PhD scholar at The Government Sadiq College Women University, Bahawalpur. Her research interest includes Fisheries, Microbiology, Molecular Genetics and Bioinformatics. She has published 22 research papers in national and International well-reputed journals. She has also reviewed many research papers.

Email: ssaba5306@gmail.com ORCID: 0000-0002-0452-8027

Arooj Fatima earned Bachelor in microbiology from Cholistan university of veterinary and animal sciences (CUVAS) Bahawalpur Pakistan. Currently she is doing M.phil in Microbiology from Cholistan university of veterinary and animals sciences (CUVAS) Bahawalpur Pakistan. Her research interest in Microbial genetics, Molecular biology, soil microbiology, plant Microbiology and food quality and its application. She has published more than 3 articles and 6 in national and international journals.

E-mail: aroojfatima31202@gmail.com ORCID:0000-0002-4709-4177

Miss Kiran Ashiq graduate from Cholistan university of veterinary and Animal sciences, Bahawalpur. Now she is a PhD Scholar at the CUVAS, Bahawalpur. Her research interest includes in fisheries, microbiology, molecular genetics and Bioinformatics. She has published 15 research paper in national and international well reputed journals. She has also reviewed many research papers.

Email: kiranashiq820@gmail.com ORCID:0009-0005-0397-6273

Miss. Salma Bibi, received her BS degree in Animal Sciences from Cholistan University of Veterinary and Animal Sciences, Bahawalpur, Pakistan. Her main areas of interest are Animal Genetics, Breeding and Reproduction. She has written 8 book chapters in international journals.

Email: salmamalik6809129@gmail.com ORCID: 0009-0003-0798-9886

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QUANTITATIVE GENETICS: UNRAVELING THE COMPLEXITIES OF LIVESTOCK TRAITS

Safdar IMRAN

Hafiz Ishfaq AHMAD

Sidra BIBI

Muhammad SAFDAR

Introduction

The trait in animals usually is parameter to describe specific phenotype or character. It may be a trait which can be observed in general without any technical aid (organism level expressions e.g., color, height, behavior, production etc) and it may also be a trait which need to be observed through molecular tools aid (cellular level expressions e.g., blood groups, immune factors, pathways regulation etc). In animal sciences including birds, livestock, fisheries and even pet and wild animals, the traits are generally divided into different groups based on nature of expression, ease of measurement and genetic control of each trait. The traits may also be categorized as single gene controlled or polygenic traits. The major categories of traits include qualitative traits and quantitative traits. The qualitative traits in general follow simple Mendelian inheritance patterns except a few traits. Yet, the quantitative traits follow a complex inheritance pattern due to complexities of genetic control and possible associations.

Basics of trait variations

The quantitative traits are measured or recorded in animals and presents a continuous variation in the population as compared to qualitative traits. The numerical values for any continuous trait usually present normal distribution for whole population when measured at each individual level. Quantitative traits are controlled by many gene pairs and the genetic interactions (both intra-allelic and inter-allelic) also contribute to the possible observed variation in any trait in a population. These quantitative traits also get influenced by the environment when compared to qualitative traits. The environmental variations, thus, shall be recorded and analyzed in calculating the actual genetic control for quantitative traits. The standard method includes estimation of the proportion of additive genetic variance out of total phenotypic variance technically termed as heritability (h^2). The values of heritability range between 0 and 1, however for most of the quantitative traits it is between 0-0.4. The numerical value of heritability is indicator of the variations due to genes in a trait's phenotype and the rest is being contributed from environmental factors. So, to calculate heritability usually management conditions are optimized at farm level as the heritability of same trait may be different for different population due to genetics as well as management.

Quantitative traits in livestock and poultry, in general, are the traits of economic importance. Although market variations have also created qualitative traits as economically important variable (color preferences, polled/horned preferences). Yet, most of quantitative traits include productive and reproductive traits and also new selection indices have been observed to include type traits as trait of economic importance. The production traits in livestock varies among dairy and beef, likewise, varies for small ruminants and poultry too. Milk production, milk composition, somatic cell count, total yield, lactation length, herd life, productive life, longevity, fertility, conception rates, calving intervals, calving ease, service period, gestation length, birth weight, feed intake, growth rate, weaning weight, mature body weight, functional appearance, age at slaughter, meat characteristics, wool traits and many relevant traits are of economic importance at farm level and are quantitative in nature. The new era has also included traits about carbon footprints of animal production, methane emissions, gut microbiota, temperament and behavior of animal in economic importance. In poultry, starting from egg weight, egg composition, fertility, hatchability, day old chick weight, growth rate, color, meat characteristics, drumstick length, shank length, height, flight characters are also recorded as quantitative traits due to continuous variations in each population.

Understanding Variance components

The inheritance patterns of these traits are usually complex as effects of some of the genes is too low to be counted directly while the effect of few other genes are established for that trait yet the underlying mechanism and genetic interactions make it difficult to exactly measure the contribution of each gene so the estimated values or predictive measures are presented in these cases also counting for the contribution of the environmental factors (feeding, housing, management, feeding, population density etc.). Earlier, the analysis and predictions have all been made on basis of phenotypic observations and their interpretation in different terms including heritability, variance, component of variance, gene frequency and dominance (Falconer and Mackay, 1996). The quantitative genetics was in action, even without molecular tools and information about specific genes, by applying statistical procedures involving partitioning of phenotypic variations (phenotypic variance) into its components. That's the reason estimation of phenotypic variations has long been used and are still being applied in animal evaluation and selection. The phenotypic variance ($\sigma2_P$) is collective result of genetic variance ($\sigma2_G$) and environmental variance ($\sigma2_E$). The interaction between genetic and environment is also counted for in calculations.

$$\sigma2_P = \sigma2_G + \sigma2_E$$

The genetic variance is subdivided into additive genetic variance, non-additive genetic variance, epistatic interactions.

$$\sigma2_G = \sigma2_A + \sigma2_{NA} + \sigma2_I$$

The environmental variance also can be categorized into temporary or permanent environmental effects.

$$\sigma2_E = \sigma2_{TE} + \sigma2_{PE}$$

These variances are quantified for calculation of heritability, that is of two types , broad sense heritability (H^2) and narrow sense heritability (h^2). In broad sense heritability proportion of total genetic variance out of total phenotypic variance is estimated using following formula.

- Broad sense heritability *Heritability* (H^2)= $\sigma2_G / \sigma2_P$

Yet, for the narrow sense heritability only proportion of additive genetic variance out of total phenotypic variance is calculated using following formula

- Narrow sense heritability *heritability* (h^2)= $\sigma2_A / \sigma2_P$

In both cases, values of heritability range from 0 to 1 and in percentage from 0 to 100.

Quantitative trait Loci

The genetic variations in the animal population are usual and natural. The phenotypic variations observed in livestock populations are due to continuous natural selection and also selection by humans for increasing desirable traits in livestock. The natural selection also contributes to the evolutionary changes in the population, and these can be traced through quantitative trait loci (QTL). The QTL are specified regions of DNA which are associated with specific trait/phenotype that present variations in a population and help resolving complex trait expressions and variation sources. The QTL are identified through QTL mapping, a statistical genetic analysis tool. That is simply leading to defining quantitative genetic as study of genetic basis causing phenotypic variations in population (among individuals). The advances in genetic and genomic analysis and improvements in molecular tools along with development in statistical tools and procedures accompanied by application of logarithm, the identification of specific gene action is becoming increasingly easy. It has opened new horizons for observing the genetic control, genetic variations, QTLs in action and possible gene interactions. The QTL analysis using inbred lines has more statistical power when compared to using outbred lines (Erickson et al., 2004) Yet, in presence of all these facilitative tools and modern prediction procedures the quantitative traits present variations which need more emphasis on exploring the source of variations, answering the question of "how genotype affects the phenotype" and bringing improvements in traits of interest in livestock.

Evolution of quantitative genetics

Quantitative genetics is also termed as genetics of complex traits. Quantitative genetics gets its basis with statistical models, although huge molecular data is currently available, yet, some trait expressions need more precise predictive models for estimation genetic variation in future generations and for designing breeding programs. These statistical methods have been proposed, developed and applied much earlier than invent of molecular tools. R. A. Fisher (1918) invented and introduced statistical method analysis of Variance (ANOVA), and S. Wright (1921) invented and introduced statistical methos named as path coefficients method, both methods were used for partitioning of variations and to explain the resemblance between relatives (Hill, 2010). It has been more than a century now, yet both of these methods are still applicable and work as core of many large techniques in data analysis. Although genetics as a discipline come into force right after the publication of Mendel's work (Mendel, 1951) and Galton's ideas of heritability of traits (Galton, 1876; Galton, 1877). Right after rediscovery of Mendel's work, there started the debate between Mendelian school of thought (Mendelian genetics) and biometrical scientists (leading to Biometrical genetics). The quantitative genetics has matured (Henderson, 1953) in past century and have gone through tremendous changes with wide applications in both plant and animal breeding and genetics (Nelson et al., 2013). However, in current scenarios it is evident that genomic data is taking over the old methods of animal evaluation because of limitations and also with advent of the new tools and techniques.

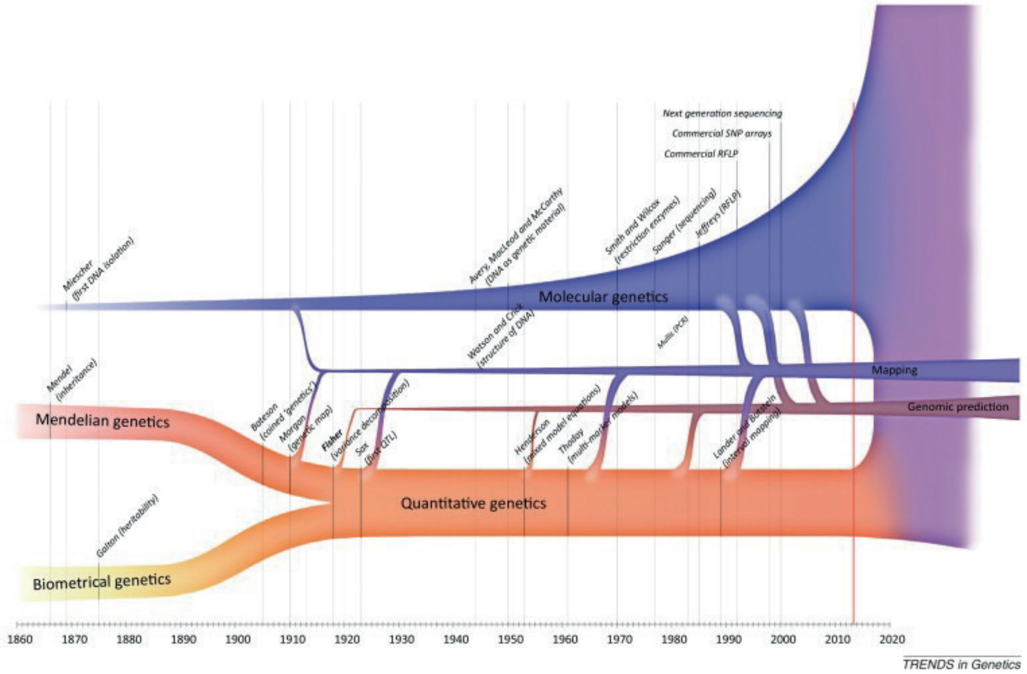

Figure1. Adopted from (Nelson et al. 2013).

The quantitative genetics in earlier days dealt with additive genetic variance and component of variances, yet later shortcomings of additive genetic approaches became evident in try to understand complex trait's genetic architecture from outcomes of genome wide association studies (GWAS) at the time (Hindorff et al. 2013). GWAS helped in identification of QTL, as this method uses whole population data for estimation of natural genetic variation in quantitative traits. Quantitative genetics is used in evolutionary genetics, as it deals with variations, through most general equation

$$\bar{\Delta}z = GP^{-1}S$$

Where,$\bar{\Delta}$z represents changes in trait mean values, G represents genetic variance–covariance matrix while P^{-1} represents inverse of the phenotypic variance–covariance matrix and S as vector of selection differentials (Roff, 2007). The comparisons of the different populations represent the genetic expression differential that help in understanding the variations and evolutionary changes which can be analyzed through threshold models, where at some point of development, traits values termed as liability is used to observe subsequent trajectory, so values of liability above threshold of trait presents one trajectory and liability below trajectory represent alternate path. Such analysis can be completed through threshold models which represents one of the applications of quantitative genetics.

Quantitative genetics helps in understanding the genetic basis of variations in population, the heritability values of same trait may vary in field and lab studies, possibly due to different in environmental component of variations, yet few studies in wild animals have estimated genetic parameters through offspring on parent regression (Roff et al., 2004). Although, the simple methods such as half-sib or offspring–parent regression can't be generally applied in wild populations of animal or birds, it leads to need of new techniques in quantitative genetics and these techniques are animal models. The animal model does not require specific pedigree (Knott et al., 1995; Kruuk, 2004), so animal model can equally be applied to wild animals and livestock for estimation of genetic variance (Charmantier et al., 2006), maternal effects (Wilson et al., 2005), genotype by environmental interactions (Nussey et al., 2005) and even effects of age, sex for variations in genetic parameters.

Quantitative genetics in era of molecular genetics is helping in understanding the variations at transcriptional level from DNA, as transcription arrays helps in visualization of transcription rates, the transcription rates vary among individuals in populations and thus also have own heritability and can be associated with the phenotypes. The transcriptional data can also be analyzed using statistical models approach of quantitative genetics, particularly mixed models which can resolve both genetic as well environmental variations (Wolfinger et al., 2001; Nettleton, 2006). The cost of microarray development and huge data results from analysis, pose some difficulties in finding statistical significance yet the solution to this technique was collapsing the microarrays data into manageable number of variables (uncorrelated) through principal component analysis.

Tools and techniques helping in quantitative genetics

Quantitative genetics is primarily a statistical description of gene actions and it in itself does not have anything to do with genetic mechanisms. The models used in quantitative genetics talk about the mathematical approximation of gene actions, univariates, bivariate, multivariate analysis, breeder equations, all have mathematical approximation about the variations and gene actions. The advent of supercomputers and powerful workstations has provided aid to quantitative genetics for in refining the statistical models to the next level. The unbalanced data from natural populations including livestock have been analyzed using powerful computing tools over the time. Few of these tools include residual/restricted maximum likelihood (REML), facilitated by the availability of general packages such as ASREML (Gilmour et al., 2008). Bayesian methods are increasingly being employed, enabled by Markov Chain Monte Carlo Methods (MCMC) methods (Sorensen and Gianola, 2002) and general packages (e.g. Bugs or Jags), WOMBAT. The results of REML can easily be used for best linear unbiased prediction (BLUP) of breeding values (Hill, 2012), advancement in tools and availability has made data analysis easier as BLUPF90. The advancement in techniques has also helped in developing GBLUP that presents estimation of the weighted proportion of genome in analysis and also the single-step genomic best linear unbiased prediction (ssGBLUP). The estimation of breeding values (EBV) and genomic breeding values (GEBV) are also part of applied quantitative genetics in livestock industry. Single nucleotide polymorphism (SNP) genotyping (Raschia et al., 2024) to understand genomic region effects on trait of economic importance in cattle. The gene associated with milk yield and fat yield were studied in multibreed dairy cattle populations (Laodim et al., 2024). The advanced gene sequence tools (e.g., eneSeek Genomic Profiler (GGP) chips, 9K, 20K, 26K, or 80K), imputation tools (e.g., FImpute version 2.2), and quality control tools (e.g., PLINK software version 1.7) has increased the selection of animals for productive traits through association studies and weighted application of quantitative genetics. Likewise, annotation tools for quantitative trait analysis using R package Genomic Annotation in Livestock for Positional Candidate Loci (GALLO) (Fonseca et al., 2020). Use of RNA sequence data for association studies for mapping expression quantitative traits applied Genome Analysis Toolkit (GATK, v. 4.1.9.0) software for analysis (Diniz et al., 2024). The quantitative genetics in evolving with the time as the computing tools and molecular tools are advancing which collectively increases the application of quantitative genetics in resolving the complexities of quantitative trait inheritance patterns.

Summary

The quantitative genetics is a wonderfully productive approach in analysis of quantitative variations in the population. The application of quantitative genetics is evident right after from the days of introduction of genetics. The statistical tools, biometrical records, phenotypic data, genotypic data, DNA and RNA sequences, transcriptional analysis, translational analysis, microarray analysis, principal component analysis, all have been used for estimation of variance, component of variance especially genetic variance and its components, association studies, genetic interaction, genetype by environment interactions, maternal effects and effects of other variables on quantitative trait variation. The quantitative genetics deals with the best mathematical approximations of the gene actions through statistical analysis. Application of quantitative genetics in evolutionary studies is very important and exemplary. Quantitative genetics helps in understanding complexities of polygenic traits. Quantitative genetics will continue as a major discipline in future also in encompasses statistical models, predictive models, animal models, mixed models, genome wide association studies, quantitative trait loci, genetic interactions, evolutionary studies and many more aspects of breeding, genetics and genomics of which many are necessary for bringing robust changes and precision in animal breeding, selection and genetic improvement of livestock.

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About The Authors

Dr. Safdar Imran received his PhD in 2021 from University of Agriculture Faisalabad, Pakistan. He is Assistant Professor of Animal Breeding and Genetics at the Islamia University of Bahawalpur, Pakistan. His research interests include predictive breeding models, Genetic selection, Genomics, reproductive biotechnology and selection and judging of animals for beauty attributes. He has published ten research articles in well-reputed national and international journals. He also has written book chapters.

Email safdar.imran@iub.edu.pk ORCID 0000-0001-5030-2267

Dr. Sidra Bibi received her degree as Doctor of Veterinary Medicine from Bahauddin Zakariya University, Multan in 2023. She is a professional veterinarian with interests in genetic improvement of livestock with particular emphasis on pets breeding and genetics. Currently, she is pursuing her Masters at the Islamia University of Bahawalpur, Pakistan.

Email malikdrsidra315@gmail.com ORCID 0009-0005-7266-3705

Dr. Muhammad SAFDAR earned his PhD in Molecular Biology and Genetics from Gaziantep University, Turkey. He is Lecturer in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, nutrigenomics, nano-genomics, bioinformatics, biotechnology, and their applications. He has published more than 70 research articles in national and international journals. He has also written many book chapters as well as an edited book. He is an associate editor for international journals.

E-mail msafdar@cuvas.edu.pk ORCID 0000 0002 3720 2090

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GENOMIC TOOLS AND TECHNOLOGIES: REVOLUTIONIZING LIVESTOCK IMPROVEMENT

Sehar ASLAM

Muhammad Shareef MASOUD

Usman Ali ASHFAQ

Mahmood-ur Rahman ANSARI

Nazia NAHID

Mubara IMRAN

Samman MUNIR

Mohsin KHURSHID

Muhammad QASIM

In recent years, advancements in genomic tools and technologies have catalyzed a revolutionary breakthrough in the area of livestock improvement, providing unprecedented opportunities for precision breeding and genetic enhancement. This chapter presents an outline of the transformative impact of genomic tools on various aspects of livestock improvement, including breeding strategies, genetic selection, disease resistance, and production efficiency. The integration of high-throughput sequencing, genotyping, and bioinformatics has enabled researchers and breeders to unravel the genetic makeup underlying complex traits and to identify key genomic markers associated with desirable phenotypic traits. Genomic selection, a revolutionary breeding approach, harnesses genetic data to anticipate individuals genomic quality, accelerating the pace of genetic gain and enhancing the efficiency of breeding programs. Additionally, genomic technologies have facilitated the discovery of novel genes and genetic variants associated with disease resistance, resilience, and adaptation in livestock species, thereby offering potential solutions to mitigate the impact of infectious diseases and environmental stressors. Furthermore, genomic tools have revolutionized reproductive technologies, such as marker-assisted selection and genomic editing, enabling precise manipulation of the livestock genome to introduce beneficial traits or to mitigate deleterious ones. However, the widespread adoption of genomic technologies in livestock improvement presents challenges related to data management, ethical considerations, and regulatory frameworks. This chapter explores the current trends, challenges, and future directions in the application of genomic tools and technologies for enhancing livestock productivity, sustainability, and resilience in response to changing environmental and socioeconomic pressures.

Introduction

1. Background on Traditional Livestock Breeding Methods

Livestock breeding has been a fundamental practice for thousands of years, essential for human survival and development (Aguzzi et al., 2008). Traditional livestock breeding methods have evolved over time, shaped by cultural practices, environmental conditions, and the needs of agricultural communities (Adli, 2018). These methods, although diverse across different regions and cultures, share common principles aimed at improving the productivity, resilience, and suitability of livestock for various purposes (Aida et al., 2016). One of the earliest forms of traditional livestock breeding is selective breeding, where humans intentionally mate animals with desirable traits to produce offspring with similar characteristics. This process often involves observing and selecting animals based on traits such as size, strength, milk production, meat quality, or resistance to diseases.

Over generations, selective breeding can lead to distinct breeds development adjusted to particular environments and purposes (Anzalone et al., 2020).

Another traditional breeding method is crossbreeding, which involves mating individuals from different breeds to combine desirable traits from each parent. Crossbreeding can introduce genetic diversity and hybrid vigor, resulting in animals with improved performance or adaptation to new environments. This method has been used to develop new breeds or improve existing ones by incorporating desired traits from different genetic backgrounds (Anzalone et al., 2019). In addition to selective breeding and crossbreeding, traditional livestock breeding methods may also include practices such as line breeding, inbreeding, and folk breeding techniques, which vary in their objectives and implementation depending on cultural traditions and local knowledge (Banan, 2020).

Traditional breeding methods have played an essential par in shaping the diversity of livestock breeds worldwide and have contributed to the resilience of agricultural systems against environmental challenges and changing conditions (Bi et al., 2016). These methods have been passed down through generations, often through oral traditions and cultural practices, and have sustained livelihoods and food security for communities around the globe. While modern technologies and scientific advancements have revolutionized livestock breeding in recent decades, traditional breeding methods continue to be relevant, particularly in resource-constrained settings where availability to advanced technologies may be limited. Moreover, there is growing recognition of the value of indigenous knowledge and traditional practices in sustainable agriculture and biodiversity conservation (Bischoff et al., 2020).

Conclusively, traditional livestock breeding methods represent a rich heritage of knowledge and practices developed by agricultural communities over centuries. These methods have contributed to the diversity, adaptability, and productivity of livestock breeds worldwide and continue to play a vital role in shaping the future of livestock agriculture in an increasingly complex and interconnected world.

2. Emergence and Significance of Genomic Tools and Technologies

In recent decades, the emergence of genomic tools and technologies has revolutionized various fields of science, profoundly impacting research, medicine, agriculture, and beyond. Genomic tools encompass a wide range of techniques and methodologies designed to analyze, manipulate, and understand the genetic information encoded within an organism's DNA. These advancements have unlocked unprecedented insights into the complexities of life, offering new avenues for exploration, discovery, and innovation (Bogliotti et al., 2018). One of the most significant breakthroughs in genomics is the evolution of high-throughput sequencing technologies, also termed as next-generation sequencing (NGS). These revolutionary techniques facilitate efficient and economical sequencing of whole genomes, transcriptomes, and epigenomes, providing researchers with vast amounts of genetic data in a fraction of the time and cost compared to traditional sequencing methods. High-throughput sequencing has paved the way for numerous discoveries, from unraveling the genetic basis of diseases to deciphering the evolutionary history of species (Cameron et al., 2017).

In addition to sequencing technologies, genomic tools encompass a diverse array of methodologies for genome editing, functional genomics, and bioinformatics analysis. Genome engineering techniques, such as CRISPR-Cas9, have empowered scientists to precisely modify DNA sequences within living organisms, offering unprecedented opportunities for genetic engineering, gene therapy, and agricultural improvement. Functional genomics tools, such as microarrays and RNA interference (RNAi), enable researchers to elucidate the functions of genes and their regulatory networks, providing insights into biological processes and disease mechanisms (Carey et al., 2019). Furthermore, bioinformatics tools and computational algorithms contribute significantly in analyzing and interpreting genomic information, enabling researchers to identify genes, predict protein structures, and unravel complex biological phenomena. The integration of genomic, transcriptomic, metabolomic, and proteomic data has enabled systems biology approaches to understanding the interconnectedness of biological systems, leading to new insights into health, disease, and environmental interactions (Carroll, 2017).

The significance of genomic tools and technologies extends far beyond the realms of basic research, with profound implications for human health, agriculture, conservation, and beyond. In medicine, genomic approaches hold promise for personalized medicine, disease diagnosis, and targeted therapies tailored to an individual's genetic makeup (Bogdanovich et al., 2002). In agriculture, genomic tools offer opportunities for crop improvement, livestock breeding, and sustainable food production to address global challenges such as climate change and food security. Moreover, genomic technologies have implications for biodiversity conservation, environmental monitoring, and biotechnological innovation, offering solutions to pressing challenges facing society (Chandler et al., 2013). However, alongside these transformative opportunities, genomic technologies also incite ethical, legal, and social implications associated with privacy, equity, and governance, highlighting the need for responsible stewardship and ethical oversight.

However, the emergence of genomic tools and technologies represents a paradigm shift in our understanding of biology and the natural world, offering unprecedented opportunities for exploration, discovery, and innovation. These powerful tools hold the potential to revolutionize various fields of science and society, shaping the future of medicine, agriculture, and beyond. However, realizing the full potential of genomics requires interdisciplinary collaboration, ethical reflection, and responsible stewardship to ensure that these technologies benefit humanity and the planet (Chen et al., 2015).

3. Basics of Genomic Tools

3.1. High-throughput Sequencing Technologies

NGS, a high-throughput sequencing technology, have transformed the landscape of genomics, revolutionizing our ability to sequence and analyze vast amounts of genetic information rapidly and cost-effectively. These innovative technologies have opened new frontiers in research, medicine, agriculture, and beyond, providing unparallel perspective on the intricacies of the genome and its role in health, disease, and evolution. One of the hallmark features of high-throughput sequencing technologies is their ability to sequence DNA at an unprecedented scale and speed. Unlike traditional Sanger sequencing, which sequences DNA fragments one at a time, high-throughput sequencing platforms can simultaneously sequence millions to billions of DNA fragments in parallel. This massive throughput enables researchers to sequence entire genomes, transcriptomes, and epigenomes quickly and efficiently, unlocking a wealth of genetic data that was once unimaginable (Chen et al., 2021).

Several key technologies power high-throughput sequencing platforms, each with its unique advantages and applications. Illumina sequencing, depending on reversible dye-terminator chemistry, is among the most broadly used NGS technologies, known for its high accuracy, scalability, and cost-effectiveness. Ion Torrent sequencing, based on semiconductor sequencing technology, offers rapid sequencing with simple workflows and minimal sample preparation requirements. Other platforms, such as Oxford Nanopore Technologies, and Pacific Biosciences (PacBio) utilize single-molecule sequencing approaches, offering long read lengths and real-time sequencing capabilities. The implementation of high-throughput sequencing technologies are extensive and diverse, covering various areas of science and medicine (Cho et al., 2018). In genomics, these technologies have facilitated genome-wide association studies (GWAS), comparative genomics, and population genetics, leading to new discoveries in evolutionary biology, human genetics, and biodiversity research. In medicine, high-throughput sequencing has revolutionized clinical diagnostics, enabling the identification of disease-causing mutations, personalized cancer therapies, and prenatal screening for genetic disorders (Cho et al., 2014).

Furthermore, high-throughput sequencing technologies have revolutionized transcriptomics, enabling the comprehensive analysis of non-coding RNAs, alternative splicing and gene expression at a genome-wide scale. Epigenomic studies have also benefited from high-throughput sequencing, allowing researchers to map histone modifications, DNA methylation, and chromatin accessibility patterns, offering insights into gene modulation and epigenetic mechanisms underlying development, aging, and disease. Despite their transformative impact, high-throughput sequencing technologies also present challenges and limitations, including data management, computational analysis, and quality control issues. Moreover, ethical, legal, and social implications associated with privacy, permission, and data sharing must be carefully tackle to assure responsible use and interpretation of genomic data (Ciccarelli et al., 2020).

However, high-throughput sequencing technologies represent a groundbreaking advancement in genomics, empowering researchers with unprecedented capabilities to decode the mysteries of the genome and its role in health, disease, and evolution. As these technologies continue to evolve and improve, they hold the promise to revolutionize various fields of science and medicine, molding the future of personalized medicine, agricultural biotechnology, and beyond. However, realizing the full potential of high-throughput sequencing requires ongoing innovation, collaboration, and ethical reflection to harness its power for the benefit of humanity and society (Coelho et al., 2020).

3.2. Genotyping Techniques

Genotyping techniques are essential tools in modern genetics, enabling the study of genetic disparity and the identification of specific GMs (GMs) within an individual's genome. These approaches are essential across broad range of applications such as biomedical research, personalized medicine, agriculture, and forensic science (Clark et al., 2000). By decoding the genetic blueprint of organisms, genotyping techniques provide valuable insights into genetic diversity, disease susceptibility, and evolutionary relationships. One of the most extensively employed genotyping techniques is polymerase chain reaction (PCR), which amplifies specific DNA sequences of interest using thermocycling. PCR-based genotyping allows researchers to detect deletions, insertions, single nucleotide polymorphisms (SNPs), and other genetic variations with high sensitivity and specificity. Allele-specific PCR, multiplex PCR, and quantitative PCR (qPCR) are variations of PCR commonly used for genotyping applications (Cong et al., 2013).

Another commonly used genotyping approach is restriction fragment length polymorphism (RFLP) analysis, which relies on the detection of DNA sequence variations that result in differences in the lengths of restriction fragments generated by restriction enzymes. RFLP analysis has been widely used in genetic mapping, linkage analysis, and population genetics studies. Other genotyping techniques include allele-specific oligonucleotide hybridization, in situ hybridization, and DNA sequencing-driven technologies such as NGS and Sanger sequencing. NGS technologies, in particular, have revolutionized genotyping by enabling the parallel analysis of thousands to millions of GMs across entire genomes, transcriptomes, and epigenomes (Cowan et al., 2019).

Genotyping techniques are invaluable tools in personalized medicine, where they are used to identify genetic variants linked with drug response, disease susceptibility, and treatment result. Pharmacogenomics, the study of how genetic variability impact drug response, relies on genotyping to guide the selection of optimal drug therapies for individual patients depend on their genetic genetic makeup. In agriculture, genotyping techniques are employed for marker-assisted selection (MAS) and genomic selection to accelerate the breeding of crops and livestock with desired characteristics which includes nutritional quality, yield potential and disease resistance. By identifying GMs associated with trait variation, genotyping allows breeders to make rational choices in selecting superior genotypes for breeding programs (Crispo et al., 2015).

Furthermore, genotyping techniques play a crucial role in forensic genetics, where they are used for criminal investigations, paternity testing and DNA profiling. Short tandem repeat (STR) analysis, a variation of PCR-dependent genotyping, is commonly used in forensic DNA analysis due to its high sensitivity and discriminatory power in identifying individuals based on their unique genetic profiles (Davis & Maizels, 2016). However, genotyping techniques are powerful tools for unraveling the genetic basis of traits, diseases, and evolutionary relationships. From biomedical research to agriculture and forensic science, these techniques provide valuable insights into disease susceptibility, genetic disparity, and individualized treatment strategies. As genotyping technologies keep on advancing, they hold the promise to revolutionize our knowledge of the genetic underpinnings of life and to drive innovations in healthcare, agriculture, and beyond (DENG et al., 2014).

3.3. Bioinformatics and Data Analysis Methods

Bioinformatics and data analysis methods play a critical role in processing and deciphering the large amount of genetic data obtained from modern genomic technologies. Bioinformatics encompasses a diverse array of computational tools and techniques for accessing biological data, such as gene expression profiles, protein structures, and DNA sequences. These methods enable researchers to derive valuable insights from complicated datasets, identify genetic variations, predict protein functions, and unravel the molecular mechanisms behind biological processes (Eaton et al., 2019). From sequence alignment algorithms to machine learning models, bioinformatics tools facilitate the integration and interpretation of genomic data, driving discoveries in fields such as genomics, systems biology, and personalized medicine (Derscheid & Ackermann, 2012).

Data analysis methods in bioinformatics are characterized by their adaptability to different types of biological data and research questions. Statistical approaches like differential gene expression evaluation and pathway enrichment analysis, are generally used to detect significant patterns and associations within genomic datasets. Machine learning algorithms such as random forests, neural networks, and support vector machines increasingly employed for tasks such as disease classification, protein structure prediction, and drug discovery. As genomic datasets continue to grow in size and complexity, advances in bioinformatics and data analysis methods will be essential for unlocking the full potential of genomic research and translating genetic insights into clinical and agricultural applications (Fan et al., 2018).

3.4. Role of Databases and Genomic Resources

Databases and genomic resources play a fundamental role in facilitating access to vast amounts of genetic information and enabling research across diverse fields of biology. These resources serve as repositories for genomic information such as genetic variability data, gene annotations, DNA sequences, and functional annotations of genes and proteins. By providing centralized access to curated and standardized data, databases such as GenBank, Ensembl, and the National Center for Biotechnology Information (NCBI) enable researchers to explore the genetic diversity of organisms, compare genomes across species, and investigate the molecular basis of biological processes (Fang et al., 2018).

Moreover, genomic databases serve as invaluable tools for hypothesis generation, experimental design, and data interpretation in genomic research. Researchers can leverage genomic resources to identify candidate genes associated with specific traits or diseases, annotate gene function, predict protein structures, and explore evolutionary relationships between species (Fischer et al., 2016). Furthermore, genomic databases facilitate data sharing, collaboration, and reproducibility in scientific research, promoting transparency and accountability in the scientific community. As genomic datasets continue to expand and evolve, the role of databases and genomic resources will remain pivotal in driving discoveries and advancements in genetics, genomics, and related disciplines.

4. Applications of Genomic Tools in Livestock Improvement

4.1. Breeding Strategies

4.1.1. Traditional Breeding vs. Genomic Selection

Traditional breeding and genomic selection are two approaches used in animal and plant breeding to improve desired traits, but they differ significantly in their methodologies and applications. Traditional breeding, also known as conventional breeding, relies on phenotypic selection based on observable characteristics which includes quality, yield, and disease resistance. Breeders select parent organisms with desirable traits and cross them to produce offspring with a combination of these traits. Through repeated cycles of selection and crossbreeding, breeders gradually improve the genetic composition of populations to achieve their breeding goals. While traditional breeding has been successful in developing new crop varieties and livestock breeds over centuries, it is often time-consuming and labor-intensive, requiring multiple generations of selection and evaluation (Foley et al., 2011).

In contrast, genomic selection is a modern breeding method that utilizes genomic data to anticipate the individual genetic attributes for particular characteristics. Genomic selection relies on high-throughput genotyping technologies to genotype thousands of GMs scattered throughout the genome of individuals within a breeding population. These GMs are linked with interested phenotypic characteristics, allowing breeders to predict the individual genetic value depending on their genotypic profiles. By incorporating genomic information into breeding programs, genomic selection facilitates more efficient and precise selection of superior individuals, accelerating the genetic gain rate and reducing the generation interval (Gaj et al., 2013). While both traditional breeding and genomic selection aim to improve desired traits in plants and animals, they differ in several key aspects. Traditional breeding relies on phenotypic selection and may be limited by the availability of accurate phenotypic data, whereas genomic selection leverages genomic information to make predictions about genetic merit, reducing the need for extensive phenotypic evaluation. Additionally, genomic selection allows breeders to select individuals at an earlier stage of development, potentially accelerating the breeding cycle and enhancing genetic development rate. However, genomic selection requires access to high-quality genomic data, sophisticated statistical models, and computational resources, which may pose challenges for breeders in some contexts (Gao et al., 2017).

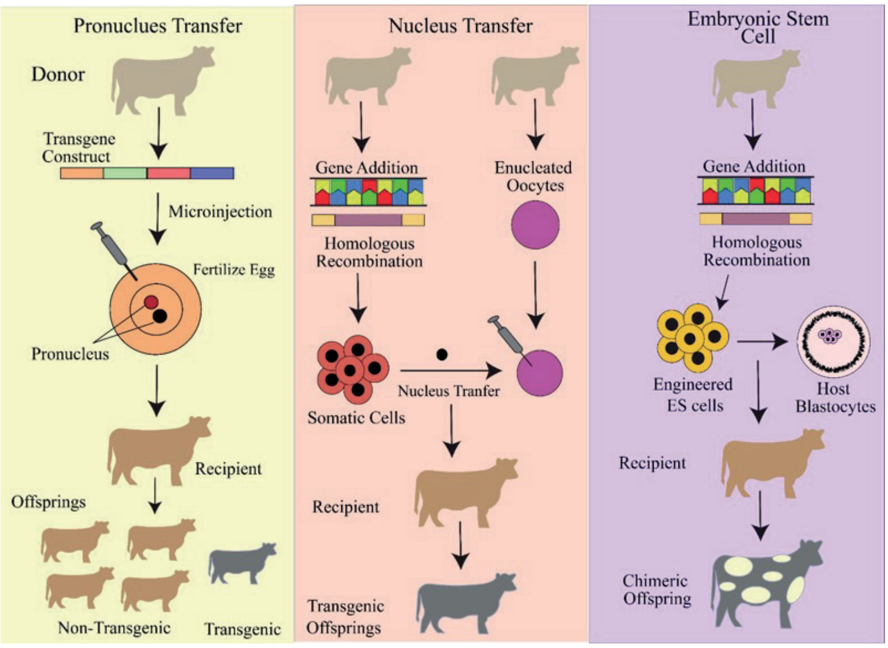

Figure 1. Different strategies of improving and modifying livestock at germline level

In summary, both traditional breeding and genomic selection are valuable tools in plant and animal breeding, each with its advantages and limitations. Traditional breeding relies on phenotypic selection and has been the cornerstone of breeding programs for centuries, whereas genomic selection harnesses the power of genomics to accelerate the rate of genetic improvement. By combining the strengths of both approaches, breeders can develop more resistant, high yielding, and sustainable crop varieties and livestock breeds to meet the problems of feeding a amplifying global population.

4.1.2. Genomic Selection Methodologies

Genomic selection (GS) methodologies represent a revolutionary technique in plant and animal breeding, leveraging genomic information to estimate the genetic value of individuals particular characteristics. GS has gained prominence due to its ability to accelerate the rate of genetic gain, enhance breeding efficiency, and enable the selection of superior individuals at an earlier stage of development. Several methodologies and statistical models are employed in genomic selection, each tailored to the unique characteristics of different breeding populations and species (Gaudelli et al., 2017). One of the key methodologies in GS is the use of high-density genotyping arrays or single nucleotide polymorphism (SNP) chips to genotype individuals within a breeding population. These genotyping arrays contain thousands to millions of GMs scattered throughout the genome, providing dense coverage of genetic variation within individuals. By genotyping individuals at thousands of loci simultaneously, breeders can capture a comprehensive snapshot of the genetic architecture underlying complex traits, enabling more accurate predictions of genetic merit (Georges et al., 2019).

Once genotypic data is obtained, various statistical models are employed to anticipate the genetic value of individuals for particular characteristics. One commonly used model in genomic selection is the genomic best linear unbiased prediction (GBLUP) model, which combines genomic information with phenotypic data to estimate breeding values for individuals. The GBLUP model assumes that genetic effects are distributed across the entire genome and that genetic similarity between individuals can be inferred from their genotypic profiles. Other statistical models, such as Bayesian methods, ridge regression, and machine learning algorithms, are also used in genomic selection, offering flexibility and robustness in predicting genetic merit (Grünewald et al., 2019).

In addition to statistical models, genomic selection methodologies may incorporate various genomic parameters and features to improve prediction accuracy. These include genomic relationship matrices, genomic selection indices, marker-based haplotypes, and genotype-by-environment interactions. By integrating multiple sources of genomic information and accounting for genetic heterogeneity and environmental factors, genomic selection methodologies can enhance the reliability and precision of genetic predictions, leading to more effective breeding strategies and improved breeding outcomes. Moreover, genomic selection methodologies are continually evolving with advances in genomic technologies, computational algorithms, and statistical methodologies. Emerging techniques such as genomic selection for multiple traits, genomic prediction of breeding values for non-additive genetic effects, and genomic selection across multiple environments hold promise for further enhancing the efficiency and effectiveness of breeding programs (Haeussler, 2020).

Hence, genomic selection methodologies represent a paradigm shift in plant and animal breeding, harnessing the power of genomics to accelerate genetic improvement and enhance breeding efficiency. By integrating high-throughput genotyping technologies, sophisticated statistical models, and genomic information, genomic selection enables breeders to make rational choices in choosing superior individuals for breeding programs, ultimately leading to the production of more resistant, productive, and sustainable cultivars and livestock breeds to meet the problems of feeding a amplifying global population (Hai et al., 2017).

4.2. Genetic Selection for Desirable Traits

4.2.1. Identification of Genomic Markers Associated with Phenotypic Traits

Identification of genomic markers associated with phenotypic traits is a fundamental aspect of genomic selection and genetic improvement in plants and animals. This process involves the identification and characterization of genetic variants, such as SNPs, deletions, insertions, and structural variations that are linked with particular phenotypic traits of interest. Genomic markers can be identified through genome-wide association studies (GWAS), linkage mapping, and other statistical approaches that examine the relationship between genetic variation and phenotypic variation across individuals within a breeding population. By analyzing large-scale genomic datasets, researchers can pinpoint genomic regions or loci that harbor candidate genes influencing target traits, offering unparallel insights into the genetic makeup and molecular mechanisms underlying complex phenotypes (Hamernik, 2019).

Once genomic markers linked with phenotypic characteristics are determined, they can be used to inform breeding decisions and accelerate genetic improvement through genomic selection. Genomic markers serve as molecular tags or signatures that enable breeders to anticipate the individual genetic quality for particular characteristics based on their genotypic profiles. These markers are integrated into statistical models and prediction algorithms used in genomic selection, allowing breeders to estimate the breeding values or genetic potential of individuals for target traits with high accuracy and precision. By incorporating genomic markers into breeding programs, breeders can expedite the selection of superior individuals, increase the genetic gain rate, and develop crop varieties and livestock breeds with enhanced productivity, resilience, and adaptability to changing environments (Han et al., 2017).

4.2.2. Application of Genomic Information in Breeding Programs

The application of genetic data in breeding programs has revolutionized the way plants and animals are bred, leading to significant advancements in crop productivity, livestock performance, and genetic improvement. By leveraging genomic technologies and bioinformatics tools, breeders can access detailed information about the genetic makeup of individuals within breeding populations, ensuring for more accurate and targeted selection of superior genotypes for desired traits. Genomic information enables breeders to identify genomic markers linked with essential agronomic characteristics such as yield, disease resilience, and abiotic stress resistance. These markers serve as molecular signatures that facilitate MAS and GS, enabling breeders to make informed decisions in selecting individuals with the highest genetic potential for desired traits (Hao et al., 2018).

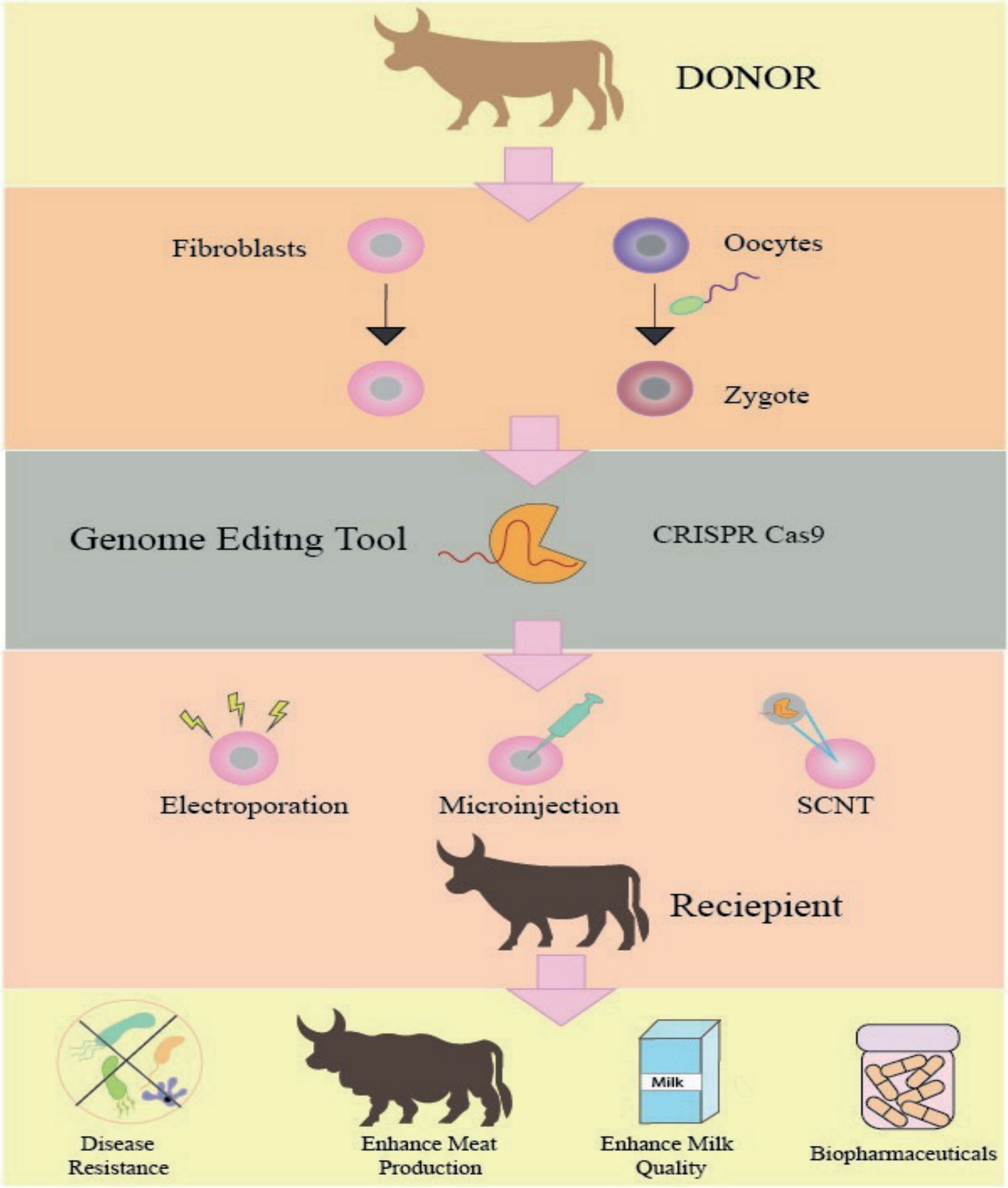

Figure 2. Representing the importance of genome editing tools for the improvement of Livestock

Furthermore, the implementation of genetic data in breeding programs enables breeders to accelerate genetic gain rate, shorten breeding cycles, and develop crop varieties and livestock breeds with improved performance and resilience. Genomic selection, in particular, has arisen as a potent breeding tool, allowing breeders to anticipate the individual genetic quality depend on their genomic profiles, aside from only phenotypic data. By integrating genomic selection into breeding programs, breeders can increase the efficiency and effectiveness of selection, leading to faster genetic progress and more sustainable agricultural production systems. Overall, the implementation of genetic data in breeding programs has the potential to transform agriculture by unlocking the genetic potential of plants and animals, enhancing food security, and addressing global issues which includes population growth and climate change (Harmsen et al., 2018).

Table 1. Techniques of Genome Editing in Livestock

Technique	**Description**	**Applications**	**Advantages**	**Limitations**
CRISPR-Cas9	A versatile tool for targeting specific DNA sequences to induce mutations.	Disease resistance, muscle growth enhancement	High precision, cost-effective	Off-target effects, ethical concerns
TALENs	Uses engineered nucleases to target specific DNA sequences.	Genetic disease correction, trait enhancement	Customizable, high specificity	Complex design, higher cost
ZFNs	Zinc Finger Nucleases that create double-strand breaks in DNA.	Disease resistance, increased milk production	High specificity, long-term stability	Technical complexity, off-target effects
MegaNucleases	Uses naturally occurring nucleases for precise gene editing.	Enhancing meat quality, disease resistance	Highly specific, efficient	Limited targeting scope, complex design

Table 2. Applications and Benefits of Genome Editing in Livestock

Application	**Species**	**Target Trait**	**Benefits**	**Current Status**
Disease Resistance	Pigs	PRRSV resistance	Reduces economic losses, improves animal welfare	In experimental stages
Muscle Growth Enhancement	Cattle, Pigs	Myostatin gene editing	Increased muscle mass, improved meat yield	Early trials, regulatory review
Enhanced Milk Production	Dairy Cows	Beta-casein gene modification	Higher milk yield, improved nutritional quality	Field trials, awaiting regulatory approval
Heat Tolerance	Cattle	Slick gene incorporation	Improved resilience to heat stress	Field trials, some commercial use
Wool Quality Improvement	Sheep	Keratin gene editing	Finer and more abundant wool	Research phase, potential commercial applications
Reproductive Efficiency	Sheep, Goats	GDF9 and BMP15 gene modification	Increased fertility rates	Experimental, promising initial results

4.3. Disease Resistance and Resilience

4.3.1. Genomic Approaches for Disease Resistance

Genomic approaches for disease resistance have emerged as powerful tools in combating infectious diseases and pathogens that threaten the health and productivity of plants, animals, and humans. These approaches leverage genomic technologies, bioinformatics tools, and molecular techniques to understand the genetic basis of disease resistance, identify resistance genes or markers, and develop strategies for breeding or engineering resistant genotypes. By unraveling the genetic mechanisms underlying host-pathogen interactions, genomic approaches provide valuable insights into the molecular pathways involved in disease resistance and susceptibility, paving the way for innovative solutions to mitigate the impact of diseases in agricultural, medical, and environmental settings (Harrison & Hart, 2018).

In plant biology, genomic approaches for disease resistance have revolutionized plant breeding and crop protection strategies, enabling breeders to develop crop varieties with enhanced resilience to pathogens and pests. GWAS, quantitative trait locus (QTL) mapping, and transcriptomic analysis are commonly used to identify genomic regions or genes associated with disease resistance traits in crops. Once resistance genes or markers are identified, breeders can incorporate them into breeding methods through MAS or GS, allowing for the rapid development of disease-resistant crop varieties with improved yield potential and sustainability. Moreover, genomic approaches facilitate the discovery of novel resistance mechanisms and the development of biotechnological interventions, such as genetic engineering or genome editing, to enhance plant immunity and combat emerging pathogens.

Similarly, genomic approaches for disease resistance play a crucial role in veterinary medicine and animal breeding, where infectious diseases pose significant threats to animal health, welfare, and productivity. Genomic studies in livestock species have identified genetic variations associated with disease resistance characteristics which includes resilience to infection, parasitic infections, and production-related diseases. With insight into genetic basis of disease resistance, breeders can implement selective breeding strategies to breed livestock populations with improved disease resilience, decreasing the requirement of antibiotics and chemical interventions in animal agriculture. Furthermore, genomic approaches enable the development of vaccines, diagnostics, and targeted therapies for controlling infectious diseases in livestock populations, thereby enhancing animal health and food safety (Hashimoto et al., 2016).

In human health, genomic approaches for disease resistance have the potential to revolutionize disease prevention, diagnosis, and treatment by determining genetic changes linked with vulnerability to infectious diseases and vaccine response. GWAS, whole-genome sequencing, and functional genomics approaches are used to identify genetic factors that influence individual susceptibility to infections such as viral and bacterial infections, and parasitic diseases (Hendel et al., 2015). By elucidating the genetic basis of disease susceptibility, genomic approaches enable the generation of personalized medicine approaches customized to an individual's genetic profile, including vaccination strategies, drug therapies, and targeted interventions to reduce the risk of infection or disease progression. Moreover, genomic approaches facilitate the discovery of novel drug targets, vaccine candidates, and diagnostic biomarkers for infectious diseases, accelerating the development of new treatments and interventions to combat emerging pathogens and antibiotic-resistant microbes (Hoellerbauer et al., 2020).

Overall, genomic approaches for disease resistance represent a transformative paradigm in disease control and management across diverse fields of biology and medicine. By integrating genomics, bioinformatics, and molecular biology, these approaches provide powerful tools for understanding host-pathogen interactions, identifying genetic determinants of disease resistance, and developing strategies for disease prevention, diagnosis, and treatment. As genomic technologies continue to advance, genomic approaches for disease resistance hold promise for addressing global health challenges, enhancing agricultural productivity, and improving the ecosystems resistance for emerging infectious diseases and environmental threats (Hsu et al., 2014).

4.3.2. Identification of Genetic Variations linked with Resilience

Identification of genetic variations linked with resilience is a crucial aspect of genomic research aimed at understanding the mechanisms underlying the ability of individuals to withstand and recover from adversity, stress, and trauma. Resilience, defined as the capacity to adapt positively in the face of significant challenges or adversity, is influenced by a complicated interaction of genetic, environmental, and psychological factors (Hsu et al., 2014). Genomic studies leveraging high-throughput sequencing technologies, GWAS, and functional genomics approaches have determined genetic variants linked with resilience traits across diverse populations, species, and contexts. These genetic variants may affect various biological pathways and systems involved in stress response, neurodevelopment, immune function, and psychological resilience, offering insights into the molecular mechanisms underlying resilience and susceptibility to stress-related diseases such as anxiety, post-traumatic stress disorder (PTSD), and depression (Hu et al., 2018).

By elucidating the genetic foundation of resilience, genetic research has the potential to inform the development of targeted interventions, treatments, and preventive strategies for promoting resilience and mitigating the impact of stress-related disorders. GMs associated with resilience traits can serve as biomarkers for identifying individuals at risk for stress-related disorders and tailoring personalized interventions to enhance resilience and mental well-being. Moreover, genomic approaches enable the discovery of novel drug targets, therapeutic agents, and psychosocial interventions that modulate resilience-related pathways and systems, offering new avenues for precision medicine and resilience-focused healthcare (Huang et al., 2020). Overall, the determination of genetic variations linked with resistance represents a promising avenue of research with implications for mental health, personalized medicine, and public health strategies aimed at promoting resilience and well-being across diverse populations and settings.

4.4. Production Efficiency Optimization

4.4.1. Genomic insights into Production Traits

Genomic insights into production traits have revolutionized agricultural breeding programs by providing a deeper understanding of the genetic factors influencing traits such as yield, growth rate, feed efficiency, and product quality in livestock and crops. Genomic technologies, including high-throughput sequencing, genotyping arrays, and bioinformatics tools, enable researchers to determine genetic variations linked with yield characterisitcs through GWAS, QTL mapping, and genomic selection approaches. By pinpointing GMs or regions associated with desirable production traits, genomic insights allow breeders to make rational selection choices, accelerating the genetic improvement of breeding populations and the development of high yield and sustainable crop varieties and livestock breeds (Huang et al., 2017).

Moreover, genomic insights into production traits facilitate the implementation of precision breeding strategies aimed at optimizing production efficiency, minimizing environmental impact, and addressing the needs of a amplifying world population. By comprehending the genetic architecture of yield characteristics, breeders can select individuals with superior genetic potential for desired traits, such as higher yield, improved nutritional value, or enhanced disease resistance, leading to more resilient and profitable agricultural systems (Ikeda et al., 2017). Additionally, genomic insights enable the identification of genetic interactions and networks underlying complex production traits, offering opportunities for targeted genetic engineering, gene editing, and molecular breeding approaches to further increase the performance and resistance of agricultural crops and livestock species. Overall, genomic insights into production traits represent a powerful tool for advancing agricultural productivity, sustainability, and food supply amidst of global problems such as climate change, population growth, and resource constrains (Hales, 2019).

4.4.2. Strategies for Enhancing Production Efficiency of Livestock

Livestock production plays an essential role in addressing global food requirement, but improving production efficiency while minimizing environmental impact remains a significant challenge. Genomic tools offer innovative strategies to enhance livestock production efficiency by leveraging genetic information to breed animals with superior traits, optimize breeding programs, and improve management practices. Through targeted breeding and precision management, genomic tools empower producers to maximize productivity, profitability, and sustainability in livestock operations. One key strategy for enhancing production efficiency is genomic selection, which utilizes genomic data to anticipate the genetic quality of animals for particular characteristics which includes feed efficiency, growth rate, and disease resistance (Jiang & Doudna, 2017). By genotyping animals and incorporating genomic data into breeding programs, producers can identify individuals with the highest genetic potential for desired traits at an early age, accelerating genetic progress and reducing the generation interval. Genomic selection enables more accurate and efficient selection of breeding stock, leading to increased productivity and profitability in livestock operations.

Another strategy for enhancing production efficiency is marker-assisted selection (MAS), which targets specific GMs linked with cost-effectively important traits such as meat quality, milk yield, and reproductive performance. By identifying GMs linked to desirable traits through GWAS and QTL mapping, producers can select animals with desired genetic profiles for breeding purposes, leading to the development of superior breeding lineage with improved performance and productivity. MAS allows for more accurate and targeted selection of animals with superior characteristics, minimizing the need for extensive phenotypic evaluation and accelerating genetic improvement in livestock populations (Jin et al., 2019). In addition to genomic selection and MAS, genomic tools can also be used to implement genomic-enhanced management practices aimed at optimizing nutrition, health, and environmental conditions in livestock production systems. By integrating genomic information with data on nutrition, health status, and environmental factors, producers can tailor management practices to the specific needs of individual animals, optimizing feed efficiency, disease resistance, and overall performance. Genomic-enhanced management strategies enable producers to identify and address potential health issues, nutritional deficiencies, and environmental stressors, maximizing productivity and well-being in livestock operations (Ryczek et al., 2021).

Furthermore, genomic tools facilitate the development of genomic breeding values (GBVs) and selection indices that incorporate multiple genetic and phenotypic traits to guide breeding decisions and optimize selection strategies. By considering the genetic merit of animals for a range of traits simultaneously, GBVs and selection indices enable producers to balance competing objectives such as growth, reproduction, and health, leading to more comprehensive and efficient breeding programs. Genomic tools also enable producers to monitor and manage genetic diversity within breeding populations, reducing the risk of inbreeding and preserving genetic resources for future generations (Joung & Sander, 2013). However, genomic tools offer powerful strategies for enhancing production efficiency in livestock systems, enabling producers to breed animals with superior traits, optimize management practices, and improve overall productivity and sustainability. By leveraging genomic information to inform breeding decisions, implement precision management practices, and optimize selection strategies, producers can maximize profitability, minimize environmental impact, and meet the growing demand for high-quality, nutritious livestock products. As genomic techniques are advancing, the potential for enhancing production efficiency in livestock systems will only continue to grow, driving innovation and progress in the livestock industry (Kalds et al., 2020)

4.5. Challenges and Ethical Considerations

Improving livestock production through genomic tools presents a promising avenue for enhancing productivity, health, and welfare. However, this approach has various constrains and ethical concerns that require careful attention to assure responsible and sustainable implementation. One significant challenge is the potential for unintended consequences on genetic diversity and breed integrity. Intensive selection for specific traits using genomic tools may lead to the loss of genetic variation within livestock populations. This reduction in genetic diversity can decrease resilience to diseases, environmental stressors, and changing climatic conditions. Preserving genetic diversity is crucial for maintaining breed resilience and adaptability, as well as safeguarding cultural heritage and traditional livestock breeds. Ethical considerations arise regarding the preservation of genetic diversity and the equitable distribution of benefits and risks associated with genomic tools, particularly for marginalized communities and small-scale livestock producers who rely on locally adapted breeds (Kalds et al., 2020).

Equitable access to genomic tools and technologies poses another challenge, particularly for resource-limited livestock producers and developing countries. The high costs associated with genotyping, data analysis, and infrastructure requirements may create disparities in access to genomic information and breeding technologies. Limited access to genomic tools can exacerbate existing inequalities within the livestock industry, favoring large-scale commercial operations over smallholders and subsistence farmers. Ethical considerations arise regarding equity, fairness, and social justice in the distribution of benefits and risks associated with genomic tools, necessitating efforts to ensure inclusive participation and capacity-building initiatives for all stakeholders in the livestock sector (Kalds et al., 2019). Ethical considerations also encompass animal welfare and the potential impacts of genomic selection on livestock health, behavior, and well-being. Intensive selection for production traits such as growth rate, milk yield, and carcass quality may lead to unintended consequences such as increased susceptibility to diseases, metabolic disorders, and welfare issues in livestock populations. Ethical considerations arise regarding the trade-offs between productivity and animal welfare, as well as the responsibility of producers and breeders to prioritize the welfare of animals in breeding programs. Strategies to address these ethical concerns may include incorporating welfare-related traits into breeding objectives, implementing animal welfare standards and guidelines, and promoting holistic approaches to livestock management that prioritize animal health, welfare, and quality of life (Kan et al., 2017).

Furthermore, ethical considerations extend to environmental impacts associated with genomic-enhanced breeding programs, including concerns related to resource use, waste management, and greenhouse gas emissions in intensive livestock production systems. Intensive selection for production traits may exacerbate environmental degradation, leading to concerns about sustainability and ecosystem health. Ethical considerations arise regarding the responsibility of producers and breeders to minimize the environmental impacts of genomic-enhanced breeding programs through sustainable management practices, resource conservation, and mitigation strategies to reduce environmental pollution and degradation (Kelly et al., 2020). However, while genomic tools offer significant opportunities for improving livestock production, they also present constrains and ethical concerns that must be overcome to assure responsible and sustainable implementation. By proactively addressing these challenges and integrating ethical considerations into breeding programs, producers, breeders, and policymakers can enhances the advantages of genomic tools by reducing potential risks and encouraging the fitness of animals, people, and the environment. Ethical, equitable, and sustainable approaches to genomic-enhanced breeding are essential for building a resilient, inclusive, and ethical livestock industry that meets the needs of present and future generations (Khan et al., 2018).

5. Future Perspectives

Current trends in genomic livestock improvement reflect a shift towards precision breeding and data-driven decision-making. With advancements in genomic technologies and bioinformatics tools, breeders can now determine and choose animals with interested characteristics more efficiently and accurately than ever before (Khan, 2019). Genomic selection and marker-assisted breeding programs have become commonplace, enabling breeders to accelerate genetic progress, improve production efficiency, and enhance animal health and welfare. Moving forward, the combination of multi-omics data, including genomics, transcriptomics, and metabolomics, holds promise for unraveling complex biological pathways and identifying novel genetic targets for further improvement (Kim et al., 2019). Additionally, the development of genomic editing technologies such as CRISPR-Cas9 opens up new possibilities for precise genetic modifications to introduce beneficial traits or enhance disease resistance in livestock populations. These trends signal a future where genomic tools continue to revolutionize livestock breeding, driving advancements in productivity, sustainability, and animal well-being (Kurt et al., 2021).

In conclusion, the transformative potential of genomic tools in revolutionizing livestock improvement is profound and far-reaching. These tools have reshaped the landscape of animal breeding by providing breeders with unprecedented insights into the genetic makeup of livestock populations. By leveraging genomic information, breeders can make more rational choices, accelerate genetic progress, and develop livestock breeds with enhanced characteristics which includes productivity, disease resilience, and environmental adaptability. The integration of genomic tools into breeding programs holds promise for resolving global food security constrains, sustainability, and animal welfare, paving the way for a future where livestock populations are more resilient, productive, and ethically managed. As genomic technologies continue to evolve, their transformative impact on livestock improvement is poised to drive innovations and advancements that benefit both producers and consumers alike.

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About The Authors

[1]Sehar Aslam, [1]Muhammad Shareef Masoud, [1]Usman Ali Ashfaq, [1]Mahmood-ur Rahman Ansari, [1]Nazia Nahid, [2]Mubara Imran, [1]Samman Munir, [3]Dr. Mohsin Khurshid, [1]Dr. Muhammad Qasim.

[1]Department of Bioinformatics and Biotechnology, Government College University, Faisalabad.

[2]National Institute for Biotechnology and Genetic Engineering (NIBGE), Jhang road, Faisalabad.

[3]Institute of Microbiology, Government College University, Faisalabad.

Correspondence qasemawan@gmail.com

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METAGENOMICS: SEQUENCING TECHNOLOGIES AND BIOINFORMATICS TOOLS

Ali RAZA

Ayesha SHAHZAD

Dua GULZAR

Kaneez RUBAB

Maryam FATIMA

Rabia GHAFFAR

Alishba JAMIL

Haseeb Raza

Hafiz Ishfaq Ahmad

Safdar Imran

Metagenomics has transformed microbial community studies by allowing analysis of both culturable and unculturable organisms in various environments. This chapter reviews current sequencing technologies, including high-throughput platforms such as Illumina and Oxford Nanopore Technologies (ONT), and their applications in metagenomics. This underscores significant advancements in bioinformatics tools that facilitate strain-level microbial detection, taxonomic classification, and metagenome functional analysis. Integrating computational pipelines, such as MEGAHIT, metaSPAdes, and Kraken2, has greatly improved the efficiency of genome assembly and functional profiling in metagenomic research. This chapter also discusses the challenges of large-scale metagenomic datasets and examines new hybrid methods for improved genome reconstruction. By linking microbial taxonomy with functional genomics, this study highlights the crucial role of metagenomics in the advancement of ecological, clinical, and biomedical research. Declining sequencing costs and novel methods continue to drive advancements in the understanding of microbial diversity, antibiotic resistance, and pathogen detection.

1. Introduction

Microbial communities encompassing habitats, such as soil, oceans, and the human body, are essential for determining microbial distribution and environmental interactions. J. Handelsman defined “metagenomics” as the functional and sequential analysis of the collective microbial genomes in 1998. Recent developments have made strain-level community detection possible (Anyansi et al., 2020; Handelsman et al., 1998). Antibiotics, hydrolytic enzymes, antibiotic resistance genes (Riesenfeld et al., 2004), and novel enzyme-coding genes (Ferrer et al., 2007) have been identified through functional metagenomics, which focuses on biochemical and metabolic aspects. Large-scale metagenomic data from various hosts are used to study species interactions, such as parasitism and mutualism (P. Gomes et al., 2024). Two high-throughput sequencing techniques were used Amplicon Metagenomics, which examines specific gene areas for taxonomic classification and biodiversity assessment, and Whole Metagenome Shotgun Sequencing, which offers comprehensive genetic insights and minimizes bias in the identification of novel genes (Anyansi et al., 2020; Pérez-Cobas et al., 2020a).

Traditionally, 16S rRNA analysis has dominated bacterial research (DeSantis et al., 2006), but rising antibiotic resistance in aquatic and terrestrial ecosystems (Ahmad et al., 2021) highlights the need for whole metagenome sequencing (Che et al., 2019), such as Nanopore and Illumina, to facilitate research on antibiotic failure and antibiotic resistance gene transfer (Pehrsson et al., 2016). Metagenomic analyses link microbiome composition to human, animal, and plant health (Wei et al., 2019), that is, the impact of metabolites such as short-chain fatty acids on human health (Wu et al., 2021). Advancements in sequencing technology have led to reduced costs, enhanced throughput, and accelerated speeds; however, conventional screening methods have limitations such as low throughput, labor-intensity, and heightened catalytic promiscuity (Riesenfeld et al., 2004; Simon & Daniel, 2011). Beyond the limitations of Moore's law (Wetterstrand, 2013), next-generation sequencing (NGS) has revolutionized genome sequencing, allowing for comprehensive genome analysis (Kumar et al., 2019), enhanced diagnosis, elucidated genotype–phenotype correlations, and aided novel gene discovery (Heremans & Freson, 2018).

Illumina sequencing provides in-depth read coverage facilitating larger sample sizes, microbial diversity with additional bar-coded time-points (Lazarevic et al., 2009), cost efficiency, and accuracy; however, it is constrained to approximately 500 nucleotides per paired-end read (K. D. Curry et al., 2022). In contrast, Oxford Nanopore technology (ONT), despite its high error rates (5–15%) (Kono & Arakawa, 2019; Rang et al., 2018), facilitates genetic research, that is, epigenetic modification and gene expression (Lee et al., 2020), offering high throughput and long read lengths (Gwak et al., 2021), making it advantageous for genome assembly of repetitive and structurally variant regions (Michael et al., 2018; Zhou et al., 2019). Having achieved read lengths of 1 M base pairs (Miga et al., 2020), ONT significantly impacts fields such as oncology, immunology, and neuroscience by enabling the analysis of phase genetic variants and novel isoforms (Ahumada-García et al., 2019; Libermann & Zerbini, 2006; Suzuki et al., 2017; Williams et al., 2020; Zalvidea & Claverol-Tinturé, 2011; Zheng et al., 2016). Its portability and real-time data analysis assist environmental research, i.e. biodiversity assessment, pathogen identification and wildlife conservation, in both laboratory and field settings (Krehenwinkel et al., 2019; Pomerantz et al., 2018; Reddington et al., 2020)

Next-generation sequencing (NGS) technology has revolutionized microbial profiling by providing extensive metagenomic data on both culturable and unculturable microbes. In addition, the reconstruction of genome assembly and its challenges have prompted the creation of algorithms for contig binning (contig grouping from the same genome) and advanced software tools to classify individual metagenomic reads or contigs and profile bacterial proportions (Gwak et al., 2021). Rapid species detection and discovery in both environmental and clinical contexts is made possible by accurate microbial identification and abundance estimation, which offers unbiased insights into metagenomic sequencing.

2. Sequencing technology

Approximately 25 years after the DNA structure was uncovered, the first DNA sequencing method was introduced (Sanger et al., 1977). Sanger and Maxam-Gilbert have developed first-generation sequencing technologies (Thudi et al., 2012). Sanger terminator sequencing uses dideoxyribonucleotide triphosphates (ddNTPs) as terminators to create DNA fragments, which are size-separated and analyzed via gel electrophoresis (Crossley et al., 2020). These fragments were subsequently size-separated and analyzed by gel electrophoresis to determine the nucleotide sequence. Sanger sequencing has advanced with capillary electrophoresis and has been widely adopted.

Between 2004 and 2006, next-generation sequencing (NGS) technologies revolutionized biomedical research, increasing sequencing data output (Mardis, 2013). NGS is a rapidly evolving field that significantly advances research and clinical applications by transforming nucleic acid sequencing and increasing data volume cost effectively (Wetterstrand, 2013). Second-generation techniques, known as NGS, include pyrosequencing, sequencing by synthesis, and sequencing by ligation, with read lengths of 50–500 base pairs (bp). Notable companies included Roche, Illumina, and SOLID. Short-read NGS advances beyond traditional Sanger sequencing through extensive parallel sequencing of short (250–800 bp), clonally amplified DNA molecules(Tucker et al., 2009).

Third-generation sequencing techniques allow single-molecule sequencing with read lengths of tens of kilobases (kb). Platforms such as Pacific Biosciences and Oxford Nanopore have advanced beyond Sanger and short-read methods, addressing limitations such as genome-wide repeats and structural variant detection. Recently, nanopore technology has gained prominence in life science and biomedical research.(Deamer & Akeson, 2000). This method has the potential to analyze single molecules of amino acids, DNA, and RNA. (Branton et al., 2008; Rodriguez-Larrea, 2021). NGS has drastically reduced the sequencing time from years to weeks, providing robust data with extensive coverage(Mardis, 2013).

2.1. Illumina sequencing platforms

The Solexa next-generation sequencer, launched in 2006, allows up to 1 gigabase of sequencing data per run (Cox et al., 2010). In 2005, the Illumina Genome Analyzer sequenced 10 human genomes in one year, and by 2015, 90% of global sequencing data came from Illumina's Synthesis-By-Synthesis (SBS) chemistry (Akacin et al., 2022). Illumina acquired Solexa in 2007, adopting its synthesis-by-synthesis technology with fluorescent-labeled reversible terminators (Goodwin et al., 2016; Mardis, 2013). Illumina platforms perform paired-end sequencing, achieving an error rate as low as 0.1%, making this the most precise base-by-base sequencing method available. Illumina sequencers offer a high output (1.2 to 6,000 Gb), exceptional accuracy, low cost per base, and various applications. However, they struggle to resolve repetitive genome regions, complicating the detection of genetic variants such as repeat expansion disorders and structural variants (SVs). Precise sample loading is also crucial to avoid overlapping clusters that compromise the quality, leading to an overall error rate of approximately 1% (Dohm et al., 2008).Illumina currently provides four benchtop platforms (iSeq, MiniSeq, MiSeq, and NextSeq) for smaller experiments and two production-scale platforms (HiSeq and NovaSeq) primarily used for large-scale whole-exome sequencing (WES) and whole-genome sequencing (WGS) (Liu et al., 2012).

2.1.1. HiSeq

The Illumina HiSeq platform is known for its high throughput, long read length, and low error rate, making it ideal for large-scale genomic studies (Stoler & Nekrutenko, 2021). The key features include precise temperature control, fluidic coupling, and customizable protocols (Pandit et al., 2022). In 2010, HiSeq 2000 used synthesis-by-synthesis (SBS) to offer high output at a lower cost than Roche 454 and SOLiD. HiSeq 2500 has two modes high output (up to 1 Tb in 6 days) and rapid run (up to 300 Gb in 60 h). HiSeq 3000/4000, built on HiSeq 2500, provides higher throughput at a lower cost (Cyranoski, 2016). In 2014, the HiSeq X Ten was introduced, comprising 10 HiSeq X instruments capable of producing 1.8 Tb in 3 days or 18,000 genomes per year at 30x coverage, utilizing patterned flow cell technology to enhance cluster generation and throughput.

2.1.2. MiSeq

MiSeq, Illumina’s integrated next-generation sequencing instrument, uses a reversible-terminator sequencing-by-synthesis technology for end-to-end solutions. This compact benchtop sequencer has run times as short as 4 hours and performs cluster generation, amplification, sequencing, and data analysis in a single run. It supports single- and paired-end runs with adjustable read lengths from 1 × 36 to 2 × 300 bp, making it ideal for targeted gene sequencing, metagenomics, and gene expression studies (Ravi et al., 2018). Launched in 2017, the NovaSeq 6000 platform offers exceptional flexibility with various flow-cell yields for different read lengths (Modi et al., 2021). Although limited to a maximum of 150 nt reads, it can produce over 20 billion paired-end reads or more than 40 billion total reads (6000 Gb) per run using two S4 300 flow cells. A center with ten NovaSeq 6000s can sequence at least 60,000 genomes with 30× coverage annually, potentially exceeding 70,000 at maximum capacity. With just a dozen centers using NovaSeq, nearly one million genomes can be sequenced each year.

2.1.3. MiniSeq

MiniSeq is a compact next-generation sequencing system that was developed by Illumina(Yang et al., 2014). It is designed to offer a cost-effective and efficient solution for small-scale sequencing projects, making it accessible to a wide range of research laboratories and clinical settings (Pareek et al., 2011). Utilizing Illumina sequencing-by-synthesis chemistry, MiniSeq offers high accuracy and low error rates (Kenneth Nelson et al., 2011). It generates high-quality sequencing data with read lengths of up to 150 bp, which is suitable for small genome sequencing, targeted gene panels, and amplicon sequencing. However, it is less commonly used for whole genome or exome sequencing than high-throughput methods such as HiSeq and NovaSeq.

2.1.4. iSeq100

The Illumina iSeq 100 system is a compact and cost-effective platform for small-scale sequencing projects (Yang et al., 2014). It generates read lengths of up to 2×150 bp and a maximum output of 1.2 Gb per run (Pervez et al., 2022). With up to 4 million reads per run, it is ideal for targeted gene expression analysis, small-scale metagenomics, and clinical diagnostic assays (Degnan & Ochman, 2012).

2.1.5. Mechanism of Illumina Sequencing

The Illumina Next Generation Sequencing (NGS) process involves four steps, starting with double-stranded DNA or other forms such as genomic DNA, immunoprecipitated DNA, reverse-transcribed RNA, or cDNA (Rizzo & Buck, 2012). Sequencing libraries are prepared by fragmenting the DNA into smaller pieces and ligating adapters to incorporate platform-specific synthetic DNA. Tagmentation can combine fragmentation and ligation to enhance efficiency. The adapter-ligated fragments are amplified by PCR and purified by gel electrophoresis. Standard kits provide protocols for whole-genome sequencing (WGS), RNA sequencing, and targeted sequencing. The library was loaded into a flow cell, where fragments were captured using surface-bound oligos complementary to the adapters. Each fragment is amplified into clonal clusters, with approximately one million copies per cluster. For example, 10,000 clusters would generate 10,000 single reads and 20,000 paired-end reads. Once cluster generation is complete, the templates are ready for sequencing. Illumina Sequencing by Synthesis (SBS) technology uses a reversible terminator-based approach to identify bases that integrate into DNA strands. The presence of all four reversible terminator-bound dNTPs during each cycle minimizes incorporation bias and lowers error rates, resulting in precise base-by-base sequencing, even in repetitive regions. The workflow, from DNA extraction to sequencing using Illumina, is shown in Figure 1.

2.2. Oxford Nanopore Technologies (ONT)

Nanopore-based sequencing is a promising single-molecule approach developed by Oxford Nanopore Technologies (Yue Wang et al., 2015). The ONT workflow monitors the electrical current changes as nucleotides move through a nanopore, translating them into specific DNA/RNA sequences. Unlike other methods, ONT directly detects and sequences single-stranded DNA (ssDNA) by measuring the electrical current variations of the bases (Weirather et al., 2017).

ONT offers several advantages over short-read methods, including improved phasing of polymorphic genes, accurate structural rearrangement detection, real-time data collection, and faster processing. Using native DNA avoids the errors from amplification processes that are common in short-read technologies. Additionally, ONT instruments are more affordable and portable, making them suitable for low-resource setting(Quick et al., 2016). However, ONT has signal-to-noise limitations, leading to a greater error margin (2–15%) than short-read methods. Gradual nucleotide processing adjustments can enhance data collection and reduce errors, which are mainly systematic and difficult to resolve compared with random errors (McCombie et al., 2019). In addition to MinION, ONT has released the GridION and PromethION platforms for high throughput, and the upcoming Flongle is an adaptor-based flow cell for small experiments.

2.2.1. MinION

MinION, released by Oxford Nanopore Technologies in early 2014, is the first commercially available nanopore sequencer. This portable USB-powered device can produce over 90 Mb of data from approximately 16,000 reads in an 18-hour run, with read lengths of 6 kb to over 60 kb (Ashton et al., 2015). By measuring 10 × 3 × 2 cm and weighing 90 g, MinION connects directly to a USB3 port, requiring minimal hardware. Its 512-channel flow cell allows the simultaneous sequencing of up to 512 DNA molecules (Ip et al., 2015), making it ideal for quick genome sequencing in challenging environments.

2.2.2. GridION

GridION can accommodate up to five flow cells, each with 512 channels containing four nanopores, totaling 2048 nanopores per flow cell. Only one pore per channel is active during sequencing, allowing for simultaneous sequencing of 512 DNA molecules (Ip et al., 2015).

2.2.3. PromethION

Released in 2015, PromethION offers improved throughput with two versions, PromethION 24 and 48, featuring 24 and 48 flow cells, respectively. With more flow cells than MinION, the PromethION system could output up to 7.6 Tb of data. PromethION 48 has 3000 channels and 12,000 nanopores, delivering six times the throughput per flow cell, generating 50–100 Gb of long-read data compared with 2–20 Gb from the other platforms (Logsdon et al., 2020).

2.2.4. Flongle

Flongle is a quick, accessible, and cost-efficient sequencing system for small tests, and is ideal for point-of-care clinical use. It uses the same nanopore technology as MinION, GridION, and PromethION, allowing for direct DNA or RNA analysis. Flongles are designed for small samples, such as those from microbiomes, and their single-run capability minimizes the risk of cross-contamination. It also facilitates rapid quality checks and species identification, demonstrating the accuracy of sequencing bacterial and viral genomes for diagnosing AMR genes (Ashton et al., 2015).

2.2.5. Mechanism of ONT Sequencing

Library preparation is essential for nanopore sequencing. DNA fragments must be repaired, and adapters added for compatibility with the nanopore system. Transposase-mediated tagmentation allows simultaneous fragmentation and adapter attachment. The DNA strand combines with a processive enzyme that unwinds the double helix and translocates a single strand through the nanopore, thereby disrupting the current as it passes. Current fluctuations are analyzed to identify specific bases, but noisy readout signals complicate the base calling. The resistance of the nanopore is influenced by nucleotides in its narrowest region, which requires advanced algorithms and substantial training data for effective analysis. Nanopore sequencing has three formats 1D (single strand), 2D (using a hairpin structure for dual sequencing), and 1D2 (similar to 2D without hairpins). Depth, quantified as the total number of sequenced bases relative to genome size, affects the assembly and accuracy. An optimal depth of at least 100x is recommended, with 200x an ideal. The N50 length, a widely accepted metric, should exceed that of the longest repeat sequence to achieve comprehensive assembly (Shafin et al., 2020). Nanopore sequencing relies on nanoscale pores in a membrane separating two chambers filled with an electrolytic solution. The cis side is the sequencing chamber, whereas the trans side contains the analyte (Fu et al., 2020; Stoloff & Wanunu, 2013). Each chamber is linked to a voltage bias that establishes an ionic current through the nanopores (Deamer et al., 2016). The ONT miniaturizes the detection system into portable ASIC chip configurations (MacKenzie & Argyropoulos, 2023). The flow cell consists of micro-wells containing synthetic bilayers with biological nanopores, enabling sequencing within a microchip integrated with electronic sensors. The workflow from DNA extraction to sequencing utilizing Oxford Nanopore Technologies is illustrated in Figure 1.

2.3. Metagenomics

2.3.1. Amplicon Metagenomic Sequencing Approach

Amplicon sequencing uses PCR amplification of a taxonomically informative marker, like the 16S rRNA gene, to assess the diversity of the microbiota. Sequencing and bioinformatic analysis are then used to identify the microbes and their relative abundances (Hugenholtz et al.; Pace). By comparing 16S sequence profiles across samples, one can uncover patterns of microbial diversity and their connections to environmental factors, which might provide light on host-microbe interactions and possible disease mechanisms involving the microbiota (Bulgarelli et al.; Muegge et al.; Smith et al.; Turnbaugh et al.), verified through microbial research (Smith et al.) (David et al.). Comparisons across host genotypes and treatment situations yield robust theories regarding microbiota. However, because of PCR biases, amplicon sequencing may overlook community diversity (Hong et al.) (Sharpton et al.) (Logares et al.). Second, amplicon sequencing may yield heterogeneous diversity estimates because different genomic locations have different taxonomic definitions (Liu et al.) (P. D. T. e. o. a. q. Schloss, distance calculation et al.) (Work- et al.) and unrecognizable artificial sequences are produced via chimeras or sequencing errors (Wylie et al.). Thirdly, taxonomic composition is revealed by amplicon sequencing, but the direct biological functions of taxa are not. The functions of genomes with particular 16S sequences can be identified by phylogenetic analysis (Langille et al.). How well does the genomic diversity of the community captured in databases affect the accuracy of functional inferences? It is difficult to research novel or divergent microorganisms because amplicon sequencing is restricted to taxa with known markers. Transferring the 16S locus across distant taxa through horizontal gene transfer may increase the diversity estimates (Acinas et al.).

2.3.2. Whole Metagenomic Shotgun Sequencing¨

Instead of focusing on certain genomic loci, shotgun metagenomic sequencing fragments and sequences all the DNA in a sample, thus overcoming the limitations of amplicon metagenomics. This technique produces sequences from multiple genomic sites, including coding sequences and taxonomically relevant loci, allowing for simultaneous identification of community members and their functional roles (Sharpton). Despite its benefits, genomic sequencing data pose several difficulties because of their complexity and size, which makes informatic analysis more difficult. Direct sequence comparison is made more difficult by the high diversity of communities and the challenge of identifying the genomic origin of readings, which frequently leads to distinct reads from the same gene (P. D. Schloss, and Handelsman, J. (2008). A statistical toolbox for metagenomics et al.) (Sharpton et al.). The distinct nature of genomes may still be complicated by overlapping reads (Mavromatis et al.) (Mende et al.). Although improvements in informatic software are increasing efficiency, processing the massive amount of genetic data needed for significant results may present computational challenges. Additionally, in metagenomes, host DNA frequently exceeds community DNA, making it necessary to effectively extract microbial DNA using advanced molecular techniques and bioinformatics methodologies (Woyke et al.) (Chew et al.) (Delmotte et al.) (R. Schmieder, and Edwards, R. (2011b). Quality control and preprocessing of et al.) (Garcia-Garcerà et al.). A common issue is contamination (Degnan & community diversity. ISME J. 6), beside this, contaminants are difficult to identify and remove (Kunin et al.). Diversity assessments may be affected by the identification of contaminating reads, although these sequences can be removed using software (R. Schmieder, and Edwards, R. (2011a). Fast identification and removal of sequence et al.). Although costs have fallen, genome-wide sequencing is still more expensive than amplicon sequencing, especially when dealing with complicated communities or extra host DNA. Oxford Nanopore Technologies (ONT) and Illumina have evaluated a molecular inversion probe spectrum for the detection of bacterial, viral, and parasitic diseases. With 96.7% agreement at the genus level for Illumina and 90.3% concordance for ONT, the panel successfully identified pathogens in clinical samples. Both the ONT and Illumina sequencing platforms demonstrated good predictive values for pathogen detection, with Illumina sequencing exhibiting larger read counts but lower mapping percentages. These findings demonstrate the compatibility of molecular inversion probes with several next-generation sequencing platforms for pathogen identification (Stefan).

2.4. Bioinformatics Pipelines

2.4.1. Amplicon data analysis

Next-generation sequencing (NGS) techniques provide single-end reads from 454 pyrosequencing and Ion Torrent, while paired-end reads are produced by Illumina and PacBio using the "fastq" format with quality scores or distinct "fasta" and "quality" files (De et al., 2024).

Commonly used tools for quality assessment include FastQC (v0.11.9) and SeqKit (Andrews, 2010; Shen et al., 2016). Tools for raw data trimming include the FASTX-Toolkit, PRINSEQ, and Trimmomatic (Bolger et al., 2014; Gordon, 2010; Schmieder & Edwards, 2011). Primer removal from demultiplexed fastq files is done by Cutadapt (Martin, 2011). Tools such as Fastq-Join, PEAR, and IDBA-UD are used to join trimmed reads (Aronesty, 2013; Peng et al., 2010; Zhang et al., 2014). DADA2 and Deblur handle chimera identification, quality filtering, and amplicon denoising (Amir et al., 2017; Callahan et al., 2016; Pérez-Cobas et al., 2020a). Deblur only allows single-end reads despite its ability to process large datasets (Nam et al., 2023). NanoPlot (v1.33.0) was used to evaluate the quality of the Oxford Nanopore long readings (De Coster et al., 2018). Filtlong v0.2.1 (Steinig & Coin, 2022) is used for length-based filtering, and NanoFilt v2.8.0 filters sequences with a minimum read length of 1000 bp for 16S amplicons and a mean quality score >10 (De Coster et al., 2018; Kruasuwan et al., 2023). Porechop 0.2.4 is used to trim ligation adapters and manages adapter trimming and barcode demultiplexing for readings that pass basecalling (Fu et al., 2022). The adapter is deleted from reads that have ≥85% adapter identity in the middle, splitting them into two (Chen et al., 2021). A consensus sequence for readings allocated to the same species can be produced by Medaka (v. 0.10.1) (Fu et al., 2022).

High-quality merged reads are classified into operational taxonomic units (OTUs) or amplicon sequence variants (ASVs) in amplicon metagenomic analyses, which correspond to distinct microbial species (Edgar, 2018). Depending on the sequence identity needed for clustering, reads are usually grouped de novo into amplicon sequence variants (ASVs) or denoised OTUs (Odom et al., 2023). OTUs were previously grouped using a 97% sequence identity cutoff [8, 9], although newer guidelines have proposed 99–100% identity to improve species-level identification accuracy (Callahan et al., 2017; Edgar, 2018). Despite its widespread use, the OTU technique has drawbacks, including decreased sensitivity to minute genomic variations and species misidentification (Pérez-Cobas et al., 2020a). For greater accuracy and error correction, denoising techniques that pinpoint precise ASVsare becoming increasingly popular (Amir et al., 2017; Callahan et al., 2016; Pérez-Cobas et al., 2020a). OTU clustering relies on thresholds such as 99% to reduce sequencing artifacts (Stevens et al., 2023). Filtering thresholds derived from abundance data have been employed to eliminate uncommon OTUs that are commonly linked to PCR and sequencing errors (Bálint et al., 2016; Bokulich et al., 2013). Denoising algorithms are currently the most effective approach (Stevens et al., 2023).]. Data are cleaned, clustered, and quantified using tools such as VSEARCH, DADA2, and Deblur. DADA2 is particularly good at pinpointing ASVs and generating fewer false positives (Amir et al., 2017; Callahan et al., 2016; Rognes et al., 2016). Deblur only allows single-end reads but is successful for large datasets (Amir et al., 2017; Nam et al., 2023). Sequences are clustered using ≥97% similarity by popular OTU clustering algorithms including USEARCH, UCLUST, and SWARM (Edgar, 2010; Mahé et al., 2014; Nguyen et al., 2016). Similarly, UPARSE clusters at 97% similarity but may overlook minute strain or species variations (Edgar, 2013). The ASVs in DADA2 are closer to the real sequences (Callahan et al., 2016). Denoising can be done using unoise3 in

USEARCH, Deblur in QIIME 2, or DADA2 (Bolyen et al., 2019; Edwards et al., 2015). For mock community sequencing, QIIME 2 with DADA2 provides the most accurate richness estimations (Almeida et al., 2018; Straub et al., 2020). For 16S amplicon sequencing, DADA2(Callahan et al., 2016), QIIME 2 (Bolyen et al., 2019), and Mothur(Schloss et al., 2009) are the most frequently utilized programs. (Fu et al., 2012; Li, 2009).

Aligning reads directly to reference genome libraries, as performed by PathoScope 2.0 (Hong et al., 2014), is an alternative to OTU clustering. In order to minimize sequencing errors and genetic variants, PathoScope reassigns ambiguously matched reads using a Bayesian mixed modeling approac(Byrd et al., 2014; Francis, 2012). Using k-mer searches, Kraken 2 provides an alignment-free technique for taxonomy assignment based on cumulative k-mer matches throughout a full read (Wood et al., 2019) (Odom et al., 2023). Although they avoid the inherent hazards of sequence grouping and denoising, both methods are susceptible to sequencing errors (He et al., 2015; Nearing et al., 2018). Although DADA2, QIIME 2, Mothur, Greengenes, and SILVA are specifically designed for 16S amplicon sequencing, some of the difficulties these tools solve are no longer as important because of advancements in sequencing technology, expansion of bacterial reference genomes, and increasing computational capacity. Despite being more computationally demanding and intended for a wider range of metagenomics, PathoScope provides more versatile and potent outcomes (Miossec et al., 2017; Nearing et al., 2018).

Taxonomic assignment of ASVs or OTUs is crucial for understanding the composition of the microbial community (De et al., 2024). By measuring the feature sequences in each sample and assigning taxonomy at several levels, from kingdom to species, a feature table (also known as an OTU/ASV table) is created that offers insights into the structure of microorganisms(Liu et al., 2021). In addition to reviewing 4 and 15 databases for microbial taxonomy and functional profiling, respectively, Wajid et al. examined 69 tools for taxonomic categorization (Wajid et al., 2022). For taxonomy assignment, common classifiers like SINTAX (Edgar, 2016a) and the RDP classifier(Wang et al., 2007) compare ASVs to full-length 16S rRNA gene databases OTUs/ASVs are commonly classified using tools such the RDP classifier, UCLUST, Deblur, BLAST, and SINA (Edgar, 2010; Sf, 1990; Wang et al., 2007). To infer precise ASVs, denoising algorithms such as Deblur (Amir et al., 2017), DADA2 (Callahan et al., 2016), or UNOISE3(Edgar, 2016b) are employed. Taxonomy is assigned based on comparisons to reference databases (Edgar, 2016a, 2016b; Wang et al., 2007)). Additional taxonomic assignment tools are Emu, minimap2, Kraken 2, and Bracken; Kristen D. Curry (Kristen D Curry et al., 2022) found Emu to be the best tool for taxonomic profiling. Full-length 16S rRNA amplicon sequencing from ONT devices. The first technique for taxonomic profiling using full-length 16S rRNA amplicon sequencing from ONT devices was NanoClust (Rodríguez-Pérez et al., 2021). MetaMaps(Dilthey et al., 2019) handles long-read data faults using an approximate read mapping technique and expectation-maximization (EM) approach, although it is less appropriate for substantially identical 16S rRNA genes (Bray et al., 2016; Roberts & Pachter, 2013). For taxonomic binning of ONT readings, Centrifuge(Kim et al., 2016) is utilized, and filtered results yield species relative abundance tables (Alili et al., 2021). BLAST and Centrifuge are well-known because of their incorporation into Oxford Nanopore's EPI2ME software, which provides a user-friendly interface for screening MinION fastq readings against several databases. MinION ribosomal RNA readings can also be taxonomically assigned by BLASTn and Discontiguous MegaBLAST utilizing standard or custom databases, such as EZBioCloud or NCBI 16S rRNA. (Kerkhof, 2021). Another effective instrument for taxonomic categorization in amplicon metagenomics is Kraken2 (Wood et al., 2019). Other tools for taxonomic assignment include Emu and Bracken, with Emu proven to be the best tool for taxonomic profiling by Curry (Kristen D Curry et al., 2022).

2.4.2. Whole metagenomics shotgun data Analysis

2.4.2.1. Illumina data

Although shotgun metagenomics offers accurate functional gene profiles and high-resolution taxonomy, it has drawbacks, such as high computational requirements, restricted software compatibility, and massive data volumes. Installing and maintaining tools can be made easier with Conda and the BioConda channel (Dale et al., 2018) when implementing metagenomic analysis pipelines. The Illumina HiSeqX/NovaSeq platforms generate 150 bp paired-end reads, whereas the BGI-Seq500 produces 100 bp paired-end reads for metagenomic sequencing.

Sequencing adapters, low-quality reads, and host DNA sequences present in the samples are eliminated using Knead Data (https//github.com/biobakery/kneaddata), employing the default Trimmomatic (Dale et al., 2018) settings (SLIDINGWINDOW420 MINLEN50) and the "—very-sensitive" option in Bowtie (Langmead et al., 2018). The quality and statistical features of the sequences can be evaluated using FastQC. KneadData or a Trimmomatic-Bowtie 2 combination can effectively manage quality and remove host contamination from metagenomic analyses (Langmead & Salzberg, 2012). Trimmomatic clears primers, adapters, and low-quality sequences from Illumina data; host-aligned reads are eliminated by Bowtie 2. These tools are integrated by KneadData for clean read production and quality checking. These readings are transformed into functional and taxonomy tables using metagenomic analysis; taxonomy profiling is accomplished with MetaPhlAn2 (Segata, 2018). MEGAHIT and metaSPAdes are assembly-based algorithms that generate contigs from clean reads. MEGAHIT easily handles large, complicated metagenomic datasets with few resources (Li et al., 2015), whereas MetaSPAdes can produce longer contigs but requires more computational resources (Nurk et al., 2017). Genes inside assembled contigs are then identified using metaGeneMark (Zhu et al., 2010) or Prokka (Seemann, 2014). Metagenomic datasets with millions of genes are aggregated into functional annotations, such as KEGG Orthology keywords, modules, and pathways, to reduce dimensionality (Kanehisa et al., 2016). Ten different software tools, namely (BLASTN (Johnson et al., 2008), DIAMOND (Buchfink et al., 2021), MEGAN (Huson et al., 2016), Kraken2 (Wood et al., 2019), Bracken (Lu et al., 2017), Centrifuge (Kim et al., 2016), CLARK (Ounit et al., 2015), CLARK-s (Ounit & Lonardi, 2016), Metaphlan3 (Beghini et al., 2021), and Kaiju (Menzel et al., 2016)) can be used for taxonomic profiling.. Software, namely DIAMOND and MEGAN for a single profile, is utilized with default settings according to their manuals. Tools are chosen to cover a range of database classification techniques, including DNA-to-marker (MetaPhlAn3), DNA-to-DNA (BLASTN, Kraken2, Bracken, CLARK, CLARK-s, Centrifuge), and DNA-to-amino acid mapping (DIAMOND+MEGAN, Kaiju). Numerous algorithms are used in these techniques, including taxon-specific markers, FM index, K-mer-based, Bayesian, and alignment-based markers. See (Menzel et al., 2016) for the benchmarking. It is also possible to investigate within- and between-sample contribution diversity (species contributions to a certain function) using HUMAnN2 (Franzosa et al., 2018), a functional profiling program that is frequently used. The Cross-platform Graphical User Interface (GUI) software MEGAN [48] facilitates customizable databases for effective functional and taxonomic analyses. Gene clusters associated with the biosynthesis of secondary metabolites are identified, annotated, and visualized using the antiSMASH database (Blin et al., 2019).

2.4.2.2. ONT data

Whole genome sequencing (WGS) provides phylogenetic analysis and extensive genomic variety, clarifies species relationships and functional functions, and shows genetic diversity among bacteria, viruses, plasmids, eukaryotes, and archaea (Pearson et al., 2009). NGS raw whole-genome sequencing datasets must be trimmed and their quality evaluated to exclude short- and poor-quality reads (Craig et al., 2001). To help with decisions about whether to proceed with analysis or sample cleanup, NanoPlot offers a summary of read length against quality. Prokka annotation files, a Bandage diagram enabling a graphical evaluation of assembly completeness, and a final completed genome in FASTA format are all provided by NanoForms (De Coster et al., 2018). In order to improve genome assembly continuity and remove adaptor contamination, 50 bp are clipped from both ends and sequences less than 1,000 bp with a quality score below 10 are removed using NanoFilt v2.8 (De Coster et al., 2018; Murigneux et al., 2021). Porechop (v0.2.3) (https//github.com/rrwick/Porechop) is used to eliminate adapter sequences, and NanoFilt (v2.2.0) is then used to filter low-quality reads and choose sequences based on length (De Coster et al., 2018).

Using de novo techniques, high-quality, trimmed genome fragments are assembled with or without a reference genome. De Bruijn graph (DBG) methods are particularly effective for reconstructing genomic sequences using overlap analysis with k-mers. The ideal k-mer length for these assemblies can be determined using programs such as Genome Scope, findGSE, and Kmer Genie (Chikhi & Medvedev, 2014). Other software tools used for short-read assembly include Euler-USR, Velvet, ABySS, AllPath-LG, SOAP de novo, MEGAHIT, and IDBA-UD, all of which are based on the de Bruijn graph (DBG) algorithm (Zerbino & Birney, 2008). Because the de Bruijn graph (DBG) technique is good at removing false contigs, it is frequently employed for the de novo assembly of variable-depth data. QUAST 5.2.0 and MetaQUAST are used to evaluate the quality of each metagenome assembly (Mikheenko et al., 2016). Numerous important quality measures are generated by this evaluation N50, L50, the length of the longest contig (in base pairs), the total length (in base pairs), and the number of contigs (Simão et al., 2015). Contigs from assemblies can be used for binning, which classifies genomic segments into biological categories to ascertain species abundance, characterize functions, and comprehend interactions, or for gene function assignment. Because binning may manage complexity from shorter read lengths, it can help expedite the process and lower the computing costs prior to assembly (Mallawaarachchi et al., 2021). For metagenomic research, binning techniques can be taxonomy-independent (unsupervised) or taxonomy-dependent (supervised). Without requiring prior knowledge of the genome, taxonomy-independent or reference-free approaches cluster fragments from the same species by grouping reads according to k-mer distribution. This method depends on k-mer distribution within the same genome being identical. Alignment-free statistical research has demonstrated that single-sequence noise can have a substantial impact on k-mer distance (Girotto et al., 2016). In order to efficiently detect isolated clusters and aggregate low-abundance reads, BiMeta and MetaCluster bin reads are clustered based on Euclidean distance between k-mer count vectors (Girotto et al., 2016; Wang et al., 2012). Tools such as Metawatt, SCIMM, and LikelyBin use nucleotide compositions to cluster fragments from the same genome. Other unsupervised binning methods include abundance-based, hybrid, and composition-based approaches (Pérez-Cobas et al., 2020a). Utilizing programs like AbundanceBin, Poisson distribution-based techniques, MBBC, and Canopy, abundance-based methods group contigs with comparable abundance levels within a sample (Kembel et al., 2012; Pérez-Cobas et al., 2020a; Ying Wang et al., 2015).

Both abundance-based and composition-based strategies are integrated using hybrid methodologies. MetaCluster4, CompostBin, MaxBin2, MetaBAT2, CONCOCT, and COCACOLA are notable tools that use these hybrid techniques To reconstruct draft MAGs, the MAGenie process (https//github.com/jackchen129/MAGenie) combines taxonomic classification, sequence extraction, and metagenome assembly. Flye is the best out of the five assemblers that are assessed; Shasta, Raven, Unicycler, and Canu are the next best. Canu 2.2 (Koren et al., 2017), Flye 2.9.2 (Kolmogorov et al., 2020), Raven 1.8.1 (Vaser et al., 2017), Shasta 0.10.0 (Shafin et al., 2020), and Unicycler 0.5.0 (Wick et al., 2017) are the assemblers that have been benchmarked. Sequences are categorized into taxonomic bins, and genome annotation occurs, identifying and characterizing genes, ORFs, and RNA molecules, signaling the transition from computational analysis to biological interpretation. To predict genes from fragmented genomic sequences, programs such as MetaGene, Metagene Annotator, and GeneMarkS-2 have been utilized (Noguchi et al., 2006; Noguchi et al., 2008; Pérez-Cobas et al., 2020a). Modern technologies for annotating metagenomic data include MetaProdigal and Glimmer-MG, but conventional techniques use automatic annotation followed by human curation. As numerous genomes are being sequenced quickly, fully automated workflows are crucial. PGAP, DFAST-core, and Prokka automated annotation pipelines are notable examples (Seemann, 2014; Tanizawa et al., 2018; Tatusova et al., 2016). For the functional annotation of eukaryotic genomes, specialized tools such as GenSAS and MAKER2 are employed. Metagenomic databases provide taxonomies and functional capabilities of the microbial community; BLAST is a popular tool for the functional annotation of assembled reads (Pérez-Cobas et al., 2020a). To further enhance and verify projected functional annotation, large databases like FunGene, MetaPathways, PFAM, InterPro, PRIAM, and MetaCyc are used (Pérez-Cobas et al., 2020a). For functional metagenomic investigations, comprehensive reference gene catalogs—such as those utilized by MGS-Fast for the human gut microbiome—are essential werebecause they facilitate taxonomic resolution, connect genes to MAGs, and recreate full-length 16S rRNA genes (Brown et al., 2019; Pérez-Cobas et al., 2020a). At the strain level, genome profiling of Metagenome-Assembled Genomes (MAGs) has been made possible using recently developed techniques. MetaMLST, StrainPhlAn, PanPhlAn, DESMAN, and MetaSVN are notable examples (Costea et al., 2017; Pérez-Cobas et al., 2020a; Quince et al., 2017; Truong et al., 2017; Zolfo et al., 2017). To classify metagenome assemblies taxonomically, Kraken 2 2.1.3 (Wood et al., 2019) is used mostly. A standard database can also be used with the following parameters two minimum hit groups, k-mer size of 35 bp, minimizer length of 35 bp, and minimizer spacing of 6 bp. Gene annotation can be carried out using standalone pipelines or web-based tools such as MG-RAST v.4.0, Mgnify, Edge, Micro-Scope, or IMG/M v.5.0 (Dong & Strous, 2019; Pérez-Cobas et al., 2020b). Online systems that lack specialized annotations or have slower processing speeds are typically better suited for standalone pipelines. The comparison of Amplicon and Shotgun Metagenomics workflows reveals distinct approaches in data analysis and assembly (Figure 2).

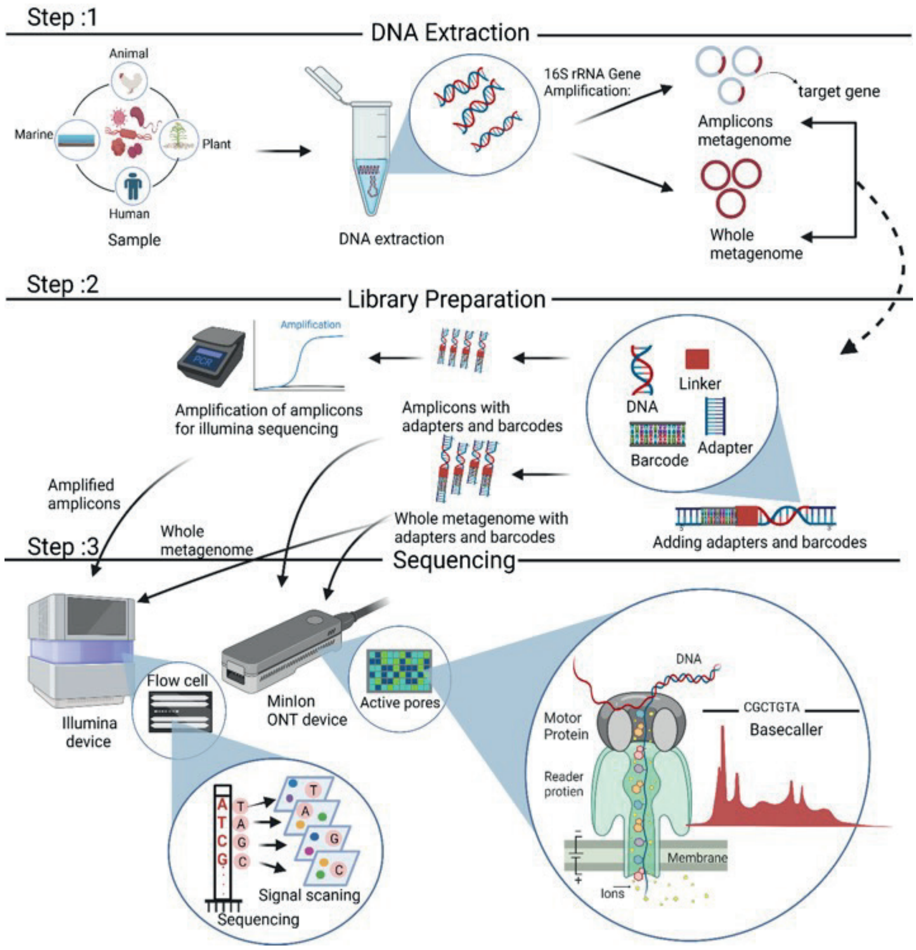

Figure 1: Step 1: DNA extraction from the sample, followed by PCR amplification. **Step 2:** Addition of adapters and barcodes for further PCR amplification. Step 3: Sequencing using Illumina and Oxford Nanopore Technologies (ONT) platforms for high-throughput analyses.

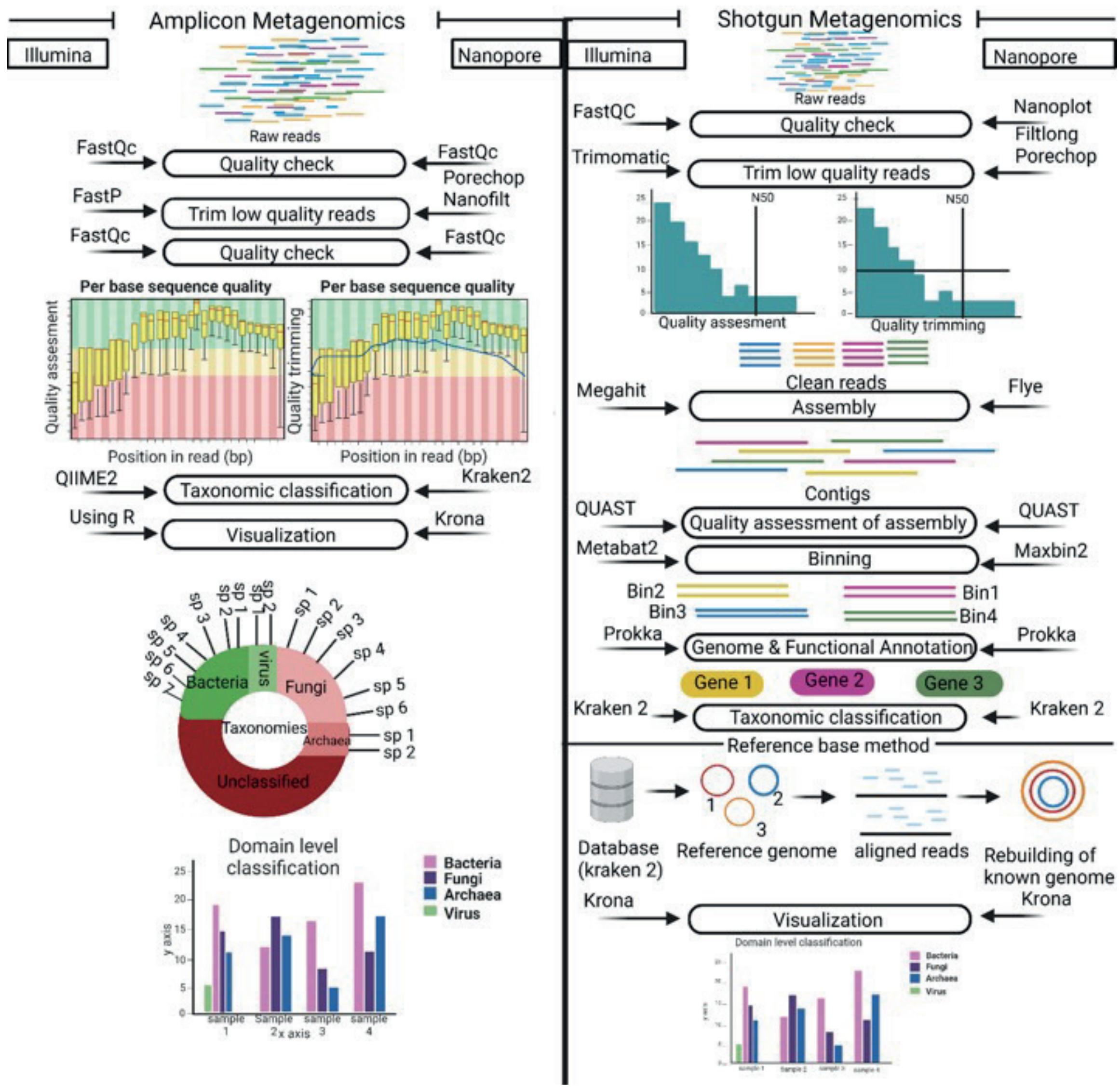

Figure 2: Comparison of Amplicon and Shotgun Metagenomics Workflows:

On the left (Amplicon Metagenomics) Raw reads are quality checked using FastQC, followed by trimming with Fastp and Nanofilt. After a second quality check with FastQC, reads are assembled with MEGAHIT. Taxonomic classification is performed using QIIME2 and Kraken2, with data visualization via R and Krona. On the right (Shotgun Metagenomics) Raw reads are quality checked using FastQC and NanoPlot, then trimmed with Trimmomatic and Porechop. Reads are assembled into contigs using MEGAHIT for short reads and Flye for long reads. Assembly quality is assessed with QUAST, followed by binning with MaxBin2 and MetaBAT2. Genome and functional annotation are conducted using Prokka, taxonomic classification with Kraken2, and visualization through Krona.

Summary

Advancements in sequencing technologies and computational biology have significantly improved our ability to conduct metagenomic research, leading to significant progress in the fields of microbial ecology, biotechnology, and medicine. The combination of Illumina and Oxford Nanopore technologies, along with advanced computational methods, has revolutionized the creation and examination of extensive metagenomic datasets, offering unparalleled precision and thoroughness. As sequencing costs continue to decrease and innovative methods emerge, the integration of metagenomics and functional genomics offers promising avenues for elucidating the roles of microbes in health, disease, and environmental systems. Advancements in hybrid techniques, long-read sequencing technologies, and real-time data analysis methods will enhance our capacity to study microbial communities and discover new genetic functions. These developments enhance our understanding of microbial diversity and have practical applications in fields such as antibiotic resistance, pathogen detection, and environmental monitoring. Consequently, metagenomics has become a leading approach in microbial studies.

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About The Authors

Ali Raza, Department of Veterinary Microbiology, Faculty of Veterinary Medicine, Ataturk University, Erzurum, Turkey

Email: sahilr21727@gmail.com ORCID 0000-0002-6575-8168

Ayesha Shahzad, Institute of Microbiology, Faculty of Veterinary Sciences, University of Agriculture Faisalabad, Pakistan

Email shahzadamnaayesha@gmail.com ORCID 0009-0008-2018-6005

Dua Gulzar, Institute of Microbiology, Faculty of Veterinary sciences, University of Agriculture, Faislabad, Pakistan

Email gulzardua42@gmail.com ORCID 0009-0001-5785-7932

Kaneez Rubab, Institute of Microbiology, Faculty of veterinary sciences

University of Agriculture Faisalabad

Email rubabbhatti512@gmail.com ORCID 0009-0009-3756-1059

Dr. Safdar Imran received his PhD in 2021 from University of Agriculture Faisalabad, Pakistan. He is Assistant Professor of Animal Breeding and Genetics at the Islamia University of Bahawalpur, Pakistan. His research interests include predictive breeding models, Genetic selection, Genomics, reproductive biotechnology and selection and judging of animals for beauty attributes. He has published ten research articles in well-reputed national and international journals. He also has written book chapters.

Email safdar.imran@iub.edu.pk ORCID 0000-0001-5030-2267

Hafiz Ishfaq Ahmad, Department of Animal Breeding and Genetics, Faculty of Veterinary and Animal Sciences, The Islamia University of Bahawalpur

Email ishfaq.ahmad@iub.edu.pk ORCID 0000-0002-9206-2596

Maryam Fatima, Institute of Microbiology, Faculty of Veterinary Sciences, University of Agriculture Faisalabad, Pakistan

Email maryamfatima2047@gmail.com ORCID 0009-0003-9458-7868

Rabia Ghaffar, Institute of Microbiology, Faculty of Veterinary Sciences, University of Agriculture Faisalabad , Pakistan

Email rabiaghaffar58@gmail.com ORCID 0009-0008-9362-4109

Alishba Jamil, Institute of Microbiology, Faculty of Veterinary Sciences, University of Agriculture, Faisalabad, Pakistan

Email alishbajamil000@gmail.com ORCID 0009-0000-3307-7133

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ROLE OF CRISPR TECHNOLOGY IN GENETIC IMPROVEMENT OF LIVESTOCK SPECIES

Muhammad TARIQ

Muhammad SAFDAR

Farhad BADSHAH

Arooj FATIMA

Salma BIBI

Saba SAEED

Kiran ASHIQ

CRISPR technology has been a breakthrough in molecular biology and especially in animal genetics given that it allows modification in DNA sequence and thus the genome of the animal. With the help of this new tool, the breeders will be able to target specific genes that are associated with such favorable traits as immune response to diseases, productivity, and feed conversion efficiency to increase the rate of animal breeding. In foundational strategies, it creates or offers the standard technique of develop a method that involves the establishment of favorable Changes of Links or the elimination of negative genetic changes. This outcome to emergence of better characterized healthier, stronger as well as more valuable breeds of cattle meant for production purposes. CRISPR also eliminates any potential of multiple genes and alters the pathways that create irreversibility of phenotypes depending on genomics. Given several reasons why the use of animals and the impact that this advancement can bring about in foods produced should not be endorsed without animal welfare as well as kind poultry and livestock productions' policy. Despite the mentioned shortcoming which restrict the efficacy of the CRISPR technology, the beneficial impacts of the method have to a considerable extent the ability to set a direction toward improving the food production and making the agriculture safe and ecological. This chapter describes the fact that the CRISPR method is utilized in the improvement of the livestock variety.

1. Introduction

The new revolution in the genetic modification of animals is by employing CRISPR which is a method that assists in the manipulation of genomes of different livestock species (Perisse et al., 2021). With the help of this great tool, new opportunities, for an advanced breeding in cattle, have emerged. It has provided response for improvement of animal welfare, disease resistance, immunocompetence of animals to diseases, efficiencies in animal production and development of superior disease resistant bio-medical models (Wang et al., 2022).

Among the fields outlined earlier as potentially useful in breeding work, the most attention is paid to the development of one or another characteristic relevant to the economy of meat, milk, and wool production. As a result, through genetic manipulation research, have found ways of increasing muscle mass by exercising, altering the quality of milk (Laible et al., 2015), improving quality of wool in different species of livestock dissected (Singh & Ali, 2021). For instance, as the analysis of myostatin gene, which plays the role of a negative regulator of muscle genes, is conducted, the animals with the extraordinarily large muscles and the increased quantity of meat in relation to bones have been obtained (Petersen, 2017).

The CRISPR technique has also been used to create cattle that is resistant to diseases via the process of altering genes that offer immunity or a tolerance to certain diseases (Islam et al., 2020). The implication is that this strategy can easily lead to some improvements in the health and well-being of animals apart from the reduced costs of outgoing that are because of infectious diseases.

CRISPR-based genome manipulation has helped to address issues affecting animal plight such as; depictions of horns from cattle (Jabbar et al., 2021) and minimizing aggression in pigs (Prosman, 2021). These lofty improvements that we are about to highlight have the propensity of improving on the health of cattle in addition to being beneficial to the farmers and producers.

Genetic manipulation, particularly of large animals, has therefore been made accurate, thus enabling the development of complex biological models that may be used for the study of human diseases, including potential treatment. Moreover, the CRISPR technique enables development of livestock products that are developed to synthesize therapeutic proteins or biopharmaceuticals in the milk or blood from the developed livestock species (Lin et al., 2022). This results in a production method that is cheap to implement as well as easy to expand.

Although chances are high that different traits in animals can be genetically enhanced using CRISPR technologies, then there are ethical issues to be considered when it comes to applying the technology and legal frameworks that should be set to best suit such processes (Singh & Ali, 2021). It is about the animals, the impact the interventions themselves have on the ecology, the health of the people and no one should take these issues lightly or vocalize about them without having gone through critical analysis and research, greater thinking, and appropriate, serious and sane debate once more.

Hence, the CRISPR technology should be looked at as a resource in improving the level of particular genetic livestock species. First, it conducted research possibly to enhance production capability, disease resistance, animal health, and/or biomedical science. It needs to be pointed out that following the examples of other industries, to promote further use of this technology in livestock farming in the extensive range, it is more proper to emphasize the positive aspects of the technology in question and come up with the ethical and legal concerns that may arise in the consecutive development of this field.

1.1 Orientation on CRISPR Technology.

CRISPR is a new addition to the world of genetic engineering and stands for clustered regularly interspaced short palindromic repeats. It also makes it possible that all kinds of genetic changes in different plants and animals are an efficient and professional process. The following is an understanding of the significance of the CRISPR technology: Here are the details of the information on the significance of the CRISPR technology:

CRISPR is a natural mode of defense that is innate in microorganisms while, rather than the use of proteins to code RNA molecules in order to direct Cas proteins to excise DNA which is severed (Pak, 2014). Key elements of the CRISPR system include the following: There are several components to the CRISPR system, (Figure 1) these are the following aspects:

1- Cas-RNA is a small RNA molecule that detracts attention to the recognizable DNA sequence and forms a complex with it (Pak, 2014).

2- Cas9 is an enzyme that had functions like molecular shears and the ability to stick to the DNA on the site where the gRNA has recognized it.

3- The last component that combines CRISPR with Cas9 enzyme is to attach a particular element called gRNA to direct the Cas9 enzyme to the DNA and fix it at a certain point that a researcher desires. This helps in chiseling of detail within the featured genetic map (Ghorbani et al., 2021).

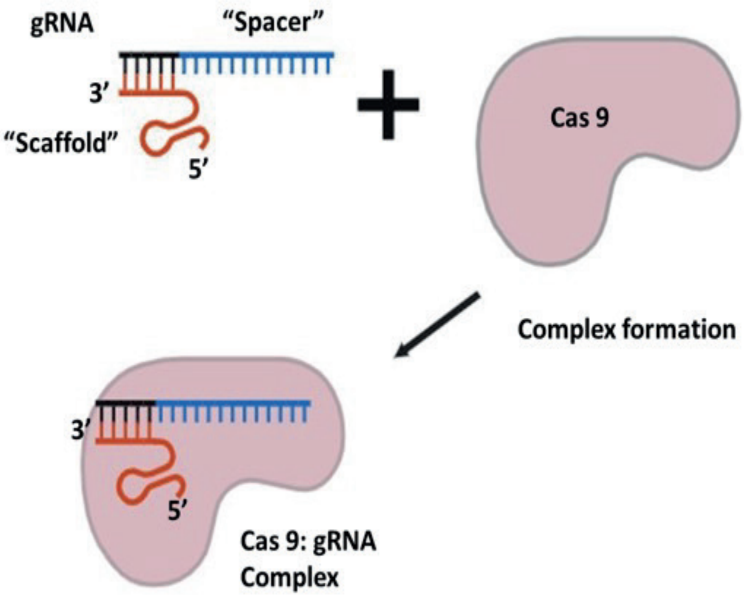

Figure 1. Component of CRISPER System

1.2 Significance in the Field of Genetic Engineering

It is more accurate to say that the CRISPR technology can be considered as one of the true revolutions in the field of genetic engineering regarding such factors as versatility, efficiency, and simplicity of the method. The significance of the product can be seen in.

1. Precise gene editing: CRISPR has the intent and the capability of creating a new style of genetic surgery, it can create targeted alterations, insertions, deletive, or correction of particular genes with an accuracy which had been so far unimaginable (Yang et al., 2021).

2. Versatility: One of the advantages that many researchers like about CRISPR is that this technique is applicable across many species, on plants, animals, and even microorganisms, these make many applications possible (Montagud-Martínez et al., 2024).

3. High-throughput screening: A tremendous advantage of CRISPR is the nature of gene editing at once at multiple positions – this has always been very useful for large physiological-genetic trials (Shalem et al., 2015).

4. Disease modeling and gene therapy: That new breakthroughs on genome editing by the application of CRISPR technique have made possible for deeper investigation and synergistic approach on a number of genetic disorders by creating disease models and gene therapies (Zhang, 2021).

5. Agricultural applications: There are views concerning the possibility that the use of this technique CRISPR might be applied in agriculture to improve yield, nutritional quality of crops, and also their ability to endure conditions, diseases, and pests (Haque et al., 2018).

6. Biomedical research: Also through CRSPR, it becomes easy to develop animal models for the study of human diseases as well as the potential treatment (Chow et al., 2008).

7. Prospects of CRISPR: However, it is imperative to address the ethical dilemmas regarding the application of the CRISPR technology further for proving the efficiency of the regulatory measures in addition to advancement in the aspects such as specificity and modes of delivery of the established regulations. CRISPR technology specifically has made a significant impact in the genetic engineering field especially through a process that allows the researcher to target genes of interest and make changes to the sequence they want at a high precision and speed as well as multiple uses. This has in turn has led to its usage across the fields including agricultural, medical and other basic research fields (Ayanoğlu et al., 2020).

1.3 - Application of genetic improvement in livestock species is vital for agriculture products and food products.

The genetic evolution of animal species plays a significant role in enhancing agricultural sustainability and guaranteeing food security. These are some crucial aspects to consider. These are some salient points:

1- Enhanced Output: The breeding and genetic selection programmed envisaged, are for improvement in traits such as gain, FCR, milk & eggs production and quality of carcass. Therefore, the pressure for resources and environment is reduced and due to this, more offspring is produced from the same or even fewer animals yield more (Maiorano et al., 2024).

2- Disease Resistance: Some of the mechanisms that can be used to introduce genes of resistance to bacterial, viral and parasite diseases in to livestock are through breeding and gene modification by techniques such as CRIPRs. Subsequently, animals acquire more health and better production rates, easy on antibiotics as well as other treatments (Söllner et al., 2021).

3- Climate resilience: It means that the development of livestock stock-breed must be suited according to the areas affected by climate change, such as heat tolerance, drought copy and adaptability to the environment. This is useful in creating an insurance policy on food to prevent situations of food shortage (Rashamol & Sejian, 2018).

4- Feed Efficiency: Feed conversion ratio is capability to feed conversion because through selection of genetic the amount of feed required per unit of animal product is in a position to be reduced hence improving the sustainability and feasibility of livestock production (Waghorn & Hegarty, 2011).

5- Animal wellbeing: It also improves the welfare of cattle since the above traits are unpleasant or have negative effects on animal health; some are deadly to the cows, or the farmers are forced to remove them or trim them often (Yunes et al., 2021).

6- Biomedical Applications: In addition to therapeutic proteins and production of antibodies and all biopharmaceutical products, and improving human life , genetically modified animals can serve as bioreactors (Bertolini et al., 2016).

7- Conservation: This way the genetically diverse Regionally Adapted Breeds are characterized and preserved in form of gene banks in order to have those breeds ready for future breeding activities and the sustainable animal production (Yaro et al., 2017). Genetic improvement programs hence have a crucial function to play in the enhancement of efficiency, greenness and sustainability by raising production efficiency, and lowering the greenness of production, while both remaining crucial during the expansion of the existing livestock production systems to meet the growing global consumption of source animal meals.

2. Fundamentals of CRISPR Technology

CRISPR has progressed to a level that the application of enhancing genes in livestock species through CRISPR based technology is revolutionized. The essential foundations of CRISPR technology in livestock are as follows: This chapter aims to define the following basic components of CRISPR technology in livestock:

CRISPR-Cas9 Mechanism

1- The foundation from which CRISPR-Cas9 system has been derived is the fundamental function of bacteria as the defense mechanisms against plasmids and viruses (Menchaca et al., 2020).

2- The system is comprised of two primary constituents: sgRNA and Cas9 which is a DNA endonuclease to provide corresponding short guide RNA molecules for endogenizing the CPE gene (Petersen, 2017).

3- The sgRNA is specific by it binds to a particular target DNA sequence and directs the Cas9 enzyme to the site of desired locus to introduce a double-strand break (DSB) within the DNA (Viotti et al., 2021).

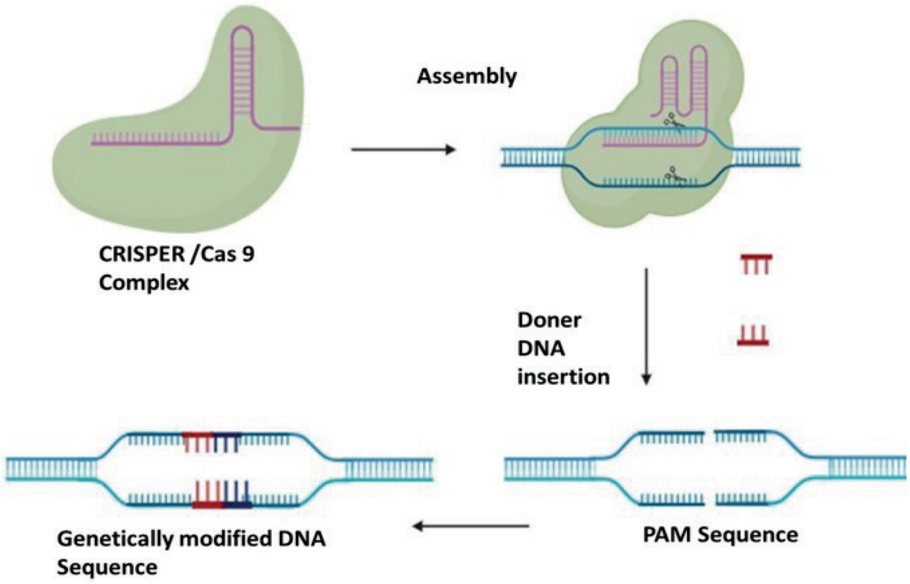

Figure 2. Mechanism of action of CRISPER

Mechanism of Action

1- Currently, the sgRNA is made of a scaffold region which is responsible for the binding of Cas9 and a 20-nucleotide sequence that is reverse complement to the target DNA (Nishimasu et al., 2014).

2- Cas9 shows preference to its binding to a specific target known as protospacer adjacent motif (PAM) which is adjacent to the target DNA (Mekler et al., 2020).

3- Cas9 has scissor like action which cutting the target DNA at two strands and leave a nick that can be repaired by intrinsic reparation system of the cell (Williams et al., 2007).

DNA Repair Mechanisms

1- The repair process that it uses is non homologous end point joining which is an error prone process and in this process insertion deletion (indels) may occur at the break points. Such occurrences may lead to their deletion or even inactivation or even alteration resulting in the disruption of the certain genes (Bennett et al., 2020).

2- As it involves the use of a supplied DNA template, homology-directed repair or HDR is precise in altering the wanted sequence to enable the precise gene insertion or correction (Budhagatapalli et al., 2015).

Applications in Livestock

1- Transgenic application of CRISPR has also been successfully done in livestock species with objectives of gene ablation, gene correction, gene insertion, transcription factor regulation and epigenetic changes (Lamas-Toranzo et al., 2018).

2- It has applications in the improvement of production parameters such as fiber traits, muscle development and lactation, for creating biopharmaceutical models, feeding parameters optimization, and most importantly, better animal ethics (Bomkamp et al., 2022).

Advantages

1- Individuals with specific DNA sequences are directly attacked with high effectiveness.

2- It is even inexpensive and considered to be relatively easier in design as compared to other previous approaches of gene editing instruments.

3- One of its possibilities is to apply itself to the simultaneous muting of several genes.

4- there is adaptability among various types of livestock species and cells (Ding et al., 2023).

Primarily, the CRISPR technology has played a very important role in the genetic enhancement of livestock as it avails accurate and effective ways of controlling the genes. Therefore, many inventions in the practice of agriculture and biomedical science have been developed.

3.1. Explanation of CRISPR-Cas systems and their mechanism of action.

CRISPR-associated CRISPR-Cas (CRISPR-Cas) systems are adaptive immune mechanisms that are present in bacteria and archaea. They function to safeguard against exogenous genetic material, including plasmids and viruses. The CRISPR-Cas system operates in three primary phases:

Stage 1: Adaptation

1- The CRISPR locus of the host genome aquisition of protospacers, short tracts of exogenous DNA which are flanked by repeats.

2- About this, the Cas1 and Cas2 proteins play a role of capturing and integrating protospacers into the Cas array.

3- However, it must also be remembered that as a genetic memory, the array aids the host in forgetting previous infections (Mohanraju et al., 2016).

Stage 2: Biogenesis

1- There is a long precursor CRISPR RNA (pre-crRNA) to be synthesized from the CRISPR array.

2- The Cas proteins inclusive of Cas6 and Cas9 possess endoribonuclease activity and consequently transcribe the pre–crRNA into crRNAs.

3- Basically, every crRNA consists of spacer sequence that targets a certain s foreign genetic element (Behler & Hess, 2020).

Stage 3: Interference

1- The Cas effector protein complex is guided to the target foreign DNA or RNA based on if the crRNA has sequence complementarity.

2- Cas effector complex has been identified to bind near a target sequence in proximity to a protospacer adjacent motif (PAM).

3- Cas effector complex eliminate the FGE through its ability to cut or degrade the target nucleic acid upon recognition (Gleditzsch et al., 2019).

The Mode of action varies depending on the specific CRISPR-Cas system involved in the case of multi type CRISPR-Cas systems. (e. g. Cas9 and its orthologs, can be classified as generalistic Type I- and Type V-REases or specialized Type II- or Type III-REases, as these systems utilize different Cas effector proteins and function on nucleic acid substrates like RNA or DNA (Makarova & Koonin, 2015). However, in all the variants of the CRISPR-Cas system, the mechanism of obtaining genetic memory, recognition of crRNAs, and the ability of Cas-gene controls to eliminate foreign nucleic acids is the same (van Beljouw et al., 2023).

3.2. Different CRISPR tools used for precise genome editing in livestock.

A variety of applications for genetic enhancement in livestock species, including sheep, goats, cattle, and pigs, have been made possible by CRISPR technology (Mehra & Kumar, 2022). Important applications consist of:

Improving Production traits

1- One potential approach to augmenting muscle mass and fiber production is through the disruption of the myostatin gene (MSTN).

2- Improving the quality of milk.

3- Increasing reproductive efficiency (Kalds et al., 2023).

Enhancing Disease Resistance and Animal Welfare

1- To enhance animal welfare and disease resistance, genetic modifications are being implemented.

2- Producing livestock with advantageous characteristics that promote animal welfare, such as the "slick" hair variant in cattle that aids in heat tolerance (Hallerman et al., 2022).

Developing Animal Models for Biomedicine:

For scientific research, developing large animal models of human diseases (Ziegler et al., 2016).

Pharmaceutical Protein Production:

Animal modification for therapeutic protein production (Dicks et al., 2015; Perisse et al., 2021). Two primary methodologies employed to produce livestock with edited genes are somatic cell nuclear transfer (SCNT) and zygote manipulation through microinjection or electroporation. Efficient gene ablation, knocking, base editing, and epigenetic modifications in livestock have been made possible by CRISPR (Menchaca et al., 2020).

However, the new CRISPR technologies themselves have a somewhat less confident, or rather more positive, potential to influence the rate of growth in stock and livestock; but it is not a bad idea to also recall the genera which pose concern on animal welfare, the impact on the environment, and moral dimensions. It is clear that this tool is rather effective and, as it can be stated with reference to the examples of the present days, it is also applied rather actively: the extended usage of CRISPR demonstrates that this tool is powerful and gradually, it is changing the field of genetics and, particularly, animal breeding at the present stage (Raza et al., 2022).

4. Applications of CRISPR CAS9

The livestock genetic enhancement industry has been changed immensely due to this CRISPR gene editing technology that creates the method that is accurate as well as efficient in having the desirable traits in the animals. Enhancing the health, and quality of life, as well as increasing production yields in many livestock species inclusive of cattle, swine, sheep, and poultry among others; this advancement has been useful.

One of the significant applications of CRISPR in livestock improvement involves leveraging on 'gain', that is, speeding up the rate of change on beneficial characteristics that would otherwise take time to disseminate through the population naturally. This is done by firstly, the introduction of alleles associated with the given traits from one breed to another with the help of selective breeding, thus negating the need for crossbreeding or secondly, by increasing the frequency of the said alleles in a particular population (Fischer & Schnieke, 2023). By using this approach it would increase the option to reduce significantly days between generations, increase the level and accuracy of selection, genetic variation (Govindaraj et al., 2015).

Also, to overcome heat stresses the CriSPr has been used to improve heat tolerance in cattle especially in the tropical and subtropical areas. Heat stress plays a great role in provoking these challenges to cattle husbandry primarily in the hot regions; nevertheless, gene editing can be employed to transfer heat-tolerant alleles to native breeds, improving yield and reducing effects of heat stress (Camargo et al., 2023).

Additionally, CRISPR has been applied in increasing yield and the quality of milk, control of the reproduction of bulls and reduction of methane emission in bovine origin (Camargo et al., 2023). Indeed, use of this technology when improving poultry breeding has made it possible to introduce such desirable characteristics as, for instance, faster growth and resistance to diseases (Upadhayay & Vishwa, 2014).

The use of genetically manipulated animals is cited to make use of the versatility of CRISPR-Cas9 system in a manner that permits the direct change on the DNA sequence within the animals. This is achieved by employing the guide molecule that pins the Cas9 enzyme to a particular position of the genomes in a cell whereby the DNA is cut open and the required changes are then made (Menchaca et al., 2020).

Further advancement in the application of CRISPR in genetic improvement in livestock cannot be only expected to expand but is already doing so in different areas. Pros towards utilizing CRISPR in this field are; high efficiency, low pollution levels, and improved wellbeing of animals. On the other hand, there are some ethical and regulation related issues which are also revealed by this technology (Perisse et al., 2021; Viotti et al., 2021).

Thus, it is seemingly reasonable to suggest that CRISPR could contribute further to the enhancement of objectives on genetic improvement of domestic animals given the ability of this technique to deliver, intentionally and with high accuracy, desirable traits to the animal's genome within a relatively quick time. Different breeds of animals have been improved by the efficacy of this method, and undoubtedly the sphere of its application in animals breeding and genetics is liberal.

5. Disease Resistance:

Thus, targeting the genes that contribute to disease resistance by using CRISPR technology has become an important aspect in breeding of livestock for disease resistance. Genetically modified cattle have also been grown using CRISPR/Cas9 to enhance the infection immunity through different germs, virus, fungus (Gao et al., 2023). This makes them healthier and more productive as it was witnessed with the animals.

Enhancing Virus Resistance using CRISPR/Cas9

Targeting plant viruses:

In the same method, CRISPR has been employed to develop plants that can be resistant to plant viruses notable as a menace to basic and novelty crop varieties. Previous study focused to cultivate edited plants harboring CRISPR mods to increase resistance against ssDNA Gemini virus genomes (Mohd Azman et al., 2022).

Applications of CRISPR/Cas9:

The CRISPR/Cas system has been investigated for its potential in fighting viral infections, namely by targeting single-stranded DNA geminivirus genomes. This research has demonstrated the effectiveness of the technique in providing resistance against viruses (Khan et al., 2022).

Resistance Against Fungal and Bacterial Infections.

One of the generic resistances that have been used to protect plants is the Fungicolous resistance and here are why CRISPR technique is used. This achievement in the genetic modification of the host through CRISPR / Cas 9 causes the genetic alteration or editing of genes has been made to intensify the immunity towards fungal pathogens (Tyagi et al., 2021).

Bacterial diseases:

CRISPR/Cas system has been revealed to possess capability to enhance plants' resistance to bacterial diseases, which in turn enhance sustainable agricultural productivity by enabling precise genetic modification to increase disease resistance (Shelake et al., 2019).

Future Prospects and Challenges.

The current applications of the CRISPR technology in bioengineering disease resistant cattle in a sustainable system of agriculture has what that can make the use of pesticides redundant and at the same time leads to increased productivity. Challenges include, the ability to transition from laboratory or greenhouse environments that uphold predetermined conditions to field conditions to verify the efficiency of disease resistance, a confirmation of agronomic performance of transgenic crops, and regulation issues on gene-edited livestock (Jhu et al., 2023).

6. Productivity Enhancement:

Genes that can be targeted to improve livestock productivity using CRISPR technology. Some of the genes that can be targeted to enhance livestock productivity under CRISPR include:

Meat production: Consequently, the deletion of MSTN gene is desirable for the growth of somatic muscles like the cattle, pigs, as well as goats. Lipoplin gene which is associated with the fat-1, transform goats into muscular and useful animal that provielt lean meat that is healthier to be consumed when preparing the diet that does not contain N-6 PUFA to N-3 PUFA ratio (Tait-Burkard et al., 2018).

Milk production: Enhancing production of the genes of interest in order to modify the milk content for the improvement of quality and quantity of the milk comprising the dairy products (Karatzas & Turner, 1997).

Egg production: Employing CRISPR in targeting those poultry' genes which are associated with matters surrounding egg-laying may help enhance the process in poultry (Barkova et al., 2022).

The genetic manipulation is also done with the intention of enhancing meat, milk and egg production livestock species as well as to find ways of feeding human beings that does not need to involve consuming animals.

7. CRISPR for edition on feed conversion ratio and nutrient utilization

CRISPR has been applied by enhancing efficiency of nutrient uptake and utilization by crops (Kumar et al., 2022; Sathee et al., 2022) This is done by genetic manipulation of certain target genes and pathways that the way it will be utilized is quite clear and happens obviously.

Effective dietary changes: CRISPR-Cas9 mediated mutation of OsHAK3 in rice resulted in decreased K+ uptake, and susceptibility to low K stress and salt stress. Genome editing techniques have been used to manipulate positive and negative nutritional signals, with the aim of improving nutrient utilization and stress indicators under deficient conditions (Sathee et al., 2022).

Nutrient absorption: The CRISPR-Cas system has been used to access genes involved in the uptake and transport of micronutrients, increasing their content in plants. The CRISPR/cas9 system has also been applied for increasing the nutritional quality of seed crops; such as rice, wheat, barley, sorghum, and vegetables; such as potatoes and tomatoes (Kumar et al., 2022).

Increase nutritional intake: The transgenic breeding has also been applied in crops enhancement to address issues to do with nutrition and crop performance through alteration of the genes that control metabolic activities (Yang et al., 2022). The Further researches have tried editing genes such as St16DOX through the use of the CRISPR/Cas9 system in which retrieval of recessive alleles of waxy, rc, rice, alc and Tomato mutants have been made possible in genome-engineered crops (Ku & Ha, 2020).

These post-editing modifications through CRISPR technology have the potential to raise quantities of nutrients in crops, enhance the efficiency of nutrient uptake and utilization, and thus to enhance world foods' nutrient density.

8. Advantages and Challenges

Efficiency: Functional benefits of CRISPR-Cas9 in animals are quite remarkable on this aspect, offering a perfect approach to easy rapid and accurate genomics (Zhu et al., 2014).

Simplicity: Compared to other methods of selective breeding in genetic engineering, CRISPR is less procedural and specific to strains and enables the altering of specific genes (Chen et al., 2019).

Cost-Effectiveness: CRISPR-Cas9 as well cheaper than other techniques in animal breeding hence making it possible to genetically improve animals (Wani et al., 2023).

Sensitivity: The advancement in technique used in CRISPR makes it more possible for people to search for better genes amongst animals by making a precise gene editing (Maximiano et al., 2021).

Prospects and difficulties in using CRISPR technology in veterinary medicine

Off-target effects: The first effect of CRISPR on Human body is the failure of specificity that causes nonspecific cleavage which creates a change in genes and there are all single exchanges and irreversible (Boutin et al., 2022).

Formation mosaic animals: Instead of introducing the genetic variation in all cells of the animal, CRISPR mutations might result in mosaic animals where only some tissues contain the variation, and can influence the stability of descendants' traits (Irion & Nüsslein-Volhard, 2022).

Regulatory barriers: Currently, there are some issues in the regulation of CRISPR-corrected livestock around the world that continues to create challenges in the approval of the CRISPR-corrected livestock for releasing to the market and the ethical questions posed by the future of the CRISPR-corrected livestock are also in the right direction (Davisson, 2019).

Ethical Issues: It is vital to be cautious on the following aspects of ethics concerning the use of CRISPR on animals; Animal suffering and welfare, manipulate genes and the ripple effects of genetic manipulation (Schultz-Bergin, 2018).

CRISPR is a promising tool in improving the livestock through enhancing the rate of genetic alterations by being precise and relatively affordable without some drawbacks like off target effects, restrictions by laws, and ethical issues regarding the use of this technology in genetic engineering.

9. Case Studies

Range of information sources on the progress in the livestock industry around the world are presented accompanied by the case and success stories, including new practices in managing livestock industry.

1. Erica and Stuart Halliday 'Ben Nevis' Angus Stud, Walcha NSW: They plant annually; diversely; rotate grazing: that sustains the health of the soil, reduces cost of investment and increases the weight of cattle They plan to achieve a net zero by 2030 (Thamo et al., 2017).

2. AACo Achievement Development Program 'Brunette Downs', Barkly Tableland, NT: Currently, AACO is the globally leading producer of beef which is involved in the sustainable development which is translated into the achievement of the company's strategic development goals that includes the application of the sustainable modeling and efficient pasture management based on the use of data analytics (Ricketts et al., 2023).

3. Andrew & Mandy Bouffler 'Trigger Valley', Lockhart NSW: The Bouffler sheep seed producers have adapted their breeding programmes in accordance with the market trends, thereby using simple techniques to improve the seed production, easy management, and increased prices of wool purchase (Bagozzi et al., 2012).

4. East Gippsland and South Coast WA: extension programs that have been learnt and adopted by farmers in Livestock farming in east Gippsland and south coast WA, Tree fencing; Sustainable grazing and sustainable grazing systems have been put into practice to enhance productivity, profit and a sustainable production has been enhanced (Nie et al., 2016).

From these case studies the realignment of livestock management practices was established indicating that the practice can lead to betterments of the soil conditions, carbon stocks, and of breeding, grazing, and of the growth of the potential livestock and enhancements of the environments all whilst using sustainable livestock management practices for sustainable development. It also raises the measure of importance of actions.

10. Applications of CRISPR in Livestock Genetic Improvement

Application of CRISPR technology in improving the genes of animals from diverse sectors are as follows.

1. MSTN gene editing for meat production: Goats were cloned in China in which the MSTN gene was modified by CRIPSR technology to get bigger muscles needed to weigh more, get meat efficiency and better quality (Zhou et al., 2022).

2. Fat-1 gene insertion in goats for healthy meat production: The study was done in United States of America. Thus, it was shown that recombinase specie CRISPR was used to clone the fat-1 gene in goats and during the experiment. These changes helped marbling development of better meats and yielded the muscle meat which has a desirable n-6 PUFA to n-3 PUFA that off-sets the negatives associated with saturated fat (You et al., 2021).

3. Introduction of UCP1 gene in mice for thermoregulation: Australian scientists and hydrologists studied how a cloning-realted tool called CRISPR-worked to beef up the UCP1 gene of mice so that their cold-regulation yardstick and fat tissue sharp declined (Michurina et al., 2023).

These examples suggest that CRISPR is a useful tool in genetic engineering and improvement of animals in various farms and proves it effectiveness, efficiency in the improvement of yield, meat quality, and animal welfare in various animal plant.

10.1. CRISPR-edited livestock as an example

CRISPR revolution can improve productivity and sustainability in agriculture and animals in the following ways.

Increase performance: The genetic engineering scientist has pointed out that way of eliminating MSTN gene could improve the quality of meat production animals such as cattle hogs and goat (Kalds et al., 2023). The MSTN enrichment using CRISPR in goat's knockout model displayed muscular build up and added weight gain when compared to the wild type animals. The MSTN knockout improves muscle growth by restraining the fat-1 gene in goat and produces muscular and crunchy meat with a favorable n-6 PUFA to n-3 PUFA (He et al., 2018).

Immunodeficiency cells: CRISPR should also be adopted to create more animals with the right sensitiveness to ailments like TB from Mycobacterium bovis that will enhance animal's health and suppress losses (Gong et al., 2020).

Improving animal welfare: Overcoming the UCP1 gene in mice could also enhance the ways through which body heat could be conserved in the cold and decrease adiposity consequently; enhancing animal welfare (Cannon & Nedergaard, 2011).

Reduces environmental Impact: It is acknowledged that CRISPR can be applied to the genes involved in methane production of animals due to the advantage of decreasing its emission capabilities (Leahy et al., 2013).

Medical supplies: The clone animals can be used in disease gene mapping in human diseases and also in the production of human proteins in Medical researches and treatment (Murray et al., 2010).

The general goal of this technology in livestock is to enhance productivity through meat and dairy yield, improve production and animal health and welfare, and decrease the amount of resources used by animals as well as the impact on the environment but the insecurities and moral implications of these technologies must be faced and sorted before they are commonly used (Murray et al., 2010).

11. Future Perspectives

Future perspectives of CRISPR/Cas9 technology in animal genetics, especially in mice and poultry research, offer exciting developments and potential challenges:

Swine Research:

Advances: CRISPR/Cas9 technology has greatly improved genome editing in mice, improving breeding, vaccine development, xenotransplantation, and disease modeling (Zhang et al., 2021).

Possible applications: The technology enables the production of transgenic mice with reduced fat content and lean meat, as demonstrated by modifying the *UCP1* gene in in the piglets (Tu et al., 2022).

Poultry Industry:

Emerging Applications: CRISPR/Cas9 technology is gaining momentum in chicken and quail and other poultry species, allowing researchers to modify gene function for transcriptional regulation, target genes and epigenetic modification (Idoko-Akoh, 2019).

Future prospects: The poultry meat industry is poised to benefit from CRISPR-powered genetically modified chickens that are more efficient in feed consumption and lean meat production, potentially appealing to consumers acceptance (Tizard et al., 2019).

Challenges and Opportunities:

Avian Species Development: Although the use of CRISPR in mammals such as pigs has advanced significantly, its use in avian species is still emerging and will soon become more competitive and will provide opportunities for genetic improvement in poultry (Khwatenge & Nahashon, 2021).

Specificity and Off-Target Effects: To increase the specificity of CRISPR in animals, it is important to overcome challenges such as target effects, ensuring that the genome is altered accurately and not inadvertently output (Epstein et al., 2021).

The future of CRISPR/Cas9 technology in animal genetics holds promise for enhancing productivity traits, improving feed efficiency, and addressing disease resistance in pigs and poultry. To fully exploit the potential of this adaptive genetic modification tool in animal agriculture, it will be important to address the challenges associated with specific cases and regulatory frameworks.

12. Summary

CRISPR/Cas9 technology has enabled genetic manipulation of animals, enabling precise genome manipulation with ease and efficiency compared to previous methods (Singh & Ali, 2021). The use of CRISPR in animal research has expanded rapidly, with more than 500 papers published since 2014.

CRISPR has enabled many genetic improvements in animal husbandry, e.g.

- Increased quality of products such as meat, dairy and fibers.
- Disease prevention and improved animal health.
- Provides large animal models for human diseases.
- Production of recombinant proteins for pharmaceutical applications.
- Analysis of gene activity involved in growth and development.

Major innovations include the ability to edit multiple genes, detect site-specific mutations, and target ancient disease cells in different species. Although challenges remain specific effects and off-target effects though ongoing research is addressing these limitation.

The future implications of CRISPR in animals are profound. It offers the potential for significantly increased yields, better feed efficiency and leaner meat in animals such as pigs and poultry. As technology advances, it becomes increasingly important to guide legal and ethical considerations.

In conclusion, CRISPR/Cas9 is a revolutionary tool that is changing animal genetics and reproduction. Its application in enhancing livestock sustainability, yield and animal welfare to meet the increasing global demand for feed holds great promise Continued research to optimize CRISPR will continue to unlock potential a it has to reshape the future of animal agriculture.

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About The Authors

Mr. Muhammad Tariq graduated from Cholistan University of Veterinary and Animal Sciences in Bahawalpur, Punjab, Pakistan. Now he is a PhD scholar at College of Animal Science and Technology Nanjing Agriculture University, Nanjing, Jiangsu, China. His research interests include Animal Reproduction, Genetics, Molecular Biology. He has published 12 research papers in national and International well-reputed journals. He has also reviewed some research papers.

Email: tariq@stu.njau.edu.cn ORCID: 0000-0001-5539-0454

Dr. Muhammad SAFDAR earned his PhD in Molecular Biology and Genetics from Gaziantep University, Turkey. He is Lecturer in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, nutrigenomics, nano-genomics, bioinformatics, biotechnology, and their applications. He has published more than 70 research articles in national and international journals. He has also written many book chapters as well as an edited book. He is an associate editor for international journals.

E-mail: msafdar@cuvas.edu.pk ORCID: 0000 0002 3720 2090

Mr. Farhad Badshah, currently doing PhD in Animal Genetics from Institute of Genomics Shenzhen, Chinese Academy of Agriculture Science China. His research focus on Functional Genomics. He has published more than 16 research articles in national and international well-reputed journals. He has also written many book chapters. He is a reviewer of many well-reputed national and international journals.

E-mail: farhadbadshah999@gmail.com ORCID: 0000 0001 6971 0957

Miss Saba Saeed graduated from University of the Punjab Lahore, Pakistan. Now she is a PhD scholar at The Government Sadiq College Women University, Bahawalpur. Her research interest includes Fisheries, Microbiology, Molecular Genetics and Bioinformatics. She has published 22 research papers in national and International well-reputed journals. She has also reviewed many research papers.

Email: ssaba5306@gmail.com ORCID: 0000-0002-0452-8027

Arooj Fatima earned Bachelor in microbiology from Cholistan university of veterinary and animal sciences (CUVAS) Bahawalpur Pakistan. Currently she is doing M.phil in Microbiology from Cholistan university of veterinary and animals sciences (CUVAS) Bahawalpur Pakistan. Her research interest in Microbial genetics, Molecular biology, soil microbiology, plant Microbiology and food quality and its application. She has published more than 3 articles and 6 in national and international journals.

E-mail: aroojfatima31202@gmail.com ORCID:0000-0002-4709-4177

Miss Kiran Ashiq graduate from Cholistan university of veterinary and Animal sciences, Bahawalpur. Now she is a PhD Scholar at the CUVAS, Bahawalpur. Her research interest includes in fisheries, microbiology, molecular genetics and Bioinformatics. She has published 15 research paper

in national and international well reputed journals. She has also reviewed many research papers.

Email: kiranashiq820@gmail.com ORCID:0009-0005-0397-6273

Miss. Salma Bibi, received her BS degree in Animal Sciences from Cholistan University of Veterinary and Animal Sciences, Bahawalpur, Pakistan. Her main areas of interest are Animal Genetics, Breeding and Reproduction. She has written 8 book chapters in international journals.

Email: salmamalik6809129@gmail.com ORCID: 0009-0003-0798-9886

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RECENT DEVELOPMENTS IN THE USE OF MOLECULAR DOCKING TECHNOLOGY IN FEED SCIENCE

Muhammad SAFDAR

Muhammad YOUNUS

Salma BIBI

Yasmeen JUNEJO

1. Introduction

A computer method called molecular docking is extensively utilized in feed science and other scientific fields to anticipate the binding mechanism and affinity of compounds. When it comes to feed science, molecular docking is essential for comprehending how bioactive substances interact with biological macromolecules like enzymes, receptors, or transporters that are involved in an animal's digestive system. By using computational simulation, the preferred orientation or binding affinity of a ligand (molecule) to a target (molecule) when they interact to create a stable complex can be predicted using a technique called molecular docking. Within feed science, targets might be proteins or enzymes involved in the breakdown and assimilation of nutrients, whereas ligands can be bioactive substances found in feed ingredients.

Since its original description in 1982 (Kuntz et al. 1982), molecular docking has evolved into the main concept of structure-based virtual screening. It consists of two main tasks, each handled by a different algorithm. The ligand can assume several forms, or postures, within the binding or active pocket, which are predicted by the sampling process. Next, for every anticipated pose, a scoring function forecasts the binding energies between the ligand and receptor.

Explaining the structural characteristics and reactions of biological systems & uncovering the mysteries of the microcosmic universe have proven difficult when research relies solely on experiments. A common technique for describing a molecule's reaction system and forecasting its macroscopic physical characteristics is molecular modeling. The field of molecular simulation (MS) technology has advanced significantly over the past 20 years, particularly after the 2013 Chemistry Nobel Prize was given out (Nie et al. 2018).

Molecular docking provides a useful framework for comprehending drug biomolecular interactions, which is useful in both mechanistic research and rational drug design as well as discovery. It works by aligning a ligand with the preferred binding site of a target-specific region of DNA or protein (receptor), primarily through non-covalent means, to form a stable complex with increased specificity and potential efficacy (Guedes, de Magalhães, and Dardenne 2014).

Since the human body needs food to obtain critical elements such proteins, lipids, carbs, and vitamins, molecular docking has broad applications in these specific fields. Furthermore, drug residues, biotoxins, and foodborne pathogens are major concerns in food safety research, which is becoming more and more concerned with molecule-level analysis (Śledź and Caflisch 2018). To investigate the connection between substrates and enzyme activity, the molecular docking method was used. Hydrophobic interaction and hydrogen bonding are two ways that protease interacts with substrates; the primary binding site is indicated by the Hydrophobic Cavity of the enzyme (Yue et al. 2017).

2. Recent Advancements in Molecular Docking

In recent years, molecular docking has emerged as a crucial component of in-silico drug development. This method entails forecasting the atomic-level interaction between a tiny chemical and a protein (Sahoo et al. 2022). This makes it possible for scientists to examine how tiny compounds, like nutraceuticals, behave within a target protein's binding region and comprehend the basic biochemical mechanism underpinning this interaction (Meng et al. 2011). For molecular docking approaches, several free and commercial computational algorithms and tools are available. These applications and resources were created and are presently being utilized in academic fields and pharmacological research (Jorgensen 2004).

According to (Sahoo et al. 2022) some of the most widely used docking applications are UCSF Dock, MC Dock, Surfex, Auto Dockgold, Glide, Discovery Studio, MOE-Dock, FlexX, DOCK, Cdcker, LigandFit, ICM, LeDock, rDock, FRED and Auto Dock Vina. Molecular docking has been essential in many drug development efforts, particularly for virtual examination of phytochemicals or nutraceuticals as potential medicinal compounds (Kitchen et al. 2004) as shown in figure 1.

The features of tiny compounds known as ADMET (Absorption, Distribution, Metabolism, Excretion, and Toxicity) can also be predicted via docking. Initially in the drug development process, the projected ADMET attributes can be utilized to weed out molecules with undesirable features (Das et al. 2020).

It is also possible to utilize molecular docking to clarify the molecular structure of proteins whose structures are uncertain. By using docking, one may forecast how tiny molecules will attach to proteins and create a protein homology model based on the predicted binding mode. Next, the constructed model can be refuted use experimental data to determine the protein's precise structure (Ferreira et al. 2015). A computational method called molecular docking validation is being applied more and more in the field of nutraceutical research to find possible targets for the treatment of different illnesses. Nutraceuticals have are naturally occurring substances that can be found in food sources such as as vegetables, herbs, and fruits that may have health benefits (Vergallo 2020).

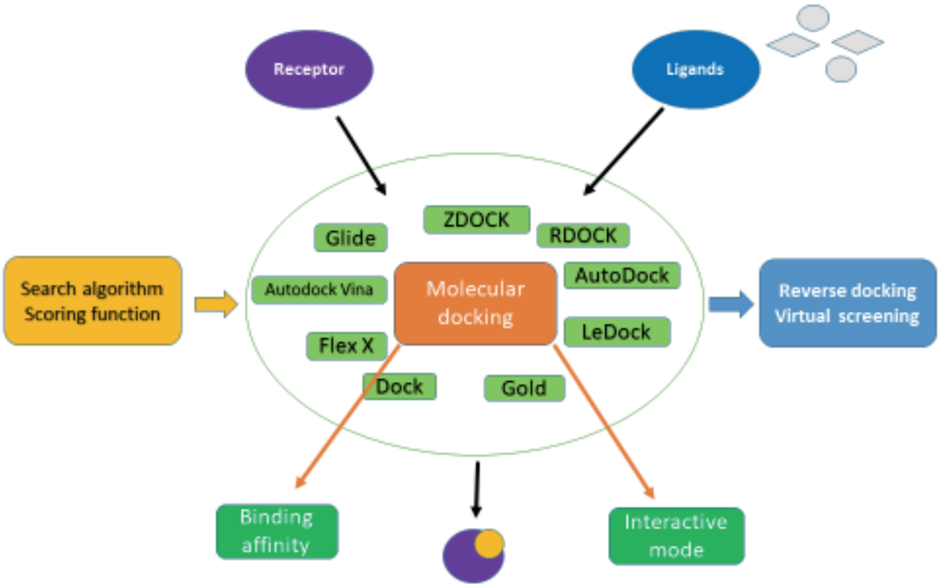

Figure 1. Recent Advancements in Molecular Docking

3. Molecular Docking Algorithms

Molecular docking algorithms provide important information on drug-receptor binding by predicting the interactions of tiny molecules with target proteins. As the field of discovery of drugs advances, scientists are always working to create docking algorithms that are more precise and effective. The current state of molecular docking approaches is reviewed, and their advantages and disadvantages are thoroughly examined.

The level of grading in the algorithm flow can be used to categorize docking algorithms into two categories: integrated and edge functions. Scoring is incorporated into the search phase of integrated algorithms, which filters out potential solutions. Scoring is applied at the conclusion of the search phase in edge algorithms. Therefore, the primary distinction is that, in integrated algorithms, the scoring function is incorporated into the solution design, but in edge algorithms, it is not. Some of the computational systems utilized in docking, such as anchoring algorithms and genetic algorithms, require integrated algorithms. A fitness score is necessary for genetic algorithms, and it is applied after each generation and employed in the selection pressure operation (Gardiner, Willett, and Artymiuk 2001).

Due to its effectiveness and precision in ligand-protein binding prediction, AutoDock Vina has become more well-known. Better docking results are a result of its increased scoring mechanism and search methodology (Trott and Olson 2010). GOLD effectively searches for ideal binding orientations by examining ligand conformations using a genetic algorithm. It is a strong docking tool due to its adaptability and capacity to manage a variety of ligand-receptor interactions (Jones et al. 1997). Advanced methods such as adjustable ligand sampling and precise scoring functions are incorporated in Schrodinger's Glide. When managing extensive virtual screening efforts, it is renowned for its accuracy and quickness (Friesner et al. 2004). Molecular docking has been profoundly affected by recent advancements in machine learning. Neural networks are used by algorithms like BindML and DeepDock to estimate binding affinities; these algorithms show better accuracy than traditional scoring systems (Jimenez et al. 2017) as shown in figure 2.

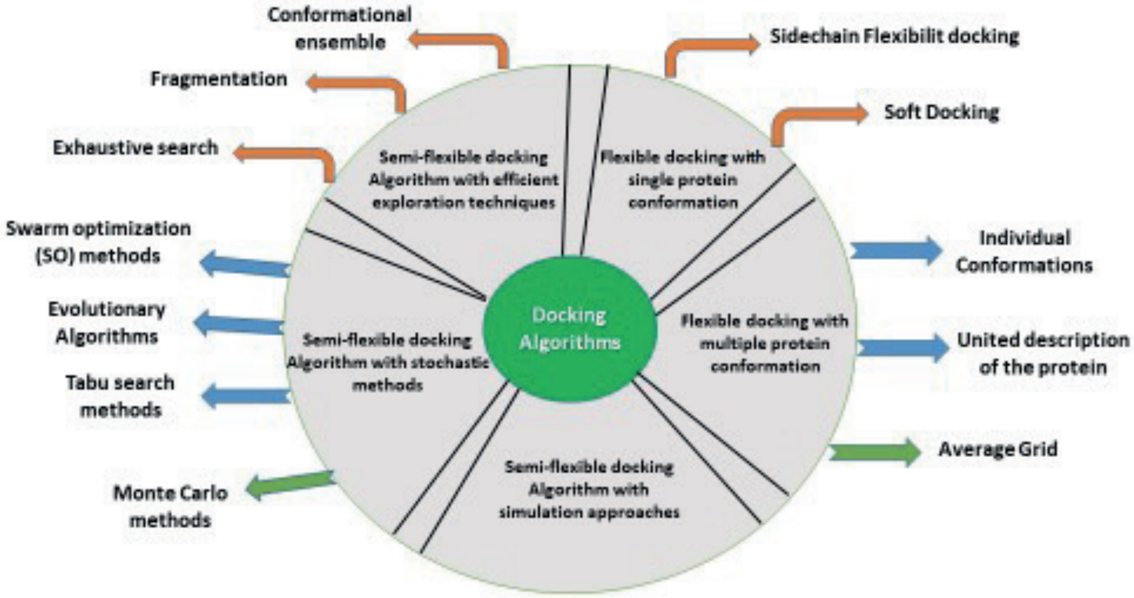

Figure 2. Different Algorithms in Molecular Docking

4. Applications in Feed Additive Design

Designing balanced ration techniques for high-yielding animals while keeping the cost-benefit ratio is one of the biggest issues encountered by farm managers, livestock rearers, animal's scientists, and nutritionists working in the animal feed sector or research field. It should also be remembered that the costs associated with meat, dairy, and animal byproducts are not constant and can change for several reasons, one of which is the cost of the feed (Thornton 2010).

The European Commission defines feed additives as goods used in animal nutrition to raise the standard of animal-derived food and feed, as well as to increase the health and performance of the animals, for example, by making feed materials more easily digested. Yeast culture or sodium bicarbonate, respectively, are two examples of the nutrients that can be found in a variety of feed additives. In terms of technicality, feed additives are neither seen as necessary nor do they provide high animal productivity or financial success in animal husbandry methods (Pandey, Kumar, and Saxena 2019).

North America or Asia-Pacific are the world's largest users of feed additives. Over 60% of the world's animal feed consumption is attributed to them (Pandey, Kumar, and Saxena 2019). According to estimates, the region with the fastest revenue growth is Asia-Pacific. Growth is especially strong in emerging economies like Brazil, China, and India because of the population's steady rise in income levels brought about by increased industrialization and the boom in the service sector. This has also helped the feed industry because per capita meat consumption has increased (Arenas-Jal et al. 2020). Due to the advantages feed additives can provide, such as promoting animal growth and controlling infectious diseases, their significance is growing daily in addition to improving feed digestibility (Pandey, Kumar, and Saxena 2019). The market for animal feed additives has a stable growth graph and is expected to continue growing in the future due to the world's rapidly rising demand for dairy, meat, and meat products (Hines 2022).

The most recent of the disruptive technologies that appear to be making a significant impact on the food and agriculture sectors is additive manufacturing or AM. By building up layers of a particular material by a design specification, it can produce a real part straight from a digital model. This gives the part's size and shape a great deal of flexibility. It produces a novel product attribute that cannot be produced with current technology (Jee and Sachs 2000). Significant advancements in the sector and bespoke food design are possible using additive manufacturing technologies. This technology's design construction is reliant on the properties of the materials and the building mechanisms. In the subject of food engineering, AM faces numerous issues, including those related to processed productivity, product innovation, and functionality (Godoi, Prakash, and Bhandari 2016).

5. Integration with Nutritional Strategies

The integration of nutritional strategies in animals involves a comprehensive understanding of species-specific requirements, life stages, health considerations, and environmental impact. For development, reproduction, and general health maintenance, animals need a certain diet. Vitamins, minerals, proteins, carbs, and fats are examples of essential nutrients. Different species have different needs, and for optimum functioning, a proper diet must be created. The nutritional requirements of infants, adolescents, adults, and the elderly change with these life phases. When it comes to treating and preventing illnesses in animals, nutrition is crucial. Eating well helps the immune system work and reduces the chance of dietary excesses or deficiencies that might cause problems.

The nutritional value of animal products is mostly determined by feeding practices. Meat, milk, & eggs are examples of goods derived from animals, and their nutritional value is directly influenced by the kind and makeup of their food. Numerous feeding techniques, both conventional and contemporary, have an impact on elements like the macronutrient balance, vital vitamins, or minerals, as well as the general safety and quality of the product. Alternative feed sources with bioactive components are being used as agents to raise the standard of animal products and promote animal health (Untea et al. 2023).

The quality characteristics of animal products are directly impacted by feeding practices. The nutritional makeup of diets greatly impacts the sensory and nutritional qualities of the finished beef products, impacting everything from fatty acid profiles to nutritional quality and tastes, ultimately influencing customer preferences and choices. Some of the studies featured in this Special Issue demonstrate the ongoing interest that academics, farmers, and producers have in the impact that animal diets have on the quality of their products (Lefter et al. 2022). The food and feed markets' increasing focus on natural products has led to a surge in demand for organic components. Research on cattle nutrition is currently trending towards formulations of diets that include organic and natural feed additives (Vlaicu et al. 2022).

Animal welfare, productivity, and health are all intrinsically linked to animal husbandry techniques. The simplest tactic to use at the farm level is undoubtedly diet composition management, which can be used to maintain ideal animal health and safely and effectively generate high-quality animal products. Significant advancements in animal genetics, animal husbandry, management, health, or nutrition have been accomplished by the dairy and beef cattle industries. Adoption of intensive production systems, however, may jeopardize the welfare and health of cattle, which would raise the prevalence of infectious and metabolic illnesses. Furthermore, because there are fewer rangeland pastures and forages available, the current changing climate phenomenon poses an extra barrier to ruminant productivity. The escalation in the frequency of extreme temperatures may potentially impede optimal health and welfare (Henry et al. 2012).

6. Applications

In feed science, molecular docking technology has become a potent tool that helps with the design and optimization of nutritional formulations, supplements, and feed additives. This thorough analysis focuses on effective case studies where feed science, animal nutrition, and sustainable farming practices have all benefited greatly from the application of molecular docking. Protein-protein interactions among feed components were examined using molecular docking techniques. Researchers have successfully created feed compositions that support the best possible protein digestibility by understanding the interactions between proteins during digestion. This solves sustainability issues with protein usage in addition to improving animal health.

In recent years, molecular docking has emerged as a crucial component of in-silico drug development. This method entails forecasting the atomic-level interaction between a tiny chemical and a protein (Sahoo et al. 2022). This makes it possible for scientists to examine how tiny compounds, like nutraceuticals, behave within a target protein's binding region and comprehend the basic biochemical mechanism underpinning this interaction (Meng et al. 2011).

The rapidly expanding subject of "in silico biology" deals with the theory, programming, and use of computational techniques to model, forecast, and clarify molecular biological processes (Palsson 2000). These days, there is a vast array of biomolecular simulation techniques that can be used to solve a variety of structural biology issues, including medication design. Biomolecular simulation approaches based on integrated bioinformatic analysis, such as molecular docking, are tools that study the interaction between molecules (such proteins and peptides) and use computer programming to anticipate their binding patterns and affinities at the molecular or atomic level (Tao et al. 2020).

In drug discovery research, they have been frequently used as theoretical simulation tools for virtual screening investigations aimed at discovering new active biomolecules, like bioactive peptides. However, complex food systems—like food emulsions with several interfaces where the protein is reacting differently to each local environment—require instrumental techniques that can directly access high-resolution molecular information (Zare, McGrath, and Allison 2015).

7. Challenges and Opportunities

Molecular docking technology has advanced significantly, offering new insights into feed science by allowing researchers to model and predict interactions between feed additives and animal proteins or gut microbiota. However, one of the major challenges in this field lies in the complexity of biological systems, especially in livestock. The variability of metabolic responses among different species, breeds, and even individual animals makes it difficult to generalize docking results. Furthermore, the accuracy of molecular docking algorithms remains limited by computational resources, simplifying assumptions in the models, and the need for high-quality, well-characterized receptor structures. Experimental validation of computational predictions remains crucial, but it is often time-consuming and expensive, creating a bottleneck in the practical application of molecular docking in feed science.

Despite the challenges, recent developments in molecular docking present exciting opportunities for innovation in feed science. Advances in high-throughput docking and artificial intelligence-enhanced algorithms allow researchers to screen thousands of feed additives quickly and efficiently, identifying compounds that may enhance animal growth, immunity, or gut health. Additionally, the integration of omics technologies (such as proteomics and metabolomics) with molecular docking enables a more holistic understanding of how feed components interact with animal physiology. These technological advancements can lead to more personalized and species-specific feed formulations, improving livestock performance and sustainability in the agricultural sector.

8. Future Directions and Recommendations

a. Integration with Multi-Omics Data: Future advancements should focus on the integration of molecular docking with multi-omics data, including genomics, transcriptomics, proteomics, and metabolomics. This would enable a more comprehensive understanding of the interactions between feed components and biological systems, providing more accurate predictions of feed efficacy and safety.

b. AI and Machine Learning in Docking Simulations: Incorporating artificial intelligence (AI) and machine learning (ML) models into molecular docking workflows can help improve the prediction accuracy and reduce computational costs. AI-driven models could streamline the analysis of large datasets, enabling rapid identification of promising feed additives for animal health and growth.

c. Personalized Feed Formulation: A future goal should be the development of personalized feed formulations based on molecular docking results, tailored to the specific needs of different livestock species, breeds, and even individual animals. This could enhance feed efficiency and optimize nutrient absorption for better overall health and productivity.

d. Enhanced 3D Structural Data: Continued efforts to enhance the availability and quality of 3D structural data of relevant proteins, enzymes, and microbial communities in livestock systems are essential. Better structural data will lead to more reliable docking simulations, reducing false positives and improving feed additive design.

e. High-Throughput Docking for Feed Additives: Developing high-throughput docking platforms to screen large libraries of feed additives can accelerate the identification of novel bioactive compounds. This would be particularly useful for discovering new phytochemicals, probiotics, and enzymes that can improve animal health and performance.

f. Validation through In Vivo and In Vitro Studies: While molecular docking offers predictive power, it is critical to validate computational predictions through in vivo and in vitro studies. Strengthening collaborations between computational scientists and experimental researchers will ensure that predictions translate into practical, real-world applications.

g. Regulatory Considerations and Standardization: As molecular docking becomes more widely used in feed science, regulatory bodies should establish standardized guidelines for the acceptance of computational predictions. This could streamline the approval process for new feed additives while ensuring safety and efficacy.

h. Sustainability and Environmental Impact: Future research should explore how molecular docking can contribute to the development of sustainable feed solutions that reduce environmental impact. For instance, docking could help identify feed additives that improve nutrient absorption, reduce waste, and minimize greenhouse gas emissions from livestock production systems.

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About The Authors

Dr. Muhammad SAFDAR earned his PhD in Molecular Biology and Genetics from Gaziantep University, Turkey. He is Lecturer in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, nutrigenomics, nano-genomics, bioinformatics, biotechnology, and their applications. He has published more than 70 research articles in national and international journals. He has also written many book chapters as well as an edited book. He is an associate editor for international journals.

E-mail: msafdar@cuvas.edu.pk ORCID: 0000 0002 3720 2090

Mr. Muhammad YOUNUS earned his M.Phil. in Zoology from CUVAS Bahawalpur Pakistan. He is a Research Associate in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, bioinformatics, biotechnology, and their applications. He has published more than 06 research articles in national and international journals. He has also written book chapters.

E-mail: younus31302@gmail.com ORCID: 0009 0005 5392 7031

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PRECISION LIVESTOCK FARMING AND THEIR APPLICATIONS FOR DAIRY ANIMALS

Muhammad YOUNUS

Muhammad SAFDAR

Jawairia Mehrin NASIR

Afshan KHADIM

Muhammad SAJJAD

Salma BIBI

Precision Livestock Farming (PLF) is an emerging technology-driven approach that utilizes advanced sensors, data analytics and automation to monitor and manage livestock farming systems with enhanced precision and efficiency. This chapter explores the potential applications of PLF that is associated with dairy farming in Pakistan. It discusses how the integration of PLF technologies improve the animal health, productivity and welfare while optimizing resource utilization and reducing environmental impact. Moreover, the chapter emphasizes the significance of adopting PLF practices in dairy sector to address the challenges faced by farmers and enhance the sustainability and profitability of dairy operations.

1. Introduction

Milk and dairy products have been a major source of dietary energy, protein, and fat for the global population throughout generations. Milk is currently the EU's top agricultural product, accounting for roughly 15% of the agricultural product in terms of value (TROPEA, 2015). Precision livestock farming (PLF) is the use of contemporary information and computer technology (ICT) for real-time animal monitoring and management. PLF systems can be useful tools in dairy production to supplement and enhance the farmer's skills in monitoring and assessing cow health and welfare. Dairy farmers may manage larger herds more efficiently with automated PLF systems. (Rutten et al., 2013). Previously, scientists have not taken into account soil factors, when combined with animal behavior that could lead to the development of realistic models to improve grazing practices and, as a result, increased productivity (Garcia et al., 2020). According to (Banhazi & Black, 2009), one key advantage of implementing a PLF system is that "every process within a livestock enterprise, which can have a large positive or large negative effect on productivity and profitability, is always controlled and optimized within narrow limits. While the potential of PLF to improve animal well-being has been highlighted, it is unclear whether the purpose of PLF development in poultry has been to promote welfare or to increase production efficiency. These two criteria are not mutually exclusive; gains in welfare can be connected to increases in output, for as by lowering 85 mortality. PLF systems might thus strive to increase both animal welfare and production (Dawkins, 2016) Precision livestock farming is a branch of precision agriculture that focuses on improving livestock farming operations by designing and developing multiple software as well as hardware technologies for automatic tracking, monitoring, and identification of diseases, record keeping, feed management, and other livestock farming operations (Lima et al., 2018). The cattle sector plays critical economic, social, and cultural functions in helping farm families improve their income and well-being. The cattle sector's economic output could be significantly increased if it was properly incorporated into new technologies and practices. Keeping livestock is an important risk-reduction strategy for vulnerable communities since animals can serve as insurance in times of need and provide a source of income diversification to assist deal with times of stress (Thornton, 2010). Precision livestock farming (PLF) is the use of information and communication technology to increase the management of fine-scale animal and physical resource variability in order to optimize farm economic, social, and environmental performance (Eastwood et al., 2012) as shown in Figure 1.

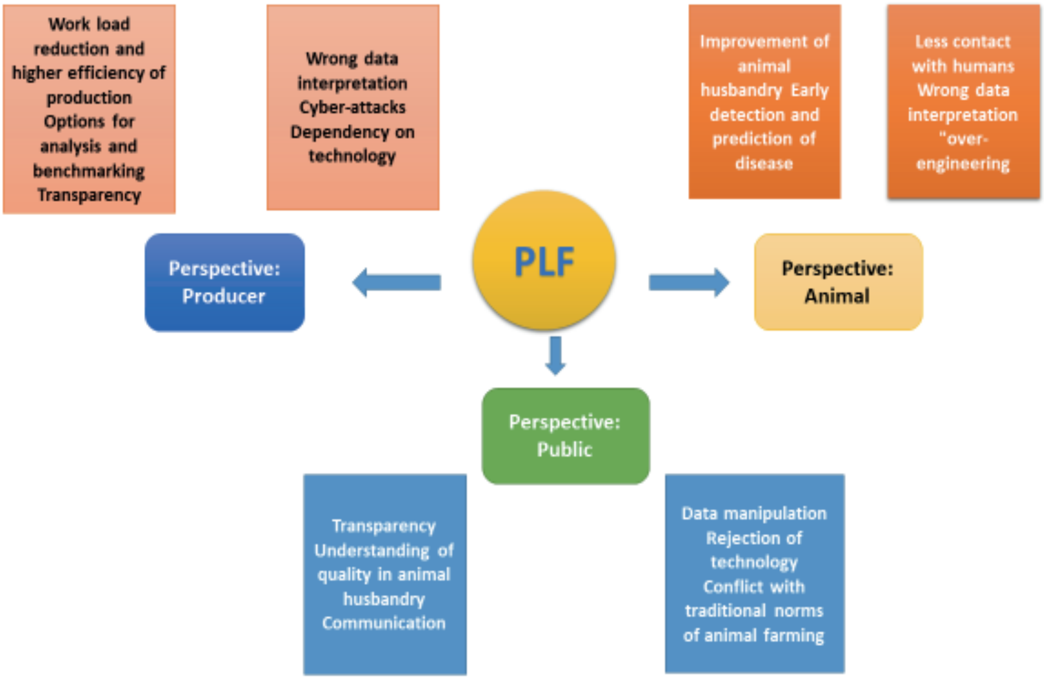

Figure 1. Assessment of the Opportunities and Hazards associated with PLF

2. Advancements in PLF

Livestock production is regarded as a key route out of poverty for developing-country rural poor. Livestock farmers face a variety of management issues, including sickness, a lack of feed resources, and a scarcity of grazing grounds. The term "Innovation System" refers to the collection of organizations, businesses, and individuals focused on putting new goods, processes, and organizational forms into economic usage, as well as the institutions and regulations that influence the systems' behavior and performance (Hall et al., 2006). PLF technologies can assist farmers in increasing livestock production potential and product quality in a sustainable manner. A computerized management system provides us with unbiased, real-time data that may be summarized into relevant, actionable insights. Data-driven decision-making results in better, more efficient, and timely decisions that increase animal herd productivity. Artificial insemination is often regarded as the most effective biotechnological method for enhancing reproductive capability. However, due to several technological, financial, infrastructural, and managerial issues, its application in Africa has yet to match its success in industrialized countries (van Arendonk, 2011). Improving both the quantitative and qualitative value of livestock products necessitates a high potential for technology adoption through increasing the potential for investment in the industry through public-private partnerships and the promotion of appropriate regulations for value addition. The main technologies that are widely employed are artificial insemination and sperm storage. If procedures and protocols are followed correctly, reproductive technology can also be utilized to control reproductive illnesses (Madan, 2005). PLF technology has the ability to improve animal welfare as well as increase output. PLF enables non-intrusive welfare assessment, where information can be gathered without the stress of disturbing or handling animals (Wathes et al., 2008). Precision livestock production technology acceptance and uptake is complex and influenced by a range of parameters like demographics and socioeconomic (age, education), financial resources, and farm size, with these variables having varying effects on adoption. The adoption of livestock production technology is one of the most established fields of research in information systems (Sharma & Mishra, 2014). In response to this challenge, PLF technologies are being developed to regularly and autonomously monitor livestock welfare and health indices, allowing for enhanced productivity and the early detection of health issues (Schillings et al., 2021). Precision livestock farming (PLF) techniques are now being developed for the benefit of modern livestock industries. Several writers reported on the use of novel PLF technologies to detect heat stress, the quality of the environment around the animals, and their physiological state. (Eigenberg et al., 2008). The potential of applying PLF approaches to give accurate heat stress modeling output will be discussed. It is widely acknowledged that PLF technologies involve model or software-based developments in addition to hardware-based developments (Black et al., 2016) as shown in figure 2.

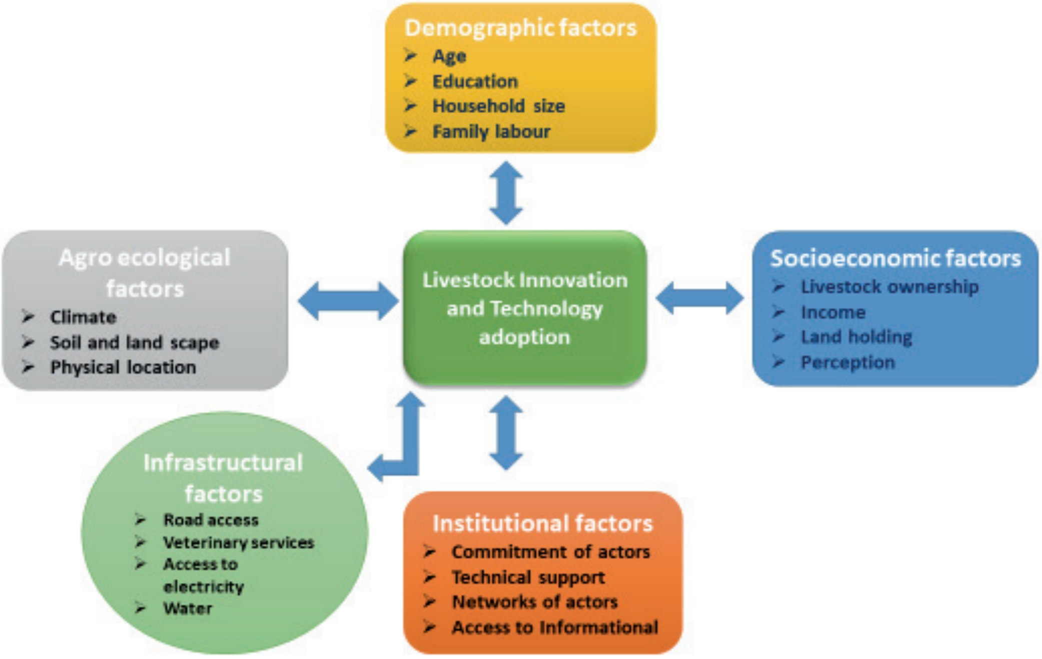

Figure 2. Conceptualization of Determinant Factors for Livestock Production Technology

3. Automated Feeding Systems

Feeding automation utilizing automatic feeding systems (AFS) is also growing more common, with an estimated thousand systems in operation around Europe in 2013 (Bonsels et al., 2013). According to (King et al., 2016) The feeding system in modern dairy farms is an essential issue in terms of animal welfare; also, choosing between the various types available on the market necessitates economic and technological considerations. Due to the high cost of feed required for high-yielding herds, optimal feed efficiency is critical for profitable farms. Feeding a total mixed ration (TMR) diet is currently a favored practice, which has influenced the development of mechanized feeding systems, which are usually represented by manually driven mixer-feeder wagons.

AFS allows for enhanced feed distribution frequency (up to 15 cycles per day), which optimizes dry matter intake by the animals and helps to maintain ruminal pH stability, which has major health and productivity benefits (DeVries et al., 2005). The incorporation of AFSs into the layout of new or existing barns creates concerns about the position and capacity of AFS components. Even though a reasonably wide range of models varying in complexity and cost have become available on the market, transitioning to an automated TMR feeding system involves costly investments. Robots, on the other hand, appear to require less room and power than a traditional tractor-drawn mixer wagon (Nydegger & Grothmann, 2009). Robotic dairy farms, also known as Automated Milking Systems (AMS), are the result of the use of cutting-edge robotics technology to boost the production of milk through increased efficiency and automation (Britt et al., 2018). Dairy land must be managed properly, with the annual output of digestible nutrients being a key indicator of the contribution that home-grown feeds may contribute to total herd nutrition. However, there is great variance in pasture production and consumption on farms within dairying regions, reflecting in part the intrinsic capabilities of the soil or access to water (Armstrong et al., 2000). In their most basic form, automation systems include a control panel, a programmed command manager, a scale, a communication interface, and lastly all of the necessary equipment to organize the process of feeding and supplying feed to animals of varied ages (Brito et al., 2020). Different software has been developed in recent years by computer scientists in order to provide the best alternative for farmers in ration formulation. To construct ideal feeding regimens, sophisticated tools such as live weight, racing, lactation period, and animal feedstock information can be used. Feed preparation, mixing equipment, and feed distribution installations are all part of automated feeding systems. The systems will load, mix, and deliver feed components like as grass and maize/corn silage to the feed table, as well as mineral feed and feed concentrate (Braun et al., 2013). Individualized feeding that is automated. Given the differences between individual animals, it is logical to believe that by using data relevant to each animal, we can make better decisions about what and how much to feed. As previously said, model-based feeding helps optimize farm productivity because individuals are likely to have different and distinct requirements. Individual feeding necessitates the ability to collect data unique to each animal, as well as analytics capable of estimating individual needs based on that data (Rue & Eastwood, 2017). A regular supply of good quality feed and fodder assures enhanced productivity, as feeding accounts for around 60%-70% of the entire cost of milk production on dairy farms. Therefore, nutrition management is critical in unlocking the true potential of dairy animals; a well-balanced feed (green and dry fodder, and also a concentrated ration) is beneficial to the farm's sustainability and profitability; and a minor improvement in animal nutritional status through additional supplemental funding can improve animal productivity with a minimal cost increase (Asmare, 2014) as shown in Figure 3.

Figure 3. Flowchart of Important Dairy Farm Management

4. Health Monitoring and Disease Detection

Global livestock production methods have become more productive per animal in recent years. 37 Intensification involves social considerations that influence consumers' perceptions of food security and safety 38 as well as sustainability, animal welfare, and animal and human health issues (Charlton & Rutter, 2017). Most nations are seeing a decrease in the number of farms with a limited number of 63 animals, to the benefit of large and efficient farms with a great amount of area for crop 64 cultivation and slurry dispersion, as well as a large number of bred animals (Fournel et al., 2017). Nutrition, husbandry, and health constraints, as well as the limited availability of vaccines and veterinary extension services, all have an impact on the productivity of Pakistan's dairy business (Warriach et al., 2018). Due to poor husbandry practices and inadequate resources, the productivity of dairy animals on small-scale farms might be suboptimal, posing a greater biosecurity risk for the spread of livestock and zoonotic illnesses than commercial dairy farms (Hayes et al., 2017). Livestock animal infections are critical in the lives of dairy producers since they not only reduce productivity but also monetarily hurt the farmers. Disease-related mortality deprives producers of dairy earnings. Disease morbidity causes both short-term and long-term product losses. These losses are more economically significant than mortality (Hasnain & Usmani, 2006). Disease-related losses are one source of reduced milk output and farm revenue. Foot and Mouth disease (FMD), Parturient Hemoglobinuria, Bovine Viral Diarrhea (B.V.D.), and a black quarter are among the many lethal diseases in Pakistan. Farmers do not vaccinate their animals against these deadly diseases, which reduces dairy production. Mastitis affects one out of every three cows or buffalo, considerably contributing to milk output loss. Ticks and other parasites are also reducing sector output (Saleem & Ashfaq, 2009). Ticks are blood-sucking parasites that live on mammals, birds, and reptiles. Ticks are regarded as a significant danger to economic animal production around the world due to the multiple direct and indirect effects they have on their hosts. Tick infestation and tick-borne diseases threaten around 80% of the world's cattle population. The economic losses caused by ticks and tick-borne diseases are estimated to be worth up to $18 billion each year (de Castro, 1997). Parturient Hemoglobinuria is a serious and economically significant illness of dairy animals. It is a severe sporadic disease that affects both pregnant buffaloes and cows globally. Intravascular hemolysis, hemoglobinuria, straining while defection, labored breathing, and death are among the symptoms (Jubb et al., 1985). FMDV (Foot and Mouth Disease Virus) is the causal agent of FMD in the Aphthovirus genus and family Picornaviridae. It is a non-enveloped, single-strand RNA virus with a diameter of 26 nm that comes in seven primary serotypes and over 60 sub-serotypes (Admassu et al., 2015). FMD is an extremely contagious disease. Pigs, cattle, goats, sheep, and buffalo are among the animals infected. FMD affects cloven-hoofed wild animals such as antelope, wild pigs, elephants, camelids, and deer. Resistance to spontaneous infection with some strains may be found in old-world camels. Llamas and alpacas from South America are somewhat sensitive. The FMD strain that infects deer and wild pigs can potentially infect cattle. Guinea pigs, rats, mice, and armadillos can all be experimentally infected (Yakobson et al., 2014) as shown in Figure 4.

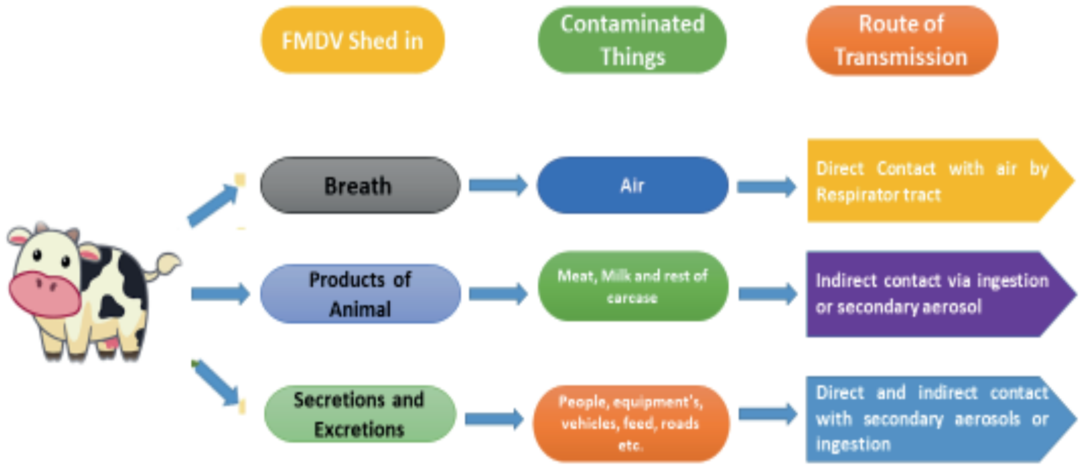

Figure 4. The Primary Pathways of FMD Transmission among Vulnerable Animals

5. Reproduction Management and Heat Detection

The goal of PLF is to manage individual animals while continuously monitoring their health, welfare, production/reproduction, and impact on the environment in real-time. The term "continuous" refers to the fact that PLF technology is always measuring and analyzing (Berckmans, 2015). Dairy product demand is expected to climb steadily as the world population rises from 7.7 billion in 2019 to 9.7 billion in 2050. In recent years, intensive farming practices have been widely employed to meet consumer expectations and requirements. Despite the fact that the size of dairy farms worldwide is increasing due to rising costs and the additional benefits of economies of scale, the ratio of animal caregivers to total animals is decreasing (Simitzis et al., 2021). The application of research and technology breakthroughs in farm animal breeding around the world has sparked the creation of PLF farming. Sensors (cameras, microphones, and accelerometers) are employed in this new technology to construct algorithms to identify the welfare of animals without disturbing them with sounds and movements, as well as to estimate productivity (Greenwood et al., 2014). PLF incorporates digital technology. It tries to reduce environmental effects by carefully monitoring agricultural activities in order to maximize productivity, reproduction, animal welfare, and targeted resource usage. PLF focuses on digital technologies to collect data about single animals, animal species, or the environment. The use of technology has made daily duties in the agriculture sector easier (Groher et al., 2020). Global livestock production systems' productivity per animal has lately increased. Customers' perceptions of animal welfare, human health, food security, safety, and sustainability are influenced by social issues. An intensive production system with a high level of organization and efficiency is stated to have the best possibilities of long-term viability (Lovarelli et al., 2020). Livestock farms vary greatly in terms of size, housing, nutritional practices, labor, genetics, record keeping, sexual management, herd welfare and health, overall replacement strategies, and individual goals, so when there are PLF systems, the concept of "one size fits all" is not applicable to all. Even if the crucial activity is the same, the ROI (Return on Investment) may differ depending on the program used to enforce the action (Carillo & Abeni, 2020).

Many studies have been undertaken to determine the potential installation and validation of monitoring systems, which are constantly evolving. Behavioral and physiological monitoring of animal characteristics can be difficult because the method used to gather data can change and there will always be interindividual variations. Several methods were used to monitor animal characteristics, including image and sound analysis utilizing cameras, sensors, or other equipment such as water/feed consumption, scales, and so on (Norton et al., 2019). PLF technologies also allow breeders to detect and control animal health and well-being at any time through continuous, direct monitoring or observation of animals. In this approach, there will surely be long-term increases in the efficiency and quality of goods from healthy and "prosperous" animals (Berckmans, 2014). Precision livestock farming technologies can inform animal caregivers in real-time, allowing them to provide tailored care to an animal exhibiting altered behavior as a result of disease, injury, or a stressor. PLF can also be used for a variety of other applications to increase the efficiency of livestock operations, such as detecting estrus in beef and dairy cattle for optimal herd reproductive management, precision feeding by monitoring daily feed intake and weight gain, and so on. Furthermore, PLF systems can detect novel phenotypes or indicator features for application in advanced breeding programs (Rosa, 2011) as shown in Figure 5.

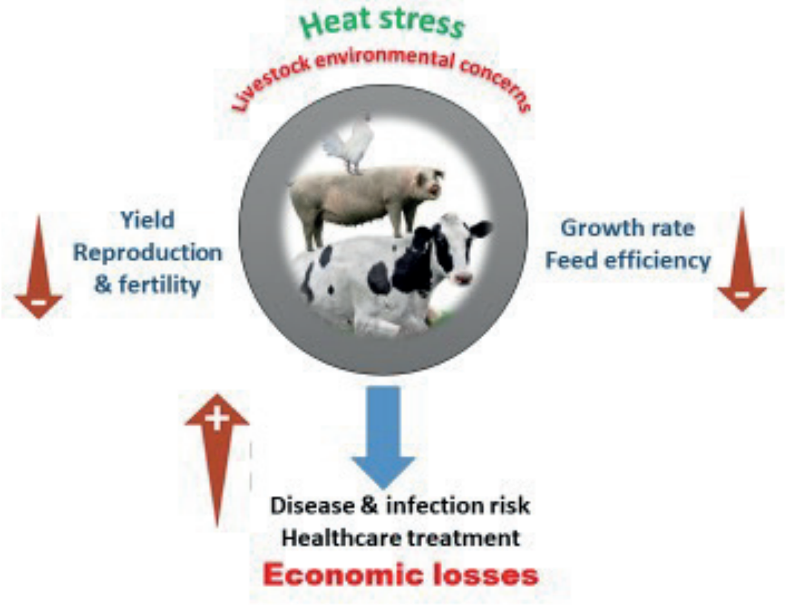

Figure 5. The Effects of Heat Stress on Animal Health, and Productivity

6. Milk Quality Monitoring and Management

Milk is widely regarded as a full diet because of the presence of important components such as proteins, lactose, milk fasts, minerals and vitamins, and so on. Livestock farming is an essential component of Pakistan's rural economy since it is the only sector that offers agricultural families almost consistent income and readily cashable assets (Agrihunt.com). Pakistan is the world's third-largest milk producer, trailing only India and the United States. On the consumption side, milk and its products account for 26% of Pakistan's food expenditure (Farooq, 2016). Pakistan has a sizable cattle population that is well-suited to the local environmental conditions. There are 41.2 million cattle, 35.6 million buffaloes, 29.4 million sheep, 68.4 million goats, 1 million camels, and 932 million poultry in our national herd (Rafique & Ahmad, 2018). Pakistan's dairy industry contributes significantly to the national economy. In 2013-14, 41.1 million tons of milk worth Rs.1766.51 billion were produced, which is nearly equal to the whole value of wheat, maize, cotton, and their byproducts produced in the country. According to (Farooq, 2016) 80% of production took place in rural areas, 15% in semi-urban areas, and 5% in urban areas. Milkmen gather approximately 90% of the total milk entering the milk marketing channels from subsistence farms. Total milk production does not meet the population's milk needs. The primary cause of this situation is that the human population is growing at a quicker rate (3% per year) than milk production (Bilal et al., 2006). Despite policymakers' lack of interest, the dairy industry is increasingly a commercial one. Despite being the world's leading milk producer, Pakistan nevertheless imports powdered milk to meet domestic demand. In 2011-12, the value of imported milk and allied products was $134.4 million, while in 2012-13, it was $112.4 million (Shoaib, 2013). Punjab produces over 73% of the country's milk, while Sindh contributes approximately 23%; the remainder is produced by different other provinces (Hashmi et al., 2007) as shown in Figure 6.

Figure 6. Factors that influenced the Cost of Milk Production

7. Environmental Monitoring and Control in Dairy Farming

Climate change affects cattle productivity in both direct and indirect ways. Livestock are homotherms, which means they regulate their body temperature to keep themselves healthy and productive. Animals get stressed when the ambient temperature is above or below the thermo-neutral range. A rise in temperature combined with humid conditions can cause heat stress in livestock, causing behavioral and metabolic changes as well as a reduction in feed (Sirohi & Michaelowa, 2007). Climate change has major repercussions for several sectors of the economy, most notably crops, animals, and human health. Because of their over-reliance on low-input rain-fed agricultural production, developing and underdeveloped countries are expected to suffer the most damage. The bulk of rural inhabitants in these countries rely largely on livestock raising for a living. The livestock industry has been reported to be extremely vulnerable to climate change (Moreki & Tsopito, 2013). Regionally, Pakistan ranks second in carrying the second biggest number of dairying animals in South Asia (138.12 million heads) after India (517.08 million heads), and the dairy sector's annual growth rate is positive, indicating a good climate for dairy in Pakistan (Siddiky, 2017). Temperature and humidity are combined into a single variable and assigned a single value via the temperature-humidity index. This is thought to be a valuable tool for forecasting the effects of the environment on farm animals. It is well known that the daily maximum and lowest values for the temperature-humidity index are 80 and 70, respectively, above which the heat-induced fatality rate increases. It has also been discovered that changes in the temperature-humidity index stimulate the emergence of new bug species, which has a direct impact on the health of dairy animals (Lacetera, 2019). Because of rising temperatures, livestock productivity in Pakistan is expected to fall by 20 to 30% in the future. Finally, a dairy and meat industry crisis will raise the pricing of products that are out of reach for middle-class consumers (Abbas et al., 2019). The cattle industry helps to alleviate poverty and add value to the economy, raising foreign exchange reserves of 1333 billion rupees (8.495 billion USD). Climate change and a lack of natural resource endowment are the most important development challenges confronting dairy production in Pakistan. Small and marginal farmers produce more than 70% of milk, and they are especially exposed to unforeseen extreme weather events (Abbas et al., 2019). Climate change is the main cause of weather-related hazards that adversely affect livestock production systems, especially in developing countries. Policymakers and researchers agree at this point that climate change significantly impacts the livestock sector

(Naqvi & Sejian, 2011). The primary externality of climate change is warmth, which, if it exceeds the ideal level, impairs the operations of biological systems in dairy animals. Warming has a direct impact on dairy production methods. Excess heat created by warming causes heat stress in dairy animals, which results in decreased milk production immediately. When the temperature rises above the animal's thermo-neutral zone, it undergoes inherited physiological changes to cool its body and maintain a steady body temperature (Rhoads et al., 2009) as shown in Figure 7.

Figure 7. Techniques that are being used in Environmental Scanning & Monitoring

8. Data Analytics and Decision Support Systems

The Precision Animal Farming (PLF) method envisions sustainability in animal production operations (Banhazi et al., 2012). PLF is one of the most powerful breakthroughs in the livestock farming business, providing farmers with real-time monitoring and management capabilities. PLF encompasses a broad range of technologies that are used in tandem with modern technologies such as microfluidics, sound analyzers, image-detection techniques, sweating and salivary sensing, serodiagnosis, and others (Neethirajan, 2017). Different terms, such as precision livestock farming (PLF), smart livestock farming, and smart animal agriculture, to name a few, have been assigned to the same paradigm in the animal science community: how to sustainably increase food production while maintaining animal welfare and reducing environmental burden by combining data acquisition (sensors), storage (IoT), and transformation with prediction analytics using artificial intelligence (AI) tools (Tedeschi et al., 2017). There are no evidence-based methods to enable herd-level strategy development. To facilitate advisor input on herd health, several streams of sensor data can be merged in a time-efficient, automated, and objective method. Climate change, with its growing frequency of environmental disturbances, places strains on the livestock industry (Hansen et al., 2012). The Moss system involves the systematic acquisition, investigation, analysis, and up-to-date information on animal and human health/production/reproductive data. Surveillance systems are used for a variety of objectives, including monitoring and identification of pandemic diseases of alien origin, such as corona. These programs help determine effective preventative and control techniques. It also monitors the development and completion of response initiatives and indicates the noninfectious and nonhazardous status of animals and animal-derived products in the field of animal health. Ultimately, ensuring that surveillance plans are on target is superior (Drewe et al., 2012). Improved management with PLF provides for an increase in the efficacy of medications used in food-producing animals; as a medication, it is only used as an adjunct to a good management system with public health responsibilities in livestock. Early detection of individual changes in disease-related health markers is critical for both early diagnostic interventions and successful chemotherapeutic therapy (Lhermie et al., 2017). Although PLF has a good impact on industrial farming and is appealing to young people, it can also have a negative impact on farmers and animals if the tools are not matched to farmers' requirements and talents. To promote farmers' acceptance of these new technologies, it is necessary to address the various facets of their labor (Hostiou et al., 2017). These complicated processes can be described using advanced statistical and mathematical modeling approaches, machine learning (ML), and data mining. As a result, they are increasingly being used in novel algorithms for predictive analytics in animal health and welfare (Vázquez-Diosdado et al., 2019).

9. Economic Benefits and Sustainability

The dairy industry in Pakistan is an important component of the agricultural sector, contributing significantly to the country's economy and providing livelihoods for millions of people. It is a significant source of income, particularly for small-scale farmers and rural communities, accounting for more than 12% of the country's agricultural GDP (Tariq & Singh, n.d.). In Pakistan, dairy production systems are divided into two categories: traditional and contemporary. Over 12,000 commercial dairy farms are believed to exist in Pakistan, with approximately 75% operating on a modest scale (Tahir et al., 2019). The most significant difficulty confronting Pakistan's dairy sector is a lack of access to high-quality feed resources (Tariq, 2020). Since Pakistan's inception, livestock (animal agriculture) has been regarded as the most important component of the national economy. During 2010-11, livestock contributed around 55.1% of agricultural value added and 11.5% of GDP. The livestock sector plays an essential part in the development of rural economies, as evidenced by the fact that 35-40 million rural populations rely on livestock (Abdullah, 2010). Livestock is the agricultural sector's backbone; although being a neglected industry, it nevertheless plays a vital role in our national economy by providing draught power, high biological value animal proteins, and by-products (hides, skin, wool, mohair, bones, and manure). The development of the dairy sector is required not only to meet the increasing demand for animal protein, but also for social and economic reasons, as dairy animals are a good source of regular cash income, economically utilize family labor, produce social security, and supply growing markets (Sarwar et al., 2002). Economic concerns are not the only ones driving dairy farmers to adopt new technologies. Economic models have been created to assess the worth of investing in PLF technologies (Schewe & Stuart, 2015). Modern farmers will face increasing pressure to care for a higher number of animals per farm in order to run a profitable company, which will become more intense in the coming years (Marquer et al., 2014). Economic losses caused by these diseases have been estimated to be Rs. 79 billion, which is roughly equivalent to one billion US dollars in Punjab alone, and economic losses caused by various livestock diseases have been estimated to be Rs. 8.4 million per district per year in Punjab by dairy farmers and others (Nazir & Khan, 2009). Human preferences and environmental influences are reducing livestock variety. Dairy farming is typically altering farming or production systems in response to the local economy and the significance of a certain breed in the evolving economic and farming system (Afzal & Naqvi, 2004).

10. Challenges and Future Directions

The livestock sector provides employment opportunities, and the livestock labor force in Pakistan is estimated to be approximately 8 million individuals, including both full-time and part-time workers (Hussain et al., 2019). In Pakistan, livestock breeding procedures differ based on the species and region (Tariq, 2013). To improve the genetic potential and productivity of livestock through the adoption of modern breeding technologies, the government implemented a number of policies and programs, including the National AI Program, the Livestock Breeding and Development Project, and the National Animal Genetic Resources Management and Conservation Programme (Tariq, n.d.). Livestock, as a significant sector of Pakistan's economy, need increased government support for its various tasks. One of the most significant issues for livestock farmers in Pakistan is a lack of financial facilities (Ullah et al., 2020). The government has also failed to provide enough training and extension assistance to livestock farmers (Idrees et al., 2007). In Pakistan, the livestock healthcare system is mostly dependent on governmental and commercial veterinarian services. The federal and provincial governments provide public veterinary services through the Livestock and Dairy Development Department. Private veterinarians and pharmaceutical firms provide private veterinary services (Afzal, 2009). Lack of proper resources, obsolete infrastructure, limited awareness, and inadequate illness surveillance are some of the primary issues in healthcare (Shaikh et al., 2022). In Pakistan, livestock breeding procedures differ based on the species and region (Tariq, 2013). Because there is no unified marketing structure dominated by intermediaries and brokers, the livestock market is fragmented, resulting in low prices for farmers and high prices for consumers (Khan, 1991). There is a lack of adequate infrastructure, and farmers must frequently travel vast distances to have their livestock treated (Rehman et al., 2017). There are no subsidies for high-quality animal feed and veterinary treatments, which limits the sector's expansion (Tariq et al., 2021). Many farmers are unable to obtain extension services. However, livestock extension services in Pakistan face a number of challenges, including a lack of access to information and training, limited resources, poor infrastructure, a lack of coordination, and a lack of farmer participation (Qamar, 2004).

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About The Authors

Dr. Muhammad SAFDAR earned his PhD in Molecular Biology and Genetics from Gaziantep University, Turkey. He is Lecturer in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, nutrigenomics, nano-genomics, bioinformatics, biotechnology, and their applications. He has published more than 70 research articles in national and international journals. He has also written many book chapters as well as an edited book. He is an associate editor for international journals.

E-mail: msafdar@cuvas.edu.pk ORCID: 0000 0002 3720 2090

Mr. Muhammad YOUNUS earned his M.Phil. in Zoology from CUVAS Bahawalpur Pakistan. He is a Research Associate in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, bioinformatics, biotechnology, and their applications. He has published more than 06 research articles in national and international journals. He has also written book chapters.

E-mail: younus31302@gmail.com ORCID: 0009 0005 5392 7031

Jawairia Mehrin NASIR is a graduate of the Government Sadiq College Women University Bahawalpur, Punjab-Pakistan, where she focuses on improving the yield of livestock to combat food shortages.

E-mail: jawariamehreen@gmail.com ORCID: 0009 0005 1899 5610

Afshan KHADIM is an ambitious final year student pursuing a BS in Zoology at Cholistan University of Veterinary and Animal Sciences, Bahawalpur. With a passion for Animal Nutrition, Breeding, Genetics, and Genomics, she has ventured into the captivating world of Molecular Modeling. Embarking on a journey into research, she aspires to merge his varied interests to contribute innovative insights to the scientific community.

afshankhadim719@gmail.com ORCID iD: 0009-0005-9875-682

Muhammad SAJJAD completed did his Graduation from Cholistan University of Veterinary and Animal Sciences Bahawalpur Pakistan. He continues his post graduate study in Zoology Cholistan University of veterinary and animal’s sciences Bahawalpur. He continues to work on molecular genetics and biotechnology as his area of interest

sajjadsaqi125@gmail.com ORCID iD: 0009-0002-6494-5161

Miss. Salma Bibi, received her BS degree in Animal Sciences from Cholistan University of Veterinary and Animal Sciences, Bahawalpur, Pakistan. Her main areas of interest are Animal Genetics, Breeding and Reproduction. She has written 8 book chapters in international journals.

Email: salmamalik6809129@gmail.com ORCID: 0009-0003-0798-9886

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UTILIZATION OF PROBIOTIC IN POULTRY DIET AND ITS EFFECT ON PERFORMANCE

Muhammad Tahir KHAN

Muhammad Waseem AFZAL

Introduction

Over the past two decades, the poultry industry has experienced tremendous growth and has become one of the most dynamic global industries. It plays a crucial role in meeting the increasing demand for high-quality protein for human consumption. However, there is a growing need for a safer protein source that is free from infectious pathogens. Unfortunately, the poultry sector has faced various challenges, particularly infectious diseases caused by viruses, bacteria, fungus, or protozoa. The economic losses resulting from these diseases and the cost of preventative medicine have been significant. As a result, antibiotics have been widely used in the poultry business for medicinal purposes, to prevent diseases, and to promote growth. However, the presence of antibiotic residues in poultry meat and eggs can potentially harm consumers. This risk is especially high during the early stages of a chick's life when it hasn't yet developed a stable gut microbiota. Therefore, there is a growing interest in finding alternatives to antibiotics in poultry production. This interest is driven by concerns about antibiotic resistance, the restrictions on the use of subtherapeutic antibiotics in Europe, and the possibility of a ban in the United States (Edens, 2003). One potential alternative is the use of probiotics.

Probiotics, also known as "living microorganisms," have been used as a major feed supplement in animal production for decades. Administered in appropriate quantities, they provide the host with health benefits (Reszka et al., 2020). By enhancing the activity of digestive enzymes, maintaining the delicate balance of bacteria in the gastrointestinal tract, and promoting gut integrity, probiotics can improve feed intake and digestion efficiency in chickens. As a result, the birds' performance and health are enhanced (Abd El-Hack et al., 2020). Research by Iriti et al. (2019) demonstrated that adding Lactobacilli to chickens' diets increased the levels of antibodies that inhibit hemagglutination after three to four weeks of feeding. Vinayasree et al. (2012) investigated the effects of probiotic treatment on broiler performance and found that the level of fecal coliform bacteria in the experimental group was significantly lower than in the control groups at the end of the sixth week. Fazelnia et al. (2021) conducted a study and discovered that the addition of potential probiotics Bacillus subtilis, Bacillus licheniformis, and Saccharomyces cerevisiae to the feed of broiler chicks improved their performance and immune responses. Furthermore, the inclusion of synbiotic and probiotic supplements reduced the harmful effects of S. typhimurium on broiler chick growth and immunity. Numerous studies have also documented the benefits of various probiotics for broiler growth (Rehman et al., 2020).

Effect of probiotic on production performance

Numerous studies have demonstrated the positive effects of different probiotics on the production efficiency of laying hens (Yörük et al., 2004; Neijat et al., 2019; Mikulski et al., 2020). In a study by Bozkurt et al. (2011), the impact of probiotic treatments on the performance of broiler breeder and layer hens was examined. The microbial cultures resulted in changes in egg production rate and egg weight, but had no effect on mortality or body weight. Some probiotics enhanced egg production rate, egg weight, and egg mass, ultimately improving the ability of layer hens to convert their nutrition into eggs. One of the three probiotic supplements significantly increased egg production rate in broiler breeders. Pilyukshina et al. (2020) found that a dosage of 1.0 kg/t of probiotic Levusell SB Plus improved chicken livability, overall egg production, and optimized egg weight. Similarly, Sultan and Abdul-Rahman (2011) reported that probiotic treatment significantly increased egg weight and production percentage compared to the control. Other studies by Softon (1990) and Hargis and Creger (1978) also showed that probiotic supplementation improved egg production qualities. Khan et al. (2011) and Panda et al. (2008) found that probiotic treatment enhanced egg production in white leghorn layer breeders. Probiotics have been shown to improve the performance of layer hens and broiler chickens in terms of body weight in various trials (Timmerman et al., 2004; Khan et al., 2007; Olnood et al., 2015; Tang et al., 2015). Likewise, research specifically focusing on layers and breeders demonstrated that adding probiotics to the diet increased egg production and feed conversion (Güçlü, 2011; Sultan and Abdul-Rahman, 2011). Furthermore, multi-strain probiotics have been found to reduce feed consumption and improve feed conversion ratio (Balevi et al., 2001).

Some research has shown that the addition of probiotics has little impact on chicken performance. Aalaei et al. (2018) found that dietary probiotic treatments did not have a significant effect on total production (hatching egg), egg weight, mortality, or body weight. Michel et al. (2017) investigated the effects of administering a combination of organic acids and a probiotic based on lactic acid bacteria on the production characteristics of broiler breeders. They found no difference in body weight or uniformity between females and males across the three trials ($P>0.05$). However, breeders that received the combination of organic acids and probiotics had significantly lower weekly-cumulative mortality compared to the control group in all three trials. Aalaei et al. (2019) found that broiler breeder hens fed a probiotic-rich diet did not significantly increase in body weight, feed conversion ratio ($P>0.05$), rate of egg production, egg weight, or egg mass compared to the control group. Similarly, adding commercial probiotic supplements did not affect the performance of laying hens or white leghorn layer breeders (Panda et al., 2008). Several studies (Pedroso et al., 2001; Kurtoglu et al., 2004; Panda et al., 2003; Mahdavi et al., 2005) have also shown that adding probiotics to laying hen feed does not have any negative effects on feed consumption, egg weight, or feed efficiency.

Effect of probiotic on hatching traits

Bozkurt et al. (2011) conducted a study to examine the effects of three different probiotic treatments on the performance of broiler breeder and layer hens. One of the probiotic supplements led to an increase in settable egg production rate and chick yield in broiler breeders. However, it is worth noting that probiotics generally tend to reduce the weight of settable eggs. Additionally, probiotics showed improvement in hatchability but did not have a positive impact on fertility. In another study published in 2011, Güçlü investigated the impact of prebiotics and probiotics on the performance of quail breeders. The results indicated a slight increase, although not statistically significant, in hatchability and the percentage of fertilized eggs with probiotic and prebiotic treatments. Shashidhara and Devegowda (2003) fed broiler breeders 0.5 kg/ton of MOS and observed an increase in the proportion of fertile eggs and hatchability. Similarly, Narushin and Romanov (2002) concluded that probiotics improved the hatchability of eggs in laying hen breeders. Ramasamy et al. (2009) reported that a mixture of 12 Lactobacillus spp. cultures appeared to enhance hatchability of eggs. Finally, Pilyukshina et al. (2020) investigated the effect of probiotics on the production performance of broiler breeder hens. They found that a probiotic dose of 1.0 kg/t resulted in a higher yield of hatching eggs and an increased number of hatched chicks.

Several studies have shown that probiotic supplementation has little to no impact on the reproductive performance of layer hens. For example, in a 2018 study, Aalaei et al. examined the performance and gastrointestinal health of broiler breeders using both single- and multi-strain probiotics. The findings revealed that these treatments did not have any noticeable effect on hatchability and fertility. Similarly, in another study conducted by Aalaei et al. in 2019, the performance of broiler breeders was assessed in relation to the use of multi-strain and mono-strain probiotics. The results showed that broiler breeder chickens that were fed a diet containing either multi- or mono-strain probiotics did not exhibit significantly higher fertility or hatchability rates compared to the control group ($P>0.05$). Furthermore, a study by Nickolova et al. in 2004 concluded that probiotic treatment had no impact on the reproductive efficiency of Muscovy ducks.

Effect of probiotic on egg quality traits

Several studies have demonstrated that probiotic microbial cultures can improve various egg quality features in laying hens (Yörük et al., 2004). Specifically, Tortuero and Fernandez (1995) found that probiotic microbial cultures, particularly Lactobacillus, improved the egg weight of laying hens. Similarly, Mikulski et al. (2012) concluded that probiotic treatment led to improved egg weight and shell quality, while also reducing the number of broken eggs. Peebles et al. (2000) reported that probiotics enhanced the weight of eggs produced by laying hen breeders. Similarly, Ramasamy et al. (2009) observed an increase in egg weight when laying hen eggs were exposed to a mixture of 12 Lactobacillus spp. cultures. Probiotic treatment was also found to increase eggshell weight and thickness, according to Panda et al. (2008). Studies specifically focusing on breeders and layers have shown that probiotic supplementation can enhance overall egg quality (Sultan and Abdul-Rahman, 2011). In quail breeders, Güçlü (2011) found that both probiotic and prebiotic treatment improved eggshell thickness. Furthermore, research conducted by Panda et al. in 2003 revealed that probiotic treatment led to improved eggshell thickness in laying hens. Similarly, Panda et al. (2008), Mutuş et al. (2006), and Mikulski et al. (2012) concluded that probiotic supplementation improves eggshell quality by increasing serum calcium concentration, as well as calcium and phosphorous retention. Additionally, Abdelqader et al. (2013) observed that probiotic supplementation enhanced the qualities of the eggshell.

However, studies conducted by Mahdavi et al. (2005) and Mohebbifar et al. (2013) did not find any significant probiotic effect on egg quality indicators. In a more recent study published in 2018, Aalaei et al. examined the use of single- and multi-strain probiotics in broiler breeders and their impact on performance and gastrointestinal health. The results showed that dietary modifications did not result in any changes in egg weight, yolk color index, or shell weight. Similarly, Güçlü (2011) investigated the effects of probiotic and prebiotic supplements on quail breeder performance, egg quality, and hatchability, and found that indicators such as egg specific gravity, egg weight, yolk index, albumen index, and Haugh unit were not significantly influenced by the diets supplemented with either probiotics or prebiotics. Consistent with these findings, Kurtolu et al. (2004) concluded that probiotics had no impact on egg specific gravity. Additionally, Yalçin et al. (2000) and Mahdavi et al. (2005) reported no impact of probiotic supplementation on the Haugh unit in their investigations on laying hens.

Effect of probiotic on blood biochemistry

Probiotics have been used in studies to enhance the biochemical parameters of broilers (Sallh and Al Hussary, 2009; Abdulmajeed, 2010). Sultan and Abdul-Rahman (2011) conducted a study on broiler breeders to investigate the effects of probiotics on certain physiological markers. The results indicated that probiotic supplementation significantly reduced levels of blood triglycerides and increased levels of serum uric acid compared to the control group, but had no effect on glucose levels. Beski (2010) observed a significant decrease in serum triglyceride levels with probiotic administration. Kurtoglu et al. (2004) found that probiotic supplementation in layers led to a dramatic reduction in serum cholesterol levels. Tortuero et al. (1975) reported that supplementing with L. Acidophilus resulted in decreased serum cholesterol in laying hens. Probiotic inclusion has also been linked to lower blood cholesterol levels in broilers (Sohail et al., 2010) and layers (Sobczak and Kozowski, 2015). According to several studies (Jin et al., 1998), probiotics may decrease the amount of cholesterol in serum and egg yolks. Zhang et al. (2012) found that a probiotic dietary level of 400 g/t significantly ($P<0.05$) reduced blood triglyceride levels compared to the control group.

Studies conducted by Mateova et al. (2008) and Beski (2010) revealed that probiotics did not have a significant impact on serum glucose levels. Aalaei et al. (2019) examined the performance of broiler breeders in relation to the effects of multi-strain and mono-strain probiotics. The study found that there were no differences in blood haematology and cholesterol levels across the different dietary regimens ($P>0.05$). Zarei et al. (2011) reported that the levels of blood cholesterol and triglycerides were not affected by dietary probiotics and prebiotics. Additionally, Dimcho et al. (2005) found that the addition of probiotics did not impact the serum total protein content of mule ducklings. Moreover, Alkhalf et al. (2010) discovered that probiotic supplementation did not affect the serum levels of total protein and albumin. Similarly, Kurtoglu et al. (2004) and Mohebbifar et al. (2013) concluded that probiotic treatment did not have any effect on blood triglyceride or cholesterol levels.

Effect of probiotic on immune response

Probiotics play a crucial role in maintaining a healthy diet. They are known to support intestinal health, prevent metabolic diseases, improve digestion, and boost immunity (Forte et al., 2016; Park et al., 2016; Ramlucken et al., 2020; Wang et al., 2020). Corthésy et al. (2007) have highlighted the various effects of probiotics on the immune system, including increased antibody production, enhanced cell-mediated immunity, improved T-cell movement, and strengthened TLR signaling. Research by Apata (2008) indicates that chicks fed with probiotics had higher levels of specific antibodies after receiving the New-Castle disease (ND) vaccine. Similarly, Forte et al. (2016) found that a group provided with a meal supplemented with Lactobacillus acidophilus produced more antibodies against the ND virus compared to the control group. Gao et al. (2008) also discovered improved gut immunity in chickens fed probiotic-supplemented diets. Similarly, Sohail et al. (2010) observed that dietary probiotic supplementation enhanced humoral immunity against the infectious bursal disease virus and ND virus in chickens exposed to heat stress. However, Balevi et al. (2001) found that probiotic supplementation did not affect the generation of specific antibodies to the ND vaccination antigen delivered through drinking water. Aalaei et al. (2019) also found no differences in the immunological response of broiler breeders to phytohemagglutinin (PHA-P) injection among different dietary regimens that included multi- and mono-strain probiotics (P>0.05).

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About The Authors

Dr. Muhammad Tahir Khan earned his PhD in poultry production from the University of Veterinary and Animal Sciences (UVAS), Lahore, Pakistan. He is a lecturer in the Department of Poultry Science, Faculty of Animal Production and Technology, Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interest includes nutritional manipulation of indigenous chicken and poultry waste management. He has published 27 research articles in national and international journals. Moreover, he is also a reviewer of some important international journals.

Email mtahirkhan@cuvas.edu.pk , ORCID 0000-0002-4734-3428

Muhammad Waseem Afzal completed his BSc Honours in Animal Science in 2012. Transitioning to the livestock industry, he served as Breeding Farm Manager at Pakistan Poultry Farms. Since 2015 he has been the Manager of Artificial Insemination (A.I) at Zubair Feeds Pvt. Ltd., where he has excelled in optimizing breeding outcomes through advanced A.I techniques. Waseem earned his M.Phil in Poultry Science from Cholistan University of Veterinary and Animal Sciences, Bahawalpur, in 2023. His expertise encompasses managing breeds such as Hubbard Classic and Arbor Acres, achieving impressive hatchability rates, and implementing comprehensive flock management practices. He is dedicated to enhancing poultry production and ensuring the health and performance of livestock.

Email waseemafzal85@gmail.com

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GREENHOUSE GASSES EMISSION AND CLIMATE CHANGE

U. YOUNAS

M. M. AYAZ

F. HASSAN

M. Z. FAROOQ

A. FATIMA

G. JILANI

Z. AHSAN

Climate change is one of the major threats to public health. While, climate changes deeply impact on the natural and social environments. The greenhouse gases (CH4, N2O, H2O and CO2) are emitting at high rate and are one of the major cause of climate changes. In 21st century, decreases of cold extremities and increases of warm extremities are reported over Pakistan. In the north region of Pakistan, the highest increase in temperature with more frequent intense precipitation is reported. By this climate change, Pakistan is facing prospect endangerment to economy, social and environmental development. Livestock yields were directly impacted by changes in climatic variables such as temperature, precipitation, frequency and intensity of severe occurrences like droughts. Many studies have examined the current and potential impacts of climate change on many forms of infectious diseases, such as water-borne, air-borne, vector-borne, and food-borne illnesses. A big challenge is emission of greenhouse gases (GHG) environmental degradation and welfare and economy issues. There is rapid growth of population in every country, that directly or indirectly leads to the excessive amount of GHG emissions and waste generated by house hold combustion increasing at about 10-16% per annum basis. According to United Nation Framework Convention on Climate Change, zero emission of GHG are needed to reduce the global temperature and avoid the worst climate changes.

1. Climatic changes in Pakistan

Climate change is the alteration in the environmental conditions naturally as well as by human intervention. Due to the climate change elevation of sea level, melting of ice glaciers, global warming, and irregular weather patterns are increasing across the globe (Lipczynska-Kochany 2018). Climate changes involve changes in rainfall patterns, variations in temperature, increases of precipitation, water-related diseases due to highly impact on water resources (Brubacher et al., 2020). Climate change is one of the major threats to public health. While, climate changes deeply impact the natural and social environments (Caminade, 2019). Great changes in the climate influence water resources, groundwater contamination, health, and subsequently human life (Tong, 2019).

The temperature, humidity, pressure, and precipitation of the atmosphere express the global environmental situation (NASA, 2018). The greenhouse gases (CH4, N2O, H2O, and CO2) are emitted highly and these GHG emissions are one of the major causes of climate change (Roy 2018). Continual human intervention (deforestation, agricultural activities, vehicle use, combustion of fossil fuel, and industrial development) and natural phenomena like volcanic explosions, seismic activities, and solar cycles have a great role in climate change (Ahmed et al. 2020). In the past 139 years, September of 2017-18 was recorded as the warmest September with the fourth highest temperature (CO2, Earth 2018). The effects of the climatic change will be destructive in the agricultural country (Pakistan), where the per capita income is already low. Due to its geographic location, Pakistan is becoming a victim of climate change effect (Balkhair et al. 2018). Multiple Asian countries including Pakistan are facing interference, due to urbanization, industrial development, and resource depletion (Chan et al. 2018). The misuse of non-renewable resources excessive use of natural sources and overgrowth of industries have a great impact on climate change in Pakistan (Waraich, 2024). The extreme exploitation causes adverse effects on the atmospheric change in Pakistan (Farah et al., 2023). In the 21st century, decreases of cold extremities and increases in warm extremities have been reported in Pakistan (Ali et al. 2019a). In the north region of Pakistan, the highest increase in temperature with more frequent intense precipitation (Amin et al. 2018).

Of this climate change, Pakistan is facing prospect endangerment to the economy and social and environmental development (Khan et al. 2016). The faster rate melting ratio of the Himalayan Glacier of Pakistan ever recorded in history (Bibi, et al. 2023), unpredictable flooding, droughts, lack of water resources, abrupt rainfall, and intense heat waves (Abid et al. 2016b). Due to global warming, climate change and its effects are quite visible and will prevail more intensely in the future (Shahvari et al. 2019). By 2020 until 2050, Pakistan's temperature is going to rise from 0.9 to 1.5 °C (Hussain and Mumtaz 2014; Arshad et al., 2021). In the worst drought period of Pakistan, 84% population of Pakistan's largest province Baluchistan was badly affected and the killing of the highest ratio of livestock by massive floods faced the central and northern parts (Ullah et al. 2018). Immediate attention is needed against the ever-growing climate change (Perkins et al. 2018). By the interpretation in climatic events, all regions in the world are projected to have natural ecosystems that affect the economic system of highlands (Fahad, 2020). Multiple researchers have predicted how climate changes in the future may affect the hydrological responses located in the Karakoram and Himalayan ranges (Baig et al., 2022). In the past few years, natural hazards have caused climate changes in most countries (Japan, Hong Kong, Taiwan, Bangladesh, and India). Weather-related events (storms, drought, heat waves, and flooding) make the country's climate-vulnerable (Ahmed, 2020). In the upcoming years, great expectations of high variations in temperature and rainfall have been reported in studies (Ahmed, 2020).

Table 1. List of climate change vulnerabilities faced by Pakistan (Hussain et al., 2020)

Serial No.	**Climate change vulnerabilities**	**Reference**
1	Continuous flooding (post-2010)	(Abid et al. 2016b)
2	Severe droughts across country (1999–2003), temperature rise, lack of water resources, and pest-diseases	(Hussain et al. 2018)
3	Recent drought in Tharparker and Cholistan	(Change, M. of climate 2015)
4	Intense temperature rise (heat wave) in Karachi	(Chaudhry et al. 2015)
5	In 2015, nearly all main types of natural disasters, earthquake, drought, flood, heat wave, and cyclone, were faced by Pakistan	(Hassan and Adnan 2016)
6	Substantial rainfalls with hail storm on March 4, 2016.	(Ghazala Qaiser 2016)

Table 2: The list of the top countries most affected in the Climate Risk Index (CRI; annual averages; adopted between 1995 and 2014 (Ahmed, 2020).

CRI 1995–2014 (1994–2013)	**Country**	**CRI Score**	**Total Losse (Million US$)**	**Losses/Unit GDP in%**
1	Honduras	11.33	570.35	2.23
2	Myanmar	14.17	1140.29	0.74
3	Haiti	17.83	223.29	1.55
4	Philippines	19.00	2757.30	0.68
5	Bangladesh	22.67	2438.33	0.86
6	Vietnam	27.17 361	2205.98	0.70
7	Pakistan	31.17	3931.40	0.70

2. Impact of climate change on agriculture

One of the most important environmental issues facing the modern world is becoming climate change. The global climate is changing as a result of greenhouse gas (GHG) emissions and a rise in gases such as carbon dioxide (CO2), methane (CH4), and nitrous oxide (N2O) (Wei, Dong et al. 2016). Variations brought about by climate change will include rising sea levels, altered rainfall patterns, and the shift of climatic areas as a result of rising temperatures. Climate trends are predicted to change, leading to a rise in the intensity of storms, floods, and droughts. The average global temperature increase will be 2.8°C, with variations ranging from 1.8°C to 4°C (Impac 2011).

Humans are to blame for the recently discovered CO2-enriched planet as, as a result of deforestation and extensive fossil fuel usage, CO2concentrations have increased from 280 parts per million to 380 parts per million since pre-industrial time (Stern 2006, Uprety, Reddy et al. 2019). A major economic activity that is reliant on weather conditions is agriculture. The agricultural industry is now more susceptible to the economic and physical effects of climate change due to the danger posed by changing climatic conditions on its production (Carleton and Hsiang 2016).

Numerous elements related to climate change are affecting productivity, such as variations in rainfall patterns, rising temperatures, altered planting and harvesting dates, accessibility to water, and appropriateness of the terrain. While the overall consequences of change in climate might not be very great, the regional effects are more widespread. While some areas will gain from climate change, others will be negatively impacted. The production of agricultural commodities will be impacted by climate change, which will also disrupt economic stability and have an impact on the supply plus on-demand balance, profitability, trade, and pricing of these commodities (Kaiser and Drennen 1993). Compared to rich countries, agriculture farms in low-developing nations would be impacted by rising greenhouse gas emissions (Kurukulasuriya, Mendelsohn et al. 2006, Seo, Mendelsohn et al. 2009). Because they depend more on labor-intensive technologies, developing economies are more susceptible to climate change than developed ones, which can adapt to it better due to the availability of technology and higher adoptions (Omerkhil, Kumar et al. 2020). From an Asian perspective, there has been a steady rise in regional warming. Climate models predicted a rise in tem premature in this region of the planet. The colder areas are warming up. Asia is becoming wetter due to fewer predictable changes in precipitation. While the likelihood of flooding increases during wet seasons due to heavy rainfall, the dry season is becoming drier. The agricultural production is now threatened by these climatic changes, which will lower agricultural output and slow down the increase of revenue (Arora 2019). Farmers in Asia who reside in remote, marginal regions with few natural resources, such as mountains, arid plains, and deserts, face grave risks from climate change. In the dry regions of western China, northern Pakistan, and India, higher temperatures are predicted. The bulk of Asia's 500 million rural impoverished are farmers who make a living by cultivating rain-fed land (Srinivasa Rao, Gopinath et al. 2016). The last several decades have seen a decline in rice, maize, and wheat production as a result of increased water stress, mostly brought on by rising temperatures (Srivastav, Dhyani et al. 2021). South Asia is more severely affected by the effects of climate change, which might lead to a 50% decrease in wheat output by 2050 (Habib-ur-Rahman, Ahmad et al. 2022). Climate Change's capricious nature poses a threat to Pakistan's agricultural sector. Pakistan is an agrarian nation, with 47% of the population dependent on it for their livelihood. The GDP is contributed by this industry by 21%. Rainfall is decreasing and temperatures are rising as a result of climate change (Asif 2020). Temperature increases are predicted to be 3^{o}C by 2040 and up to 5–6 ^{o}C by the end of the century. The agriculture industry is now economically fragile as a result of these climatic changes. Pakistan is ranked 28th out of the nations that would be severely impacted by climate change given that 22 of the 28 nations are in Africa. Among the top 10 non-African countries is Pakistan (Malik, Ahmed et al. 2023). World Bank has identified 12 nations that are most vulnerable to climate change, including Pakistan. Pakistan can anticipate increased heat, heavy rainfall, droughts, and decreased agricultural productivity as a result of climate change. Without realizing it, Pakistan has been experiencing the effects of climate change. The IPCC Fourth Assessment Report (2007) predicted that Pakistan's northern areas would see more intense precipitation (Munir and Munir 2023).

Pakistan is now experiencing floods as a result of severe, erratic precipitation. According to earlier research, arid regions are significantly impacted by climate change (Hussain, Butt et al. 2020). Crop yields are showing significant losses, which lowers the income of the dry land farmers. Due to their heavy reliance on the natural climate, Pakistan's dry regions are similarly impacted by climate change (Fahad and Wang 2020). The earnings and production of agriculture have been disrupted by climate change. Arid regions are now more susceptible to climate change due to increased warmth and less rainfall. The topic of how local farmers in dry areas will be affected by rising temperatures emerges. Given how catastrophic global warming is, what financial losses might be expected, and what changes can be implemented to help their farms' bottom lines? Farmers in dry regions are now more vulnerable to climate change as a result of the warming, which has led to notable variations in predicted yields (Deryng, Conway et al. 2014). From this angle, the study's goal is to discuss how climate change is affecting desert region agriculture. The project will examine how climate change is affecting these regions economically. The study fills in knowledge gaps about how various climatic factors have impacted agricultural productivity and profitability. It also discusses the adaptive strategies that farmers in dry regions will employ to mitigate the peculiar effects of climate change.

It also discusses the adaptive strategies that farmers in dry regions will employ to mitigate the peculiar effects of climate change.

3. Impact of Climate Change on Livestock

Global warming in particular is changing the environment and may have a significant impact on farm animal productivity worldwide (Rojas-Downing, Nejadhashemi et al. 2017). Heat stress seems to be one of the interesting environmental variables that affect animals and make animal production difficult in various parts of the world. Livestock yields were directly impacted by changes in climatic variables such as temperature, precipitation, and the frequency and intensity of severe occurrences like droughts. Every animal has a range of ambient temperatures that is referred to as its "thermo-neutral zone" (Biswal, Vijayalakshmy et al. 2020). Temperatures that fall or rise above this range put animals under stress. A dairy cow's ability to produce milk is significantly influenced by its temperature environment, particularly in animals with exceptional genetic quality (Sesay 2023).

The thermal humidity index (THI) increases by 0.2 kg per unit increase in milk production when the index rises above 72. A rise in milk output causes animals to become more susceptible to heat stress and lowers the temperature at which milk loss occurs(Bouraoui, Lahmar et al. 2002). When it came to heat sensitivity, mid-lactating dairy cows were more sensitive than their early- and late-lactating counterparts. Furthermore, when exposed to heat, mid-lactating dairy cows had a greater decrease in milk output (-38%). Although animals may adapt to the hot climate, their reaction mechanisms are damaging to their ability to reproduce and be productive in the long run(Kaufman 2019).

When an animal is in proper equilibrium, reproduction is often a sumptuous process. Most farm animals become infertile owing to heat stress brought on by high ambient temperatures and excessive humidity, which also negatively impacts the reproductive health of farm animals. Climate change directly affects the growth of palatable grass species, and because of decreased rainfall, the regeneration of fodder species in grassland and forests is declining, resulting in a scarcity of high-quality, diverse cattle fodder. The number of cattle has decreased as a result, which has further impacted the production of meat, milk products, and dairy goods.

By drying out wetlands, grazing areas, water supplies, and streams, and reducing the amount of drinking water available to cattle, the drought also had an impact on them (Barkema, von Keyserlingk et al. 2015). An increase in temperature caused the emergence of new illnesses, and a shortage of feed caused the patterns of animals to shift. Variations in the frequency of severe events, together with variations in rainfall and temperature regimes, can impact the distribution and quantity of disease-causing vectors. Climate change-related higher temperatures may hasten the development of some pathogens and parasites that go through one or more life cycle stages without an animal host. This might result in shorter generation durations and possibly more generations annually, which would increase the size of the disease or parasite population (Yadav and Upadhyay 2023).

Consequently, to adapt to climate change Different adaptation tactics are used by farmers in developing nations, include breeding livestock species that are suited to the local environment, diversifying livestock breeds, using appropriate resource management techniques, and using alternative feed production technology. The population of the world is predicted to increase from 5.5 billion in the present to around 8 billion in 2020. Consequently, it is reasonable to anticipate that the significance of cattle production will rise during the ensuing decades (Herrero, Grace et al. 2013). Around the world, large-scale livestock production is carried out in dry and semi-arid regions (McCarthy, Kamara et al. 2001). For at least 20 million pastoral households and at least 200 million stalk-holding farmer families in Asia, Africa, and Latin America, livestock is their only source of income (Devendra, Morton et al. 2005). Many people in marginal regions of sub-Saharan Africa still depend on extensive livestock raising for their livelihood. However, during the past three decades, very little progress has been made, and these regions continue to be marked by poor production and great climate vulnerability (McCarthy, Kamara et al. 2001). Even while the connection between the livestock industry and climate change is far more nuanced and rarely discussed, animals play a significant role in reducing poverty and promoting rural development in Africa (Herrero, Wirsenius et al. 2015). In rural African communities, pasture and water are the two main natural resources that are used for livestock production (Bekele 2017). For this reason, climate change will have an influence on livestock output in two ways: directly via effects on livestock performance and indirectly through effects on the ecosystem (Cheng, McCarl et al. 2022).

4. Impact of Climate Change on Humans

Variations in temperature, precipitation, wind, and sunshine can have an impact on the environment in which disease pathogens and hosts survive, reproduce, and spread, as well as the conditions in which they spread. These health impacts show themselves as variations in the incidence and severity of infectious illnesses, as well as changes in their seasonal and regional patterns. Many studies have examined the current and potential impacts of climate change on many forms of infectious diseases, such as water-borne, air-borne, vector-borne, and food-borne illnesses (Paz, Linares et al. 2020). Human health may be impacted by climate change, particularly in the case of infectious illnesses (B. Yeh, M. Fair et al. 2020). For the majority of infectious illnesses, three elements are necessary: a host (or vector), a pathogen (or agent), and a transmission environment. Certain diseases need intermediary hosts to finish their life cycle or are transmitted by vectors

(Engering, Hogerwerf et al. 2013). Without a suitable habitat and weather, disease germs, vectors, and hosts cannot live, reproduce, spread, or transmit. Therefore, variations in climate or weather may impact infectious disorders by modifying pathogens, vectors, hosts, and their living habitats (Sarwar 2015).

Studies have shown that long-term climate change causes many infectious diseases to spread regionally (Liang and Gong 2017). Temperature, precipitation, wind, sunlight, and host and pathogen conditions are all impacted by climate change, as is the environment in which diseases are transmitted. Changes in illness patterns, frequency, and severity are among these health impacts (Yadav and Upadhyay 2023). This study examines how host, pathogen, and transmission components of infectious illnesses are impacted by climatic factors.

Extreme weather events and weather changes brought on by climate change have a major negative impact on human health by spreading infectious illnesses. Climate factors limit the spread of these illnesses and have an impact on the growth, survival, reproduction, and quality of life of hosts and pathogens as well as their interactions with people. Although many infectious illnesses are significantly impacted by extreme weather events and meteorological risks, it is still difficult to forecast these events' patterns and health implications because of our limited understanding of them (Ebi, Vanos et al. 2021). Forecasting the effects of large-scale extreme weather events on disease pathogens, hosts, and transmission is more difficult since these events frequently entail coupled alterations in many climatic factors.

Humans are not passive recipients of climate change-induced health effects, but can actively contribute to their control and alleviation (Karimi, Mohajerani et al. 2023). Climate change changes vary globally, making it necessary to project health implications on infectious diseases regionally. Some populations are more vulnerable to these risks due to their lack of resources. Developed countries and less capable societies should collaborate to reduce their vulnerability to climate change-induced health risks (Anukwonke, Tambe et al. 2022). To alter human vulnerability to changing infectious disease risks, proper adaptation measures can be implemented. This includes continuously improving public health programs and reallocating resources based on spatial-temporal changes in health risk. Early warning systems based on these projections have proven effective in helping societies take proactive measures to prevent or alleviate health impacts. By adopting proactive adaptation measures, we can work together to mitigate the negative health impacts of climate change.

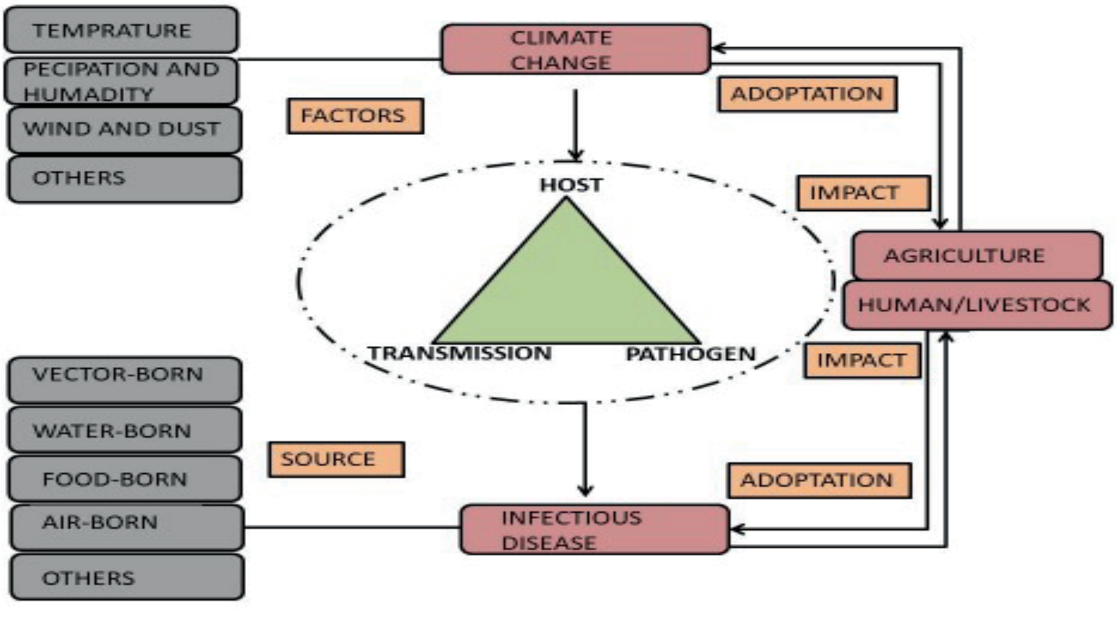

Figure 1. Impact of Climate Change on Human Infectious Diseases

Two scientific studies on the effects of climate change on human infectious illnesses and health are revealed by this review of the literature. While the other focuses on identifying favorable climatic conditions for disease pathogens, hosts, or transmission, the former focuses on forecasting climate factors that may result in heightened health risks. Nevertheless, there is a lack of cooperation between these two groups, which makes it difficult to foresee how the landscape of health hazards for infectious illnesses will evolve and comprehend patterns of climate change.

Meanwhile, as discussed previously in this article and pointed out by (Page and Howard 2010) Accurate predictions of spatial-temporal shifts and climate variables' magnitude can be linked to understanding how these changes may impact infectious disease risks. This combination can lead to effective proactive adaptation measures to prevent and minimize the negative health effects of climate change.

According to the literature, the majority of research examines how climate change affects health risks and finds an empirical correlation between changes in infectious disease morbidity or mortality and weather. There are differences in how climate change affects health, though, as several research studies are unable to demonstrate a cause-and-effect link. It is common for various research to link comparable weather circumstances to varying health risks. This might be because of limits in scientific understanding or scientific ambiguity about the overall impact of climate change on health. This is due to the possibility of distinct influences on the three components of infectious diseases: pathogen, host, as well as transmission.

5. Reasons of Global Climate Change

These days, world climate change is a significant issue. It causes the globe's overall yearly temperature to gradually rise, a trend that started at the start of the Industrialization process which occurred at the turn of the millennium. The current spate of severe weather has intensified discussions on the globe's temperature rise. Significant amounts of production along with economic activity, that involve the release of the principal warming gases (methane, carbon dioxide, etc.), account for the planet's temperature shift (Albergel et al., 2010).

The freezing environment (chilled water plus snow), the biological world, the ground, the sea, as well as the surrounding environment, are all included in the climate system of the globe. Numerous factors, including weather, rainfall, dry land or wind moisture, icy along snowy conditions, as well as several more, define the environment. Numerous diverse natural phenomena cause the weather to fluctuate frequently. The activities of humans have emerged to be a major fresh component that has been affecting the planet's climate in increasing amounts during the past two centuries. The "greenhouse effect" describes its effects (Alirezaei et al.,2017; Bayer, 2015; Moumen et al., 2019; Chehabeddine, Tvaronavičienė, 2020).

The impact of activities that are natural is to blame for changes in the atmosphere. But in terms of global warming, human-related issues are starting to matter. The two main causes of changes in the atmosphere worldwide include follows: Variations in the planet's magnetic field as well as the release of greenhouse gases in the planet's lower atmosphere (Chen and Chen, 2016).

The greatest global issue of the last 10 years has been the challenge of climate change brought on by anthropogenic activity. Additionally, manufacturing along with the usage of manufacturing products, globalization, destruction of forests, increasing numbers of people, as well as expansion of the economy are all related to this issue (Chen et al., 2015; Cloy, 2018).

The surface temperature of the globe rises as a result of greenhouse gas collection warming the inner atmosphere's regions. This phenomenon is known as the phenomenon of the greenhouse effect. Because of this, the air temperature is higher than it is supposed to be, which has permanent effects like global warming along with changes in the environment (Huanget al., 2016).

Each notable variation in environmental measures (such as moisture, temperature, and air) that lasts for an extended duration (years even more) is referred to as environmental change (Nda et al., 2018). The atmosphere has been a major factor affecting the existence of evolution, modifications, or variety among creatures from the first environment's existence to the current (Wisz et al., 2013). Changes in the environment lead to changes in both land and marine habitat, which in turn affect the ecological equilibrium of these habitats.

Since agriculture is eventually responsible for 20% release of greenhouse gases, it is both a major contributor as well as a victim of environmental change. A number of instances of extreme rain events are having a significant impact on agricultural business productivity in addition to agro-environmental along with climate-related variables including drought, floods, & blazes in forests (Chivangulula et al., 2023). Furthermore, the flames are fed by an excessive dependence on limited assets, rendering agriculture globally susceptible to devastation. Since the availability of food and water is being negatively impacted by changes in the climate (Zhang et al., 2023), Reduced agricultural output challenges landowners' standard of living which is a major contributor to impoverishment (Li, 2023). Agriculture platforms, particularly in developing countries, are essential to national economies including the financial stability of people's communities (Chikafa et al., 2023).

Since climate change is one of the main factors contributing to the loss of creatures, it has a catastrophic impact on species worldwide. World organism changes have been demonstrated to have a high correlation with a variety of weather events (Manes et al., 2021). The speed as well as intensity of changes in the climate are causing a modification in the ranges of aquatic clean water, or land creatures that may thrive in their respective settings. A variety of factors, including the number of species dispersion, movement patterns, timing of activities, along the use of tiny ecosystems, are all impacted by shifts in typical environmental conditions (Allan et al.,2021). All the factors contributing to the decline of biodiversity are interconnected with changes in the climate.

It is often known that changing the climate has an immediate influence on the well-being of people (Sasai et al.,2023). According to estimations from the World Health Organization, changes in the climate could result in an additional 250 thousand fatalities yearly between 2030 and 2050 as well (Watts et al., 2015). Okoro et al. (2023), indicated that a primary reason for such fatalities was the worldwide transmission of illnesses carried by vectors. Concern, anxiety, or psychological disorders are on the rise among individuals due to warming temperatures. Repeated exposure to

significant climate crises, such as natural crises, can potentially result in traumatic illness.

According to Barati et al. (2023), the regional as well as worldwide climates are impacted by modifications to the environment in forestry. The growth and production of overseas forests are significantly impacted by worldwide warming because of the altered patterns of rain or temperature, among other factors. The changing climate has a detrimental influence on the state of the forest. It additionally results in various terrible repercussions, such as insect epidemics, shortages, and fires in trees, which endangers the lives of societies that depend on trees for life. Dry conditions are just one of the many repercussions of the changing climate that are beginning to jeopardize the future well-being of forests across the globe. The world's woods are under more pressure to survive due to increased storm intensity carried by changes in the climate.

Reducing impoverishment is seriously threatened by climate change, which has the potential to destroy years of developmental work. Although the effects of climate change are being felt globally, they are more acutely by the impoverished as well as in developing nations. Due to their heavy reliance on resources from nature along with their poor ability to adapt to fluctuations in the environment, they become more susceptible. Important species should be preserved as well as restored in order to promote lifestyles that rely on the environment's resources in addition to aiding societies in their attempts to evolve. Reducing greenhouse gas emissions, enhancing the quality of life for people, plus generating environmentally friendly employment are all possible with the shift to a carbon-free society.

Variability in ocean circulation, that may alter how warmth or rainfall are distributed, so massive eruptions of volcanic material, that can occasionally raise the amount of air molecules and hence filter a greater amount of direct sunlight, are two examples of the naturally occurring causes of worldwide warming. Nevertheless, the planet's environment hasn't altered much over billions of ages. For the survival of all living things, the temperature as well as the equilibrium number of heat-trapping emissions of greenhouse gases have stayed precisely perfect. However, maintaining this equilibrium is becoming more and more difficult. We are increasing the number of atmospheric pollutants in the environment by burning fossil fuels to warm our houses, power vehicles, and make a wide range of other things. We have increased the naturally occurring greenhouse effect's capacity for heating by producing more of those gases (Adedeji, 2014).

6. Technological Advancements in GHG Emissions

A healthy society is established by environmental stability. It reflects on the activities that do not disturb the integrity and stability of nature (Ainou et al., 2022; van der Aalst et al., 2023). The global world is facing several kinds of challenges like poverty, injustice, climate change, and inequality (Bai et al., 2022). A big challenge is the emission of greenhouse gases (GHG) that degrade the environment, destroy welfare, and create economic issues (Leal Filho et al., 2020; Hassan et al., 2024). There is rapid growth of population in every country, that's leads to excessive amounts of GHG emissions, and waste generated by household combustion will increase by about 10-16% yearly (Lin et al., 2022). Impacts of the population growth through the increased use of green growth and sustainable development are investigated (Abid et al., 2022). Zero emissions of GHG are needed to reduce the global temperature and avoid the worst climate changes (UNFCC, 2015). Reducing the anthropogenic emission of GHG and introducing of advance technologies are necessary for a safe environment (Williamson, 2016; Goglio et al., 2020). With energy technology innovations reduction of greenhouse gas emissions is possible (Jordaanet al., 2017; Haseeb et al., 2024).

The country is moving towards sustainable development through technological advancements and saving from GHG emissions (Sadiq et al., 2023a). Impacts of the technological advancements on the environmental condition have been examined. However, the innovative technologies with the use of recycling energy let to perform business processes without GHG emissions (Suki et al., 2022). High technological advancements in a country's economic entities implement eco-efficiency and GHG reductions is positively connected with sustainable development (Zhang et al., 2023).

The GHG emissions can be reduced without affecting human activities by the eco-friendly projects (green financing) (Fonseca et al., 2020). For the social and economic betterment, technological advancements in GHG emission have been introduce. GHG emissions can be decreased by the use of ecologically friendly technology and the environment can be protected (Chien et al., 2022c; Shulla et al., 2021). The major components of energy efficiency are renewable energy output and energy consumption. It helps to overcome energy use and lessen the harmful effects by energy usage. It can lessen the GHG emissions (Chien et al., 2022b). Decreasing the fossil fuel share in the energy and replacement by green initiatives helps to decrease GHG emissions (Dinh et al., 2022). There is a great contribution of green finance to sustainable development by reducing GHG emissions (Sadiq et al., 2022b).

The recent advanced technologies like smart agriculture farming. This technology increases the crop yield and reduces the environmental GHG emission (Islam et al., 2020). In livestock farming, smart and advanced technologies help to monitor the animals, detect air quality, and ventilation in farms, and lessen the GHG emission (Saravanan, 2018; Qi et al., 2023). Effective utilization of smart farming in the livestock sector has proven to reduce GHG emissions. Controlling multiple parameters on the livestock farms influences the GHG emission. Best management practice on farms reduces the CH4 emission on farms (Bell et al., 2014; Eckard, 2014: Panchasara et al., 2021).

Land use and its management have a great impact on the soil condition and it has an indirect impact on climate change. Climatic conditions can be changed by the changing of human activities (S. Vijaya., 2012). Recent advanced techniques can reduce CO2 emissions and could lead to a clean environment (Yoro, 2020).

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About The Authors

Prof. Dr. Muhammad Mazhar Ayaz is a distinguished academic and administrator currently serving as the Vice Chancellor of the Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. He has made significant contributions to veterinary education, research, and the development of the livestock sector in Pakistan. Under his leadership, CUVAS has advanced in areas such as research innovation, industry-academia linkages, and community outreach. Dr. Muhammad Mazhar Ayaz has a strong academic background, holding a PhD in Veterinary Science with a specialization in Parasitology. He has published numerous research articles and has been a key figure in promoting sustainable livestock practices and the latest trends in veterinary sciences. His work emphasizes the importance of livestock in the economic sustainability of small farmers and has been instrumental in fostering collaboration between academic institutions and the livestock industry

E-mail: mmazharayaz@cuvas.edu.pk ORCID: 0000-0002-7301-7386

Arooj FATIMA earned Bachelor in microbiology from Cholistan University of Veterinary and Animal Sciences (CUVAS) Bahawalpur Pakistan. Currently she is doing M.phil in Microbiology from her parent institute (CUVAS) Bahawalpur Pakistan. Her research interest in Microbial genetics and food quality and its application. She has published more than 3 articles in national and international journals.

E-mail: aroojfatima31202@gmail.com ORCID:0000-0002-4709-4177

Zarva AHSAN earned Doctor of Veterinary Medicine (DVM) from Riphah College of Veterinary Sciences Lahore Pakistan. She is doing M.phil in livestock management from Cholistan University Of Veterinary and Animal Sciences (CUVAS) Bahawalpur, Pakistan. Her research interests are managemental practices in livestock farm, milk quality, milk supply chain and heat stress.

E-mail: dr.zarva.ahsan@gmail.com ORCID:0009-0004-3473-7454

Dr. Umair YOUNAS received his DVM and Mphil (Livestock Management) degree from the University of Veterinary and Animal Sciences, Lahore. During M.Phil, Dr. Umair got training from PTC+ institute (Netherlands) on dairy farm practices and milk processing. After completing his M.Phil., Dr. Umair secured his Ph.D (Livestock Management) degree from the same university along with research work from the University of Florida as Sabbatical. Dr. Umair younas has vast experience in academics and since 2008 he has been working on various academic posts. Dr. Umair has more than 35 publications and Currently, he is working as Head of the Department (Livestock Management) in CUVAS as well as ORIC member and Deputy director QEC (Quality Enhancement Cell).

Email: umairyounas@cuvas.edu.pk ORCID: 0000-0002-5107-9391

Dr. Farooq Muhammad ZAHID; In 2009, he was introduced to the Faculty of Animal Production and Technology University of Veterinary and Animal Sciences Lahore Pakistan as a full-time teacher, his research direction is Molecular Nutrition, Poultry Intestinal health utilization of beneficial microbial resources and mechanism of interaction in prebiotics, probiotics and gut microbiome. More than 20 research papers have been published in authoritative journals such as Autophagy, Journal of Animal Science and Biotechnology, International Journal of Food Science & Technology, Journal of Zhejiang University-SCIENCE B (Biomedicine & Biotechnology), Mediators of Inflammation. He published two book chapters under exclusive license to Springer Nature Switzerland AG 2023 , Climate Changes Mitigation and Sustainable Bioenergy and on nutrient sensing. He is also working as Associate Editor for the Journal of Ethology & Animal Science (JEASc). He presented his papers in China, Sri Lanka and Malaysia.

Email: zahid.farooq@uvas.edu.pk ORCID: 0000-7309-9553

Ghulam JELANI earned Bachelor in Livestock Management from Cholistan University of Veterinary and Animal Sciences (CUVAS) Bahawalpur Pakistan. Currently, he is doing M.phil in Livestock Management from her parent institute (CUVAS) Bahawalpur Pakistan. His research interest in production of livestock. He has published more than 7 articles in national and international journals.

E-mail: gjelani3035@gmail.com ORCID: 0000-0001-7771-4763

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ENVIRONMENTAL IMPACTS ON ANIMAL HUSBANDRY

Saba SABA

Furqan ALI

Muqadas KANWAL

Kainat WAHEED

Abid HUSSAIN

Animal husbandry, a cornerstone of agriculture, involves managing domestic animals for products like meat, milk, eggs, wool, and work services. Originating around 11,000-15,000 years ago with dog domestication, this practice has expanded to include livestock such as sheep, goats, cattle, and poultry. These animals play a crucial role in human nutrition, the economy, and environmental management. However, modern animal husbandry faces significant challenges, particularly due to climate change. Rising temperatures and altered precipitation patterns are affecting feed availability, productivity, and animal health. Changes in climate impact the growth and quality of feed crops, leading to reduced feed availability and increased competition for resources. Water scarcity, elevated feed costs, and more frequent extreme weather events further stress livestock systems. Heat stress impairs animal health by reducing feed intake, growth, and reproductive efficiency, while increasing susceptibility to diseases. Additionally, climate change influences the distribution and prevalence of vector-borne diseases, potentially expanding the range of pathogens affecting livestock health and productivity. The industry's expansion, particularly post-World Wars, has intensified environmental issues such as greenhouse gas emissions, habitat loss, and biodiversity decline. With the global population expected to reach 10.4 billion by 2067, adopting sustainable practices is crucial. Innovations in feed alternatives, such as insects and microalgae, along with advancements in genetics, nutrition, and feed efficiency, are essential for improving livestock resilience and reducing environmental impacts. Future strategies must focus on enhancing production efficiency, managing climate risks, and integrating innovative feed solutions to ensure the sustainability of livestock systems amidst ongoing climate challenges. This chapter highlights the intricate relationship between animal husbandry and environmental sustainability, emphasizing the need for balanced, innovative solutions to address the industry's future.

Introduction

Animal husbandry is a branch of agriculture which is basically associated with provision of the necessary life supplies to the animals and domesticates them. The word domestic is actually originated from a Latin word “domesticus” which means “belong to home” and husbandry means “to care for” or “to manage carefully” so when collectively combine these terms with animals, it lead to care for the animals to belong it to home. Animal husbandry relates to the provision of food, shelter, healthy practices, animal management and breeding of all the household animals e.g., horse, dog, cat, especially livestock, such as sheep, goat, cow, chicken, duck etc. (Briganti & Mezei, 2012; Copeland et al., 2018).

Although the word husbandry was introduced in English language much later but roots of livestock management in domestic settings lies in history approximately 11,000-15000 years back, when humans started to keep dogs in houses as commensals for security and for helping the humans to hunt down the wild animals. Sheep are considered the first livestock to be domesticated followed by goat, cattle, cat, pig, horse and poultry. This concept of domestication set the foundation for evolution of human being from hunters who hunt the animals to gather resources to a friendlier lifestyle which led to the develop complex societies (Frantz, Bradley, Larson, & Orlando, 2020; Vigne, 2011). Livestock is not only raised for animal welfare but also to accomplish the human nutritional, financial and environmental requirements. Animal husbandries provide care and manage the domestic animals and in return obtain various products from these animals such as eggs, meat, milk, cheese, other dairy products, wool, and not only this but they also use them for work, to carry heavy stuff and for transportation purposes sometimes, particularly in rural areas. They participate in the human welfare and livelihood of lots of people in many ways (Frantz et al., 2020; Vigne, 2011).

Livestock Farming

Livestock farming or raising various animals such as buffalo, cattle, sheep, goats, camels and pigs for their products is a common practice of livelihood around the agricultural world. In response to the food shortage after the World Wars, the livestock industry grew larger and more intense to produce enough affordable food and income. About 29 percent land surface of the world is used for livestock production in the form of pastures for grazing or croplands to feed the animals and make money from animals sourced food (meat, milk, fats, cheese, yogurt, cream) and non-food products (hides, wool, clothes, leather) and organic fertilizer (livestock manure) at small scale personal farming level and at large scale industrial level (Eijrond, Claassen, Van Der Giessen, & Timmermans, 2019).

Poultry Farming

Raising live animals like chickens, ducks and pigs is the main concern of this type of agriculture farming industry. In the last few decades, the performance of pig and poultry production system has achieved very high levels. These systems collectively deliver a huge amount of inexpensive and nutritious food, especially high-grade protein in the form of eggs and meat that contribute to the security of food globally. It requires great amount of feed resources to feed pigs and poultry, additionally, poultry animals excrete hefty amounts of nitrogen and phosphorus in the environment, these circumstances put the sustainability of these sectors at risk (Andretta et al., 2021).

Fish Farming

In this farming approach, fish are raised using waste products from cattle without need for extra nutrients. Products of fishery and aquaculture include all parts of fish either farmed or captured (meat, head, fins, scales, skin, bones, and viscera) and also crustaceans removed from shellfish during processing (filleting, canning and packaging) and used as an alternate source of protein (Yu et al., 2019). These by-products of fish are rich in nutrients, and they can also be used to extract fish oil and use for animal nutrition. However, usage of these products is still inadequate resulting in economic and environmental problems (Gasco et al., 2020). Aquaculture is very precious and essential for the welfare and the economic sustainability of the world. The rapid increase in global demand intensive aquaculture production builds situations in which farmed fish are prone to pathogens exposure so frequent use of antibiotics is required to deal the condition (Mavraganis, Constantina, Kolygas, Vidalis, & Nathanailides, 2020).

Dairy Farming

This kind of farming produces milk for human use over an extended period. In 2018, there were more than 290 million dairy cows worldwide, producing about 700 million tons of milk (Alvåsen, Dohoo, Roth, & Emanuelson, 2018). Cow's milk is a valued source of multiple micro and macro nutrients which provide proteins, essential minerals, vitamins and energy to the consumers. Furthermore, dairy farming is the main source of income for a lot of farmers worldwide by milk and milk products i.e., yogurt, cheese, cream, fat, butter etc. Modern day dairy farming is facing major sustainability challenge, most persistent being emission of greenhouse gases (GHGs) to the atmosphere. Dairy farming is a threat to water channels due to emissions of nitrogen and phosphorus from manure spreading and over-grazed fields. Production of feed involves environmental impact and resource use, with the severity depending on the crop production system and local conditions (Arvidsson Segerkvist, Hansson, Sonesson, & Gunnarsson, 2020).

Honeybee Farming

The honeybee is a very valuable insect because it produces honey. Other than that, honeybee farming is also important for securing food, providing job opportunities to get income, helps in plant pollination, environmental protection and actively participate in human welfare. Recently these actions are affected by various living and non-living factors, in combination or alone (Wakgari & Yigezu, 2021). The climate changes like temperature variations, water scarcity, rise in humidity, cutting of plants, lack of pollination of flowering plants, poor agricultural practices, use of pesticides and antibiotic resistance led to the reduction in honeybee colonies and their products. The global demand for honey & other by products (wax, pollen, royal jelly, propolis and venom) has increased massively in recent years due to numerous uses and applications (AU-IBAR (Africa Union Inter African Bureau for Animal Resources, 2019).

Livestock roam freely in pastures and feeding places in intensive livestock farming and it is considered one of basic reasons for loss of biodiversity. The exposure of intensive livestock to the residential areas in vicinity could be a complex issue characterized by inadequate understanding and unpredictability of the possible effects on health of residential community, along with value driven concerns unsustainable and inappropriate management of livestock has added to environmental degradation, loss of biodiversity, evolving infections and disease, and more emission of gases from (Van Zanten, Van Ittersum, & De Boer, 2019). The severity of these impacts has increased parallel to the increase in human population, purchasing power, and urbanization since the mid-20th century (Philip K Thornton, 2010).

A huge portion of world’s population reside in rural areas, it is estimated that by 2050, more than 50% of the population will still be living in the rural areas and almost 75% of them will be dependent on agricultural, farming and other rural activities to earn livelihood (Guresci, 2022). Livestock constitutes around 40% of the agricultural gross domestic product (GDP) worldwide and adds roughly 30% of the agricultural GDP in developing countries round the globe. Despite that, livestock production and supplying in industrialized countries contributes for 53% of agricultural GDP globally (Yitbarek et al., 2019).

Food security is defined as an adequate amount of quality food to be available through domestic products or import from outer sources to reach a level of nutritional welfare where the physiologic requirements are fulfilled all the time. Food security requires a stable availability, access consumption, and sustainability of food and its sources. In the last 50 years, the trend of food source has shifted globally from grains to animal proteins, which has significantly amplified the production of livestock to meet demand. With global populations rising rapidly, global agriculture faces the challenge of producing enough food to meet increasing demand in conditions of changing climate and natural resources depletion (Descheemaeker et al., 2016). Exploitation of natural resources (destructive & unnecessary usage) ends up in greater depletion of natural resources and pollutes our environment, which threatens the food security well-being for all the consumers worldwide, in long run (Sekaran, Lai, Ussiri, Kumar, & Clay, 2021).

Small- and large-scale livestock farms, poultry and pig farms, honeybee farms, fisheries, forest-dependent populations are most affected communities hit by environmental changings and weather-related disasters, which are increasing in number and getting intense over the time with environmental change. It can volatility increase poverty and hunger, as livestock food security is compromised and there will be a need to find other feasible options or practices to reduce the risk posed on livestock welfare and ultimately human welfare (Rahman, Alam, Islam, Bhuiyan, & Rahman, 2016).

Environmental Issues

The environment on the land of the earth is responsible for the existence of living organisms which are suited to it. After a living being comes into existence, it struggles to be capable of living in congruence with its immediate environment to thrive. This environment is responsible for harmony, wellbeing and the existence of every living organism. If there is a change in environmental conditions, it will affect the wellbeing of living organisms including livestock especially who cannot cop up with the changings and might lead to affect the very existence of them. There are many factors which can affect the livestock industry for example resources availability and disease prevalence (Adopted, 2014; Escarcha, Lassa, & Zander, 2018; Rojas-Downing, Nejadhashemi, Harrigan, & Woznicki, 2017).

Resources Availability

The world population is expected to reach around 10.4 billion in 2067, and approximately 81% of the total population will belong to Africa or Asia. This enormous increase in population will lead to affect the dynamics of demand and supply and cause a reduction in the amount of arable land per capita for food and feed to 0.15 ha per person. Countries which have fewer arable lands per capita will certainly use the available arable land to grow food for humans rather than producing feed for livestock. Also, the pastures and grasslands would be converted to arable land to meet the requirements of growing populations which will further limit the land for grazing by dairy cattle. At this rate not even half of the population in developing countries would access the livestock or its products (Herrero et al., 2015). Fresh water is a necessity for existence of humans and livestock. It is used to fulfil the drinking, cooling, cleaning requirements of livestock as well as for crop cultivation to produce feed and for processing of livestock products. Scarcity of resources and environmental degradation as growing challenges, pose a serious risk for the sustainability of livestock sector globally. Water stress caused by depletion of fresh water resources and droughts has been very common, and it directly affects the food production areas related to animal husbandry, and result in huge agricultural damages, severe economic loses and social impacts (Getirana, Libonati, & Cataldi, 2021).

Disease Prevalence

Livestock products constitute about half of world's agricultural production value which includes meat, eggs, cheese, yogurt and organic fertilizer and other items such as hides, clothes, leather etc. which are source of income from low economic status individuals to many big companies which generate huge revenue from it. Livestock disease has strong effect on economy, animal welfare, environment and the public health. Animals are prone to multiple diseases and health conditions that could affect their welfare e.g., foot-and-mouth disease, bluetongue, brucellosis in bovine, porcine, sheep and goat, bird flu, swine fever theileriosis, porcine reproductive and respiratory syndrome (PRRS) etc. (Barman et al., 2020). Health and sustainability of livestock and its products' commercial markets, smallholder farming systems, as well as the growth to support demand are all vulnerable to a disease outbreak in livestock. Different practices to manage livestock diseases can induce unsustainable and harmful outcomes i.e., antibiotic resistance which might be given to animals to promote growth or management of some persistent infection. Likewise episodic or unpredictable disease outbreaks decrease animal production and can impose inadvertent consequences on demand and supply dynamics of various products (Kappes et al., 2023).

Climate Change

The US National Climate Assessment in 2018, concluded that the "earth's climate is now changing faster than at any point in the history of modern civilization, primarily as a result of human activities" (Dietz, Shwom, & Whitley, 2020). Throughout the world global warming has a profound impact on animal husbandry and livestock production ability via physiological changes in animals and their habitations. In some areas of the tropical regions, due to high temperatures and relative humidity, the environmental conditions are not feasible for agriculture and animal production which affects the competitiveness of economic activities. Based on intensity and time period these environments have declined livestock production, by affecting reproduction, causing weight gain, and reducing meat and milk production (Naranjo-Gómez et al., 2021).

Climate Change and Animal Production and Reproduction

The animals' body temperature increases in hot environmental conditions, including high humidity, high solar radiation, predominantly when atmospheric temperature (cattle core body temperature 38.0 to 39.3 °C) exceeds the upper critical temperature. Heat stress give rise to problems in animal's body and keep them from executing normal physiological functions as animals couldn't dissipate the heat (Idris, Uddin, Sullivan, McNeill, & Phillips, 2021). Reproduction of livestock is affected by the prevailing climatic conditions during different seasons, especially in summer and rainy seasons. The fertility in animals, both male and female, is affected by climatic heat and precipitation due to weather changes and via food also. Unexpected changes in environment temperature and relative humidity above a certain level fairly reduce the conception rates (Bronson, 2009).

Rise in temperature change heat exchange between environment and animal which reduce the feed intake, growth and leads to decrease in animal production i.e. milk production, egg, wool production. Animals in production are especially susceptible to heat stress and rise in environmental temperature due to climate change add to the problem. Even though the animals, like any other living being, try to adapt to high temperatures, but only at the cost of production efficiency. Heat stress affects the hypothalamic center of appetite negatively and reduces the food intake to get rid of heat stress by reducing the production of heat due to the metabolism. If the biological and behavioral responses are inadequate to cope with heat stress the animal, try to minimize the internal heat load by cutting off the feed intake which reflects in production yield. The impact of resource depletion, animal disease and climate has posed a serious threat on food security, human health and world economy (ÇAM, Habibi, & YILMAZ, 2024).

Extreme Weather Events

Global climate has seen unexpected variations in previous 2 decades that have caused the earth temperature to rise by 1 °C. This phenomenon has caused severe irregularities in weather which gave birth to extreme weather events such as tornados, hurricanes, thunderstorms, blizzards, higher sea level leading to tsunami and floods, wildfires and desertification and increase in CO2 level of atmosphere. The effect of weather variations on animal husbandry is dependent on deviation of weather patterns from normal, duration of exposure to the livestock, frequency and intensity. Animals have innate ability to cope up with the weather and climate changings if it is for shorter period of time, but if the change is persistent or for longer time the result of these drastic changings will cost us the welfare of animal husbandry (Churchill et al., 2022).

Floods, tornados, hurricanes and thunderstorms deprived the soil of all the necessary minerals it requires to grow the crops for human and animal feed. Likewise, deforestation or desertification due to wildfire accidents in forests further narrows the natural available resources for animals and further cause low level of atmospheric O2 and higher level of CO2 which could lead to respiratory issues in humans and cattle. Livestock is at a loss if it must compete with humans for food which consequently endangers the wellbeing of animal husbandry. The climatic threats along with other socioeconomic factors escalations the vulnerability and causes the loss of livelihoods to many people who earn from the animal husbandry industry (Hertel, Baldos, & van der Mensbrugghe, 2016).

Changes in Temperature and Precipitation Patterns

As discussed in the above section the livestock is affected by climatic heat and precipitation directly (weather changes) and indirectly (via feed and fodder). There are multiple changes in the environmental factors like optimum temperature, precipitation, wind speed and solar radiation but, temperature-humidity index (THI) is single factor that define combine effect of temperature and precipitation related to heat stress level (Habeeb, Gad, & Atta, 2018).

Impact on Grazing Lands

As the climate is the main driving force of ecosystem, any change in it would affect the ecosystem positively or negatively. Global warming has changed the temperature, precipitation and rain fall patterns worldwide that affect the soil moisture and nutrients level which is required for proper growth of plants and grass in grasslands which are source of food for cattle (Cansler et al., 2022). As our climate is facing continuous increase in temperature, precipitation and humidity levels it disturbs the moisture, nutrients, carbon storage and microbiota of soil. Microbiota of soil get hyper active by weather changings and decompose organic material of soil at higher rate and leech off the essential nutrients of vegetation growth which leads to desertification of pastures (Y. Zhang et al., 2021). Variations in water cycle by shift in precipitation pattern, due to global climate changes, have been observed in various geographic regions. Grasses cover more of the earth's surface than any other vegetation type and provide food to the cattle. Precipitation is a crucial factor for grassland productivity because grasslands are solely dependent on rainfall and precipitation to fulfill their water requirements. But it can only happen if grazing lands receive ambient water supply for proper growth aeration. If there is more precipitation it will deprive the soil of essential nutrients and it will become barren and productivity of soil will be low, similarly if there are low levels of precipitation there will not be enough water for plants and grass to carry on photosynthesis, which will reduce the grass yield of grassland. If the situation persists a major section of grassland could be lost at the hands of change in precipitation pattern of world (Barnett & Facey, 2016).

Water Availability

Water is a basic life necessity without which life cannot exist as by volume, more than half of the human body is made of water. Water is a mandatory factor in the agricultural industry, for livestock as well as for crops and vegetation. But the availability of fresh water is endangered by global climate change and deforestation which caused a reduction in rainfall in many areas of the world. On estimation 2.50% of all the water present on land is fresh water but about 1.7 % is captured in the form of ice bergs and glaciers, which are not available for regular drinking purpose. Which means only 0.77% of all the water on earth is available in aquifers, soil pores, lakes, swamps, rivers and the atmosphere for drinking, washing, farming, cultivation, industrial and all other purposes (Akinmoladun, Muchenje, Fon, & Mpendulo, 2019).

Availability and sustainability of appropriate good quality water, especially for drinking purpose of all living organisms is a global concern. Water must be supplied to the livestock and crops in adequate amounts, for animals to be healthy and to perform physiological functions, and for crops and vegetation for photosynthesis and their survival. Livestock water requirement vary from animal to animal and breed to breed also with environment temperature and humidity levels, in arid and semiarid regions (Naqvi, Kumar, De, & Sejian, 2015). Constant depletion of natural freshwater reservoirs and rainfall due to climate changes has put the animal husbandry at risk as water deficiency exert harmful effects on livestock welfare directly (insufficient water supply for drinking and other operations i.e. to alleviate heat stress, producing livestock food products, non-food products) and indirectly (inadequate supply for crop cultivation) (El Sabry, Romeih, Stino, Khosht, & Aggrey, 2023).

Greenhouse Gas Emissions and Livestock

The release of various harmful gases in the atmosphere e.g. carbon dioxide, methane, nitrous oxide and ammonia which trap heat in the atmosphere layer and create a greenhouse effect is called greenhouse gas emission (GHG). The gases are released from five main sources such as:

1. Energy sources: combustion of fossils and fuels i.e. coal, petrol, wood etc. to obtain energy

2. Industrial source: fossil fuel burning for energy, and chemical reactions to obtain valuable product e.g. paper industry, metal industry, mining industry
3. Transportation source: emissions from the burning of petrol and diesel from road vehicles, aviation, ships and trains
4. AFOLU source: agriculture, forestry and other land uses
5. Residential and commercial source: release of energy from appliances, electricity, cooking in residential and commercial building (Lamb et al., 2021).

Feedback Loop Between Emissions and Climate Impact

Livestock produces huge amount of greenhouse gases by various physiological process i.e. cattle and ruminant livestock produce methane ($CH4$) and carbon dioxide ($CO2$) from enteric fermentation (anaerobic and aerobic) to decompose manure, nitrous oxide ($N2O$) and nitrogen oxide are released from the use of nitrogen (nitrification and denitrification of feces) containing fertilizer (Eisen & Brown, 2022). Release and accumulation of these gases in the atmosphere are a reason of damaging environment by trapping heat which led to climate fluctuations which in response put livestock at risk by returning the favor in the form of heat stress, droughts, hurricanes, precipitation and rainfall pattern changings, desertification, soil infertility etc. which all are capable of threatening animal husbandry welfare alone or in combination.

Biodiversity and Habitat Changes Affecting Livestock

Bio means “life” and diversity means “variation” which means biodiversity is the network of variety of living organism i.e., animals, plants, fungi and microorganisms on earth that make up the natural world (Medvet, Bartoli, Pigozzi, & Rochelli, 2021). All these living organisms work parallel in the ecosystem in a balanced way to support life on the land. Biodiversity is the base of sustainable development and well-being of all living organisms including humans, because it performs various functions and renders numerous services to the ecosystem (Assessment, 2005). These services range from primary production, nutrient cycling, water & air purification, climate variation and mitigation of greenhouse gas emissions, to plant pollination, food & genetic resource supply and disease control (Mi et al., 2021).

Global biodiversity loss is caused by habitat deterioration and shift in the land use practices (Pereira et al., 2010). Human overpopulation is the key factor of loss of biodiversity, because the increase in human number has led to the unfair sharing of natural available resources with other species and unequal distribution of habitat. People are displacing wild nature so exhaustively that they are causing many species to go extinct and thus degrading our ecosystem (Cafaro, Hansson, & Götmark, 2022). Climate changes, habitat fragmentation and modern infrastructure are also the significant contributing factors (Alkemade et al., 2009). So, considering the services ecosystem provides to animals and other living beings, loss of biodiversity can affect health of livestock drastically in variety of ways.

Reduction in Nutritional Resources

The biodiversity ecosystem has a variety of feeders, fodder and medicinal plants which not only fulfil the nutritional requirements of livestock but also work as veterinary medicine source to cure animal’s ailments. The negative impact on biodiversity will end up to the loss of these natural resources and limiting natural antibiotic remedies causing nutritional deficiencies and higher incidences of livestock infections which will lead to reduced growth and productivity of livestock (Hanazaki et al., 2023; Tilman et al., 2001).

Increased Disease Susceptibility

Loss of biodiversity can fluctuate the host pathogen dynamics because high diversity means more available options for pathogens which reduce the disease burden on any species, also in greater specie variety there exists poor pathogen hosts which dilute the impact of infectious agents and slow down the disease transmission. Biodiversity decline also reduce genetic diversity which makes available livestock's more susceptible to disease as genetic defenses also decrease in such cases which will affect animals health and reduce their productivity (Keesing, Holt, & Ostfeld, 2006; Ostfeld & Keesing, 2012).

Impact on Ecosystem Services

Pollination

The plants which provide feed for the animals depend on various flying insects like bees and butterflies, loss of biodiversity can lead to decline of pollinator species which are inevitable for plats pollination. Low biodiversity weakens ecosystem resilience, spoiling pollination services vital for plants and crops reducing livestock food source (Dicks et al., 2021).

Pest Control

Diverse ecosystem maintains the level of pesticides in balance with pest population to minimize crop damage and maximize yield. Loss of biodiversity put predator species and parasitoids on decline trend as well, leading to increase in pest outbreaks in crops spoiling majority of food source for livestock. The changes in biodiversity have affected the available habitats of beneficial insects further exacerbating pest problems (Letourneau & Davidson, 2022).

Nutrient Cycling

Soil fertility is dependent on nutrients which are provided by various microbes by decomposing the organic matter fertilizers and keeping soil healthy. Decrease in biodiversity has decreased these microbes not only in variety but also in number. The density of population of decomposers is in continuous declining trend so nutrient cycling mechanisms have slowed down as well which deprives soil of essential nutrients and reduced ecosystem productivity. Additionally, the loss of plant diversity affects root structures and organic matter and soil fertility, further impairing nutrient cycling, land productivity and its ability to support livestock (Delgado-Baquerizo et al., 2016).

Breeding Programs

Conservation of wild relatives and diverse breeds is essential for breeding programs intend to improve livestock health and productivity. Biodiversity loss can limit the genetic pool available for these programs (FAO, 2016).

Introduction of Invasive Species

The animal, plant, fungi or microorganism species which move from their native habitat to a new place by human activities opportunities and try hard to settle there to the point when they start damaging its new surroundings and ecosystem are known as invasive species. Not every newly introduced species develops into an invasive species, but those that do can have a significant impact on agriculture industry, farming & conservation land (Eisen & Brown, 2022). Invasive species are known to have certain characteristics which help them to thrive in new habitat, they have higher growth rate, and better ability to adapt to new environment and reproduce rapidly that's why they outcompete the native species for available resources and thus disturb the biodiversity conservation and ecosystem. Invasive species affect the biodiversity and are a major reason for biodiversity and economic loss. Invasive species could be source of pathogen contamination and could induce a disease outbreak if they carry a new pathogen to new premises and infect native livestock species, or they could be used as vectors of the local pathogens if they are not vulnerable to it and transmit the pathogen to native livestock or plant species which leads to decrease in crop and livestock yield (Chinchio et al., 2020).

Environmental Influence on Livestock Feed Availability

Climate alteration presents a major obstacle to the sustainability of livestock systems worldwide. The increase in global temperature and fluctuations in the climate condition affect feed and water resources along with the livestock wellbeing and productivity. Additionally, atmospheric alteration affects various stages of livestock products production, including manufacturing, preservation, shipping, selling, and utilization. This jeopardizes the capacity of existing livestock system to support the livelihood and satisfy the increasing demand of animal products. The livestock sector is currently essential for food distribution and food resilience. Animal resources such as meat, milk, and eggs contribute 15% and 31% respectively, per capita calorie and protein intake around the globe with regional variations. Studies on livestock and climate instability frequently emphasize the capacity of livestock in atmospheric mitigation as well as describing adaptation strategies. However, when these studies address climate impacts, they often have a limited scope, focusing on livestock species, primary agricultural outputs, or specific aspects of climate related risks like weather threats. These studies typically do not comprehensively consider the vulnerability levels of different communities (Adopted, 2014; Escarcha et al., 2018; Rojas-Downing et al., 2017).

Changes in Feed Crop Yields

Livestock influence on the food supply chain involves the heightened level of atmospheric carbon dioxide (eCO2) and tropospheric ozone (O3), alongside the alteration in both the mean and variability of climate warmth and rainfall patterns. Additionally, livestock contribute to concerns such as coastal inundation, seaward deluge, and heightened risks also frequencies of catastrophic climate occurrence (Peñuelas et al., 2019). Territories currently facing water stress are anticipated to endure extreme repercussions. High-latitude zones may see increased crop yields due to diminished cold patterns and extended growing periods. Shoreline regions might encounter elevated soil salinity caused by increasing sea levels and more vigorous surge inundation. Alteration in the rainfall patterns, especially in arid areas, exacerbate saline concentration issues. Changes in climate conditions and higher temperature could results in dispersal of disease and pests increasing additional pressure on essential pollinizer fauna. Under hotter and moist conditions insufficient storing facilities are expected to results in escalated post-harvest losses on farms. Increasing atmospheric carbon dioxide levels can enhance output, nevertheless these benefits may not be uniform across all crops. Moderate C3 crops could experience the most favorable effects, although these benefits are constrained by nutrient and water supply. Conversely, raised tropospheric ozone levels are expected to have a detrimental impact on crop yields. Higher temperatures and drier environments are likely to benefit C4 plant breed and may increase hazardousness in certain vegetation, particularly in preservation. Increased atmospheric carbon dioxide might reduce plant protein and minerals content, while harmfulness increased in certain organisms. Rising atmospheric carbon dioxide levels are anticipated to benefit C3 plants and promote the spread of woody vegetation, potentially displacing grasses (Godde, Mason-D'Croz, Mayberry, Thornton, & Herrero, 2021). Global projections suggest that annual climate variability is projected to increase, likely impacting feed production negatively. Alteration in seasonal climate patterns will lead to specific impacts in different regions, conceivably resulting in either constructive or adverse consequences. Nevertheless, heightened fluctuation is expected to reduce the predictability of feed availability. Severe weather incidents may limit animals' pasture access and profoundly disturb the feed production process (LeMonte et al., 2017).

Impact on Feed Crop Productivity

Hotter and arid conditions are foreseen to increase the water requirements of both plants and animals, exacerbating pressure on water resources, especially in regions already facing water scarcity. Moreover, higher temperatures will result in greater glacier melting, disturbing established patterns of surface water supply. Increased temperatures and extreme events like deluges and dry spells are expected to degrade water quality for animal consumption by raising levels of pathogens, sediments, salts, nutrients, or pollutants in water sources (Legesse et al., 2017). Livestock production, animal well-being, and lifespan are anticipated to endure negative impacts due to diminished availability and quality of fodder, thermal stress, heightened vulnerability to illnesses stemming from compromised immune systems, and fatalities resulting from severe climatic occurrences like tempests, inundation, heat waves, and cold spells. Overall, these impacts are anticipated to be detrimental worldwide. However, in regions with frosty winters, higher temperatures might mitigate cold strain in animals, reduce their energy requirements for maintenance and heating in housing facilities (Filipe, Herrera, Curone, Vigo, & Riva, 2020). Impacts of environmental alteration on resources will continue to cause shifts in global agricultural zones and alter seasonality and suitability for cultivation and animal husbandry. Research of king et al. A northward shift of up to 1200 km for viable agricultural areas prior to the century ends, though several new regions may face fluctuating water ratios (King et al., 2019). Across the past 6 decades, drylands expanded, particularly in semi-arid regions, and this trend is expected to continue (Huang et al., 2017). In sub-Saharan Africa, over 20% of mixed farming in arid and semi-arid regions could become unfit for crop farming by the middle of the century (Jones & Thornton, 2009). Forage production are expected to experience fewer impacts from global warming compared to crop yields. This could favor grazing systems and possibly lead to a shift away from the current trend towards more intensive farming systems (Havlík et al., 2015). Environmental change may diminish the accessibility, excellence, and safety of livestock products by causing contamination with pathogens or pesticides and diminishing their nutritional value and sensory allure. This could lead to increased and more fluctuating prices. Moreover, changing societal standards could impact eating habits, especially in affluent nations.

Competition for Feed Resources

Current intensive livestock production systems heavily depend on purchased feedstuffs like maize, wheat, and soybeans, but this reduces the availability of grain for human consumption. Mixed farming, which integrates animal and crop enterprises, offers a more balanced approach, yet even these systems often feed animals grain that could otherwise nourish people. As demand for animal products rises globally, particularly in Asia and South America, an additional 300 million tons of grain will be needed by 2050 just for livestock, while human demand for arable crops also increases due to population growth. The push towards eco-efficient livestock systems in response to rising feed costs will likely result in higher greenhouse gas emissions per unit of production, highlighting the sustainability dilemma (Pollock, 2008). As climate variability increases, species niches shift, resulting in plant and crop substitutions that can impact animal diets and pose challenges for smallholders in managing feed shortages. For example, in East Africa, maize is being replaced by sorghum and millet, which are more suitable for drier climates. Similarly, in semi-arid marginal regions of southern Africa, farming systems are transitioning from integrated farming to pastureland-based systems. The effects of climate instability on plant productivity vary by location, system, and species, with C4 crops benefiting from temperature increases up to 30-35°C, and C3 crops responding positively to higher CO2 levels, provided water and nutrients are adequate. However, in semi-arid rangelands where growing seasons may contract, productivity is likely to decline, impacting the availability of stover and metabolisable energy for dry season feeding (P. Thornton & Herrero, 2008).

Alternative Feed Sources

Animal husbandry can convert proteins into premium food for human intake, however it is essential to identify substitute protein source to replace high-energy protein (HEP) feeds like soybean meal (SBM). Insects and microalgae show potential as sustainable alternatives, with insects being part of poultry's natural diet and algae offering efficient production on marginal lands. Seaweed, although containing high-value compounds, faces challenges in production and nutritional variability. By-products from human food crops, such as camelina sativa and guar, can also replace SBM in livestock diets. The transition to human-inedible protein sources (HIP) is recognized as necessary, but standard experimental designs are needed to evaluate their impacts effectively across different livestock species (Te Pas, Veldkamp, de Haas, Bannink, & Ellen, 2021).

Sustainable Feed Alternatives

Insects can be cultivated on substandard bio waste, transforming it into top graded protein. While insect farming doesn't require land, producing feed for insects might, necessitating careful consideration of energy use and environmental impact. Insects are a natural part of poultry diets and provide a suitable protein composition (Khusro, Andrew, & Nicholas, 2012). Algae can be an efficient, highly productive protein source, particularly on marginal land, avoiding competition with traditional agriculture. Although production is currently limited by the use of open-pond systems prone to contamination and low productivity, alternative systems might become viable on a larger scale despite their higher costs. Algae's protein content varies by species, and while they match conventional feeds in crude protein and amino acid composition, widespread use is restricted due to logistical and economic challenges, as well as potential contamination issues (Lamminen, Halmemies-Beauchet-Filleau, Kokkonen, Jaakkola, & Vanhatalo, 2019; Taelman, De Meester, Van Dijk, Da Silva, & Dewulf, 2015).

Heat Stress and Livestock Health

Stress inclusively refer as negative implication and describes the growing harmful effects on variety of animal health and performance factors. Animals face heat stress when there is imbalance between heat produce within their bodies and their ability to dissipate it. When environment faces unexpected changes stress appears. It can be activated by multiple factors. Temperature is one of the crucial factor that trigger heat stress in animals. Increased environmental temperature can lead to significant heat gain and loss and major reason for animals heat exhaustion (BV, Ajeet, & Meena, 2011). Thermal strain is aggravated by global warming progressively impacting livestock and poultry. It is a common issue of domesticated animal feeding in tropical and sub-tropical region. Livestock and poultry faces severe decline in food consumption, delayed growth, instability in intestine, reduced reproducibility, endocrinal and immunological disruption (Chen, Yong, & Ju, 2021). Globally, dairy industry face heat stress as a challenge particularly in growing economic communities ascribed to leap up temperature accompanying by number of animal production and escalated agriculture (Renaudeau et al., 2012; Von Keyserlingk & Hötzel, 2015). Frequent decrease in the milk production has been associated with the heat stress, for instance reduce milk production could occur from the combine effect of heat strain on dairy cattle physiology, metabolic activities, and feed accretion. In addition, selection of dairy sheep have lower heat resistance for increased milk production (Finocchiaro, Van Kaam, Portolano, & Misztal, 2005). When animals feel ill or unable to control the environment something like dehydration or shade to lower their body temperature possibly endanger their welfare and these risks might not have direct connection with their biological function (von Keyserlingk, Amorim Cestari, Franks, Fregonesi, & Weary, 2017). Livestock owners in tropical countries seems heat stress as main challenge because of elevated lipid peroxidation level, alteration in electrolyte concentration, antioxidants and decline in cell mediated immune response (BV et al., 2011). Heat stress also have clear connection with host biological pathways like apoptosis, autophagy, MAPK signaling pathways, epigenetic modifications, cytokine imbalance heat shock proteins and neuroendocrine system that have consequential impact on poultry and livestock health (Chen et al., 2021).

Physiological and Behavioral Responses to Heat Stress

Animal’s metabolism and production respond differently to acute and chronic heat stresses. Overproduction of oxidative stress agents and reactive oxygen radicals, coupled with reduced antioxidant defenses, due to variance in pro-oxidants and antioxidants causes oxidative imbalance, particularly in domesticated animals during summer and ultimately leads to cell damage (Bernabucci, Ronchi, Lacetera, & Nardone, 2002; Ganaie et al., 2013). When environmental temperature exceeds the optimum temperature, consumption of feed decreases notably among animals experiencing heat strain. The cause of reduced feed intake due to heat stress involves the activation of receptors in pro-opiomelanocortin (POMC) similar to capsaicin receptor 1 (TRPV1) in hypothalamus arcuate nucleus. Hypothalamus is the appetite control center of animals (Jeong et al., 2018). Heat stress extends stomach clearance time and undermine intestinal peristalsis disturbs the digestion process, leading to accretion of chyme and appetite suppression (He et al., 2018). Unbalance endocrine homeostasis has direct or indirect impact on hen's reproduction that leads to lesser egg production, poorer egg quality along with thinner egg shells and low weighted eggs (Franco-Jimenez et al., 2007). Mortality rate also increases in layer breed and broilers due to escalated temperature. Lesser feed intake lowers the calcium digestion of diet also the significant contributing factor of reduced egg quality and production during heat stress (Quinteiro-Filho et al., 2010). Intestinal epithelium is also affected by the triggering of MAPK and NFK B signaling pathways due to heat stress. Moreover, activation of JNK and P38 by heat stress leads to apoptosis of epithelium cells as well as damage promotion (Hou et al., 2015). Heat stress damages the immune system of livestock and poultry. This damage leads to reduced drug resistance, higher susceptibility to infection, immune suppression and consequently higher morbidity and mortality among animals (Netea & van der Meer, 2017). Meat quality is encompass by overall physical and chemical attributes associated with nutritional value, taste, and texture. Efficacy of animal husbandry has been directly related to quality of meat. Organs, muscle metabolism and fat deposition affected by thermal stress decline the meat standard and production (Cui et al., 2016; M. Zhang et al., 2020).

Impact on Productivity and Health

The livestock sector is rapidly expanding as part of agriculture, contributing 33% to the agricultural GDP and compelled by population expansion, urbanization, and increasing income levels in developing nations. By 2050, requirements for all farm products is expected to increase twofold in sub-Saharan Africa and South Asia. Globally, agricultural production face reduction of 1 to 5 % per decade due to climate change (Abdela & Jilo, 2016; Bekele, 2017). Climate factors for instance environmental temperature and rainfall patterns significantly impact pasture and food resources for animal reproduction, annually. Mannerly, during rainy seasons pastures are abundant and have good nutritional content. Contrarily, grassland during the dry season have low nourishing value, high in fiber, have low protein content, often leading to decline in animal production (Abebe, 2017). Fertility rate can decrease 20 to 30 % during the summer, with noticeable seasonal patterns in estrus. Rising ambient temperature negatively affects cow's natural matting behavior by reducing both duration and estrous expression intensity. A dairy cow measuring 635 kg produces 36 kg milk daily need 22% of more energy at 32˚C than at 16˚C. With this rising temperature, dry matter consumption decreases to 18% and milk production to 32% (P. Thornton & Herrero, 2008). Livestock and climate change are closely interconnected. The spatial distribution and accessibility of grazing area and water heavily rely on precipitation patterns and availability. Variations in precipitation and temperature influence the accessibility of fodder, grazing area, feed quality as well as weed, pests, and disease occurrence. Consequently, fluctuation in environmental factors such as temperature, rainfall, frequency and intensity of extreme events like drought directly influence the livestock production (Aklilu, Desalegn, Mesfin, & Negash, 2013; Mendelsohn & Neumann, 2004). A rise in temperature of 2 to 3°C nationwide, coupled with heightened moisture from environmental change, is expected to worsen the heat strain in dairy animals, resulting in decreased growth and milk output. Analysis of Bekele De Wit Stankiewicz et al expected that reduction in continuous water run-off would have substantial impact on access to surface water across 25% of Africa by the close of this century. Morton et al., 2007, widely held that climate changes disproportionality impact developing nation, especially rural farmers. Moreover, small scale farming and low capitalization are expected to heighten the vulnerability of livestock production in these nations. Climate change threatens water supplies from rivers, lakes, and precipitation, thereby diminishing water accessibility for livestock farming (Bekele, 2017; De Wit & Stankiewicz, 2006).

Impact of Climate Change on Pathogens and Vector-Borne Illness

Climatic shifts impact the outbreak and spread of pathogens, as well as their hosts and vectors, affecting their transmission, development and breeding. This is in turn influence the distribution, disease spread to new areas and host parasite relationships. Vector borne diseases are more conspicuous for affecting animal health directly, these are linked to the soil, water, floods, rodents associated diseases and those sensitive to air temperature and humidity (Grace, Bett, Lindahl, & Robinson, 2015). Vectors are the host that carry and transmit disease causing agents to the living organisms, which then become host. Significant disease vectors of livestock such as flies, tick mosquitoes midges, tsetse flies, are affected by climate changes in multiple ways. The spatial dispersal and demographic dynamics of these insects' vectors are linked to climate pattern and changes. As a results climate changes alter the range, duration, extent of the infectious diseases through its impact on these vectors (Phillip K Thornton, van de Steeg, Notenbaert, & Herrero, 2009; Wu, Lu, Zhou, Chen, & Xu, 2016).

Shifts in Vector Distribution and Disease Prevalence

Climate change's ecological structure leads to both geographical and phonological shifts. It can affect the transmitting pattern and efficacy of pathogens make their range broad among host. The expanded range of pathogens increases animal's susceptibility to disease thereby enhancing the pathogenic potential of disease agents. Consequently, animal husbandry are susceptible to changes in intensity and spread of animal diseases (Getachew et al., 2009). Precipitation pattern and temperature changes influence the distribution and abundance of disease vectors. With temperature shifts, ability of the insects vector to retain or acquire viral infection also varies (Wittmann & Baylis, 2000). Climate change can significantly impact the onset, propagation, and dissemination of animal diseases. For instance, the allocation of vector-borne diseases like Rift Valley Fever, African Horse Sickness, and Bluetongue varies greatly with periodic and long-term environmental changes. Climatic variability can influence contagious diseases in livestock in numerous ways such as influence of disease agents due to elevated temperatures can accelerate the development of pathogens or parasites. The influence of the host is that shifts in disease distribution can affect the susceptible animal population, vectors affected by changes in rainfall and temperature pattern can influence the distribution and abundance of disease carriers and epidemiology is effected by change transmission rates between hosts (Oluwayelu, 2014). Although there is no agreement that a hotter planet is inevitably more susceptible to diseases, the likelihood of disease risks may be rising due to other factors such as the expanding intricacy and magnitude of market networks and the unavoidable escalation of production systems in particular regions (Randolph, 2008). In hot summer months, dairy cows encounter heightened milk somatic cell counts and a greater occurrence of clinical mastitis. Minimizing heat stress with air conditioning or shade administration leads to reduced instances of clinical mastitis in comparison to cows exposed to natural conditions. The elevated occurrence of clinical mastitis during warm and humid conditions is linked to heightened heat strain and an increased fly population associated with these circumstances. Additionally, hot and humid weather intensifies cattle tick infestations, including Boophilus microplus, Haemaphysalis bispinosa, and Hyalomma anatolicum, which act as carriers for various protozoan diseases (Sanjay Kumar, Prasad, & Deb, 2004; Singh, Nauriyal, Oberoi, & Baxi, 1996).

Impact on Animal Health and Productivity

The initial problem puts forth a biological challenge, whereas the second one presents a technological. Solving both problems requires an understanding of descriptive and numerical reactions of animals to multiple levels of heat strain. Encouraging local breeds for raising is another adaptation strategy, since these breeds exhibit greater heat tolerance compared to crossbred and exotic breeds. For instance, indigenous cattle breeds like Sahiwal and Deoni showed minimal adverse effects of thermal strain, such as reduced milk production, compared to Jersey and Red Sindhi crossbreeds. Livestock husbandry entails optimizing the animal environment to maximize efficient production of beef, dairy, and wool. Insight into climatic stress and adaptations is crucial for enhancing management skills (Stott, 1981). Various operational procedures exist to mitigate heat strain, along with pros and cons. Dwelling offers significant control over environmental stressors, albeit with higher initial costs per animal. Sheds are essential for minimizing losses in milk yield and breeding effectiveness. Well-designed sheds enhance livestock welfare and efficiency by optimizing air flow and providing protection from sunlight. It is documented that a well-planned shed can decrease heat stress on animals by 30-40%. The design and operation of dairy cattle shelters vary depending on local climates; a space allocation of 60 square feet per animal is typically deemed sufficient. Larger space allocations enhance air circulation, which is vital in warm, humid climates (Armstrong, 1994).

Studies comparing shed materials and influence of roof dimensions and alignment on micro-environment have found hay to be a cost-effective roofing material for cattle sheds. However, corrugated steel sheets are popular due to their durability and low maintenance requirements. In hot and humid climates, increased space allocations provide more open areas for airflow, which is crucial for managing heat stress in cattle. These studies have observed that the positioning of cows within the shed also plays an important role (Das, Karunakaran, Barbuddhe, & Singh, 2015). Satellite data are increasingly utilized to assist in disease prediction, particularly for epidemic-prone diseases like Rift Valley Fever (RVF) and malaria (Grace et al., 2015). However, accurate prediction relies on a solid understanding of disease transmission patterns and epidemiology. It has been noted that satellite data tends to overstate precipitation in arid regions and underreport it in mountainous areas (Dinku, Chidzambwa, Ceccato, Connor, & Ropelewski, 2008). Promoting elimination and management of key illness involves employing various innovation with the capability to enhance management of climate-sensitive diseases, for instance, Utilizing multivalent vaccines capable of providing immunity against various illness, deploying heat-resistant vaccines that do not depend on refrigeration for storage, focusing on breeding disease-resistant livestock breeds that can withstand multiple diseases, and by using insecticides like pyrethroids that effectively target multiple vectors. Enhancing the resilience of livestock systems is crucial in adapting to climate change and variability. Unlike crop agriculture, livestock husbandry offers flexibility because animals are relocated to areas along with access of feed and water resources as needed (Friedman, Voet, Reznikov, Dagoni, & Roth, 2011; Grace et al., 2015).

Advances and Future Opportunities in Animal Productivity

Future agricultural changes may take three forms: rapidly and sustainably increasing production to meet growing demand, developing alternatives for livestock and poultry, and implementing novel food production strategies. The UK's scientific community is robust enough to make significant contributions to all three phases. To improve the sustainability of animal production systems and lessen their environmental footprint, three primary goals must be tackled: maximizing the quantity of viable offspring per breeding pair, enhancing the effectiveness of converting feed and water into animal products, and reducing waste and losses caused by disease and stress. Relevant scientific disciplines include genetics, immunology, nutrition, physiology, and reproductive biology, with effective research requiring cross-disciplinary collaboration with experts in mathematics, physics, and computing. While the UK has strengths in genetics, genomics, and disease research, it lacks sufficient expertise in whole animal biology, such as physiology, reproductive biology, and nutrition (Hume, Whitelaw, & Archibald, 2011). The availability of human edible protein sources for livestock may become limited soon. Enhancing protein efficiency in human inedible protein sources can reduce reliance on HEP sources, though HIP sources can only partially replace them currently. It's crucial to consider the land use requirements of HIP sources. A transition in protein resources may require multiple actions, including precision feeding to minimize waste. However, there is still much to learn, particularly at the individual animal level (Te Pas et al., 2021).

Production Efficiency

While pigs and poultry have seen significant productivity gains, ruminants have not kept pace (Crowley et al., 2010). Genetic data on beef cattle indicate that continued selection can enhance feed efficiency and other characteristics, enabling animals to better adapt to specific feeds or environments. Successful precedents for this approach exist, such as the US Beefmaster and the Australian Droughtmaster cattle, which were selected for traits like weight, fertility, and environmental adaptation. Progress in genomics will aid in creating new specialized breeds and optimizing hybrid vigor. Feed efficiency can also be enhanced through additives and treatments, though these face opposition due to concerns about residues and safety. Rational, evidence-based research may demonstrate their acceptability, similar to GMOs (Hayes et al., 2009). Other solutions to improving efficiency include advancements in production systems, feedstock, and animal breeding, particularly for ruminants. Current reliance on grains and cereals is unsustainable, competing with human food and biofuels. Alternatives like new plant varieties optimized for marginal land and genetically modified plants with higher nutritional value are being explored. Unconventional feed sources, such as algae, and genetically modified plants designed to reduce environmental impacts, like greenhouse gas emissions, are also being considered (Zhou, Hernandez-Sanabria, & Guan, 2009).

Addressing greenhouse gas production in ruminants is crucial. New technologies aim to monitor and reduce methane production through manipulation of rumen microorganisms. Efficient animals produce less methane, suggesting that selection for improved food efficiency and altered rumen environments could reduce emissions.

Innovations in Farming Practices

Efficient resource utilization and waste handling in livestock agriculture, addressing the pressing environmental challenges posed by the global livestock sector. Key factors in improving resource efficiency and waste management in livestock farming are precision agriculture technologies, like sensor-based monitoring and automated systems, significantly enhanced resource use and reduced waste. Stringent regulatory frameworks, especially in regions like Europe, positively influenced sustainable waste management practices. The adoption of circular economy principles, such as repurposing animal manure, effectively promoted both waste management and resource efficiency. Moreover, farmer education and awareness were crucial, as informed farmers were more likely to adopt sustainable practices, emphasizing the need for tailored outreach initiatives (Wang'ombe, 2023).

Technological Advancements

Food sustainability is closely tied to sustainable agriculture, which involves methods that fulfill human food requirements, improve environmental conditions, and effectively utilize resources while sustaining agricultural activities aimed at enhancing long-term human well-being (Kok et al., 2019; Searchinger et al., 2019). However, sustainability of food and agricultural systems faces pressures from global population growth, rising food demands, climate change, limited water resources, and the shift to alternative energy sources. Addressing these challenges requires an integrated strategy incorporating advanced technology, ecosystem services, and human resources to promote sustainable agriculture (Nadathur, Wanasundara, & Scanlin, 2017). As the global population is projected to reach 10 billion by 2050, unprecedented pressure will be placed on water, fertile land, energy, and climate, raising concerns about ecological damage and sustainability. Emerging technologies like IoT, AI, and gene editing, along with government and non-government policies promoting plant-based protein, are crucial for optimizing protein sources and enhancing food system sustainability (Foley et al., 2011; Nadathur et al., 2017).

Genetics

Advancements in animal breeding through genome-wide selection and complete genome sequencing are expected to enhance the efficiency of identifying high genetic merit sires. This approach will be complemented by sophisticated progeny testing and tracking, making the prediction of breeding values more precise. Cloning of productive animals will become more accessible, necessitating careful management to maintain genetic diversity and mitigate risks during pandemics. Additionally, genomic technologies will address challenges in livestock productivity, such as increasing fecundity in animals like pigs and sheep, and understanding the epigenetic links between maternal nutrition, stress, and offspring productivity (Coleman, Pierce, Berry, Brennan, & Horan, 2009; Hill, 2010).

Selective Breeding and Genetic Modification

Improving crops is crucial for ensuring food security, sustainability in agriculture, and developing resilient plant varieties. Key strategies focus on enhancing traits like yield, disease resistance, adaptability to diverse environments, and nutritional value to meet increasing global food demands amidst climate challenges (Zakari, Khan, Tan, Alvarado, & Dagar, 2022). Selective breeding plays a foundational role in this effort, involving deliberate selection and propagation of favorable plant characteristics for improved varieties that fulfils the demand of growers and customers alike. Contemporary methods like marker-assisted breeding and genetic modification complement traditional methods, expanding the capacity to enhance crops. These advancements are pivotal in boosting agricultural productivity, quality, and resilience to environmental stresses, thereby benefiting farmers economically and providing consumers with better nutritional options (Singha & Singha, 2024).

Conservation of Genetic Resources

Genetic variability in plant genetic resources (PGRs) plays a crucial role in crop enhancement, enabling breeders to cultivate varieties with desired characteristics such as yield, quality, and resilience to environmental stresses. This diversity originates from natural variability and includes mutated strains, indigenous species, and breeding populations. Preservation of new genes resistant to pests and environmental stresses is essential for cultivating resilient crop varieties. Techniques such as phenotypic, biochemical, and molecular analyses are used to characterize and utilize genetic diversity effectively in breeding programs, ensuring the sustainability and adaptability of agricultural crops (Begna & Begna, 2021; Montalvo et al., 1997; Swingland, 2001). Historically, the practice of selecting and conserving locally adapted plant seeds, known as landraces, persisted until Gregor Mendel's principles of inheritance were rediscovered during the twentieth century. This renewed interest resulted in the creation of breeding initiatives focused on producing high-yield and stress-resistant crop varieties, essential for beginning of Green Revolution and significantly boosting global agricultural output (Panis, Nagel, & van Den Houwe, 2020). However, this period also saw a decline in landraces and the dominance of monoculture farming, resulting in the loss of more than 75% of genetic variation in plant genetic resources and Nine out of ten crop varieties once cultivated by farmers. Today, conservation efforts are critical to maintain the remaining PGRs amidst challenges like climatic shifts, weather deterioration, and population growth. International initiatives involve over 17,000 institutions worldwide, including gene banks, safeguarding more than 5.4 million accessions of crop species, their wild counterparts, landraces, and breeding materials to ensure their sustainable use and equitable benefit-sharing in accordance with international treaties aligned with the Convention on Biological Diversity (CBD) (Bélanger & Pilling, 2019).

Resource Management and Sustainability

Land Use and Habitat Management

Sustainable land and habitat management is essential for global development, as it affects both the natural environment and economic prosperity. For example, forests are home to 80% of the world's terrestrial biodiversity, supply clean water, prevent soil erosion and flooding, and can provide one-third of carbon mitigation efforts (Baskent, 2021). In order to maximize long-term benefits, it is essential to establish and carry out practices that uphold the enduring health and adaptability of agricultural and livestock resources, as these have a substantial impact on soil health and functionality (Baronti et al., 2022) Thus, Sustainable land management practices and conservation strategies is an essential mechanism that manage land and its natural habitat, ensure that there is a future of natural resources and livelihoods.

Sustainable Land Management

Sustainable land management (SLM) is vital for addressing both current and future human needs while ensuring the long-term sustainability of ecosystem services and livelihoods. It integrates the management of land, water, and biological resources through policies, strategies, and technology. According to the World Bank, SLM is critical for meeting the demands of a growing population. It aims to halt and reverse land degradation, enhance land productivity, and ensure sustainable outcomes for ecosystems and human well-being (Baskent, 2021).

Sustainable Land Management Practices

A variety of SLM practices (e.g., rotational grazing, agroforestry systems, wildfire control etc.) which support sustainable livestock farming (Baskent, 2021).

Rotational Grazing

Rotational grazing is a method where livestock are moved through different fenced grazing areas (paddocks) to regulate forage production, improve forage quality, promote animal health, and maintain environmental quality (Whitt & Wallander, 2022). Grass plays a crucial role in safeguarding soil from erosion by water and wind. Additionally, it nurtures essential biological processes, such as the decomposition of organic matter and the accumulation of soil organic carbon (Baronti et al., 2022).

Impact of Grazing on Soil Health

1. **Impact of Grazing:** Grazing removes photosynthesizing leaves, affecting soil's physicochemical processes and can lead to soil erosion if not managed properly.
2. **Excessive Grazing Pressure:** These conditions lead to muddy terrain, compacted soil, decreased presence of preferred grazing plants, and an increase in weed growth.
3. **Insufficient Grazing Pressure:** Results in increased biomass production but leads to forage waste and reduced net profit due to selective grazing by animals (Baronti et al., 2022).

Key benefits of rotational grazing include:

1. **Soil Health:** Protects soil from erosion, supports biological activity, and prevents degradation by maintaining optimal grass height (15 cm).
2. **Environmental Benefits:** Increases grazing production, reduces greenhouse gas emissions, and minimizes soil compaction(Baronti et al., 2022).
3. **Enhanced Soil Ecosystem Services:** Improves soil ecosystem services, including regulation, supply, and support (Galindo et al., 2020).
4. **Prevents Overgrazing:** Implementing short intervals of high-intensity grazing followed by extensive recovery times is critical for herb recovery and increased fodder production. (Dong, Zheng, Martinsen, Liang, & Mulder, 2022)
5. **Intensive Rotational Grazing (IRG):** Promotes high stocking rates with short grazing periods and long recovery times, increasing soil organic carbon, reducing soil

compaction, enhancing water retention, and improving soil aggregation(Teutscherová et al., 2021).

Agroforestry

Agroforestry is an innovative and sustainable agricultural approach that holds the potential to transform the way we produce food. By diversifying agro-ecosystems with a variety of components such as woody perennials, palm trees, crops, forages, and animals, agroforestry not only enhances biodiversity but also improves soil health, water conservation, and overall ecosystem resilience(Rosati, Borek, & Canali, 2021). Agroforestry integrates trees with crops and/or livestock, enhancing agricultural diversity and resilience against climate risks (Quandt, Neufeldt, & Gorman, 2023). Agroforestry systems are classified as silvopastoral (trees and pasture), silvi-agriculture (trees and crops, such as alley cropping, windbreaks, shelterbelts, etc.), and agro-silvopastoral (trees, crops and animals) (Fahad et al., 2022).

Species Selection

It's important to carefully consider the selection of tree species and the procedures for establishing them before starting an agroforestry project. Species like Moringa oleifera and gliricidia offer multiple environmental benefits such as drought tolerance and nitrogen fixation, enhancing soil quality and agricultural productivity (Boumenjel, Papadopoulos, & Ammari, 2021).

Impact of Agroforestry

Soil Protection and Improvement: Agroforestry systems mitigate soil erosion and nutrient loss through reduced runoff. They enhance soil physical properties like water-holding capacity, permeability, and drainage. Tree cover improves soil fertility by adding organic matter and recycling nutrients effectively (Salimath et al., 2022).

Role of Soil Microorganisms: Soil microbial communities in agroforestry systems contribute significantly to soil fertility and productivity. These systems support diverse and functional microbial populations, promoting nutrient cycling and enhancing biological soil fertility compared to sole cropping (Li et al., 2020; Marsden, Martin-Chave, Cortet, Hedde, & Capowiez, 2020).

Microbial Abundance and Functionality: Agroforestry increases microbial abundance through presence of organic accumulation, drainage from roots, and different waste quality. Various organisms like nematodes, earthworms, and insects play crucial roles in nutrient cycling and soil structure maintenance (Marsden et al., 2020).

Resource Use Efficiency: In agroforestry systems, trees and crops compete for resources like light, water, and nutrients. This competition can result in complementary or competitive effects depending on species and spatial arrangement, ultimately enhancing overall productivity and sustainability (Salimath et al., 2022).

Carbon Sequestration: Agroforestry is vital for soil development and health as it reduces erosion, air pollution, and natural disturbances while promoting soil health and carbon sequestration to combat climate change (Pantera, Mosquera-Losada, Herzog, & Den Herder, 2021).

Wildfire Mitigation: Agroforestry reduces wildfire incidents by managing fuel loads and enhancing landscape resilience, particularly in regions like the European Mediterranean basin experiencing increased fire risks due to climate change. Compared to forests and shrublands, agroforestry and grasslands exhibit lower average fire incidences, highlighting its potential as a sustainable land management strategy (Pantera, Mosquera-Losada, Herzog, & Den Herder, 2021).

Conservation Strategies

Actions like deforestation, wildfire, mining, urbanization, and habitat fragmentation are drastically altering the conservation status of many species. Increasing agricultural activities driven by population growth pose significant threats to global biodiversity through habitat loss, pollution, and the introduction of invasive species. Conservation efforts aim to preserve species diversity, protect habitats, and maintain ecological relationships essential for ecosystem services (Frouz, 2020).

Major Strategies

1. **The in-situ (on-site) conservation** involves protecting, managing, and monitoring natural habitats, including wildlife reserves, farms, and communities. Protects natural habitats directly where biodiversity thrives, such as wildlife reserves and community-managed areas. This approach prioritizes preserving local biodiversity and ecosystems, crucial for long-term species survival and sustainable development.

2. **The ex-situ (off-site) conservation** Involves techniques applied outside natural habitats, like captive breeding and gene banks, to safeguard species at risk, particularly those threatened by factors like climate change and overexploitation. It complements in-situ efforts and supports biodiversity through scientific research and public education.

These strategies aim to maintain biodiversity, protect natural habitats, and enhance ecosystem resilience against threats like habitat loss, pollution, and climate change, promoting sustainable land use and human-wildlife coexistence (Mestanza-Ramón et al., 2020). The first National Policy for species Management prioritizes both on-site and ex-situ conservation methods at the national, regional, and local levels to protect species and their ecosystems. Key conservation efforts include:

1. **In-Situ Conservation:** Prioritizing the National System of Protected Areas to protect ecosystems that are at risk and integrate conservation into land management plans.
2. **Mitigating Environmental Impacts:** Evaluating and implementing measures to minimize the impact of development projects on wildlife at various governmental levels.
3. **Ex-Situ Conservation:** Establishing wildlife rehab centres in accordance with national and international criteria to help in-situ conservation activities.
4. **Local Conservation Initiatives:** Developing and executing conservation plans, programs, and projects at the local level, focusing on endangered species.
5. **Education and Awareness:** Conducting ongoing communication, education, and public participation activities to highlight the importance of biodiversity conservation, especially focusing on wildlife.
6. **Collaborative Planning:** Coordinating conservation efforts among decentralized governments to align local initiatives with national conservation goals (Mestanza-Ramón et al., 2020).

Water Conservation and Management

Efficient Water Use Practices

Agriculture is the major global water user, accounting for 69% of freshwater withdrawals. Increasing challenges due to water scarcity, exacerbated by competition with crops and non-agricultural sectors (Cheng, McCarl, & Fei, 2022). Key methods to achieve this include improved irrigation techniques and water recycling.

Improved Irrigation Techniques

1. Drip Irrigation:

Drip irrigation, or trickle irrigation, involves supplying water directly to the plant root zone using emitters or drippers. This method ensures efficient water and fertilizer management by minimizing evaporation and seepage losses. It significantly enhances crop productivity and reduces water consumption compared to traditional methods like furrow irrigation (Moursy, ElFetyany, Meleha, & El-Bialy, 2023; Shi, Lu, Zheng, Zhang, & Zhangzhong, 2022).

Principles of Drip Irrigation Method

Drip irrigation delivers water slowly through small plastic pipes equipped with drip emitters, ensuring precise delivery close to plants' roots. This method optimizes water use by wetting only the soil around the plant as needed, based on soil texture and emitter flow rates. Applications are frequent (every 1-3 days) to maintain optimal soil moisture levels for plant growth (Ambomsa, 2020).

Fundamentals of Drip Irrigation

1. Water source and pump options include open wells, bore wells, and canals. A pump can be built based on the availability of water and the area to be watered.
2. Filtration Unit: Uses various filters (e.g., hydro-cyclone, sand/media, screen/disc) to remove pollutants from water.
3. A customized network of pipes, including main lines, sub-main lines, laterals, and emitters, to meet agricultural water requirements. The design of a system defines the diameter and length of these elements, and emitters are chosen based on the crop's water requirement (Arshad, 2020).

Advantages of Drip Irrigation

1. The use of drip irrigation improves water saving, nutrient delivery, and reduces evaporation (Bansal, Mahajan, Verma, & Singh, 2021).
2. Reduces water loss through seepage and evaporation, leading to significant increase in water production (Flores, Faria, Rettore Neto, Diotto, & Colombo, 2021).
3. Improve crop output, increase soil moisture in the root zone, and save up to 56.4% on irrigation water usage compared to furrow irrigation (Moursy et al., 2023).
4. Promotes environmental preservation by reducing water and fertilizer consumption.
5. Adaptable to various land forms and soil types, improves vegetable hygiene in dry soils, and eliminates the need for drainage (Ambomsa, 2020).

2- Smart Irrigation Systems: Advanced irrigation systems use real-time sensor data to change watering schedules in response to soil moisture and weather conditions. This technique optimizes water use by delivering irrigation precisely when and where it's needed, saving water resources efficiently (Abedin, Chowdhury, Hossain, Andersson, & Karim, 2017). Fig.1 shows the SMART irrigation system that can be used in IoT devices(Obaideen et al., 2022).

Components and Benefits

- Data Acquisition (Sensors): Monitors soil moisture, weather parameters (humidity, temperature), and other environmental factors.
- Irrigation Control: Automates irrigation based on sensor data, reducing water wastage.
- Wireless Communication and Data Processing: Enables remote monitoring and control.
- Fault Detection: Identifies and addresses system malfunctions promptly (Abedin et al., 2017).

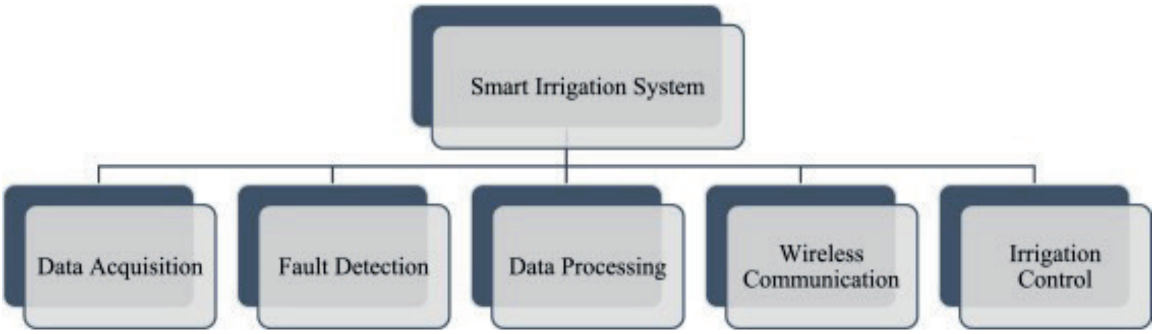

Figure 1.:Smart Irrigation System (Obaideen et al., 2022)

Water Management

Effective irrigation water management hinges on understanding the relationship between soil, crops, and water. This knowledge is essential for optimizing agricultural activities, ensuring that processes and products are well-informed. Various methods are employed in agriculture for water management, each with its own advantages and limitations:

1. Precise measurement and management techniques to monitor water use efficiently.
2. Using water-smart landscaping and irrigation
3. Control reverse osmosis for water purification
4. Recover rainwater by capturing and utilizing
5. Build reservoirs to store water for irrigation

IoT systems play a crucial role in modern irrigation, Fig.2 (Obaideen et al., 2022) shows the benefits of using IoT in irrigation systems:

1. Reduced water consumptions and cost-efficiency
2. Improved performance efficiency
3. Lower energy consumption
4. Minimized crop wastages (Obaideen et al., 2022).

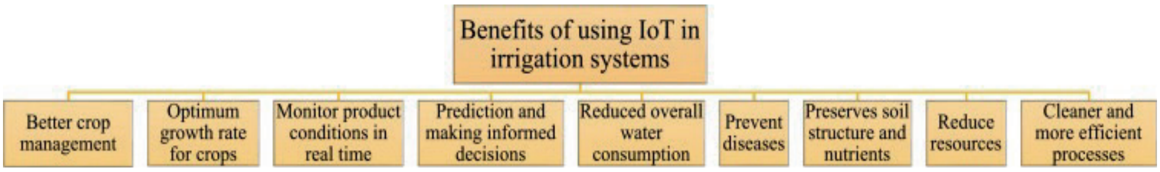

Figure 2. Benefits of IoT in irrigation systems

Water Recycling

Water recycling, particularly the reuse of treated greywater, offers a sustainable solution to alleviate water scarcity in agriculture (Filali et al., 2022). Treated greywater offers agriculture a cost-effective, locally sourced water supply that matches specific water quality needs, alleviating strain on the national water grid (Al-Mashaqbeh, Ghrair, & Megdal, 2012).

Grey Water Recycling:

Greywater comprises wastewater from household activities excluding toilets and kitchen wastes. It can be treated and reused for irrigation after filtration and disinfection processes. Greywater contributes 50-80% to household sewage capacity and contains 18-22%, 20-32%, and 9-14% of potassium (K), phosphorus (P), and nitrogen (N), respectively, allowing it to be reused after basic treatment (Filali et al., 2022).

Table 1. Sources of Grey water

Grey Water Source	Constituents
Bathroom	Shampoo, soap, toothpaste, lint, traces of urine, body care products, hairs, skin, hair oil, body fats, hot water and sand/clay particles
Hand basin	Toothpaste, soaps, body care products, shaving waste, hairs and skin cells
Kitchen	Dish washing detergents, oil and fats, food residue, hot water, raw meat washing, fruit and vegetable peels, tea or coffee, traces of food preservatives, sand and clay particles
Laundry	Chemicals from detergents, oils, solvents, bleaches, paints, hot water, non-biodegradable fibres from clothing

Components of a Gray Water Recycling System

1. **Collection:** Gray water is collected from various sources as shown in Table 1 (Elhegazy & Eid, 2020).

2. **Filtration:** Collected greywater undergoes filtration to remove solids, hair, and large particles using methods like sand filters, activated carbon filters, and membrane filters.

3. **Treatment:** After filtration, greywater is treated to remove pathogens and reduce organic matter through:

4. **Biological Treatment:** These processes might be aerobic, anaerobic, or mixed. Utilizing processes such as filtering marshes, sequenced batch reactors, and anaerobic sludge blankets, where plants and microorganisms break down organic matter and contaminants. Membrane bioreactors (MBRs) were also regarded as revolutionary technologies due to their stability and capacity to eradicate infections.

5. **Chemical Treatment:** Methods like coagulation, electrocoagulation, ion-exchange resin processes, and disinfection (e.g., chlorination) are employed to enhance water quality (Filali et al., 2022).

6. **Pretreatment:** Preliminary processes like sieving and decantation are conducted to reduce particulate load of oil etc. and regulate untreated greywater flow (Filali et al., 2022).

Hybrid Systems

Innovative hybrid solutions for greywater recovery, such as bioreactors with membranes paired with filters made of membranes (the use of nanofiltration or ultrafiltration), or aerated biofilter systems combined with filter marshes, were successfully tested. These combinations effectively purify greywater both physiochemically and microbiologically. Studies have demonstrated significant reductions exceeding 95% for turbidity, 75% for total suspended solids (TSS), 93% for biochemical oxygen demand (BOD5), and 85% for chemical oxygen demand (COD) (Filali et al., 2022).

Benefits of Gray Water Recycling

1. Cost Savings by using less fresh water reduce
2. Reduced Strain on Septic Systems and Treatment Plants
3. Improved Treatment Efficiency
4. Lower Energy and Chemical Usage
5. Enhanced Groundwater Recharge
6. Promoted Plant Growth
7. Nutrient Reclamation
8. Increased Environmental Awareness and Sensitivity (Al-Mashaqbeh et al., 2012)

Pollution Control Measures

Livestock contributes significantly to agricultural emissions, primarily through methane (CH4) emissions from enteric fermentation and manure management, as well as nitrous oxide (N2O). These emissions are a major factor in agricultural pollution, alongside fertilizer use. Agricultural water pollution, caused by inadequate treatment of pollutants discharged into water bodies, harms aquatic plants, organisms, and ecosystems (Baronti et al., 2022; Wato, Amare, Bonga, Demand, & Coalition, 2020).

Waste Management Systems

Strategies to reduce water pollution from livestock, including waste management systems, encompass several key components. It can have three different components:

1. Manure handling refers to the process of removing or managing manure in animal housing or grazing areas.
2. Manure storage refers to the infrastructure and methods for storing and applying manure.
3. The way manure is administered to the land for crop fertilization.

However, within these three broad categories, there are various technologies, structures, and equipment, which in combination comprise a suite of methods, or a system (MMS) that farmers can utilize to manage manure (Niles et al., 2022).

1. Manure Storage and Handling:

Manure includes voided feces and urine, spilled feed and water, wash water, bedding, and other wastes. Livestock producers manage manure through methods like solid, slurry, or liquid handling systems. Effective storage, such as covered anaerobic lagoons, helps control nutrient release and minimize runoff (Zong Liu, 2020).

2. Manure Treatment: Techniques such as solid-liquid separation and anaerobic digestion are employed. Solid-liquid separation improves nutrient management and pathogen control, while anaerobic digestion produces biogas for energy and reduces odor.

- **Manure solid-liquid separation:** Solid-liquid separation is a method used to treat slurry or liquid manure, separating it into a low-moisture solid fraction and a low-strength liquid fraction. This process enhances handling and transport of the manure while also allowing for better nutrient management. Techniques such as sedimentation, filtration, or centrifugation are employed, sometimes with chemical aids, to achieve separation.

- **Pathogen reduction in manure treatment:** Pathogen reduction in manure can be effectively achieved through composting, which requires maintaining temperatures above 50°C to deactivate pathogens. Anaerobic digestion with external heating is also effective in reducing pathogens, resulting in digestate with lower pathogen risks. Additionally, practices like liming and ammonia treatment are commonly used to deactivate microorganisms in manure (Janni & Cortus, 2020; Zong Liu, 2020).

3. Composting

Composting is a widely used method for treating solid manure. Microorganisms break down organic matter in manure under aerobic conditions, generating heat, carbon dioxide, and water. This process removes moisture, volatile organic matter, and reduces manure volume. Composted manure is easier to handle, transport, and less likely to emit odors or pollutants. The heat produced kills pathogens and weed seeds, producing a safe-to-use product that releases nutrients slowly, reducing water quality impacts.

4. Anaerobic digestion system:

Anaerobic digestion converts liquid and slurry manure into methane-rich biogas using microorganisms in an oxygen-free environment. This biogas can be used for electricity and heat generation, with potential for household and industrial use after purification. Anaerobic digestion also reduces organic nutrients, eliminates weed seeds, reduces odors, and deactivates pathogens (Zong Liu, 2020).

Manure application: Manure applied as organic fertilizer can reduce reliance on mineral fertilizers, but excessive application may increase nutrient levels like phosphorus and potassium to undesirable levels.

Mitigation of Greenhouse Gas Emissions

Livestock production faces significant challenges from climate change, including increased temperatures, erratic precipitation patterns, and rising carbon dioxide levels. Greenhouse gas (GHG) emissions from livestock primarily consist of methane (CH4), nitrous oxide (N2O), and carbon dioxide (CO2) from both direct and indirect sources such as feed production and land use changes (Cheng et al., 2022).

The GLEAM results indicate that greenhouse gases from farm animals' distribution networks consist of 50% the gas methane (CH4), 24% nitrous oxide (N2O), and 26% carbon dioxide (CO2). Emissions by category are shown in Figure.3(Cheng et al., 2022), where methane (CH4) emissions are portrayed in yellow, nitrous oxide (N2O) in green, and carbon dioxide (CO2) in red.

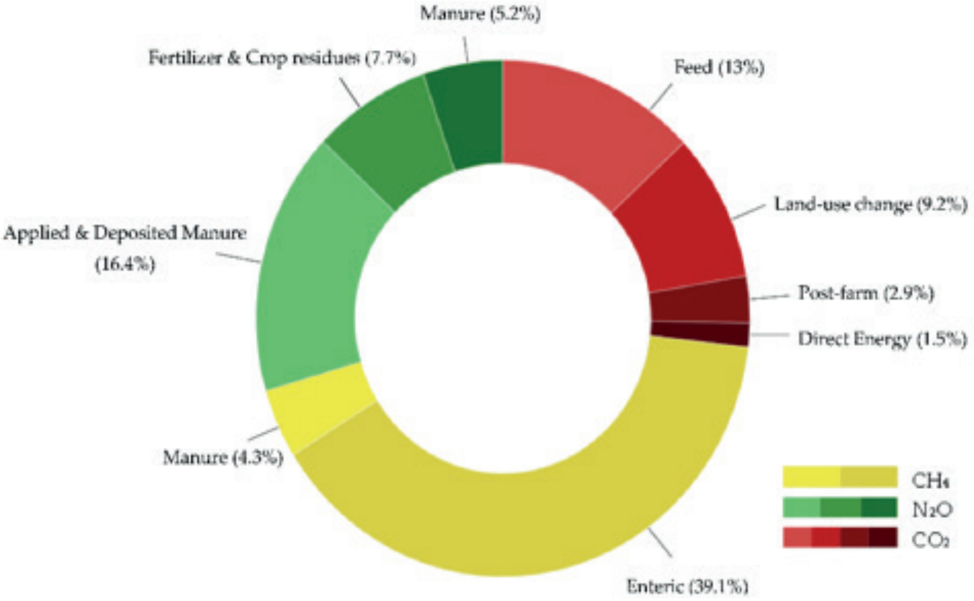

Figure3. Emission of gases from livestock

Strategies

Mitigation strategies to reduce livestock GHG emissions include effective manure management practices like anaerobic digestion and composting.

Manure Management Practices

Livestock manure generates both N_2O and CH_4 emissions, and most of these are related to storage and handling methods. Altered manure storage practices can reduce manure GHG (CO_2, CH_4, N_2O) emissions. These include shortened storage duration, lowered storage temperature, solid–liquid separation, and less use of water (Cheng et al., 2022). Anaerobic digestion and composting play a major role in reducing GHG emissions.

1. Anaerobic digestion

Anaerobic digestion captures methane from manure in anaerobic conditions, converting it into biogas for renewable energy production, thereby reducing methane emissions significantly. The technique comprises four major steps: hydrolysis, acidogenesis, acetogenesis, and methanogenesis (Yao et al., 2020).

- **Reduction of GHG emissions:** Anaerobic digestion breaks down manure using microorganisms in oxygen-free conditions, producing biogas (mainly CH_4 and CO_2) and digestate. This biogas can be used for generating heat or electricity, reducing greenhouse gas (GHG) emissions by replacing fossil fuels and by changing the composition of emissions from the traditional combination of N_2O and CH_4 into a combination of CO_2 and CH_4 (Cheng et al., 2022).

Steps of Anaerobic Digestion

The process involves four steps shown in Fig.4 (Yao et al., 2020): hydrolysis breaks down organic substrates into smaller compounds; acidogenesis converts these compounds into volatile fatty acids, CO_2, and H_2; acetogens further convert VFAs into acetic acid; and methanogens produce methane and CO_2 from acetate and hydrogen (Yao et al., 2020).

Overall, anaerobic digestion can reduce GHG emissions from manure by over 30% compared to traditional methods. Dietary adjustments for animals can also help reduce emissions by altering the volume and composition of manure (Cheng et al., 2022).

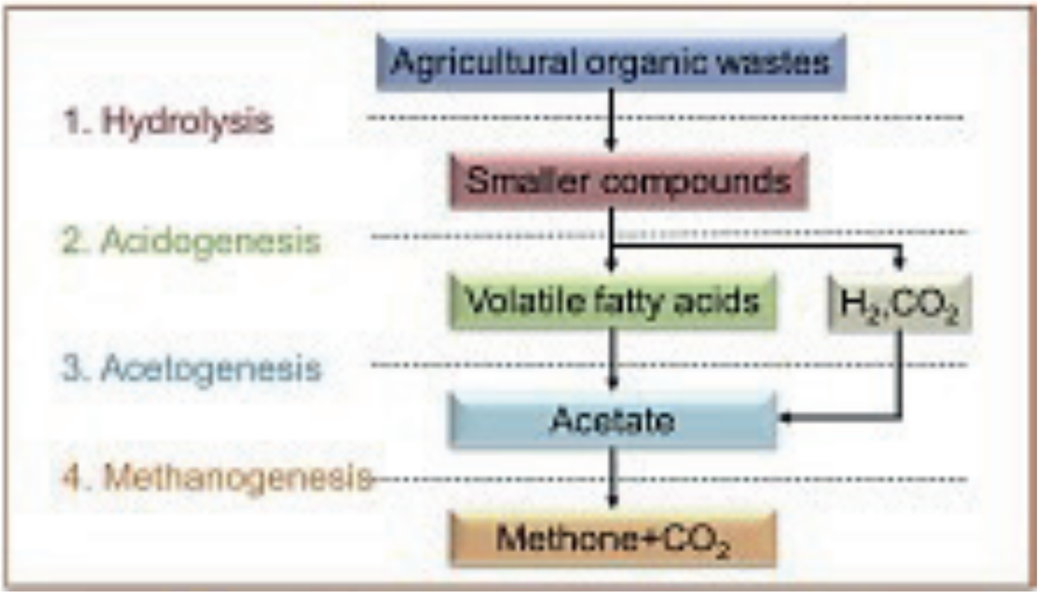

Figure 4. Steps of Anaerobic Digestion

Biochar Composting

Biochar composting combines manure with biochar, offering an effective alternative to traditional methods like stockpiling or composting separated manure solids. It can significantly reduce CH4 emissions by 84% compared to composting without biochar. This approach is particularly beneficial for smaller farms and those without digesters, potentially increasing the CH4 mitigation potential of dairy manure globally (Harrison et al., 2022).

2. Adoption of Renewable Energy Sources

Utilizing biogas plants in livestock farming significantly reduces greenhouse gas (GHG) emissions by capturing methane (CH_4) from manure and converting it into renewable energy. In this process, dewatered digested manure is repurposed as recycled bedding material in barns. The cycle begins with mixing excreted manure and recycled bedding material in a fermenter, where anaerobic fermentation occurs over 30 days. After fermentation, the digested manure undergoes solid-liquid separation using a screw press separator, resulting in solid compostable material used for bedding. This integrated approach reduces CH_4 emissions by 43.0% from organic fertilizer storage and recycled bedding material production through solid-liquid separation in biogas systems. Furthermore, the use of sealed tanks for digestate storage prevents additional gas emissions into the atmosphere, contributing further to greenhouse gas (GHG) reduction. Studies indicate that closed tank systems can significantly minimize CH_4 emissions compared to open storage methods (Setoguchi et al., 2022). Research by Battini et al. (2014) indicates a 67% reduction in CH_4 emissions from stored biogas digestate compared to raw slurry, further enhanced by solid-liquid separation that minimizes organic matter entering storage storage. Additionally, Setoguchi et al. (2022) emphasize that anaerobic biogas processes yield digestate with reduced nitrous oxide (N2O) emissions post-application, while also mitigating odor, pathogens, and weed seed germination in animal manure. The use of sealed tanks for digestate storage further prevents GHG emissions, providing comprehensive environmental benefits in livestock farming practices (Setoguchi et al., 2022). Moreover, biogas production offers additional benefits such as reducing nitrous oxide (N_2O) emissions compared to raw slurry after field application, as well as mitigating odor, pathogens, and weed seed germination in animal manure (Setoguchi et al., 2022). This integrated approach not only enhances energy sustainability in livestock farming but also addresses environmental concerns associated with manure management.

10. Addressing Antibiotic Resistance

Antibiotics have been used in animal husbandry since the 1950s to promote growth, treat diseases, and prevent them. The indiscriminate use of antibiotics has resulted in the rise of multidrug-resistant bacteria that harm both animal and human health (Low et al., 2021).

Impact of Antibiotic Use in Livestock

The use of antibiotics in livestock farming has led to the development of antimicrobial-resistant bacterial strains, posing significant risks to both environmental and public health. This situation creates a reservoir of resistant bacteria within animal populations, which can spread to humans through direct and indirect contamination.

Individuals in direct contact with livestock, such as farm workers, veterinarians, and slaughterhouse workers, are at high risk of being contaminated with resistant bacteria. Once contaminated, these individuals can transmit resistant bacteria or their genes into their communities and healthcare settings, potentially leading to infections that are difficult to treat. Consumers of animal products are also at risk. They can contract antibiotic-resistant bacteria through the handling and consumption of contaminated meat, such as poultry. The extent of this risk, however, remains a debated topic.

Resistant bacteria can spread from farms into the environment through manure application on agricultural fields. These bacteria can be transported via dust, water, and food products, further disseminating resistance genes and contaminating natural ecosystems. This environmental spread not only affects wildlife but also increases the risk of human exposure through various pathways, amplifying the public health threat (Hosain, Kabir, & Kamal, 2021).

Strategies to Mitigate Antibiotic Resistance

Improved Farm Management Practices: Implementing rigorous hygiene practices can prevent infections, reducing the need for antibiotics. Providing balanced diets to livestock enhances their immune systems, making them less susceptible to infections. Proper handling, adequate space, and appropriate environmental conditions can decrease disease incidence.

Vaccination and Probiotic: Vaccines protect livestock from bacterial infections, reducing the need for antibiotics. These improve gut health and boost immunity, making animals more resistant to infections and reducing the need for antibiotics.

Selective Breeding and Alternative Therapies: Breeding programs focused on enhancing genetic resistance to diseases can reduce the need for antibiotics. AMPs, also known as host defense peptides, are an alternative to traditional antibiotics. These peptides, found in various life forms, contribute to intrinsic mucosal immunity and protect against microbial infections).

Education and Public Awareness: Training and educating farmers about the risks of antibiotic overuse and the benefits of alternative practices. Raising awareness among consumers about the importance of antibiotic-free meat and encouraging demand for sustainably produced products.

Research and Development: Advances in biotechnology, such as the use of carbohydrate-modified compounds and combination therapies, are being explored to develop new antibacterial agents that can overcome antibiotic resistance. Increasing the production of AMPs in the body to boost immune responses can help combat infections. For example, Vitamin D supplements are being evaluated for their role in modulating AMP expression and treating bacterial infections.

Integrated Pest and Environmental Management: Integrated pest management strategies can reduce the need for antibiotics by controlling parasites that might otherwise lead to infections. Promoting sustainable agriculture practices that focus on maintaining ecological balance and reducing reliance on chemical interventions (Mann, Nehra, Rana, & Dahiya, 2021).

Soil and Air Quality Impact

Soil Degradation by Conventional Agriculture and Livestock

Conventional agricultural practices can significantly degrade soil by reducing soil organic matter (SOM) and nutrient content. Moreover, these practices lower microbial diversity and biochemical activity in the soil. Within the agricultural sector, livestock is responsible for nearly 80% of all agricultural emissions, primarily from enteric fermentation (methane-CH4 emissions) and manure management, which release methane (CH4) and nitrous oxide (N2O) into the atmosphere.

Grazing and Soil Erosion

Grazing has an immediate effect on the condition of the soil. Grass protects soil from erosive forces like water and wind, while also supporting biological activity including organic matter decomposition and soil organic carbon buildup. However, improper grazing can remove photosynthesizing leaves, disrupt natural physicochemical processes, and trigger soil erosion. Excessive grazing leads to muddy conditions, soil compaction, and the spread of weed species that thrive under these conditions.

Methods for Soil Restoration

Pasture Management and Sustainable Practices

To mitigate the negative impact of livestock on soil quality and enhance land health and productivity, it is essential to adopt sustainable pasture management practices. Proper pasture management helps maintain soil health and function, ensuring long-term benefits such as water conservation and carbon stock accumulation.

1. **Optimal Grazing Pressure:** Grazing at the ideal level (15 cm) optimizes new grass output while also promoting plant regrowth. This practice ensures that livestock receives the optimal nutritional value from the grass while preventing soil degradation. Maintaining optimal grazing pressure involves adopting a pastoral plan that balances livestock food demands with minimal forage wastage.

2. **Maintaining Soil Coverage and Botanical Composition:** Adequate management of domestic herbivores is crucial for maintaining good soil coverage and the botanical composition of meadows. This includes adjusting stocking rates to avoid overgrazing and under grazing, which can both lead to soil degradation and loss of productive species.

3. **Reducing Livestock Emissions:** Implementing practices that reduce livestock emissions, such as improving feed efficiency and manure management, can also benefit soil quality. These practices help decrease the environmental footprint of livestock farming, contributing to overall land health and productivity (Baronti et al., 2022).

Impact on Air Quality and Strategies for Improvement

Livestock farming significantly contributes to air pollution through the release of ammonia (NH3), which acts as a precursor to fine particulate matter. Fine particulate matter originates from various sources, including traffic, power plants, industry, household energy use, and agriculture (Martins et al., 2015). Ammonia reacts with sulfuric and nitric acids in the atmosphere to form fine particulate matter. Approximately 80% of ammonia emissions in Europe are attributed to agricultural activities, with the main sources being livestock urine and manure storage. The emission levels of ammonia depend on the type of livestock, with beef and sheep producing higher amounts compared to pigs and poultry.

Strategies to Mitigate Air Quality Effects

To address the impact of livestock farming on air quality, several strategies can be implemented to reduce ammonia emissions and improve ventilation in farming operations.

1. Increased Livestock Production Productivity: Enhancing the efficiency of livestock farming can reduce the environmental impact. This can be achieved by supporting local farmers' markets and community gardens, which reduces the need for long-distance transportation of goods. Decreasing the demand for deforestation can also lower atmospheric CO2 levels, further mitigating climate change.

2. Manure Management Optimization: Effective manure management is crucial for reducing emissions of ammonia, methane (CH4), and nitrous oxide (N2O). Strategies include: Lowering the dietary crude protein content in animal feed to reduce nitrogen excretion. Acidifying external slurry storage to decrease ammonia volatilization. Frequently removing manure to minimize emissions. Using covers such as straw or artificial films over manure storage to limit gas release.

3. Eliminating the consumption of fossil fuels: Reducing the agricultural sector's dependence on fossil fuels can help lower greenhouse gas emissions. This includes minimizing the use of oil for producing nitrogenous fertilizers, promoting a shift towards renewable energy sources.

4. Reduction in the Production and Consumption of Foods from Animal Sources: Promoting healthier diets with lower consumption of animal-based foods can decrease the environmental impact of livestock farming. Reducing the demand for meat and dairy products can lead to a decrease in ammonia emissions and overall air pollution (Sofia, Gioiella, Lotrecchiano, & Giuliano, 2020).

5. Technological and Management Improvements: Implementing advanced technologies and better management practices can significantly reduce ammonia emissions. Examples include installing grooved floor systems with teeth scrapers in animal confinement facilities. Creating tree shelterbelts around confinement zones to function as barriers to ammonia dispersal. Applying precise fertilizer management techniques to avoid overapplication and runoff.

6. Optimized Ventilation Systems: Improving ventilation systems in livestock facilities can help disperse and dilute ammonia and other emissions, reducing their concentration and impact on air quality. Effective ventilation is essential for maintaining air quality within and around livestock operations (Domingo et al., 2021).

Future Perspectives

Precision Livestock Farming (PLF)

Precision Livestock Farming (PLF) is the application of cutting-edge approaches for customized livestock management, with continuous real-time monitoring of health, welfare, production/reproduction, and environmental effect. PLF collects and analyses livestock data using a variety of techniques and technologies, including wearable sensors, data collection systems, and behavioral analysis tools.

- **Wearable Sensors:** These devices monitor an animal's physiological and reproductive status, behavior, and health. They provide continuous, non-intrusive data collection, enabling early detection of health issues and timely interventions.
- **Integrated Systems for Data Harvesting:** These systems combine data from various sensors and make it accessible to farmers on smartphones and laptops. Real-time data allows for better management of production inputs, improving efficiency and reducing waste.
- **Electronic Milk Meters:** These early PLF applications measure milk production

electronically, providing accurate measurements of milk yield and enhancing dairy farm productivity.

- **Rumination Monitoring:** Devices that monitor chewing activity to assess health and well-being. Early detection of digestive and feeding issues leads to timely interventions and improved animal welfare.
- **Behavior Analysis Tools:** These tools analyze livestock behavior to detect abnormalities or changes, helping identify stress or discomfort in animals and allowing for prompt corrective actions to ensure better welfare (Monteiro, Santos, & Gonçalves, 2021).

Genomic Selection in Livestock Farming

Genomic selection uses DNA markers across the genome to predict the breeding values of animals. This allows for the early and accurate selection of animals with desirable genetic traits, surpassing traditional methods that rely on observable traits and phenotypic records.

Benefits:

- **Increased Genetic Gain:** Genomic selection can achieve up to 143% higher genetic gain compared to traditional methods by identifying superior genetic traits early.
- **Reduced Phenotyping:** Fewer phenotypic records are needed, allowing resources to be redirected towards genotyping more animals, which enhances genetic gain.
- **Higher Selection Intensity:** More candidate animals can be genotyped, increasing the intensity of selection for desirable traits.
- **Improved Accuracy:** The accuracy of genetic evaluations improves, especially for non-phenotyped candidates and proven females, leading to better breeding decisions.
- **Shorter Generation Intervals:** Early identification of superior genetics reduces the time between generations, accelerating genetic improvement.

Practices

- Using an initial training population enhances genetic gain by leveraging existing genetic data from the start.
- Prioritizing genotyping over phenotyping results in higher genetic gains as more animals are evaluated genetically.
- Reducing the number of phenotypic records per lactation allows for more extensive genotyping, significantly boosting genetic gain.
- Genotyping a larger pool of candidates increases selection intensity, ensuring only the top performers are chosen for breeding, thus maximizing genetic progress (Obšteter, Jenko, & Gorjanc, 2021).

Innovations in animal husbandry are crucial for the future of sustainable livestock farming. By embracing these technologies and practices, the livestock industry can significantly reduce its environmental impact, improve animal welfare, and ensure a sustainable supply of animal products. These developments are a step towards a more robust and sustainable food system that benefits both producers and consumers.

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About The Authors

Dr. Saba Saba

Affiliation: Department of Microbiology and Molecular Genetics, The Women University Multan, Multan, Pakistan

Email: saba.6395@wum.edu.pk ORCID: 0000-0002-9182-4667

Furqan Ali

Affiliation: Central and Diagnostic Laboratories, K&Ns Food Poultry PVT. Ltd (ISO/IEC 17025) & Department of Microbiology and Molecular Genetics University of Okara, Okara, Pakistan

Email: malikfurqan001@gmail.com ORCID: 0009-0005-0444-6434

Ms. Muqadas Kanwal

Affiliation: Department of Microbiology and Molecular Genetics University of Okara, Okara, Pakistan

Email: muqadasmuqadas685@gmail.com ORCID: 0009-0000-4832-3544

Ms. Kainat Waheed

Affiliation: The University of Lahore, Pakistan

Email: kainatwaheed15@gmail.com ORCID: 0000-0001-8937-8605

Dr. Abid Hussain

Affiliation: Department of Microbiology and Molecular Genetics, University of Okara, Pakistan

Email: abihqureshi@gmail.com ORCID: 0000-0001-8661-9522

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SECTION II:

ANIMAL HEALTH

THE IMPACT OF PROBIOTICS ON ANIMAL HEALTH

Bruno TILOCCA

Sina Salajegheh TAZERJI

1. The Impact of Probiotics on Animal Health

Microorganisms are ubiquitous living systems harbored in all sections and anatomic districts of the animal body. Nevertheless, microbial communities associated to the gastrointestinal tract (GIT) are nowadays accounted as the most abundant and biodiverse, and their massive featuring highlighted concern in many physiological processes of most superior animals, humans included. In this light, the focus of the present chapter is GIT-associated microbial communities and the functional assets they are associated with, although pivotal roles and potentials are recognized to the microbial communities inhabiting other anatomical districts (Deusch, Tilocca, Camarinha-Silva, & Seifert, 2015).

In recent years, the use of probiotics in animal health has garnered significant attention and interest among researchers, veterinarians, and animal owners alike. Probiotics, defined as live microorganisms that confer health benefits when administered in adequate amounts, have shown promising results in enhancing the well-being and performance of various animal species. Primarily consist of beneficial bacteria and yeast strains, such as Lactobacillus spp., Bifidobacterium spp., and Saccharomyces spp., among others (Abd El-Hack et al., 2022; Abdelbasir, McCourt, Lee, & Vanegas, 2020).

GIT microorganisms are naturally present in all animals and play crucial roles in maintaining gut health and immune function. However, factors such as stress, illness, or antibiotic use can disrupt the balance of these microbial communities, leading to digestive disorders, reduced nutrient absorption, and susceptibility to infections. In this scenario, modulating the microbial community through administration of probiotics counterbalance the above dysbiosis conditions laying at the ground of the insurgence and/or progression of system pathologies of both infective and noninfective origin (Colditz & Hine, 2016; Committee et al., 2018).

The following chapter provides an overview of the usage of probiotics to sustain animal health and production in diverse zootechnic contexts.

2. Mechanisms of Action of Probiotics

The mechanisms through which probiotics exert their beneficial effects on animals are multiple and intricated (Figure1). They competitively exclude harmful pathogens by occupying binding sites on the intestinal epithelium, thereby preventing the colonization of pathogens. Also, probiotics enhance the integrity of the gut mucosal barrier by promoting the production of mucins and strengthening tight junctions between epithelial cells. Probiotics help prevent the translocation of pathogens and toxins across the intestinal lining. This barrier function is crucial for maintaining immune homeostasis which is, as well, modulated by the metabolic activity of probiotics strains.

Altogether probiotics' mechanisms reduce the risk of gastrointestinal infections and improve overall health.

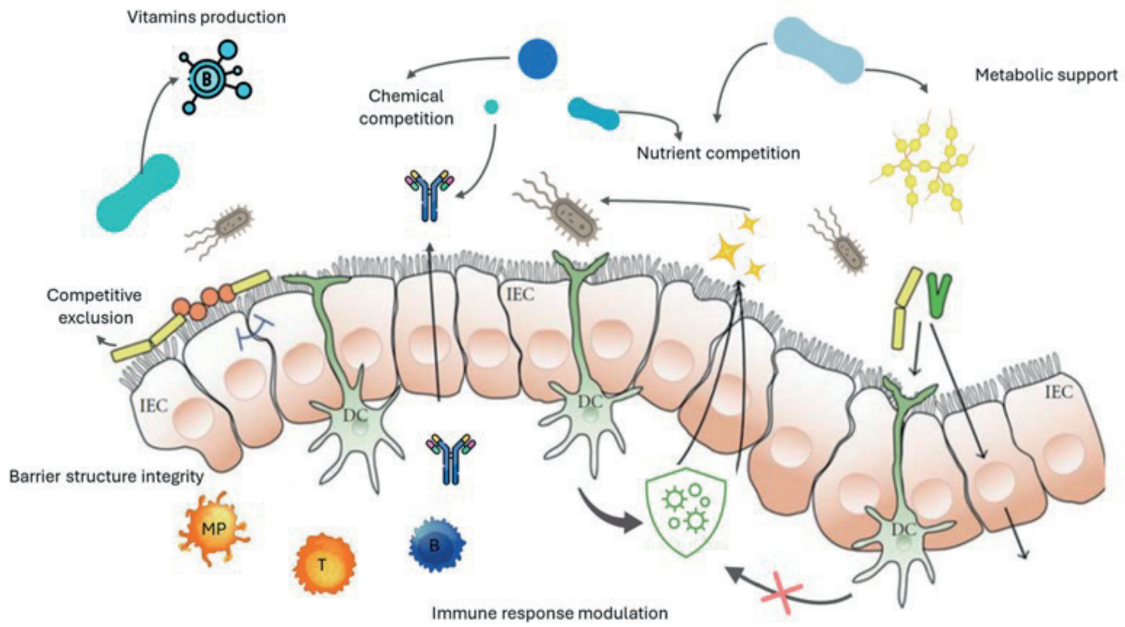

Figure 1. Mechanisms of action of probiotics. The figure summarizes the major mechanisms undertaken by the probiotic's cells administered to support animal health status. IEC: intestinal epithelial cells; DC: dendritic cells; MP: macrophages; T: T-cell lymphocyte; B: B-cell lymphocyte.

2.1 Composition of the microbial community

The direct mechanism of action of probiotics includes the modulation of the microbial community composition within the gut. This involves establishing complex interactions between the probiotic microorganisms themselves, the indigenous gut microbiota, and the host's gastrointestinal environment. It impacts the alpha-microbial diversity, microbial richness and evenness (Maftei et al., 2024). These, in turn, are mirrored as altered patterns of interactions among the microorganisms and its host, accounting for both qualitative and quantitative changes, resulting in the ameliorated tuning of the physiological functions as mediated by the hosted microbial community (Celi et al., 2017). In addition, probiotics stimulate the production of mucins, which are glycoproteins that form the protective mucus layer covering the intestinal epithelium. Such mucus layer serves as a physical barrier against pathogens and toxins, while also providing a habitat for beneficial bacteria (Paone & Cani, 2020). By promoting mucus production and maintaining barrier function, probiotics support gastrointestinal health and reduce the risk of intestinal permeability and the associated inflammatory responses.

As of today, further research into the specific mechanisms and interactions involved in probiotic-mediated microbiota modulation helped, and will continue, to uncover new therapeutic potentials for managing a wide range of health conditions in both humans and animals.

2.2 Metabolic support of the microbial community

The metabolic activities of probiotics are diverse and multifaceted, impacting various aspects of host physiology and gut microbiota composition. Through fermentation, production of antimicrobial compounds, modulation of immune responses, enhancement of nutrient utilization, reduction of oxidative stress, and metabolism of bile acids, probiotics provide a significant contribution to the gut health, improving overall well-being in animals and humans alike (Santos-Buelga, González-Paramás, Oludemi, Ayuda-Durán, & González-Manzano, 2019; Sanz & De Palma, 2009).

2.2.1. Fermentation and Acidification

Probiotic bacteria are known for their ability to ferment various substrates present in the gut, such as dietary fibers and complex carbohydrates. During fermentation, probiotics produce short-chain fatty acids (SCFAs) such as acetate, propionate, and butyrate. These, in turn, lower the intestinal lumen pH, creating an acidic environment that inhibits the growth of pathogenic bacteria. In this manner, probiotics promote a favorable ecological niche for themselves and other beneficial microorganisms, besides suppressing harmful pathogens (Dakal, Kumar, Majumdar, & Yadav, 2016; Dama et al., 2024).

2.2.2. Production of Antimicrobial Compounds

Probiotics can synthesize and release antimicrobial substances that directly inhibit the growth of pathogenic bacteria. These antimicrobial compounds may include bacteriocins, hydrogen peroxide, organic acids, and peptides. Bacteriocins are proteinaceous toxins produced by probiotics that specifically target and kill even closely related bacterial strains without exerting the toxic effect on the beneficial ones. This chemical exclusion mechanism helps probiotics to maintain dominance and prevent colonization by harmful microbes in the gut. Analogously, other antimicrobial compounds produced by the probiotics strains exert their activity by other mechanisms including pore formation and enzyme activity modulation, as well as quorum sensing after having t

2.2.3. Modulation of Immune Response

The metabolic by-products of probiotics, particularly SCFAs like butyrate, have immunomodulatory properties. Butyrate, for example, serves as an energy source for colonic epithelial cells and helps to maintain intestinal barrier function. It also regulates the production of inflammatory cytokines and promotes the differentiation of regulatory T cells (Tregs), which play a key role in immune tolerance and homeostasis. By influencing the gut-associated lymphoid tissue (GALT) and mucosal immune responses, probiotics contribute to enhancing the host's immune defense against pathogens (Zhou, Chen, Patil, & Dong, 2024).

2.2.4. Enhancement of Nutrient Utilization

Probiotics can enzymatically break down complex nutrients that are otherwise indigestible by the host's digestive enzymes. For instance, specific strains of probiotics are employed to provide enzymes like cellulase and xylanase that degrade plant cell walls and release nutrients such as sugars and vitamins. This enzymatic activity enhances nutrient absorption and utilization by the host, leading to improved growth performance and feed efficiency in animals (Yi, Pan, Long, Tan, & Zhao, 2020).

2.2.5. Reduction of Oxidative Stress

Some probiotic strains possess antioxidant properties and can scavenge free radicals within the gut environment. By reducing oxidative stress, probiotics help protect intestinal cells from damage caused by reactive oxygen species (ROS), which are generated during normal metabolic processes and under conditions of inflammation or stress. This antioxidant activity contributes to maintaining gut barrier integrity and overall health status (Al-Shawi et al., 2020; Anadón, Ares, Martínez-Larrañaga, & Martínez, 2019).

2.2.6. Metabolism of Bile Acids and Cholesterol

Certain probiotics have the ability to metabolize bile acids, facilitating their excretion from the body. This metabolic activity can lower blood cholesterol levels by reducing the reabsorption of bile acids in the intestine, thereby promoting cardiovascular health. Additionally, probiotics may directly influence lipid metabolism and bile acid synthesis in the liver through signaling pathways involving SCFAs and other metabolic intermediates (Abd El-Hack et al., 2022; Abdelbasir et al., 2020).

In summary, the mechanism of action of probiotics via their metabolic activity involves a complex interplay between the probiotic microorganisms and the host's gut environment. Probiotics exert their beneficial effects through a variety of metabolic activities; although, not all of them have yet been elucidated. Further research into the specific metabolic pathways and interactions between probiotics and host physiology will continue to unveil new therapeutic potentials and applications in

3. Probiotics Applications in Animal Health

The application of probiotics in animal health spans across various species, including livestock (such as cattle, poultry, and swine), companion animals (like dogs and cats), and even exotic animals kept in captivity. In livestock farming, probiotics have been extensively studied for their ability to improve growth performance, feed efficiency, and resistance to diseases.

3.1. Cattle

Probiotics can contribute to overall gut health in cows, promoting better digestion and absorption of nutrients. Probiotics support cow nutrition through various mechanisms. Ruminants rely on microbial fermentation in the rumen to break down fibrous plant material. Probiotics containing fiber-degrading bacteria such as Fibrobacter succinogenes and Ruminococcus flavefaciens showed enhanced metabolism of complex carbohydrates (cellulose and hemicellulose) into simpler sugar units that animals can absorb and utilize more efficiently. Here, probiotic strains, such as those belonging to the genus Lactobacillus and Bifidobacterium, resulted in improved protein digestion in the rumen. They produce enzymes that break down proteins into amino acids, which are then available for absorption and used for growth, milk production, and maintaining of the overall health status (El Jeni et al., 2023). Also, probiotics can improve the availability and absorption of minerals such as calcium, phosphorus, magnesium, and iron. For example, lactic acid bacteria and certain strains of Bacillus spp. produce organic acids that lower pH in the gut, facilitating the solubilization of minerals and their subsequent absorption (Varvara & Vodnar, 2023). Similarly, vitamins are produced by a variety of probiotic bacteria, mainly strains of Bifidobacterium and Lactobacillus. These have the ability to synthesize vitamins such as group-B vitamins (B1, B2, B6, B12) and vitamin K. These vitamins are crucial in various metabolic processes and overall health in cows (Wan et al., 2022).

Besides the production of nutritional components, probiotics are active in the degradation and/or neutralization of anti-nutritional factors naturally present in feed ingredients, such as phytates and tannins (Petrova et al., 2022). These, indeed, inhibit the absorption of minerals and reduce the digestibility of proteins and carbohydrates. By degrading these compounds, probiotics improve overall feed efficiency and nutrient utilization. Furthermore, a healthy gut microbiota, as promoted by probiotics, maintains intestinal integrity and function. This supports nutrient absorption, ensures that the gut lining is healthy, immunocompetent and capable of absorbing nutrients effectively.

In addition, probiotics actions extend to reducing the risk of infections associated with suboptimal nutrition or stress. Stress can compromise immune function in cows, making them more susceptible to infections. Probiotics have been shown to mitigate the negative effects of stress by modulating the gut-brain axis and supporting a healthy gut microbiota; in turn, enhances immune responses and resilience to infections (Binda et al., 2024).

Concerning the protective role of probiotics against infective agents, mastitis is an informative example. Worldwide, mastitis is common and among the costliest infection in dairy cows. Probiotics such as Lactobacillus spp. and Streptococcus spp. have been studied for their ability to counterbalance mastitis-causing pathogens like Staphylococcus aureus and Escherichia coli by preventing them from adhering to mammary epithelial cells (Bouchard et al., 2015). Also, selected probiotics strains can modulate the immune response in the udder, reducing the severity of mastitis (Kober et al., 2022).

Diarrheal diseases in calves can be caused by various pathogens such as rotavirus, coronavirus, and enterotoxigenic E. coli. Probiotics strains of Lactobacillus and Bifidobacterium scored an improved gut health and reduced incidence and severity of diarrhea by competing with pathogens for binding sites, production of antimicrobial substances, and enhancing mucosal barrier function (Kober et al., 2022).

Respiratory diseases such as bovine respiratory disease complex (BRDC) are of significant concerns in cattle. Oral administration of probiotics has proved to enhance immune responses in the respiratory tract; thus, reducing pathogen colonization and mitigating the severity of infections caused by bacteria like Mannheimia haemolytica and Pasteurella multocida (Andrés-Lasheras, Jelinski, Zaheer, & McAllister, 2022).

Altogether, by improving nutrient digestion and uptake, enhancing natural defenses and reducing the prevalence of pathogenic bacteria, probiotics administration in the cow industry help reduce the need for antibiotics in managing infections (Andrés-Lasheras et al., 2022). This approach supports sustainable farming practices and mitigates the risk of antibiotic resistance development.

3.2. Probiotics administration in the poultry industry

The poultry industry employs probiotics in farming practice acknowledged their ability to promote health status. Probiotic strains of Lactobacillus spp., Bifidobacterium spp., and Bacillus spp., colonize the avian intestinal tract and compete with harmful bacteria like Salmonella spp. and Clostridium perfringens, preventing system infections and the spread of foodborne diseases (Fathima, Shanmugasundaram, Adams, & Selvaraj, 2022). Immunomodulatory effects of probiotics have been documented in both innate and adaptive immune responses. They stimulate the production of immunoglobulins, enhance phagocytic activity of macrophages, and promote the proliferation and activation of T cells and natural killer (NK) cells in the GALT. This immune modulation helps chickens mount effective immune responses against pathogens, reduces the incidence of infections, and supports overall immune health and resilience.

In practical applications, probiotics are often administered through feed or water supplements to poultry flocks. This method is convenient and has shown promising results in field trials for reducing the incidence and severity of avian flu outbreaks. Also, probiotics hinder the shedding of avian flu viruses in poultry feces. This can lower the transmission of the virus within the flock and to other birds, thereby helping to control outbreaks (Parida, 2009).

Other applications of probiotics in the poultry industry include the control of Salmonella infections. Salmonellosis is a major concern in poultry due to its impact on both bird health and food safety. Probiotics, such as Lactobacillus and Bacillus, have been shown to competitively exclude Salmonella from the chicken gut colonization by means of both physical and chemical competition (Micciche, Foley, Pavlidis, McIntyre, & Ricke, 2018).

Clostridium perfringens is another impactful pathogen in the poultry sector as it can cause necrotic enteritis in chickens, leading to significant economic losses. Probiotics like Bacillus subtilis and other lactic acid bacteria have demonstrated the ability to inhibit Clostridium perfringens growth and reduce the incidence of necrotic enteritis when administered regularly in feed (Aljumaah et al., 2020). Analogously, Campylobacteriosis is a leading cause of foodborne illness associated with poultry products (Śmiałek, Kowalczyk, & Koncicki, 2021) . Probiotics have been investigated for their potential to reduce Campylobacter colonization in chickens. Studies have shown that selected probiotic strains can decrease Campylobacter counts in the chicken gut, thereby lowering the risk of contamination during processing (Śmiałek et al., 2021). The effectiveness of probiotics has been demonstrated also on parasites. Eimeria species are protozoan parasites responsible for coccidiosis. Administration of probiotics such as Saccharomyces cerevisiae and Bacillus spp. have been used to manage Eimeria infections by promoting gut health and enhancing immunity against coccidiosis (Kiarie, Leung, Akbari Moghaddam Kakhki, Patterson, & Barta, 2019).

Besides biotic insults, the poultry industry faces various stressors that can negatively impact bird health and productivity. Here, probiotics have been utilized to mitigate the negative effects of stress on chickens acquired during stressful conditions such as transportation, vaccination, or environmental changes. Administering probiotics can help maintain gut integrity, strengthen immune defenses, and improve overall resilience against infectious agents. In addition, as concerns over antibiotic resistance and consumer preferences for antibiotic-free poultry products grow, probiotics offer a viable alternative to antibiotic growth promoters (AGPs) in poultry production enabling growth performance and health without contributing to antibiotic resistance or residues in poultry meat and eggs (Kiarie et al., 2019).

Despite the numerous benefits of probiotics in poultry production, challenges remain, including the selection of appropriate probiotic strains, optimization of dosage and administration methods, and variability in efficacy under different farming conditions. Factors such as feed composition, management practices, and bird genetics can influence the effectiveness of probiotic supplementation in poultry. In this light, continued research into probiotic strains, formulations, and application strategies will further optimize their use for maximizing poultry health, welfare, and productivity globally.

3.3. Probiotics usage in pig productions

Probiotics have gained significant attention and application in the pig industry due to their potential to improve growth performance, feed efficiency, and overall health of pigs. One of the primary benefits of probiotics in pigs is their ability to promote gut health. Strains of Lactobacillus and Bifidobacterium, colonize the intestinal tract and compete with harmful bacteria for nutrients and attachment sites on the gut wall. This competitive exclusion reduces the proliferation of pathogens like Escherichia coli and Salmonella spp., thereby lowering the incidence of gastrointestinal infections and diarrhea in piglets (Attia et al., 2023). Also, probiotics help improve the digestive efficiency of pigs by enhancing the breakdown and absorption of nutrients from feed. They produce enzymes such as amylases, proteases, and cellulases that aid in the digestion of complex carbohydrates, proteins, and fibers. Facilitating nutrient utilization is crucial for optimizing growth rates and reducing production costs in pig farming (Canibe et al., 2022). Moreover, probiotics play a vital role in modulating the immune system of pigs. They stimulate the production of immunoglobulins and enhance the activity of immune cells such as macrophages and T cells in the gut-associated lymphoid tissue (GALT). This immune modulation helps pigs mount effective immune responses against pathogens and improves their resistance to infections and diseases, thereby reducing the need for antibiotic treatments. This positively impacts the marketability of the pig industry products. Indeed, with increasing regulatory restrictions and consumer concerns over antibiotic use in livestock production, probiotics offer a viable alternative to antibiotic growth promoters (AGPs). Probiotics provide similar growth-promoting effects by enhancing nutrient absorption, maintaining gut health, and boosting immune function without contributing to antibiotic resistance or residues in meat products. This shift towards probiotic supplementation aligns with sustainable and responsible farming practices in the pig industry (Liao & Nyachoti, 2017). In this view, the use of probiotics in pig farming has been associated with reduced stress levels and improved welfare outcomes. Stress factors such as weaning, transportation, and changes in diet can disrupt the gut microbiota and compromise immune function in pigs. Probiotics help maintain microbial balance, support gut barrier function, and mitigate stress-induced intestinal inflammation, thereby promoting overall well-being and resilience in pigs raised under intensive production systems (Liao & Nyachoti, 2017).

Besides the auxinic application of probiotics, they find application therapeutically in pig farming to manage infective diseases and health challenges. For instance, probiotic supplements have been shown to reduce the severity and duration of diarrhea outbreaks associated with enterotoxigenic E. coli infections in piglets (Liao & Nyachoti, 2017). Additionally, probiotics help mitigate the impact of environmental stressors and optimize growth performance during critical phases such as weaning, thereby supporting the overall health and productivity of pigs from nursery to finishing stages.

3.4. Administration of probiotics in companion animals

In companion animals, probiotics have shown promising effects in a variety of processes. Firstly, they enable managing gastrointestinal disorders, other than contributing to enhancing the overall immune response, which is particularly beneficial for older pets or those undergoing stressful situations like travel or changes in environment (Appanna & Appanna, 2018). Also, probiotics hinder infections in pets by supporting their immune system. Specifically, they stimulate immune responses in the gut-associated lymphoid tissue (GALT) and mucosal surfaces, where a significant portion of the immune system is located. Other mechanisms exploited for the probiotics include promoting a healthy gut microbiome, and directly inhibiting pathogenic bacteria. For instance, multiple species of Lactobacillus and Bifidobacterium help prevent and manage gastrointestinal infections in pets (Ellickson, 1985). They facilitate a balanced gut microbiota and excludes pathogenic bacteria as species of the genera Salmonella, Campylobacter, and Clostridium perfringens (Elbers et al., 2008; Ellickson, 1985). Along, probiotics strengthen and restore the intestinal barrier structure, reducing the risk of infections and improving digestive performances (Zinsstag, Schelling, Waltner-Toews, & Tanner, 2011). Administration of probiotics strains resulted in effective counteraction of the antibiotics side- effects. Thus, reducing the duration and severity of antibiotic-associated diarrhea and supporting overall recovery. Recent studies demonstrated that Lactobacilli, among others, can help maintain a healthy urinary tract environment by producing antimicrobial substances against uropathogens like E. coli (Song et al., 2022).

Stress can weaken pets' immune systems and increase their susceptibility to infections. Probiotics can help mitigate the effects of stress by producing neurotransmitters that regulate mood and stress responses (Madabushi, Khurana, Gupta, & Gupta, 2023).

In addition, probiotics applied orally or included in dental chews and treats can contribute to oral health in pets by reducing plaque formation, combating periodontal pathogens, and supporting gum health. This can help prevent oral infections and improve overall dental hygiene with important repercussions on the overall health status and animal wellness (Mäkinen, Mäyrä, & Munukka, 2019). Implementation of probiotics have also shown potential effects in managing dermatological conditions such as allergic skin diseases and infections caused by Malassezia yeast or Staphylococcus bacteria. Here, beneficial strains modulate the immune response by reducing inflammation, which may alleviate symptoms and support skin barrier function integrity (Bond et al., 2020).

3.5. Exotic animals

Probiotics administration in exotic animals can be applied to various species to support digestive health, immune function, and overall well-being. Unlike farm- and companion-animals, administration of probiotics to exotic animals has unique challenges and considerations, mainly linked to the animal management practices (Garcias-Bonet et al., 2024). Nevertheless, probiotics are, nowadays, administered to different types of exotic animals. In exotic avian species, probiotics administration demonstrated to support gastrointestinal health, especially during periods of stress or dietary changes. Alongside, other probiotic strains enhanced immune function in birds, helping to prevent infections and supporting animal health status. This is particularly beneficial in aviaries or breeding facilities where birds are more susceptible to stress-related illnesses (Smith, 2014).

Probiotics can aid in improving digestive function in reptiles, especially herbivorous species like tortoises and iguanas. They assist in breaking down plant fibers, enhancing nutrient absorption, and reducing the incidence of gastrointestinal issues such as constipation or impaction (Rawski, Kierończyk, Długosz, Świątkiewicz, & Józefiak, 2016). In addition, probiotics help treat microbial dysbiosis, a common condition for reptiles housed in captivity due to dietary changes or environmental stressors (Rawski et al., 2016). Similar effects have been observed in small mammals (e.g., Rabbits, Guinea Pigs) where probiotics administration benefitted herbivorous small mammals by aiding them in the fermentation of dietary fiber in the cecum and colon. This enabled enhanced nutrient utilization, prevents gastrointestinal stasis, and reduces the risk of conditions like bloating.

Exotic mammals may experience stress during transportation, veterinary visits, or changes in the environment. Here, probiotics showed supporting these animals by modulating stress responses, and maintaining immune function.

Interestingly, probiotics can be used in aquaculture settings to improve water quality and support the health of fish. Beneficial bacteria can compete with and inhibit the growth of pathogenic organisms in the aquatic environment, reducing the incidence of infectious diseases and promoting fish health (Wang, Chuprom, Wang, & Fu, 2020). Also, oral administration of probiotics enhances nutrient absorption and utilization, particularly in omnivorous and herbivorous fish species. This improves growth rates, feed efficiency, and overall performance in aquaculture operations.

4. New frontiers of probiotic administration: tailored veterinary medicine

Probiotics administration in animals through a tailored veterinary medicine approach involves drawing probiotic therapy to the individual animal's specific health needs, microbiome composition, and response to treatment; among the other interfering environmental variables one might consider depending on the specific issue. Although highly variable, tailored approaches share some common steps. Before starting probiotic therapy, veterinarians may profile microbiome composition and assess diversity of the animal's gut microbiota. This identifies any dysbiosis that may be contributing to health issues to treat or prevent. Based on the microbiome analysis and the animal's health condition, veterinarians select probiotic strains that are most likely to benefit the animal (Singh & Natraj, 2021). This selection considers the specific benefits each strain is capable of, such as promoting co-occurrence of beneficial bacteria, production of antimicrobial substances, and/or enhancing immune function. This step is crucial as it is required to forecast the role of the novel strain(s) in the biotic and abiotic mileu where it is expected to be hosted. Also, it is pivotal to determine the optimal dosage and administration method for the probiotics chosen, based on the animal's species, age, weight, health status, and the severity of the condition being treated (Jugan, Rudinsky, Parker, & Gilor, 2017). Likely to pharmacological treatments, a follow-up of the animal's response to probiotic therapy is expected, evaluating parameters such as digestive health, immune function, and overall wellness status.

Probiotics may be integrated with other personalized veterinary treatments, such as dietary modifications, medications, and supplements. This holistic approach addresses multiple aspects of the animal's health and maximizes the effectiveness of treatment. Adjustments of the probiotic regimen are to be made possible according to the animal's individual response and/or any changes in health status either correlated or independent from the probiotic treatment. In this light, veterinarians should periodically re-assess the animal's microbiome and health status to adjust probiotic therapy, if needed, to sustain beneficial effects and prevent recurrence of health issues.

Overall, tailored veterinary medicine enhances the effectiveness of probiotics administration by customizing treatment plans to meet the unique needs of each animal. This approach ensures that probiotic therapy is targeted, evidence-based, and optimized for improving the animal's health and well-being. Collaborating with a veterinarian who is knowledgeable in probiotics and personalized medicine is essential for emphasizing the uniqueness of the animals’ microbial community, modulating its finely tuned orchestration in favor of a long-lasting homeostatic balance without the administration of drugs or even the burdensome antibiotics.

In conclusion, probiotics represent a valuable tool for enhancing gut health, improving growth performance and supporting disease management in both companion animals and the animal production industry. By modulating the gut microbiota, boosting immune responses, and reducing the reliance on antibiotics, probiotics contribute to sustainable and efficient farming practices.

While probiotics offer numerous benefits, several challenges remain, including strain specificity, dosage optimization, and variability in efficacy across different production environments. Factors such as feed composition, management practices, and genetics can influence the effectiveness of probiotic supplementation. More research is needed to better understand the mechanisms of action of probiotics and to identify optimal formulations and application strategies for maximizing their health-promoting effects. As the understanding of probiotic interactions with the microbiome continues to advance, their integration into routine management practices holds great promise for promoting healthier and more resilient pig populations, worldwide.

5. Future Directions and Challenges

While the potential benefits of probiotics in animal health are substantial, several challenges remain. One critical consideration is the strain-specificity and dosage requirements for different animal species and health conditions. Moreover, the regulatory framework governing the use of probiotics in animal feed and healthcare products varies across regions, necessitating standardized guidelines for efficacy and safety assessments.

Future research directions include exploring novel probiotic strains, understanding their interactions with the host microbiota, and optimizing delivery methods to ensure viability and efficacy. Additionally, integrating probiotics with other nutritional strategies, such as prebiotics (which promote the growth of beneficial microbes) and synbiotics (a combination of probiotics and prebiotics), holds promise for synergistically enhancing animal health outcomes.

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About The Authors

Dr. Sina Salajegheh Tazerji is a veterinary medicine professional specializing in infectious and zoonotic diseases, public health, and One Health. He has extensive research experience and has published numerous papers in reputable journals. Dr. Sina has presented his findings at various national and international conferences. His expertise in research, teaching, and leadership makes him a valuable asset in the veterinary medicine field.

E-mail: sina.salajegheh@gmail.com ORCID ID 0000-0002-5259-6905

Professor Bruno Tilocca is a tenure track in animal infectious disease. His research focuses on host-pathogen interaction and antimicrobial interaction for the elucidation of biomarkers for diagnostic and prophylactic purposes. His research activity is summarized in book chapters and more than 50 peer-reviewed papers.

E-mail: btilocca@uniss.it

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HEALTH AND REPRODUCTION ISSUES IN LIVESTOCK

Abdul SAMEED SAHER

Ali RAZA

Khalid MEHMOOD

Amjad ISLAM AQIB

Kun LI

Riaz AHMED GUL

Health and reproduction are centered to be major factors influencing productivity and stability in the livestock industry. Bacterial and viral pathogens cause significant health issues in the dairy industry, among them the ability to reproduce efficiently. These issues have the potentials of leading to abortion, dystocia, retained placenta, mastitis, foot and mouth disease and parasitic infestations. Of all the infectious diseases affecting livestock, brucellosis is most notorious for causing abortion in the later stages of pregnancy, retained placenta, and post-partum metritis, and barrenness in the flock in subsequent cycles in cattle. Besides imposing a limit to low production; it persists in establishing major economic impacts and continued health threats to the population across the globe. Nutritional deficiencies, genetic factors, and environmental stress factor were also seen as the causes of these disorders in this chapter, as well. Feeding, health management, proper mating that includes selecting good stocks, observing biosecurity measures, and adopting mechanized technology are key areas to minimize and address the issues that arise when managing a healthy livestock.

Introduction

At present, the questions concerning the health of animals and reproduction in herd have become urgent since rather tangible changes as for production and stability of the received incomes in this sphere are observed. These matters are not problems of merely well-organized farms but rather can occur even in relatively easy setting with great details. This article explains the considerations surrounding animal welfare and the role that animal welfare plays in informing management practices on farms. This research highlights that any abnormality in productivity and efficiency has a negative effect on the economy as well as quantity of milk produced. Animal Fertility is also another aspect related to dairy production because it involves the ability of a cow to reproduce offspring. Observation of dairy cow is very important as it deals with the reproductive management in dairy cattle that aims at planning for the cow to conceive in such a way that she would get pregnant profitably soon after calving or after a given period. Consequently, reproductive efficiency is a key parameter in the dairy business and the calving interval should be considered in order to attain maximum milk yield by the dairy cows. Heat detection, accurate intrauterine insemination technique, high semen quality and maximal semen motility, and the environment of the female genital tract are any other factors linked with high fertility rates is very important (Tolosa et al., 2021).

The health of dairy cows is a major determinant of the general wellbeing and productivity of any livestock enterprise and some of the diseases that are common may be contagious and really keep production in check. Thus, constantly emerging dairy issues and new diseases persist to be a threat to the dairy industry as well as advancements in veterinary science and optimal animal husbandry practices. Especially due to the emergence of multi-drug resistant pathogent and formation of climate changes together with the contemporary socio-/politics it is getting more difficult in the modern world to cope with the animal health issues. In other words, they should be combined and implemented within the context of a complex strategy for profitable dairy farming (Wells et al., 1998).

The major problems in health and reproduction of livestock are infertility, dystocia, parasites infestations, retained placenta, mastitis, foot and mouth disease would be examined in this chapter, their causes connected with nutritional efficiencies, genetic factors, stress factors, environment, and the ways how to protect from these factors. Some measures and effective control strategies as well as research prospects are discussed in this chapter to control these issues regarding management and production.

Common Reproductive Issues

Abortion

Abortions in dairy cattle may be accidental and may be associated with infections or non-infections causes. Some of the known infectious diseases that commonly cause abortion in dairy cattle are brucellosis, leptospirosis, Listeriosis, Q fever, bovine viral diarrhea, mycotic condensing, and Neosporosis. Genetic and non-genetic disorders are normal causes of non-infectious abortion in dairy cattle. The various factors that play a major role in abortion incidence for dairy cattle are genetic factors, environmental factors, management factors, geographical factors and infectious agents. Consequently, abattoir influences breeding and productiveness damages towards dairy cows. Abortions cause replacement heifer losses, low milk production, increased treatment and feed costs, as well as culled productive stock, hence, enormous economic losses to dairy farms. Prevention measures can be put in place in this form: bio-security measures, vaccination, proper feeds and nutrition, genetic improvement, environmental management and health checks. These strategies assist in sustaining the health of a herd to begin with, boost reproductive rates and decrease economic loses (Tulu et al., 2018).

Brucellosis

Brucellosis is a significant human and domestic and wild animals' disease everywhere; it is also considered as zoonotically important disease. In the females the disease presents itself through abortion storms in the pregnant cows, infertility, mastitis, retained placenta and arthritis. A cow which is infected usually abort at between the 5th and the 7th month of pregnancy. Brucellosis induced abortion frequently takes place in the last trimester of pregnancy. All these manifestations result in losses in the production system. Different strains of the bacterium called Brucella are known to cause brucellosis in cattle but it is predominantly caused by Brucella abortus. Also, cattle brucellosis occurs with contaminated pastures, feed, and water, and consumption of aborted fetuses or genital secretions of recently aborted cows or normal-calving carrier cows. Although S19 and RB51 vaccination in cattle has been used in the developed countries for brucellosis control, systematic data record about the occurrence of the disease in the developing world is insufficient and the implementation of the control programmers is still limited. The following are some of the risk factors identified in bovine brucellosis; Some of reasons include size of the herd, age of the animal, sex, type of management, for example confining animals, exposure history to wildlife, location and introduction of different breeds into the same groups. Several tests have been used in diagnosing the bovine brucellosis. These are staining methods like modified acid-fast staining methods, culture and dot hybridization to PCR and nucleic acid amplification tests. However, more frequently used serological tests in most epidemiological studies include serum agglutination test (SAT), Rose-Bengal test (RBT), Buffered plate agglutination test (BPAT), fluorescence polarization assay (FPA) and ELISA. Serological tests are limited by having more false-positive results from vaccinated animals, cross reactivity to other gram negative bacteria, poor sensitivity from serological tests like SAT and RBT (Thomas et al., 2022).

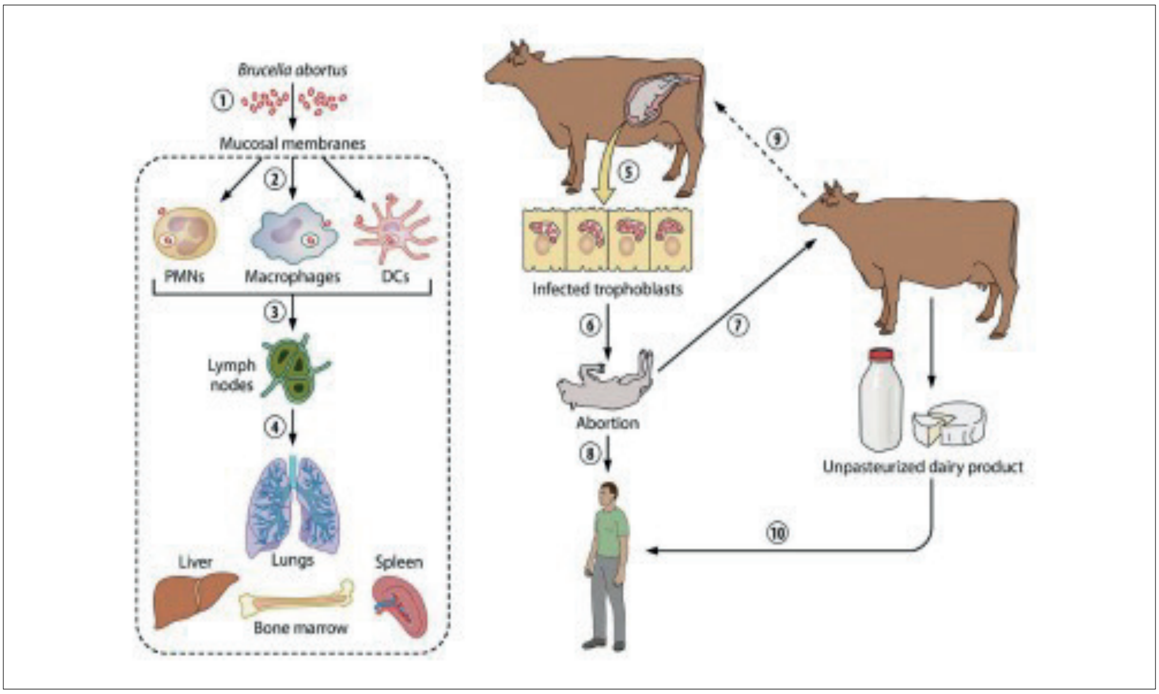

Figure 1. Visual process of Brucellosis to abortion

Infertility

A mixture of genetic, nutritional, and environmental factors affects the health of domestic animals. Particularly among all these factors, their reproductive efficiency determines their general productivity. Mating problems are common reasons for reproductive failure; they can be due to inadequate pregnancy, infection, poor quality genetics, or stress caused by the surrounding environment (Stegelmeier et al., 2020). Some of the possible factors that may lead to infertility in animals includes; the genetic factor, environmental factor, and feeding factor. Some crossbreed animal may be more prone to fertility problems as a result of their genes, while other factors such as drastic changes of weather, or poor living conditions also affects fertility. Also, deficiencies of nutrients can make fertility in animals difficult (Abedal-Majed & Cupp, 2019). With good breeding practices and nutrition, the issues of infertility in livestock farming can easily be overcome or greatly reduced. Some of the other causes that are attributed to the inability of cow to conceive includes, metabolic disorders occurring from feeding imbalance, functional problems such as luteal insufficiency and inovulation, poisonous plants intake, acquired barrenness attributed to nutrition and housing, and reproductive toxins that hinder performance. There are also other noninfectious causes of infertility in cows, these include ovarian disorders, inflammatory diseases, congenital abnormalities, which also re-emphasize the necessity of nutrition, health and genetics in conception. That is why it is important to identify and treat these various causes in order to improve the reproductive performance of animal as well as the overall production (Mikhailova et al., 2021).

Dystocia

Dystocia in livestock with specific reference to cattle and particularly to cows and buffaloes can to a certain extent be attributed to various maternal and fetal influences. Some of the factors are feto-maternal disproportion, improper cervical dilation, uterine torsion, uterine inertia and hernia of gravid uterus (Sharma et al., 2022). Anyway, uterine torsion, which is a twisting of the uterus along the length, is rather popular among buffaloes and is a cause of dystocia especially with right horn pregnancy (Juneja et al., 2023). Also, fetal maldisposition, fetal oversize, and monster babies also contribute to dystocia in of livestock farming. Dystocia is observed in mares due to improper fetal limbs formation which leads to head deviation that need to be manipulated to enable the mare give birth. Vaginal delivery may not always be possible if it fails after attempts have been made, for example, maternal pelvic stenosis, hence timely and correct handling of dystocia of animal is very crucial (G et al., 2022). Fetotomy and caesarean section are among the interventions commonly employed in cases of dystocia in cattle, with caesarean section as a standard clinical practice, there is more chances of survival of both the dam and the calf (Barrier et al., 2013). In sheep there are different treatments and they include surgeries such as cesarean section through which live or dead foetuses, according to the case are removed to minimize losses of income by farmers. Consequently, other ideas such as using hemp ropes to help in delivering the calf have been invented for the cows with an intention of handling dystocia and assuring calf survival. It is important to develop a method for early identification of dystocia and application of correct treatment and selection tools, thus preventing a high level of morbidity and mortality in cows and their calves, which would be less beneficial in terms of economical rates for the operations of livestock industry (G et al., 2022).

Retained Placenta

The phenomenon of Retained Placenta (RP) in livestock particularly in the highly productive dairy cows is quite multifactorial. Various factors contribute to RP including metabolic stress which includes hormonal and nutritional imbalances, negative energy levels, lack of proteins, minerals, vitamins, and antioxidants; high levels of cortisol and adrenaline, amongst others (Li et al., 2021). For the same reason, still birth, dystocia, abortion, twin births, induction of labor, cesarean section, shortened gestation, and infectious diseases are also known to cause RP (Mordak et al., 2017). Effects include inflammation of the uterus, suppression of milk secretion and overall diminished fertility as well as prolonged time to next calving and consequently, the livestock losses. This thus stresses the need to understand the various causes of RP to be in a position to prevent and or manage them (Amin & Hussein, 2022). The improved level of knowledge on the ways concerning RP and its costs should also focus on the attention to diet and vitamin intake. Understanding the multiple factor of RP and applying the management practices can provide different data on the pathobiology of the disease, and can help to improve the strategies for controlling and preventing the reproductive issues like dystocia in cattle (Dervishi & Ametaj, 2017).

Table 1. Summary of Reproductive Diseases in Dairy Cattle

Disease	Causes	Symptoms
Abortion	Infectious (brucellosis, leptospirosis, listeriosis, Q fever, BVD, mycotic infections, neosporosis); Non-infectious (genetic and environmental factors)	Abortion, retained placenta, metritis
Brucellosis	Brucella abortus; Contaminated pastures, feed, water, aborted fetuses, genital secretions	Abortion, arthritis
Infertility	Genetic factors, nutritional deficiencies, environmental stress, infections	Irregular estrous cycles
Dystocia	Feto-maternal disproportion, cervical dilation issues, uterine torsion, fetal malposition, oversized fetus	Prolonged calving, abnormal fetal positioning
Retained Placenta	Metabolic stress, hormonal imbalances, nutritional deficiencies, high cortisol levels, stillbirth, dystocia, twin births, cesarean section, infectious diseases	Failure to expel placenta within 24 hours post-calving, uterine inflammation, reduced milk secretion

Common Health Issues

Mastitis

Mastitis in livestock especially in the cattle and buffaloes is an infection by the bacterial, fungal, or viral pathogen that penetrates into the udder or teat canal, resulting in the contagious or the environmental type of mastitis. The factors affecting the level of cow damage with mastitis include milk yield, stage of lactation, milking and feeding operations, animal age, as well as the season when the problem was identified (Ghosh et al., 2023). Accurate management of hygiene in the milking process is effective as in the case of disinfection of the mammary gland is important after the milking process to minimize the occurrence of mastitis (Khasa et al., 2020). Also, the level of risks increases with age, so that the older cows are more risk prone to experience the mastitis (Adamu et al., 2020). Mastitis is costly in terms of production loss and requires antibiotic treatment in clinical cases and therefore effective control measures should be implemented to improve livestock health status (Viniukov & Viniukov, 2018). Mastitis prevention in livestock is the result of efforts that follow a complex of various approaches reported by different researchers. The primary prevention practices are washing and milking time, hygiene, using correct milking equipment, creating comfortable and clean lying and feeding areas, culling of chronic infected cows, giving antibiotic treatments to cows having mastitis, using dry cow antibiotic therapy, treating clinical cases of mastitis, setting udder health targets, and regularly assessing the udder health status, and reviewing the mastitis control program on a periodic basis (Zemanova et al., 2022). Further, accruing of genetic characteristics like CD14, CXCR1 genes and lactoferrin and lactoglobulin for resistance to mastitis is highly important to boost the immune status of animals against this disease. In addition, increasing hygiene in livestock housing to reduce the transfer of mastitis pathogen during milking, balance diet to stabilize the cow’s immune system, and exploring non-antibiotic preventive measures for mastitis are some of the strategies to control mastitis (Oudessa Kerro, 2020).

Foot and Mouth Disease (FMD)

FMD is an example of an infectious disease of animals with cloven-hoofed species, and widely spread all over the world (Aslam & Alkheraije, 2023). It is an animal disease that is caused by Foot-and-mouth disease virus (FMDV) and presented clinically by vesicular lesions in mouth, feet and udders making the affected animals lame and leading to mastitis (Seyoum & Tora, 2023). Trade and production losses are the two main areas affected by FMD; hence, this disease has a strong negative impact on the economy. There are direct transmission routes by droplets, aerosols, and airborne particles including consumable items and surfaces showing the necessity of enforcing biosecurity and the infection’s source control (Wulandani, 2022). There is a major focus on understanding the geographical distribution of FMD in livestock and the possibilities of direct or indirect contact of infected animals. The effectiveness of culling workouts has also been considered in these aspects. Therefore, having efficient policies that addresses the issue of prevention, control, and eradication of FMD is crucial in order to safeguard the livestock and food production industry. Various measures need to be put in place in efforts to control Foot and Mouth Disease (FMD) in livestock. Vaccination is very vital in management of FMD, decreasing the basic reproduction number and thereby preventing the spread of the disease. In caring V on the part of FMD transmission, early quarantine, vaccination, and disintegration are useful. It is necessary to implement strict biosecurity measures that include isolation of affected animals, proper cleaning and disinfected of farms and equipment’s to avoid the spread of FMD. Awareness of farmers to recognize goats with FMDV antibodies for early isolation, vaccination, screening and decontamination activities are some of the recommended prevention measures for FMD in the livestock are very important strategies to control FMD (Araghi et al., 2022). Also, by removing infected and exposed animals from other animals is very important to control FMD infection. Vaccination in livestock and other biosecurity activities, early quarantine, and vaccination followed by culling of infected animal are some of the ways through which chances of FMD transmition in animal can be reduced.

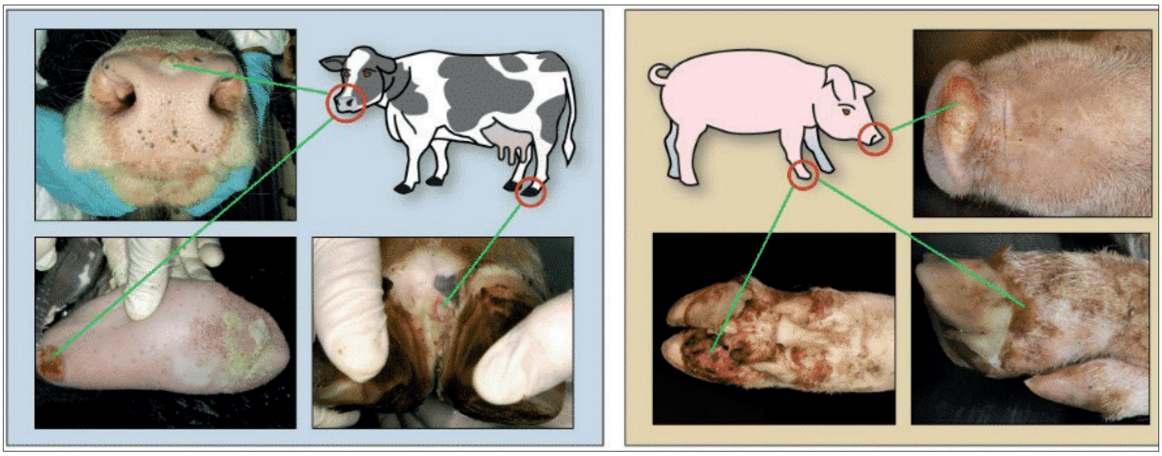

Figure 2. FMD symptoms in cattle

Parasitic Infestations

Gastrointestinal parasitic infestation is one of the most critical parasitic infestation affecting livestock around the world. Some of these are Haemonchus, Strongyloides, and Trichostrongylus whereby they have known consequences such as decreased feed conversion ratio, production costs, and mortality at the advanced stages of parasitic infestation (Inegbenosun et al., 2023; Khan et al., 2023). Research has shown that a large number of ruminant animals such as cattle and goats could be affected substantially by gastrointestinal stromal tumor (GISTs) however, among goats, both nematode such as Strongyloides papillosus and protozoa such as Eimeria are common (Verocai et al., 2020). Parasites that infect livestock produce clinical signs and pull down the economic value of the stock. Blood protozoan diseases are transmitted through vectors, some of which include ticks and flies, and they can cause anemia, fever and sometimes death in severe cases hence there prolonged carrier stages of acute chronic forms (Senapati et al., 2018). Some of the gastro-intestinal parasites include Cryptosporidium and Giardia though some of these parasites affect humans as well, a number of livestock species but the level of prevalence may differ. Pathological manifestations of strongyloidiasis that affect animal are the cause of the spread of the disease by nematodes Strongylida, and lead to the development of fever, anemia and neurological disorders in infected animals (Hopper, 2022). Infections by such parasites like Fasciola hepatica and Dicrocoelium dendriticum causes hepatic disorders and chronic wasting, whereas rumen flukes like Cotylophoron daubneyi lead to inflammation and clinical signs of diarrhea and emaciation from sheep and goats (Tariq, 2017). Furthermore, the parasitic skin disease due to mites in cattle, sheep, as well as goats lead to skin lesions, weight loss, and declination in milk yield thus incurring producer’s losses. Also, wild ranging/migratory animals have different nematodes and protozoans that are zoonotic to humans and a threat to the health of individuals. Molecular and immunodiagnostic tools are participated vital in diagnosing and accessing the parasite infections in livestock for individual farms and their herds’ health. In view of these parasitic diseases, it is very necessary to control through strategic deworming, biological control, and also environmental hygiene for better livestock production to enhance economic growth.

Bovine Respiratory Disease (BRD)

Acute pneumonia in cattle is defined as Bovine Respiratory Disease (BRD) that affects both dairy and beef cattle and is caused by different bacterial agents such as Pasteurella multocida, Mycoplasma bovis, Mannheimia haemolytica, and Histophilus somni; viruses including Bovine herpesvirus-1, Bovine parainfluenza-3 virus, and Bovine It has also been identified that the nasal mycobiome which consists of fungal such as Trichosporon and Issatchenkia could be useful in diagnosing BRD (Centeno-Martinez et al., 2023). Moreover, the identification of BRD-associated pathogens has been carried out through multiplex real-time RT-PCR and was found to be successful for early diagnosis; the bovine viral diarrhea (BVD) was often found with other bacteria and viruses (Gandhi et al., 2023). In detecting metabolites of infected cattle, 1H-NMR spectra significantly correlated with values offering the option of early diagnosis and management of an infection.

The common measures that farmers can take in order to avoid further cases of spread of BRD in their herds include the following. It is possible to eliminate the chances of outside viruses entering the more susceptible herds through the use of better external bio-security measures such as the Norwegian BRSV/BCoV control program lowers the instances of transmission greatly (Holt et al., 2022). Further, another control measures for BRD include vaccination, use of antimicrobial, and improvement of the animal's living environment and health status. Additionally, with regard to other diseases such as BVD, control programs have been able to practice strict measures that have cut the infection rates for the diseases through voluntary eradication of persistently infected animals and self-generated industry assurance (Staton et al., 2020). These practices, along with proper and regular use of disinfectant on all equipment that may be used from one animal to another such as foot trimming blades in the prevention and control of the disease, are critical in the management of BRD in cattle herds.

Johne's Disease

Johne's Disease, from Mycobacterium avium subspecies paratuberculosis or MAP, is a persistent and highly pernicious disease in cattle involving the intestines. There signs includes diarrhea, body weight loss and, as a result, impact heavily on the health and efficiency of affected cattle herds (Johnson et al., 2022). The identification of Johne's disease is even more complex as its infested herds with its subclinical infection type remains unnoticed. It has control measures which are instituted at the herd level to minimize exposure to the bacteria by creating barriers and these include proper wash and analysis of feeding and watering utensils with proper implementation of health measures, proper identification and separation of affected animals plus provision of treatment (Stabel & Collins, 2022). There is also forceful consideration being given in using vaccinations as an available form of prevention. Currently, the tools commonly used for diagnosis of the disease include serum ELISA, fecal PCR, and fecal culture, which have low sensitivity and specificity and therefore can rarely diagnose the illness in its preliminary stages (Johnson et al., 2022). In light of these scenarios, there is a need of more efficient techniques and the measures for eradicating the Johne's disease in beef herds is an urgent necessity. Procedures with regard to control the spread of the diseases includes conducting regular tests on animals, proper disposal of manure, and abstaining from using colostrum from affected cows as well as sealing off bio-security measures to curb introduction of MAP in clean herds.

Figure 3. Johne's Disease in livestock**Table 2.** Summary of Health issues in livestock

Table 2. Summary of Health issues in livestock

Health Issue	Causes	Symptoms
Mastitis	Bacterial infection (Staphylococcus, Streptococcus)	Udder swelling, decreased milk production, fever
Foot and Mouth Disease (FMD)	Viral infection (Foot-and-Mouth Disease Virus)	Vesicular lesions on mouth and feet, lameness, fever
Parasitic Infestation	Gastrointestinal nematodes (Haemonchus, Strongyloides), protozoa	Anemia, weight loss, diarrhea
Bovine Respiratory Disease (BRD)	Bacterial (Mannheimia haemolytica), viral (Bovine Herpesvirus), environmental stress	Coughing, nasal discharge, fever, rapid breathing
Johne's Disease	Mycobacterium avium subspecies paratuberculosis (MAP)	Chronic diarrhea, weight loss, reduced milk production

Causes of Reproductive and Health Issues

Nutritional Deficiencies

Due to poor feeds, it becomes very difficult for the growth of the animal, lactation, reproduction and over all animal health. That is why the products containing protein, amino acids, minerals, iodine, and selenium are vital for the body and reproductive processes. Deficiency of these nutrients leads to various issues of cattle at different physiological states such as anemia, bone disorders, cardiac abnormalities, reproduction problems, and poor growth and reproductive performance (Graham, 1991). This is true because particular nutrients cause single health problems. Deficiency of phosphorus, vitamin A and its precursor beta-carotene, protein and energy, copper and zinc, vitamins A, D, K and E, thiamin, cobalt, and iron; and inadequate intake of dietary iodine manganese and selenium leads to such metabolic complications, low feed intake rate and poor developmental and reproductive performances (Dunn & Moss, 1992; Hill & Shannon, 2019). Furthermore, the low supplemental mineral may cause a change in the general reproductive physiology of animals hence resulting to low reproductive efficiency and imbalances in animal's reproductive systems which are evident in roughages and commercial diets. The negative effects of copper in livestock are acute copper poisoning that affects sheep badly, under this circumstance copper in meat and milk has low amount while the negative effect of lack of copper is anemia, osteoporosis, cardiovascular diseases, wool and hair imperfections and infertility. Manganese is also needed in small amounts; its deficiency causes poor growth and reproduction, and slimy mouth coat of grazing animals (Alonso et al., 2019). Species with rapid development and superior body build, especially the young ones, are more vulnerable to selenium and vitamin E deficiencies, leading to nutritional myopathy. This condition is normally accompanied by weak muscles, muscle twitches, incoordination, possible reluctance to move, and rarely death (Oetzel, 1988). Moreover, protein-energy malnutrition is widely spread among different species of livestock and this disease may be accompanied by the ruminal maldigestion, hypothermia, and recumbency. These clinical symptoms need an early detection along with strict care in order to counter and manage them effectively.

Genetic Factors

Genetic factors are crucial to livestock farming since they are associative with a number of different aspects of the animal; including metabolic balance, weaning weight and reproductive performance. Genetic manipulation has been advocated in order to improve sustainable production of livestock based on research findings and the advancements in tools such as RNA-sequencing in identifying key genes associated with reproductive traits (Liang et al., 2023). That is why the links between such factors as heredity and environment were also recently established to affect weaning weight; the estimates of heritability also depend on the breed differences as well as the kind of management practices. Also, these findings explain the role of parental and environmental influence on development of fetal growth and performance of young stocks through early life environmental factors controlling the genetic factors, which play a vital role in the metabolic and physiological health of cattle. Different methods to increase productivity of livestock and to ensure food safety in animal production systems require the knowledge of and focus on genetic factors (Pala, 2004).

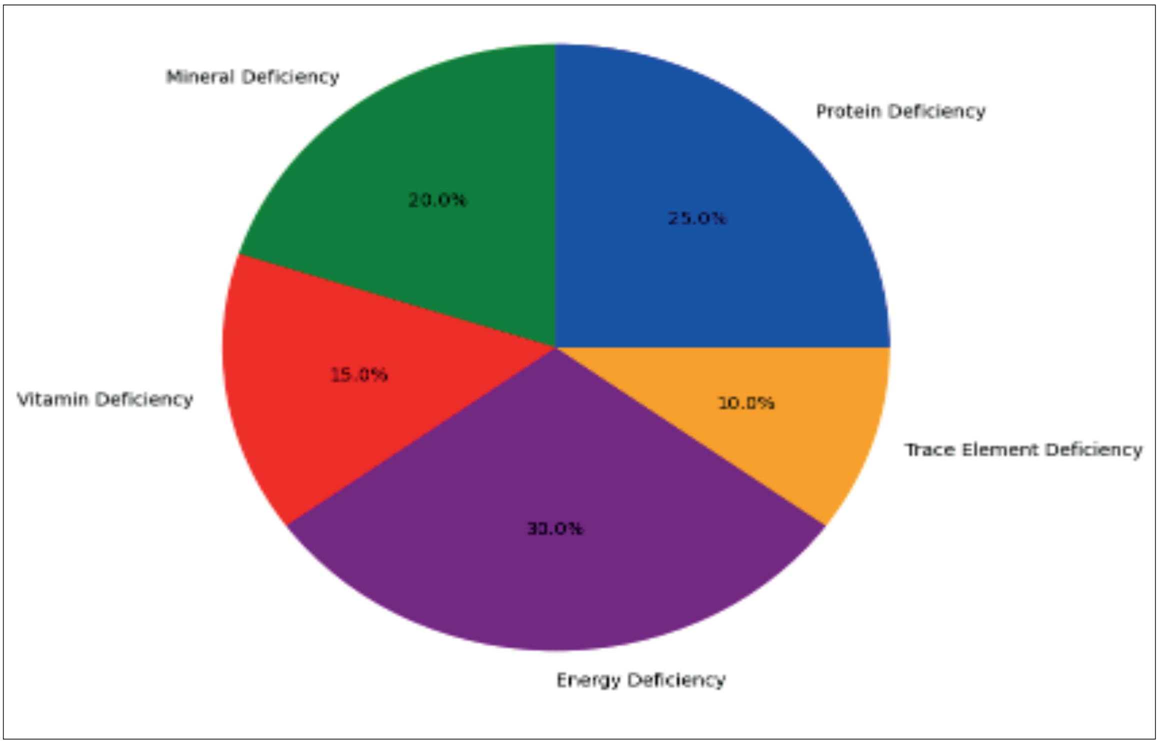

Figure 4. Prevalence of nutritional deficiencies in livestock

Thus, the process of outbreed selection in cattle can significantly affect the tendency to viral infections. Genetic information, for instance, genes in MHC and immune response pathways, is significant for disease resistance in animals; hence, animals with such genes must be protected to help prevent disease outbreaks (Hulst et al., 2022). This explains how epidemics of diseases succumb to genetic loss and was to show how disease resistance affects cow farming. Some immune displayed genetic differences are associated to disease resistance in native cow genotypes that are prevalent in India which has tropical disease resistant genes. The identification and application of genes related to disease resistance like MHC are a good example to explaining the effectiveness of genetic influence in enhancing disease resistance in cattle (Kataria et al., 2022).

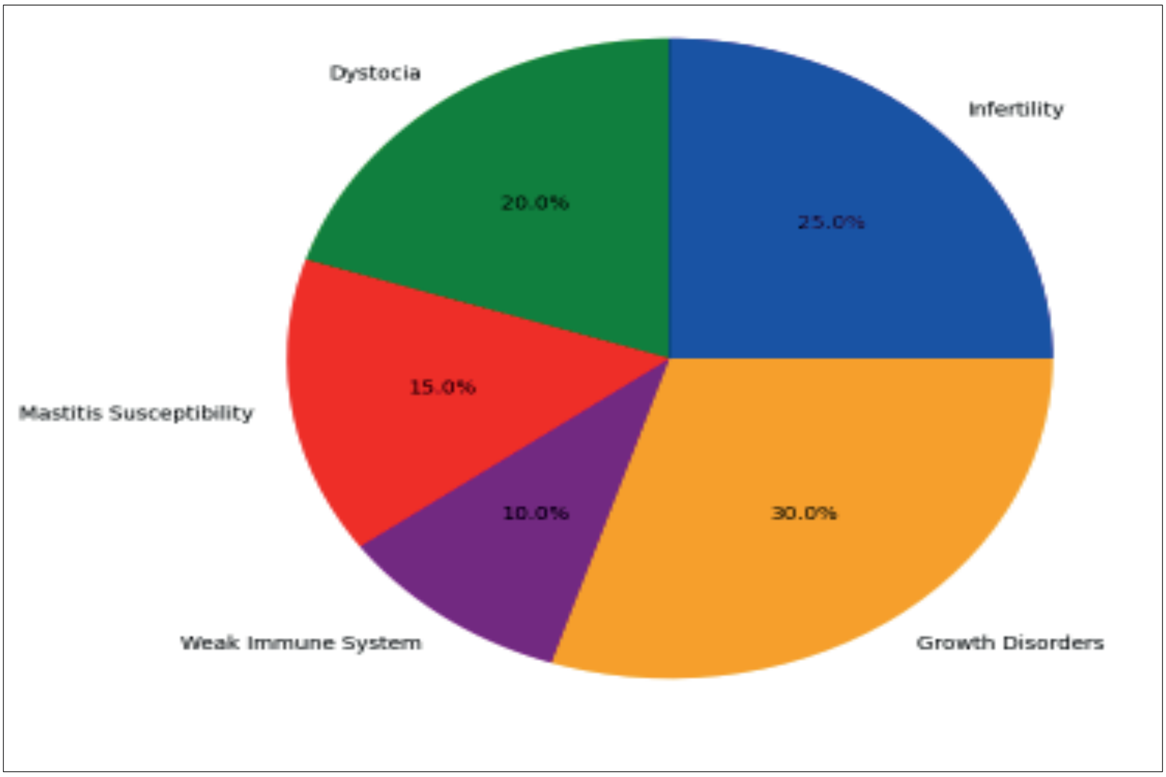

Figure 5. Distribution of Genetic Factors Impacting Livestock

Environmental Stress

Heat stress is an environmental problem infiltrating cattle production, and farm animals and their performance are negatively impacted irreparably in terms of health and fertility (Misztal, 2022). The heat stress physically affects milk yield, changes in hormones that may affect fertility, increase in mortality which are all costly to the production process. Some of the measures that can be used to address heat stress include manipulation of the animals' immediate environment in a bid to provide shades, installation of cooling systems among others. Also, use of vitamins will help reduce the physiological changes that are associated with heat stress if the animal intake is enhanced. The same can be considered as preventive steps, where use of breeds which are more heat tolerant are adopted in order to manage the stress caused by hot environment on the cattle. Temperature, immunity, and oxidative stress are some of the parameters that need to be routinely checked so as to prevent heat stress. The transforming climate systems have equally affected agricultural production; therefore, enhancing the productivity of animal production and the well-being of those animals requires data on how the climate stressors such as heat affects them. Heat tolerance tests and dedication of appropriate changes in environment, including airing and irrigation control, will help the producers to reduce the negative impact of heat stress on the cattle. This growing interconnectivity of practices does not only promote the responsible use of resources on livestock but also improves the resistance of the cattle in a fluctuating environment (Akinyemi & Adewole, 2021).

Management and Control Measures

To reduce the consequences of climate change and to reduce the impact of the dairy business in the environment management of livestock is critical. Some of these have included heat recovery, feed quality improvement, right composition of the herd, and anaerobic waste management among others (Rencricca et al., 2023). Methane production is a significant issue in ruminants, though it can be minimized through the anti-methanogen vaccination, low-CH4-emitting animal breeding, and feed (Oliveira et al., 2022). Thus, it becomes possible to adapt to the heat and cold influences by breeding animals capable of withstanding unfavorable temperatures, changing the microclimate, and regulating the diet that will help the livestock to gain healthy growth and reproduce in the period of extreme climate conditions. Moreover, promoting sustainable farming practices and enhancing people and animals' health depend on implementing the necessary policies for controlling air pollutants including particulate matter and greenhouse gases emitted from livestock buildings (Arndt et al., 2021).

Vaccination is one way of managing the health of cattle according to the data as reported by the researchers. On the same note, vaccination campaigns help the herd in terms of excluding epidemics, which in turn could be expensive for the company. Biosecurity measures are controlling animal circulation, maintaining hygiene, and isolating the new or sick animals are also crucial to preventing the entrance and spread of illnesses (Lopez-Moreno et al., 2022).

To ensure maximum health, production, and the general performance of livestock operations, nutritional management is essential. Effective nutritional practices are shaped by a number of factors, including the use of small grain forages for stocker calves, metabolic imprinting through early postnatal feeding, antinutritional components in forages, and the developing field of nutrigenomics. Modern cattle management techniques depend on an understanding of how nutrients affect gene expression, metabolic pathways, and tissue function. Furthermore, attention to the growth and intestinal health of young ruminants is indicated as an important area of research in the field of nutritional management. Livestock producers may maximize their animals' growth, reproduction, and general performance by addressing these factors with specialized dietary management (Katoch, 2023).

In order to increase production, disease resistance, and sustainability in animal agriculture, genetic improvement in cattle is essential. The area has been transformed by a number of technologies, including molecular markers, genomic selection, and gene editing, which have sped up genetic advancement and enabled precise trait alterations. Sustainable genetic development in cattle sectors has been made possible by the introduction of new technologies like genomic selection and the implementation of effective genetic assessment systems thanks to collaborative models between scientists, breeders, and industry stakeholders. Livestock breeding programs can significantly increase animal productivity annually while lowering resource inputs by concentrating on well-defined breeding objectives, efficient trait measurement, and genetic evaluation (Garcia, 2023).

Table 3. Management and control measures for Preventing Health and Reproductive Issues in Livestock

Issue Type	Specific Issue	Management Strategies	Mitigation Strategies
Reproductive	Abortion	Regular health checks, vaccination	Biosecurity, improved nutrition
	Brucellosis	Vaccination, biosecurity, regular testing	Quarantine new animals, culling infected animals
	Infertility	Genetic selection, balanced diet	Reducing environmental stress, regular reproductive health monitoring
	Dystocia	Proper breeding management, prenatal care	Timely veterinary assistance, nutritional management during pregnancy
	Retained Placenta	Adequate mineral supplementation, hygiene during calving	Prompt veterinary intervention, postpartum care

Issue Type	Specific Issue	Management Strategies	Mitigation Strategies
Health	Mastitis	Hygienic milking practices, regular udder health checks	Antibiotic treatment, maintaining clean and dry housing
	Foot and Mouth Disease (FMD)	Vaccination, strict quarantine measures	Biosecurity, regular health surveillance
	Parasitic Infections	Regular deworming, environmental sanitation	Rotational grazing, monitoring and testing for parasites
	Bovine Respiratory Disease (BRD)	Good ventilation in housing, vaccination	Reducing environmental stress, early detection and treatment
	Johne's Disease	Testing and culling of infected animals, biosecurity	

Future Directions in Livestock Health Management

The future trend for livestock health management is therefore viewed in the context of the innovation as well as effective use of advanced technologies. Exploring the techniques in genomics, biotechnology, and precision agriculture, it explores the ways on improving the health and production of livestock. For example, genomic selection help us to predict and select the genetically better animals for breeding as well as bring a better way of biotechnology solutions to the disease prevention and control (Akhigbe et al., 2021).

Special methods, like sensoring and data analysis, allowed a farmer to control their animals' health and activity level effectively. It means that various health concerns can be identified precisely, the usage of money and other resources can be controlled more effectively and the decisions can be made more adequately. Using these technologies the farmers can improve productivity of farming and make it sustainable, while keeping the animals healthy and productive on the farm that will help in sustainable livestock health management. To progress and come up with more solutions that will help the livestock industry, more funding needs to be directed to scientific research. There is need for engagement of researcher's veterinarians, and farmers since it vital in putting into practice the resultant findings in a way that will be most beneficial for the livestock industry at large (Rivas et al., 2019).

Altogether, the trends for the further development of the practices for the improvement of the health of livestock are being reported to shift towards even more integrated and environmentally friendly. Such concentration applies to animal rights, conservation, and incorporating indigenous knowledge with the contemporary world practices. Through an integrative concept, both the livestock's health and other social and environmental issues can be met by farmers (Martin, 2024).

Summary

Thus, the orientation and quality of services offered such as animal health and reproductive services impact on agricultural yields and economic returns. This chapter mirrors other chapters in this book by stressing on different reproductive and health problems in cattle; the need to apply basic management approaches thus emerges clearly. The case means that genetics, malnutrition, and stress have to be tackled in matters concerning reproductive health. Improving the elements of biosecurity, breeding, and applying the modern technologies can play a very effective role in improving the health of animals. In the future, genetic livestock improvement, and precision farming as well as technology will be part of new livestock farming methods. All these innovations do not only increase efficiency in production, but also help in the improvement of sustainability within the agriculture industry. The use of Dimensional Model guarantees that the animal on the farms is healthy and raised in the right manner regardless of the demands of the market or the environmental conservationist principles that are in place. The level of complexity depicted in the management of livestock farming requires a convergence of expertise from scientists, veterinarians, and farmers. In this way, the stakeholders can effectively engage in dialogue and share the knowledge that can enable them to apply sound practice to reduce the said health risks and to achieve the maximum yields. The cooperative form thus does not only protect the well-being of the animals but at the same time, ensure the sustainability and stability of farm businesses in the constantly changing global environment. Thus, it can with certainty be stated that the future of the livestock farming industry depends on the ability to actively control certain factors and utilize advanced technology. Thus, the focus on animal health, responsible use of resources, and cooperative relations with stakeholders may be the key to the industry's ability to meet the increased need for better-quality agricultural products and prevent harm to animals and the environment.

Scientific Ethics Declaration

The authors say that they are responsible for the scientific, moral, and legal aspects of this chapter, which is published in Animal Production and Health.

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Conflict of interest

The authors declare o conflict of interest.

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About The Authors

Dr. Amjad Islam Aqib, following earning his PhD in 2017 is working as Assistant Professor, in the Department of Medicine, Cholistan University of Veterinary and Animal Sciences, Bahawalpur, Pakistan. In addition to this he is Manager Research Operations and development ORIC CUVAS, President One Health Club CUVAS, and secretary ethical Review Committee of CUVAS Bahawalpur. Focus of his research is preventive veterinary medicine aiming further on antimicrobial resistance and vaccine development. His publications are getting milestone of 100 in numbers in addition to 25 book chapters and editor of 03 books. Dr. Aqib is academic editor of reputed ISI journals, and have successfully run special issues of Frontiers, MDPI, and Hindawi as guest editors. He is active reviewer of reputed journals of Elsevier, Wiley, Springer, Frontiers, Dove Press, Hindawi, MDPI and many more.

Email ID amjadislamaqib@cuvas.edu.pk ORCID 0000-0001-7618-3948

Dr. Khalid MEHMOOD earned his Doctor of Philosophy (PhD) from Huazhong Agricultural University, Pakistan. He is currently working as Assistant Professor, in the Department of Clinical medicine, Faculty of Veterinary and Animal Sciences (FV&AS), The Islamia University of Bahawalpur (IUB), Pakistan.

E-mail khalid.mehmood@iub.edu.pk, ORCID 0000-0003-4720-8792

Dr. Riaz Ahmed GUL earned his Doctor of Veterinary Medicine (DVM) from Faculty of Veterinary and Animal Sciences (FV&AS), The Islamia University of Bahawalpur (IUB), Pakistan. He is currently enrolled in MPhil in Clinical medicine and Surgery (CMS) in Department of Clinical Medicine and Surgery department at Faculty of Veterinary and Animal Sciences (FV&AS), The Islamia University of Bahawalpur (IUB), Pakistan.

E-mail rrriaz3032@gmail.com, ORCID 0000 0001 5556 0572

Dr. Kun Li earned his PhD in 2019 from the College of Veterinary Medicine at Huazhong Agricultural University, Wuhan, Hubei, China. From 2017 to 2019, he conducted research in the Department of Parasitology at the University of Illinois at Urbana-Champaign, USA, under the National Youth Postdoctoral Fund and other projects. He later completed his postdoctoral studies at Huazhong Agricultural University. He is currently an Associate Professor in the Department of Veterinary Medicine at Nanjing Agricultural University. His research spans a wide array of fields including veterinary infectious diseases, zoonotic diseases, veterinary pathology, veterinary microbiology, and veterinary immunology. He has authored 177 publications in prestigious national and international journals, contributing significantly to the veterinary science field. Additionally, Dr. Li has written and edited numerous book chapters and full-length books. He serves as an editor and editor-in-chief for several leading national and international journals, including Scientific Reports, Pakistan Veterinary Journal (PVJ), MDPI, and Frontiers in Veterinary Science.

E-mail lk3005@njau.edu.cn ORCID 0000-0002-2026-9969

Dr. Ali Raza received his masters in clinical medicine and surgery in 2024 at The Islamia University Bahawalpur, Pakistan. He is a research associate in a project of Pakistan science Foundation (PSF). His research interest includes molecular bacteriology, gene extraction, sequencing and phylogenetic analysis. He has published more than four articles in national and international well reputed journal. He has also written 2 book chapters recently one is being ready to get online excess.

Currently focussing on PhD admission.

Email aliraxa3014@gmail.com ORCID 0000000923017907152

Dr Abdul Sameed Saher received his master in clinical medicine and surgery in 2024 at the Islamia University of Bahawalpur, Pakistan.His research interest includes Detection of Acute Phase Proteins and Haemato-Biochemical Changes in Naturally Infected Mycoplasma Bovis Calves.He has published more than 2 articles in national and international journal.

Currently focusing on PhD admission.

Email abdulsameedsaher@gmail.com ORCID0009000693270844

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FOOT AND MOUTH DISEASE (FMD) IN LIVESTOCK

Abdul REHMAN

Muhammad Mazhar AYAZ

Momina MALIK

Umaima NADEEM

Salma BIBI

Muhammad ABDULLAH

Tanveer NASIR

Tariq ABBAS

Umair YOUNAS

Muhammad SAFDAR

History

Foot and mouth disease is a viral disease that infects cloven-hoofed animals including cattle, pigs, sheep, and many wildlife species (Thomson, Vosloo, & Bastos, 2003). The history of FMD shows that foot and mouth disease started in the 16th century and was an epidemic disease that caused serious damage to cattle disease (Woods, 2013). Frosch and Loeffler, two well-known scientists in the late 19th century demonstrated that FMD was caused by filterable transmissible agents that were sub-microscopic and were smaller than any well-known bacteria(Bos, 1999). It was considered the first virus that could infect vertebrates(Mahy, 2005). Waldman and Pape studied the Foot and mouth disease virus on guinea pigs and later in vitro cell culture in 1920 (Mahy, 2005). The chemical and physical characteristics of foot and mouth disease viruses were studied and demonstrated in the late 20th century (Grubman & Baxt, 2004). In 1989 the three-dimensional structure of the virus was described(Prasad, Yamaguchi, & Roy, 1992).

Importance and Economic Impacts of FMD

Foot and Mouth Disease has a significant impact on livestock animals (Thomson et al., 2003). It has posed serious damages to livestock industries in such a way that it has decreased the livestock productivity rate in huge amount (T. J. Knight-Jones & Rushton, 2013). It has low mortality in general but often shows high mortality in young animals because they often have myocarditis (Jonathon Arzt et al., 2011). FMD is a WOAH (World Organization of Animal Health) listed disease and must be reported to the organization (Singh, 2023). Foot and Mouth disease is not a zoonotic disease (It, 2001).

The signs and symptoms of the Foot and Mouth Disease virus show blisters on the mouth region (tongue and Lips) as well as in between the hooves and on the teats that are followed by high-grade fever (Pikul, Ilchenko, & Prylutskiy, 2019). It is a serious disease but often animals do recover from this disease but it leaves the animal body systems weakened and debilitated (Stenfeldt, Diaz-San Segundo, De Los Santos, Rodriguez, & Arzt, 2016).

Visible loss includes loss of milk production, loss of draught power, lower weight gain, and death of animals (Admassu, Getnet, Shite, & Mohammed, 2015). The invisible losses include fertility problems, changes in herd structure, and delays in sales of animals and livestock products (Souley Kouato et al., 2018). The additional costs include vaccines, vaccine delivery, Movement control, Diagnostic Tests, and culled animals while revenue foregone includes use of suboptimal breeds and denied access to markets both local and international (T. J. D. Knight-Jones, McLaws, & Rushton, 2017).

Another significant impact of Foot and Mouth Disease is its socioeconomic impact in the regions that depend on livestock production to meet their daily requirements and necessities. It creates a pessimistic effect on the farmers (Baluka, 2016).

Etiology

Causative agent

The causative agent of Foot and mouth disease is Foot and Mouth Disease virus(Grubman & Baxt, 2004). Foot and Mouth Disease Virus is a species that belongs to the genus Aphthovirus of the family Picornaviridae(Domingo, Baranowski, Escarmís, & Sobrino, 2002). This family belongs to the order Picornavirales (Zell, Knowles, & Simmonds, 2021). Foot and mouth disease virus species have 7 serotypes (Callens & De Clercq, 1997)..

Figure 1. Causative agents of FMDV

These serotypes are differentiated from each other according to the antigenic diversity (Tayo, 2011).

Characteristics

The molecular characteristics of the Foot and Mouth Disease virus denote that it is a non-enveloped virus with icosahedral symmetry(Carrillo, 2012). Foot and Mouth Disease virus consists of a positive sense single-stranded RNA molecule with 8.5kbp length(Sarangi et al., 2015). The 3' end of its RNA genome is polyadenylated while the 5' end is covalently linked to a small protein called VPg (Domingo et al., 2002). The replication occurs according to the same pattern as of other viruses of the family Picornaviruses i-e in the cytoplasm membrane-bound replication complex (Rowlands, 2003).

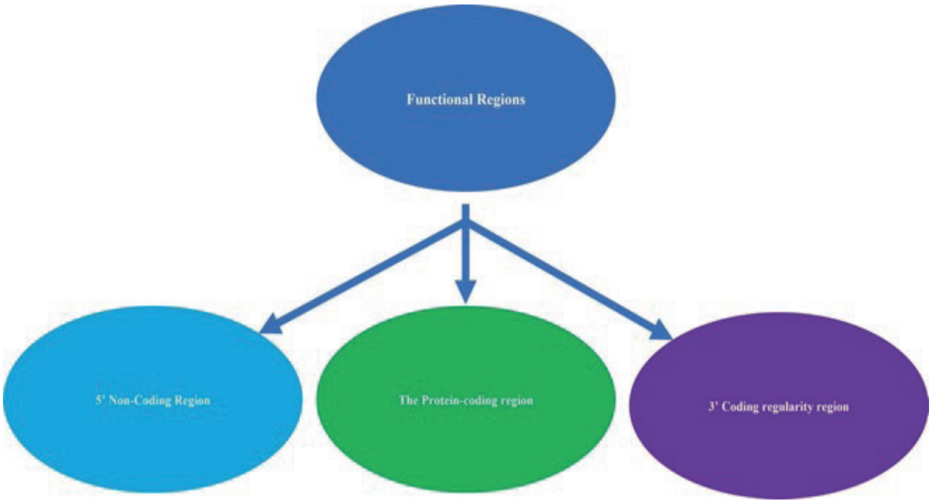

Figure 2. Functional regions of genome of FMDV

The structural characteristics of Foot and Mouth disease virus show that it has icosahedral head with 60 copies of each of 4 capsids (structural proteins) Vp1-VP4 (Zhu, 2017). The diameter of the particle of Foot and Mouth Disease Virus is 30nm (Liu et al., 2019).

Host range

Cloven hoofed animals mostly of order Artiodactyla are greatly affected by FMDV(Vosloo & Thomson, 2019). The host range of Foot and Mouth Disease includes animals such as cattle, pigs, sheep and goats (Admassu et al., 2015). It also infects some wild animals of the same order. Such as buffalo, giraffe, camel and deer (Weaver, Domenech, Thiermann, & Karesh, 2013).

Epidemiolgy

Though Foot-and-Mouth disease is highly contagious disease and is endemic throughout the Asia (Jamal & Belsham, 2013).

Distribution in Asian countries

FMDV has prevailed in different regions of Asia, these countries have a history of wide range of outbreaks of FMD (Rweyemamu, Roeder, Mackay, Sumption, Brownlie, Leforban, et al., 2008). FMD has a headache of livestock for decades (Aslam & Alkheraije, 2023). A total of 1,478 small ruminants were tested for seroprevalence and 22.8% were reported as FMD in Pakistan (Aslam & Alkheraije, 2023). In India, geographically the prevalence was reported to be 31.5%, 11.6%, 4.4%, 5%, and 4% in southern, North-eastern, western, Eastern, central and North regions (Aslam & Alkheraije, 2023). In Afghanistan, over the past few decades conflicts has been ongoing that have resulted in massive destruction of infrastructure of the country (Wajid, Chaudhry, Rashid, Gill, & Halim, 2020). Illegal transboundary movement of livestock between the Pakistan and Afghanistan border has boosted the spread of FMD (Aslam & Alkheraije, 2023). Between 1995 and 2008, the total number of outbreaks reported were 4,171 (Osmani, Robertson, Habib, & Aslami, 2019). In Bangladesh, the prevalence of FMD in Raj Shahi region was reported 25.7 million (Samad, 2019). In China, serotypes O and A were prevalent and effect 17 regions on China mainland (Guo et al., 2006). The Asia 1 serotype was eradicated in 2009, and since 2010, only serotypes O and A have been observed in northwestern and southeastern China (Aslam & Alkheraije, 2023). In Mongolia, 44 outbreaks of FMD were reported in goats, camels, sheep and cattle (Shiilegdamba, Carpenter, Perez, & Thurmond, 2008). In Kazakhstan, 76,851 cases were reported in which 8% tested positive. In Russia, high morbidity was seen in pigs and cattle (Aslam & Alkheraije, 2023).

Table 1. Prevalence and percentage of FMD in Asian countries

Countries	**prevalence**
Pakistan	22.8%
India	21%
Iran	1381 cases
Iraq	48.64%
Bangladesh	25.7%
Afghanistan	20%
Kazakhstan	8%
Russia	79%
Mongolia	Serotype O and A
Egypt	48-68%
China	Serotype O and A
Kuwait	2722 cases till 2016, still reporting
Oman	64 cases from 2011-2015

UAE	Serotype O, A and Asia1 reported
Turkey	Serotype O, A and Asia1 reported

Transmission

The transmission is facilitated when the virus sheds from ruptured vesicles into the bodily secretions and excretions (Feng, Hirai-Yuki, McKnight, & Lemon, 2014). The virus enters in the body via ingestion and also by inhalation (Pal, 2018). The transmission of FMDV occurs both directly and indirectly (Jonathan Arzt, Juleff, Zhang, & Rodriguez, 2011). The direct contact is done by animals, there secretions such as saliva, semen, milk, urine and feces while the indirect transmission occurs via air, wind, fomites and other mechanical conditions like vehicles and humans (mechanical vectors) (Sandip Chakraborty et al., 2014). Pigs are mostly resistant to the aerosol transmission of Foot and Mouth Disease virus (Alexandersen, Brotherhood, & Donaldson, 2002).

Table 2. Different routes of FMDV transmission

Transmission routes		**References**
Direct animal contact	*Most common transmission route*	*(Paton, Gubbins, & King, 2018)*
Animal products	*Through ingestion of animal products e.g. feeding of waste food or untreated milk to young animals*	*(Tomasula & Konstance, 2004)*
Mechanical transmission	*Transmission through virus particles and inanimate objects such as footwear, clothing, vehicles and instruments.*	
Wind	*It's not common, but it's possible, especially if pig farms are in the vicinity and under certain weather conditions, e.g., cool and high humidity temperatures.*	*(J. Arzt, White, Thomsen, & Brown, 2010)*

Pathıgenesis

After the transmission of the foot and mouth disease virus that is either transmitted by direct contact or indirect contact the virus enters the body and adheres to the mucosa of pharynx in the respiratory tract (J. Arzt, Pacheco, & Rodriguez, 2010). After its attachment to the mucosal cell membrane of pharynx in the respiratory tract it is spread to the secondary sites (Admassu et al., 2015). Macrophages play the role of transporting virus to the secondary sites such as epithelium, other mucosal cells and myocardium (Meidaninikjeh et al., 2021). In the secondary sites the virus replicates, it penetrates the host cells and uses its DNA to make copies of its RNA and proteins. After the assembly of the virus inside these secondary site cells the cell burst and the virus enters the blood, causes systemic infection called as viremia. After the viremia the virus infects epithelial at many other sites and within few days the vesicles develop (Fuller, Von Bonsdorff, & Simons, 1984). The process of pathogenesis takes 2 weeks and the clinical signs and symptoms appear after 2 weeks. The young animals get necrotizing myocarditis (a heart disease) and eventually dies (Błyszczuk, 2019).

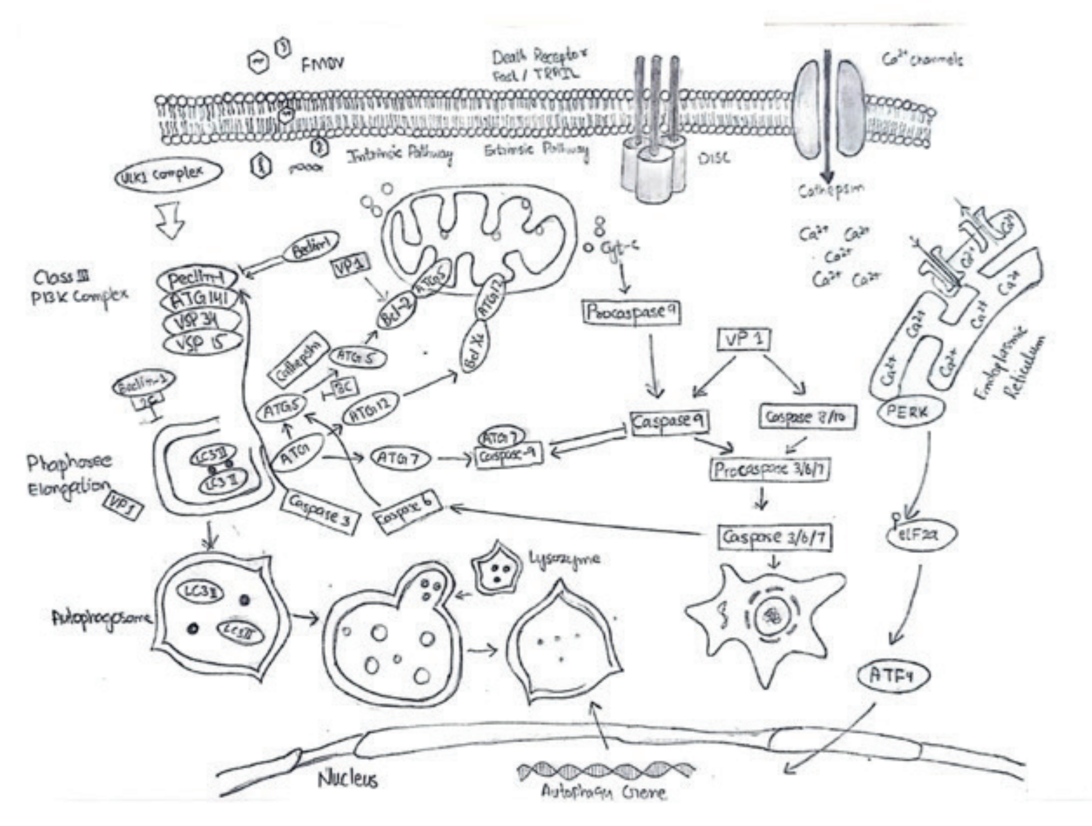

Figure 3. Immunity to Foot-and-Mouth disease virus

Clinical Signs and Diagnosis

This ssRNA virus show various signs after invading living body (Nelemans & Kikkert, 2019). The clinical signs include Lameness or ataxia, vesiculation, profuse salivation and ulceration are the common manifestation in cattle (Petrovski, 2015). Vesiculation on the nose including the snout and muzzle are the major lesions observed in infected beef cattle and pigs. The teat and feet were the second most frequently vesiculated body parts on infected pigs. Other symptoms observed are fever, loss of appetite, weight loss, hypersalivation, growth retardation, depression and severe decrease in milk production, which could persist after recovery (Attia).

Generally, FMD can be identified on the basis of clinical signs. Severity of symptoms may be due the several reasons, such as species and the age of animal, dosage of exposure, virus strains and host immunity to virus (Klein, 2009). So, diagnosis based on clinical signs are unreliable due to the other several disease share symptoms as FMD. However, confirmatory laboratory diagnosis of suspected FMD case is vital. Conventional techniques are routinely used like CFT (Complement-fixation test), VNT (Virus neutralizing test), virus isolation test and ELISA (enzyme-linked immunosorbent assay). VNT and CFT are well-established and now using to detect FMD (Binti Senawi, 2019).

Nucleic acid detection methods are used to detect the presence of viral nucleic acids (Haase, Brahic, Stowring, & Blum, 1984). As these methods involve amplification of viral nucleic acids, they have higher sensitivity compared to serological methods. Reverse Transcriptase-Loop-Mediated Isothermal Amplification capable of amplifying DNA at a single temperature at 60-65°C (Naveen & Bhat, 2020).

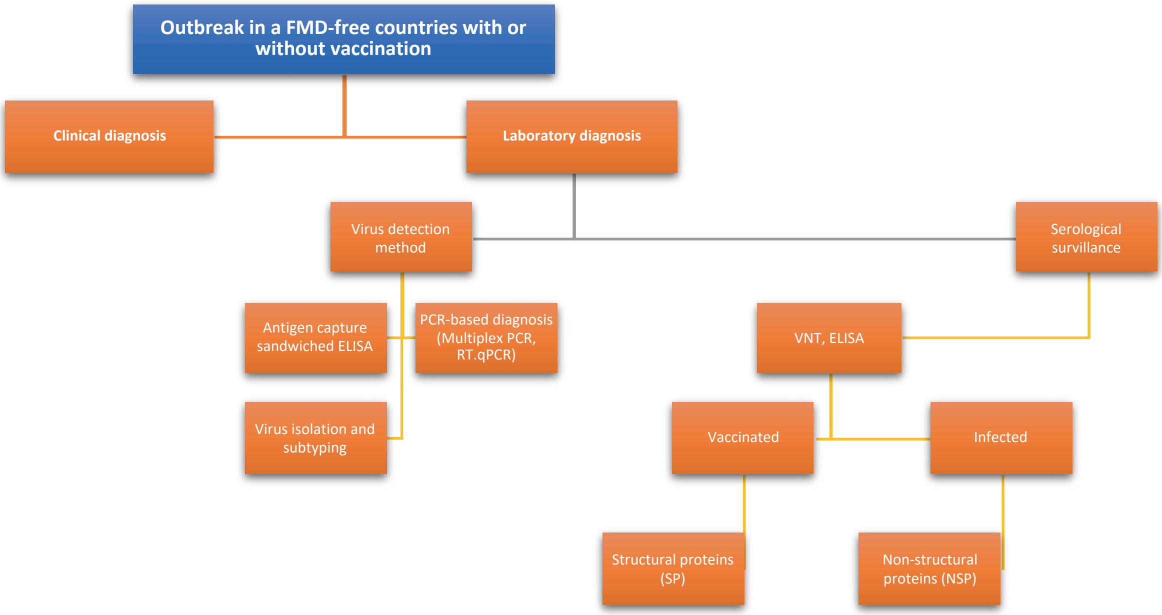

Figure 4. Laboratory tests for determining FMD

Impact on Livestock and Economy

FMD is a contagious viral disease that effect the cloven-hooved animals (deer, cattle, pigs, goats and sheep etc.) cause fever and vesicular eruption in nose, feet, muzzle and on mammary glands after which they became erosions (Sandip Chakraborty et al., 2014). It causes severe morbidity and mortality in livestock. It can reduce the productivity of animals and also effect the various ally in the entire livestock chain (Herrero et al., 2013). At micro level, it effects the primary producer due to the mortality and also causes reduction in milk yield (Lérias et al., 2014). The loss due to FMD are direct and indirect. Direct loss (80%) due to decreased production, and Indirect loss is due to the cost for FMD control and poor access to market can be indirect loss of economy. A big impact posed on world's poorest areas where people are dependent on livestock is also the major issue caused by the FMD (T. J. Knight-Jones & Rushton, 2013). FMD reduces the herd fertility leading to the less livestock production which effects the food security. FMD controls require large cost and its often difficult to discontinue control programs due to the risk of new FMD incursion (Kitching et al., 2007).

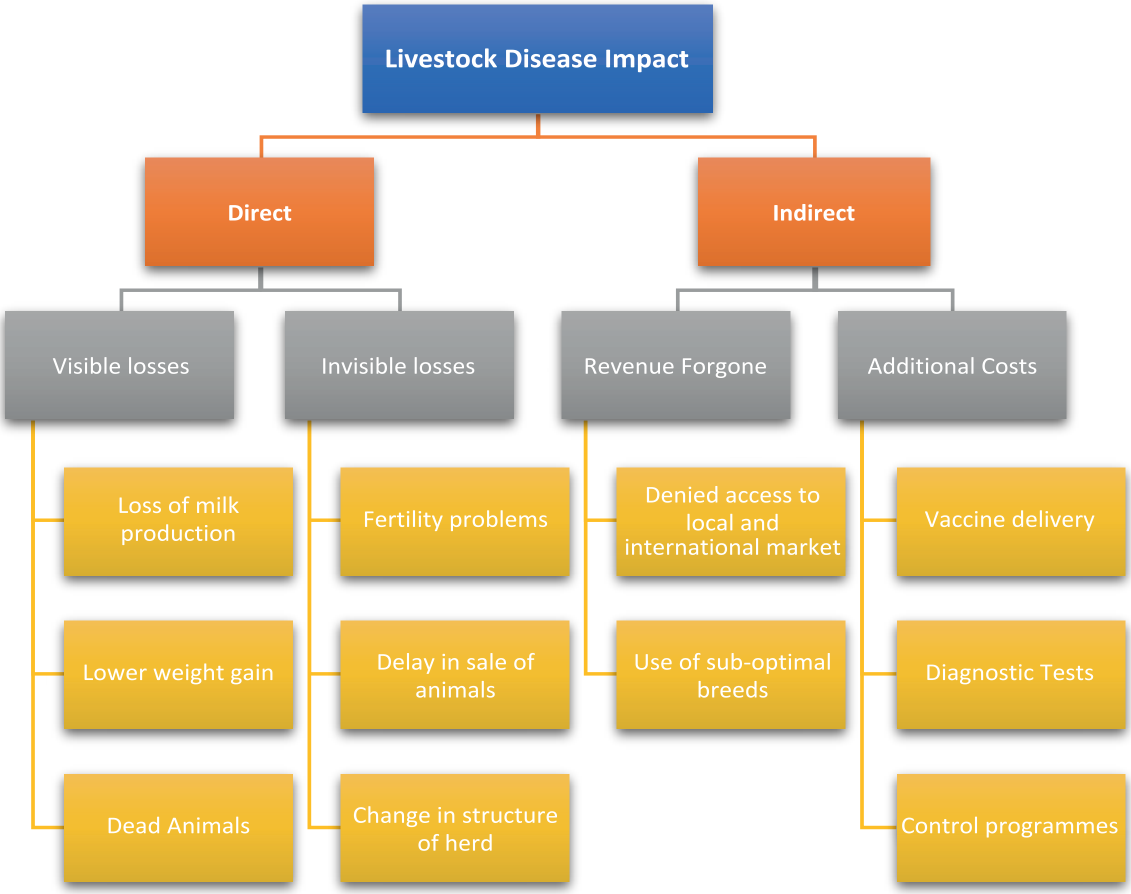

Figure 5. The impact of Foot-and-Mouth Disease.

FMD is present in the about 60% of countries in world and endemic in many countries (Rweyemamu, Roeder, MacKay, Sumption, Brownlie, & Leforban, 2008). It causes huge economic loss in livestock industry. In India 80% of the direct loss is due to the decreased milk production by the lactating animals. This disease has enormous economic consequences. In our country's production system, livestock serve multiple purpose like drought power for farming operations and milk to farm families (Herrero et al., 2013).

Thus, FMD permanently effects the productivity and health of animals and therefore can greatly affect the supply of milk, meat and dairy products (T. J. Knight-Jones & Rushton, 2013). Although many animals recover from this disease but this disease leaves them enfeeble and causes severe losses in milk and meat production (Law, 1906).

An FMD outbreak can affect the global economy by Billions of dollars by both direct and indirect losses (T. J. Knight-Jones & Rushton, 2013). To the government, direct cost would include for eradication and disease control such as maintenance of the animal movement control, disposal of infected animals, intensified border inspections, compensation to the products and costs of vaccine. FMD can also post negative impact on the food security and nutrition in developing countries (Kompas, Nguyen, & Ha, 2015). An FMD also has social impacts such as enormous physiological damage specially on families and localities directly affected by this disease.

Table 4. FMD affecting different species of animals, its symptoms, geographical distribution, percentage and impact on economy.

Species	Symptoms	Geographic Distribution	% impact on animals	Economic impact
Cattles	Shivering, slobbering and smacking lips, reduced milk yield, raised temperature, sores and blisters on feet, tender and sore feet, increased pulse and respiration	Worldwide, prevalent in Asia	Up to 90%	Loss in meat and milk production, trade restrictions affecting import and export
Pigs	Sudden lameness, blisters on snout and tongue	worldwide	100%	Loss in pork production, trade restrictions affecting export and import
Sheep	Sudden, severe lameness, lies down frequently, reluctant to move, blisters on hoof and dental pads	worldwide	90%	Reduced lamb and wool production
Deer	Mild symptoms, rarely severe	Limited cases reported	varies	Minimal economic impact due to the limited commercial importance
Goats	Fever, Blisters on tongue, mouth and feet	worldwide	90%	Lesions in meat and milk production
	varies	Africa, parts of Asia	varies	Economic impact due to the limited due to the commercial importance
Bisons	Similar to cattle	North America	varies	Economic impact varies by region affecting bison meat production

Prevention and Control

Prevention and Control have employed different means to eradicate the disease in a protective way (Almendras, 2001). The first step in any control program must be an absolute stand-still of livestock movement in the infected area. The biggest challenge is the destruction of infected animals without the spread of FMDV. Cleaning and disinfection of contaminated premises create additional hazards. So, it is difficult to control the disease because of their costly process (Carling & Huang, 2013).

If FMD enters your farm there are some steps to prevent this contagious disease. Strict biosecurity practices can help you to minimize the chances of getting exposure to disease. Use preventive measures to minimize the spread and introduction into your farm.

- Use strict biosecurity measures for animals and their products, people and equipment.
- Stop or restrict all animals to prevent spread or entry of disease.
- Observe, detect and report any clinical signs to your herd veterinarian as soon as possible

(Elbers et al., 2008).

- Limit access to your farm, keep the gate locked when not in use.
- Post signs to inform visitors to follow on your farm:
- Stay away from this farm until you get permission
- Hont before getting out of vehicle
- Check-in farm personnel upon arrival
- Follow farm biosecurity procedures
- Wear PPEs
- Avoid contact with animals specially those showing any kind of symptoms

- Educate yourself and train your employees about FMD and their ill signs (in previous mentioned chart) (Sieng et al., 2022).
- Discuss the threat of FMD with your neighbors.
- Eliminate the direct contact between animal across fence lines.
- Control normal moving animals in your farm like cats and dogs.
- Do not share equipment to other farms. (Ellickson, 1985).
- Change gloves and clothes properly and disinfect shoes when enter in to the farm. (Coronado et al., 2012).
- Wash hands after any contact with animals.
- Minimize the visitors to only those necessary for farm operations.
- Only one farm vehicle should be used.
- Record visitors on your log sheet.
- Provide the following items to visitors:
    - Clean head-covers and disposable or disinfected rubber foot wear
    - Facilities for disinfecting vehicles and all personnels
    - Pressure washers, brushes, water and EPA approved disinfectants for footwear and any equipment used
- Stop all the movements of animals on and off farm.
- Do not allow your animal to contact with neighbor's livestock.
- Fence off streams and rivers.
- Monitor animals closely
- Any animals that have recently been purchased should be quarantined for at least 30 days.
- Dispose of any bedding and manure from isolation areas. (Hutchison, Walters, Avery, Munro, & Moore, 2005).

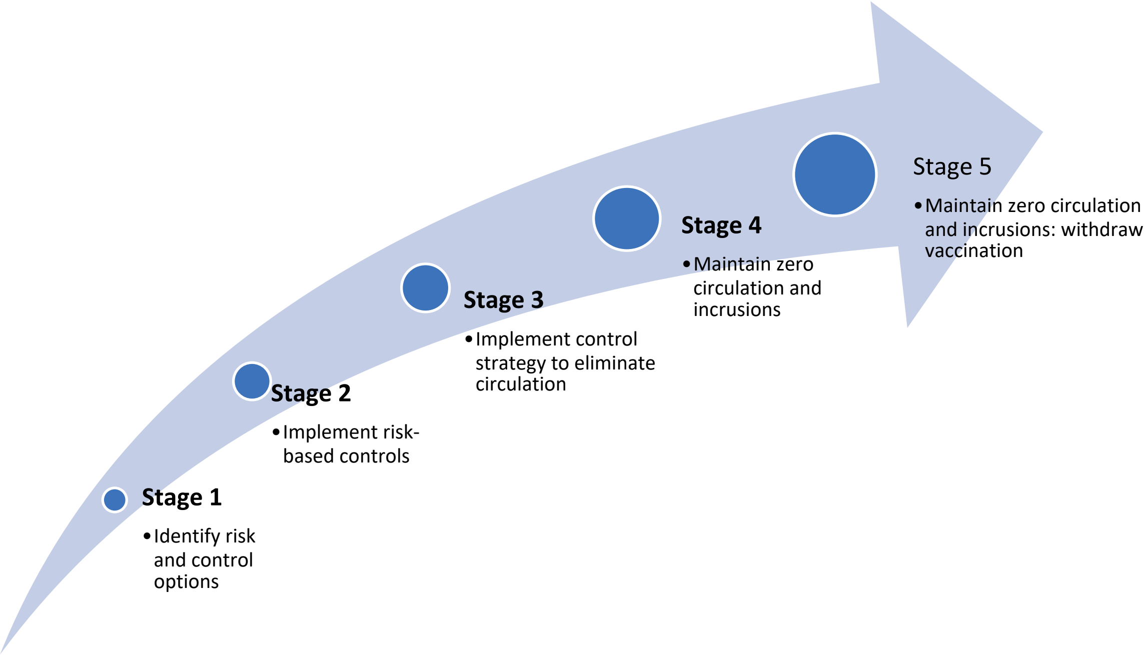

Figure 6. Stages in progressive control pathway for FMD.

Movement to a higher stage requires the completion of milestones indicated through arrows Stages 4 and 5 involve activities that lead to the submission of the application of official recognition of freedom (Donnelly, Mueller, & Gallahue, 2016).

FMD is controlled with quality vaccines containing appropriate FMD virus strains, also controlled by improving food security but it is difficult due to the existence of multiple serotypes of this virus, and multiple host species including wildlife. It is not currently possible to effectively control and eradicate FMD from the world because of a combination of technical constraints, an incomplete understanding of the epidemiology of the disease, and a lack of cost-effective disease control strategies (Kitching et al., 2007). Foot-and-mouth disease can be controlled by the cleanliness of animals and animal products. A slaughter policy was first applied in the UK in the late 19th century. Surveillance and early detection of FMD outbreaks are necessary. It involves clinical signs monitoring, conducting diagnostic tests, and reporting cases properly. During an outbreak, quarantine of animals becomes the major control of FMD from spreading. Spreading awareness to farmers, veterinarians, and community about the outbreak will help people to know the severity of disease so that it will help to cope-up with the disease rapidly (Pulla et al., 2021).

World has progressed a lot towards the control of Foot-and-Mouth disease through different eradication schemes.

Vaccination of FMD

Vaccination against Foot-and-Mouth disease is one of the control measures used during the FMD epidemic depending on the local epidemiological conditions (Rweyemamu, Roeder, MacKay, Sumption, Brownlie, & Leforban, 2008). A decision to make vaccination can be made only if there is enough knowledge on the effectiveness of the vaccination in eliminating the virus from the community. There are some points that need to be in mind are:

Immunity to FMD

Animals that are vaccinated or recovered from disease is mediated by the antibodies of which serum-neutralizing antibodies are more relevant in terms of protection (Plotkin, 2010). ELISA is quite extensively used in recent years, but this method measures the wide spectrum of antibodies.

Vaccine production environment

Production of vaccine and FMD antigens are carried out under the internationally recognized standard of GMP within the Quality assurance framework (De Clercq, Goris, Barnett, & MacKay, 2008).

Selection of Vaccine strains

After the confirmation of quality assured environment for vaccine production, selection of strain for vaccine preparation is the other major step. Although by vaccination control of FMD is complicated by the variability of antigen in virus, observers and vaccine producers are overplaying the issue (Doel, 2003).

Disease control strategy

This is difficult and controversial and there is no simple process to arrive at definite strategy for the control of FMD. The overall policy of any country and region affected by the disease will be based on the broad range of factors including cost.

Vaccine implication

The main issue in the safety of FMD vaccination is the target species. Foot-and-Mouth disease is contagious viral disease affecting livestock animals (Admassu et al., 2015). Commercial vaccines which are formulated with inactivated FMD virus, aluminum hydroxide/saponin or single or double emulsions for adjuvants are using worldwide for the control of disease in cattle. Animals immunized with high-load monovalent vaccine develop a high titer of antibodies at 7 days of postvaccination. However, it is difficult to remove all of the non-structural viral proteins that are produced during cell culture replication of FMDV and these can evoke antibodies that interfere with marker tests. Traditional vaccines remain the cornerstone for emergency and prophylactic uses.

Table 5. Importance of vaccine attributes in different situations (prophylactic and emergency vaccination).

Vaccine attributes	Prophylactic vaccination	Emergency vaccination
Rapid formulation	low	high
Rapid immunity onset	low	high
Thermostable formulation	high	medium
Antigenic broad spectrum	medium	medium
Efficacy	high	high
Negative marker	medium	high
Long lasting protection	high	low
Low production cost	high	medium
Low risk of virus release	high	high

Although current FMD vaccines can prevent clinical disease but the protection is short term (~6 months) requiring the booster doses for prophylactic control (Parida, 2009). Vaccination doesn't induce rapid protection against challenges or prevent the development of carrier state. So, it is clear that the length of protection depends on the expanse of immunization and duration of exposure methods.

World has progressed a lot towards the control of Foot-and-Mouth disease through different eradication schemes.

Table 6. Commercially available vaccines, their pros and cons.

Type	**Name**	**Pros**	**Cons**
Inactivated	Aftovaxpur DOE	Safe, no risk of disease	Booster dose required
Live attenuated	SAT2, No use due to safety concerns	Long lasting immunity	Reverse-attenuation
DNA based	Ad5-FMD	Stable and easy to produce	Need of adjuvants, less immunogenic
Peptide vaccines	VP1 synthetic peptides vaccine	Safe, no risk of disease, chemically stable	Requires adjuvants, less effective

Advances in FMD

There are more advances in the diagnosis of Foot-and-Mouth disease including the Nucleic acid detection method, ELISA, and chromatographic strip tests (Parida, 2009). Molecular-based techniques are used to detect the presence of viral nucleic acid. Up to date, improved versions of RT-PCR have been employed for the detection of Foot-and-Mouth disease virus. Multiplex RT-PCR with more advancement, automated electronic micro assay for the simultaneous detection and differentiation of different swine viruses including FMDV is used. Real-time quantitative PCR-based analysis with fluorescent emitting compounds has been used to measure the number of amplicons during amplification in real-time. RT-LAMP is needed for the detection of FMDV genomic sequence targeting the FMDV 3D RNA polymerase gene (Ranjan et al., 2014).

Serological methods including ELISA detect the presence of viral antigens or antibodies in serum or body fluids. Current ELISA is the modified version of the radioimmune assay. In this technique, the antigen is immobilized in the solid phase by either direct or indirect labeled antibody. To improve the performance of ELISA in FMD diagnosis many modifications have been made focusing on developing on the development of new coating antigens and monoclonal antibodies. Also, double sandwich ELISA further improved the sensitivity of FMDV detection to 125 times higher than the CFT. More effective and safer vaccines are created by genetic engineering using CRISPR and other gene-editing technologies (Teng, Yao, Nair, & Luo, 2021).

There are also advances in the eradication of Foot-and-Mouth disease. The Action Plan for the regional Hemispheric program for the eradication of FMD without vaccination resulted in the FMD-free status of the bovine population of South America. There have been some limited attempts to develop antiviral drug therapy that affects specific viral protein targets. The technology is used to specifically inhibit FMDV replication in cell culture. However, this technology has not been extended to be susceptible animals (McEwen & Fedorka-Cray, 2002).

Future Recommendations

Countries having FMD are facing trade barriers posed by FMD-free countries and they're having high economic losses to the livestock industry (T. J. Knight-Jones & Rushton, 2013). In the era of eradication of rinderpest, progressive worldwide control of Foot-and-Mouth disease must be regarded as a major contribution. The strategy for the control of Foot-and-Mouth disease in the endemic era should be based on seven stages.

1. Assessing and defining the FMS status
2. Vaccination and movement control
3. Virus transmission should be suppressed to overcome the disease
4. Need to achieve freedom from FMD with vaccination according to OIE standards
5. Achieve freedom from FMD without vaccination according to OIE standards

6. Extend the FMD free zones
7. Maintain the FMD freedom

These issues should be addressed to eradicate foot-and-mouth disease (Rodriguez & Gay, 2011). To effectively monitor the control program in a country, we need to place a national commission to coordinate all organizations associated with the FMD control program including the assurance of quality of vaccines. Another major aspect of the future regarding better ways to eradicate FMD is the timing of vaccination. Quality of vaccine should be the other important for the success of control programs. Make sure the use of monovalent vaccines where a particular serotype is prevalent for a long time, will reduce the cost of the operation. Maintenance of the cold chain is important as immunogenicity of antigen is lost by exposure to high temperature and repeated freezing. Susceptible livestock populations primarily cattle and buffalo, should be covered under the vaccination campaign. Centers for the Control of FMD need to enhance their surveillance strategy with target-based surveys that contribute to increasing the degree of sensitivity in the search for viral circulation in the context of the absence of clinical occurrence of FMD. These all measures will be helpful in the future for the successful eradication of Foot-and-Mouth disease (Pattnaik et al., 2012).

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About The Authors

Dr. Muhammad SAFDAR earned his PhD in molecular biology and genetics from Gaziantep University, Turkey. He is a lecturer in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, nutrigenomics, nano-genomics, bioinformatics, biotechnology, and their applications. He has published more than 70 research articles in national and international journals. He has also written many book chapters as well as an edited book. He is an associate editor for international journals.

E-mail msafdar@cuvas.edu.pk , ORCID 0000 0002 3720 2090

Dr. Umair YOUNAS received his DVM and Mphil (Livestock Management) degree from the University of Veterinary and Animal Sciences, Lahore. During M.Phil, Dr. Umair got training from PTC+ institute (Netherlands) on dairy farm practices and milk processing. After completing his M.Phil., Dr. Umair secured his Ph.D (Livestock Management) degree from the same university along with research work from the University of Florida as Sabbatical. Dr. Umair younas has vast experience in academics and since 2008 he has been working on various academic posts. Dr. Umair has more than 35 publications and currently, he is working as Head of the Department (Livestock Management) in CUVAS as well as ORIC member and Deputy director QEC (Quality Enhancement Cell).

Email umairyounas@cuvas.edu.pk ORCID 0000-0002-5107-9391

Abdul Rehman received his graduate degree in Applied Microbiology from Cholistan University of Veterinary and Animal Sciences, Bahawalpur, Pakistan. He has completed his internship at the renowned National Institute of Health Pakistan, where he worked on various microbiological studies. Abdul has written a thesis based on his work during this internship. He has also authored several research and review articles and contributed a chapter on Foot and Mouth Disease in animals and livestock, which is set to be published soon. His research interests encompass viral immune evasion, antimicrobial resistance, and diagnostic advancements.

E-mail jami.abdrehman@gmail.com ORCID 0009-0000-7588-0127

Momina Malik, a microbiologist with a degree in Applied Microbiology from Cholistan University of Veterinary and Animal Sciences, Bahawalpur (2024). Her final-year research focused on bacterial activities in different aspects. She has authored research articles and book chapters, showcasing her ability to communicate complex microbiological concepts. Her academic and research achievements reflect her dedication to advancing the field of microbiology.

Email mominamalik041@gmail.com ORCID 0009-0002-1507-2560

Umaima Nadeem, a microbiologist with a degree in Applied Microbiology from Cholistan University of Veterinary and Animal Sciences, Bahawalpur (2024). Her final-year research focused on bacterial activities in different aspects. She has authored research articles and book chapters, showcasing her ability to communicate complex microbiological concepts. Her academic and research achievements reflect her dedication to advancing the field of microbiology.

Email umn0015@gmail.com ORCID 0009-0005-4396-5923

Muhammad Abdullah is a Poultry Scientist with a degree of Applied Poultry Sciences from Cholistan University of Veterinary and Animal Sciences Bahawalpur 2020-2024. His research expertise spans various fields, of poultry. he is also a prolific author of book chapters and editor of several prestigious scientific volumes. Additionally, he worked as media secretary of poultry Science club at Cholistan University of Veterinary and Animal Sciences.

Email abdullahzahid2212@gmail.com ORCID 0009-0007-7627-4349

Mr. Tanveer Nasir is currently pursuing a BS in Biotechnology at the Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His primary areas of interest include Biotechnology, Molecular Biology, and Genetics. He has contributed three book chapters published in international journals, showcasing his growing expertise in these fields.

Email tanveernasir408@gmail.com ORCID 0009-0008-7232-1053

Miss. Salma Bibi, received her BS degree in Animal Sciences from Cholistan University of Veterinary and Animal Sciences, Bahawalpur, Pakistan. Her main areas of interest are Animal Genetics, Breeding and Reproduction. She has written 8 book chapters in international journals.

Email salmamalik6809129@gmail.com ORCID 0009-0003-0798-9886

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ZOONOTIC DISEASES AND PUBLIC HEALTH

Muhammad RAMEEZ

Aman Ullah KHAN

Muhammad FAROOQ

Zoonotic diseases, which are transmitted between animals and humans, pose significant threats to public health, agriculture, and the environment. This chapter "Zoonotic Diseases and Public Health" provides a comprehensive overview of zoonotic diseases, covering their historical perspective, epidemiology, major diseases, transmission dynamics, and prevention and control strategies. The historical section explores early observations, epidemics, and scientific advancements that have shaped our understanding of zoonosis. Epidemiological aspects highlight the global prevalence, distribution, and factors influencing the spread of zoonotic diseases. Major zoonosis such as rabies, avian influenza, and Lyme disease are discussed, emphasizing their impact on human and animal populations. Transmission dynamics, including modes of transmission and reservoir hosts, are examined to understand the complexities of zoonotic disease transmission. The chapter also discusses the One Health approach, emphasizing collaborative efforts between veterinary, medical, and environmental professionals in zoonotic disease management. Prevention and control strategies, including surveillance, vaccination, and hygiene measures, are explored to mitigate the risks of zoonotic diseases. Challenges such as emerging diseases and antimicrobial resistance, as well as the impact of climate change on disease patterns, are addressed. Case studies highlight notable outbreaks and successful control measures. The chapter concludes with a summary of key points and emphasizes the importance of continued research and collaboration in combating zoonotic diseases.

Introduction

Zoonotic diseases, also known as zoonosis, are infectious diseases that can be transmitted between animals and humans. These diseases can be caused by bacteria, viruses, parasites, and fungi, and they pose significant threats to public health, agriculture, and the environment. Zoonotic diseases can be transmitted through direct contact with infected animals or their environment, through consumption of contaminated food or water, or through vectors such as mosquitoes and ticks.

The significance of zoonotic diseases lies in their potential to cause widespread illness and even death in both animals and humans. These diseases can have serious economic impacts, affecting livestock production and trade, as well as human healthcare costs. Additionally, zoonotic diseases can have long-term environmental consequences, as they can impact wildlife populations and ecosystems (Figure 1).

Figure 1; Human, Animals and environment interaction and zoonotic diseases.

This chapter provides a comprehensive overview of zoonotic diseases, covering their historical perspective, epidemiology, major diseases, transmission dynamics, and prevention and control strategies. It explores the global prevalence and distribution of zoonosis, highlighting the factors that influence their spread. The chapter also discusses the One Health approach, which emphasizes the interconnectedness of human, animal, and environmental health in addressing zoonotic diseases.

Zoonotic diseases have been a major concern for human populations. Early observations and beliefs about these diseases date back centuries, with ancient civilizations recognizing the link between human health and animal contact. The impact of epidemics and pandemics caused by zoonotic diseases, such as the Black Death and the Spanish flu, has shaped our understanding of disease prevention and control.

Advancements in scientific research have led to significant progress in understanding and managing zoonotic diseases. The development of vaccines, antibiotics, and other treatments has helped to reduce the impact of these diseases on human and animal populations. However, challenges remain, including emerging diseases and antimicrobial resistance, which require ongoing research and collaboration to address.

Historical Perspective

Zoonotic diseases, illnesses that can be transmitted between animals and humans, have been a significant concern throughout human history. Early civilizations, such as the ancient Egyptians, Greeks, and Romans, recognized the link between human health and contact with animals (Figure 2). While their understanding of disease transmission was limited by the scientific knowledge of the time, these early observations laid the foundation for our modern understanding of zoonotic diseases.

Figure 2; Ancient Egyptian Artwork depicting their beliefs about humans and animals interaction.

Early Observations and Beliefs

Ancient cultures often attributed disease outbreaks to supernatural causes or environmental factors. However, some early observations hinted at the transmission of diseases from animals to humans. For example, the Greeks noted the transmission of rabies through the bite of an infected animal (King, A. A., et al. 2004). Similarly, the Romans observed the spread of diseases like anthrax and brucellosis from animals to humans (Tanga, C., et al., 2022). These early observations were critical in understanding the potential for diseases to cross species barriers.

In medieval Europe, the concept of "miasma" theory emerged, suggesting that diseases were spread through foul-smelling air (Kannadan, A. 2018). While this theory was not based on scientific evidence, it did lead to the implementation of some rudimentary public health measures, such as quarantine and isolation of sick individuals. These measures, while crude by modern standards, laid the groundwork for more sophisticated disease control strategies in later centuries.

Impact of Epidemics and Pandemics

Throughout history, zoonotic diseases have caused devastating epidemics and pandemics that have shaped societies and influenced human behavior. One of the most infamous examples is the Black Death, which was caused by the bacterium Yersinia pestis and is believed to have originated in rodents (Barbieri, et al. 2020). The Black Death, which swept through Europe in the 14th century, resulted in the deaths of an estimated 75-200 million people, dramatically altering the course of history (Figure 3).

Figure 3; Spread of the Black Death (from the original outbreak to its end), 1346–1353 (Cesana, D., et al., 2017).

Another notable zoonotic disease outbreak was the Spanish flu pandemic of 1918, caused by the H1N1 influenza virus. This pandemic infected an estimated 500 million people worldwide and resulted in the deaths of 20-50 million individuals (Watanabe, T., & Kawaoka, Y. 2011). The origins of the Spanish flu are believed to be avian, with the virus jumping from birds to humans. The impact of these pandemics underscores the importance of understanding and controlling zoonotic diseases.

Scientific Discoveries and Advances

The field of microbiology, which emerged in the 19th century, marked a significant turning point in the understanding of zoonotic diseases. Scientists such as Louis Pasteur and Robert Koch made groundbreaking discoveries about the causes of infectious diseases and developed vaccines and treatments for various illnesses.

Pasteur's work on rabies, a zoonotic disease transmitted through the bite of infected animals, led to the development of the first rabies vaccine (Beyene, K., et al., 2018). Koch's postulates, a series of criteria for establishing the cause of an infectious disease, revolutionized the field of epidemiology and our understanding of how diseases spread. These scientific advances paved the way for more effective control and prevention of zoonotic diseases.

Historical Control Measures and Lessons Learned

Throughout history, various control measures have been implemented to combat zoonotic diseases. Quarantine, isolation, and culling of infected animals were common practices in ancient civilizations. In more recent times, public health campaigns promoting hygiene and sanitation have helped reduce the transmission of zoonotic diseases.

One of the key lessons learned from history is the importance of interdisciplinary collaboration in combating zoonotic diseases. The One Health approach, which recognizes the interconnectedness of human, animal, and environmental health, has become a cornerstone of modern disease control efforts (Ojeyinka, O. T., & Omaghomi, T. T. 2024). By working together across disciplines, we can better understand, prevent, and control zoonotic diseases for the health and well-being of all species.

The historical perspective of zoonotic diseases highlights the significant impact these diseases have had on human history and the importance of ongoing research and collaboration in preventing and controlling them. Through a combination of scientific discovery, public health measures, and interdisciplinary collaboration, we can continue to make progress in combating zoonotic diseases and protecting the health of both humans and animals.

Epidemiology of Zoonotic Diseases

Zoonotic diseases, which are infections transmitted between animals and humans, are a significant global public health concern. They encompass a diverse range of pathogens, including bacteria, viruses, parasites, and fungi, and can be acquired through direct contact with infected animals, consumption of contaminated food or water, or exposure to vectors such as mosquitoes and ticks (Ferreira, M. et al., 2021). Understanding the epidemiology of zoonotic diseases is crucial for effective prevention and control measures.

Global Prevalence and Distribution

Zoonotic diseases are widespread and occur on every continent, affecting both developed and developing countries. However, the prevalence and distribution of these diseases vary widely depending on factors such as geographic location, climate, human-animal interactions, and socio-economic conditions (Rahman, M. et al., 2020). For example, vector-borne zoonotic diseases like malaria and dengue fever are more prevalent in tropical and subtropical regions where the climate is conducive to the breeding of mosquitoes (Chala, B., & Hamde, F., 2021). Similarly, foodborne zoonotic diseases such as salmonellosis and campylobacteriosis are more common in areas with poor food safety practices and inadequate sanitation (Abebe, E., et al., 2020).

Despite the challenges in accurately estimating the global burden of zoonotic diseases, it is believed that they account for a significant proportion of human infectious diseases. According to the World Health Organization (WHO), zoonosis are responsible for around 60% of all human infectious diseases (World Health Organization, 2014), while emerging zoonotic diseases pose ongoing threats to public health security.

Factors Influencing the Spread of Zoonotic Diseases

The spread of zoonotic diseases is influenced by a complex interplay of factors that can be categorized into environmental, ecological, socio-economic, and behavioral determinants (Rahman, M. T., 2020). Understanding these factors is crucial for developing effective strategies to prevent and control zoonotic diseases.

Environmental Factors

Environmental factors, such as climate change and habitat destruction, can have a profound impact on the spread of zoonotic diseases. Changes in temperature and precipitation patterns can alter the distribution and behavior of disease vectors and reservoir hosts, leading to changes in the prevalence and transmission dynamics of zoonosis (Caminade, C., et al., 2019). For example, the expansion of mosquito habitats due to warmer temperatures has been linked to the spread of vector-borne zoonotic diseases like malaria and dengue fever.

Habitat destruction and fragmentation can also increase the likelihood of zoonotic disease transmission by bringing humans into closer contact with wildlife. Deforestation, urbanization, and agricultural expansion can disrupt ecosystems and create opportunities for pathogens to spill over from animals to humans (White, R. J., & Razgour, O., 2020). Additionally, changes in land use can lead to the loss of biodiversity, which has been linked to an increased risk of zoonotic disease emergence.

Ecological Factors

Ecological factors, such as the abundance and diversity of wildlife species, can influence the spread of zoonotic diseases. High biodiversity has been associated with a lower risk of zoonotic disease transmission, as it can reduce the likelihood of pathogens spilling over from one species to another (Salkeld, D. J., et al., 2015). However, human activities that disrupt ecosystems can alter the balance of wildlife populations and increase the risk of zoonotic disease emergence.

The presence of certain wildlife species, known as reservoir hosts, can also influence the spread of zoonotic diseases. Reservoir hosts are species that can carry and transmit pathogens without showing any signs of illness. Identifying and understanding reservoir hosts is important for predicting and controlling zoonotic disease outbreaks (Wang, L. F., & Crameri, G. 2014).

Socio-economic Factors

Socio-economic factors, such as poverty, lack of access to healthcare, and inadequate sanitation, can increase the risk of zoonotic disease transmission. Poor communities are often more vulnerable to zoonotic diseases due to factors such as overcrowding, malnutrition, and lack of education about disease prevention (Cascio, A., et al., 2011). Additionally, limited access to healthcare can delay diagnosis and treatment, allowing zoonotic diseases to spread unchecked.

Livelihood activities, such as agriculture, wildlife trade, and bush meat hunting, can also influence the spread of zoonotic diseases (Ferreira, M. N., et al., 2021). These activities can bring humans into close contact with potentially infected animals, increasing the risk of disease transmission. Improving socio-economic conditions and promoting sustainable livelihoods can help reduce the risk of zoonotic disease emergence.

Behavioral Factors

Human behavior plays a significant role in the spread of zoonotic diseases. Practices such as the consumption of bush meat, keeping of exotic pets, and improper food handling can increase the risk of zoonotic disease transmission (Alexander, K. A., & McNutt, J. W., 2010). Additionally, cultural beliefs and practices can influence people's attitudes towards zoonotic diseases and their prevention.

Travel and migration can also contribute to the spread of zoonotic diseases, as infected individuals can carry pathogens to new areas. Globalization has facilitated the rapid spread of zoonotic diseases (Bandara, M., et al., 2014), as increased travel and trade have created opportunities for pathogens to move between countries and continents.

Antimicrobial Resistance in Zoonotic Pathogens

Antimicrobial resistance (AMR) in zoonotic pathogens is an emerging factor that significantly influences the spread and control of zoonotic diseases. The overuse and misuse of antibiotics in both human medicine and animal agriculture have led to the development of resistant strains of bacteria that can be transmitted between animals and humans (Trott, D. J., et al., 2018). This makes infections harder to treat, increases the duration of illness, and raises the risk of severe outcomes. AMR also complicates the treatment protocols for zoonotic diseases, potentially leading to higher healthcare costs and longer hospital stays (Wassenaar, T. M., & Silley, P. 2008). Addressing AMR requires coordinated efforts across human, animal, and environmental health sectors to promote the prudent use of antimicrobials, enhance surveillance of resistant pathogens, and develop new treatment options.

Challenges in Control

Controlling zoonotic diseases poses significant challenges due to their complex nature and the diverse range of pathogens involved. Surveillance systems must be strengthened to monitor the occurrence and spread of zoonosis, particularly in resource-limited settings where surveillance capacity may be limited (Carpenter, A., et al., 2022). Additionally, One Health approaches that integrate human, animal, and environmental health are essential for effective zoonotic disease control.

Major Zoonotic Diseases

Zoonotic diseases, or zoonosis, are infections that are naturally transmissible from vertebrate animals to humans. These diseases can be caused by a variety of pathogens, including bacteria, viruses, parasites, and fungi. Understanding major zoonotic diseases is crucial for public health and animal health professionals alike, as these infections can have significant impacts on both human and animal populations.

Overview of Prominent Zoonosis

Rabies

Rabies is a viral disease caused by the rabies virus, which primarily affects the central nervous system of mammals, including humans. The primary mode of transmission is through the bite of an infected animal, with dogs being the most common transmitters globally, though bats, raccoons, skunks, and foxes also carry the virus. Rabies is nearly always fatal once symptoms appear, underscoring the importance of post-exposure prophylaxis (PEP). It causes 50,000 to 100000 human deaths annually, mainly in Asia and Africa, affecting children predominantly (Pavli, A. et al., 2011). Rabies outbreaks in wildlife can also devastate local ecosystems, reducing biodiversity. Prevention includes vaccinating domestic animals, managing wildlife, and educating the public on avoiding contact with potentially rabid animals.

Avian Influenza

Avian influenza, or bird flu, is caused by influenza A viruses that primarily infect birds but can also affect humans and other animals. Highly pathogenic avian influenza (HPAI) strains like H5N1 and H7N9 can cause severe disease and high mortality in humans (Alexander, D. J., 2007). Transmission to humans usually occurs through direct contact with infected birds, their droppings, or contaminated environments. Although human cases are rare, they can be severe or fatal, posing a global health concern. HPAI outbreaks in poultry can lead to mass culling, resulting in economic losses and affecting food security (Swayne, D. E., & Suarez, D. L., 2000). Control measures include monitoring bird populations, culling infected poultry, vaccination programs, and public education for poultry workers.

Ebola Virus Disease

Ebola virus disease (EVD) is a severe and often fatal illness caused by the Ebola virus. It is transmitted to humans from wild animals and spreads through human-to-human transmission via bodily fluids (Beeching, N. J., et al., 2014). EVD outbreaks cause high mortality rates, severe social and economic disruption, and significant strain on healthcare systems. Human cases typically result from contact with infected bats, non-human primates, or their bodily fluids. The disease can devastate wildlife populations, particularly primates. Control measures include early detection, isolation of patients, contact tracing, safe burial practices, and community engagement to prevent the spread (Chowell, G., & Nishiura, H. (2014).

West Nile Virus

West Nile virus (WNV) is primarily transmitted to humans through the bite of infected mosquitoes. It can cause febrile illness, encephalitis, or meningitis, with severe cases potentially leading to death (Campbell, G. L., et al., 2002). Birds are the primary reservoirs, with the virus cycling between birds and mosquitoes. WNV impacts human health through neuroinvasive disease and can cause substantial economic costs due to healthcare expenses and vector control efforts. In animals, particularly horses, WNV can cause severe neurological disease. Prevention focuses on mosquito control, using insect repellent, and reducing standing water where mosquitoes breed.

Zika Virus

Zika virus is primarily transmitted to humans through the bite of infected Aedes mosquitoes but can also be transmitted sexually and from mother to fetus (Musso, D., & Gubler, D. J. (2016). While Zika virus infection is often mild, it can cause serious birth defects, including microcephaly, if contracted during pregnancy (Honein, M. A., et al., 2017). Zika virus outbreaks pose significant public health challenges, particularly in tropical and subtropical regions. The virus also affects wildlife, though the extent is less understood. Prevention includes mosquito control measures, using insect repellent, wearing protective clothing, and reducing mosquito breeding sites.

Hantavirus

Hantavirus is primarily transmitted to humans through contact with rodent urine, droppings, or saliva (Madai, M., et al., (2021). It can cause hantavirus pulmonary syndrome (HPS) or hemorrhagic fever with renal syndrome (HFRS), both of which can be severe or fatal (Vaheri, A., et al., 2013). Human cases often result from exposure to rodent-infested areas. Hantavirus impacts human health significantly, with high fatality rates and considerable healthcare costs. Control measures focus on rodent control, sealing homes to prevent rodent entry, and educating the public about avoiding contact with rodent excreta.

Lassa Fever

Lassa fever is a viral infection caused by Lassa virus, transmitted to humans through contact with rodent excreta or human-to-human transmission (Asogun, D. A., et al., 2019). It causes hemorrhagic fever with a high mortality rate. Lassa fever is endemic in West Africa, posing significant public health challenges. Prevention includes rodent control, safe food storage, and early detection and isolation of cases.

Crimean-Congo Hemorrhagic Fever

Crimean-Congo hemorrhagic fever (CCHF) is a viral infection caused by the CCHF virus, transmitted to humans through tick bites or contact with infected animal blood. It causes severe hemorrhagic fever with a high mortality rate. CCHF outbreaks pose significant public health risks and impact livestock health (Nasirian, H. 2020). Prevention includes tick control, using protective clothing, and educating at-risk populations.

Middle East Respiratory Syndrome (MERS-CoV)

Middle East respiratory syndrome (MERS) is a viral respiratory illness caused by MERS-CoV, transmitted to humans through contact with camels or human-to-human transmission (Azhar, E. I., et al., 2019). It causes severe respiratory illness with a high mortality rate. MERS outbreaks pose significant public health challenges, particularly in the Middle East. Prevention includes avoiding contact with camels, using protective equipment, and early detection and isolation of cases.

Severe Acute Respiratory Syndrome (SARS-CoV)

Severe acute respiratory syndrome (SARS) is a viral respiratory illness caused by SARS-CoV, transmitted to humans through respiratory droplets. It causes severe respiratory illness with a high mortality rate. SARS outbreaks in the early 2000s highlighted the global health risks of emerging zoonotic viruses (Baric, R. S., 2008). Prevention includes infection control measures, early detection, and quarantine.

COVID-19 (SARS-CoV-2)

COVID-19 is a viral respiratory illness caused by SARS-CoV-2, transmitted to humans through respiratory droplets and contact with contaminated surfaces. It causes a wide range of symptoms, from mild respiratory illness to severe pneumonia and death. The COVID-19 pandemic has had profound global health, social, and economic impacts. Control measures include vaccination, public health interventions, and global cooperation to mitigate the spread (Jo, W. K., et al., 2021).

Nipah Virus

Nipah virus is a zoonotic virus transmitted to humans from bats, pigs, or through human-to-human transmission. It causes severe respiratory and neurological illness with high mortality rates (Ang, B. S., et al., 2018). Nipah virus outbreaks pose significant public health threats in Southeast Asia. Prevention includes avoiding contact with infected animals, improving biosecurity in pig farms, and early detection and isolation of cases.

Japanese Encephalitis

Japanese encephalitis is a viral infection transmitted to humans through the bite of infected mosquitoes, primarily affecting children in Asia. It causes encephalitis, with symptoms like fever, headache, and neurological complications, leading to high mortality and long-term disability (Misra, U. K., & Kalita, J. 2010). Japanese encephalitis impacts public health significantly, particularly in rural areas. Prevention includes vaccination, mosquito control, and public education.

Lyme Disease

Lyme disease is a bacterial infection caused by Borrelia burgdorferi, transmitted through the bite of infected black-legged ticks (Ixodes scapularis) (Stanek, G., et at., 2012). Symptoms include fever, headache, fatigue, and erythema migrans (a characteristic skin rash). Untreated Lyme disease can spread to joints, the heart, and the nervous system, causing severe health issues. It is the most common vector-borne disease in North America and Europe, impacting human health through prolonged illness and economic burdens (Marques, A. et al., 2021). Lyme disease also affects animals such as dogs, horses, and cattle. Prevention involves avoiding tick-infested areas, using insect repellent, performing tick checks, and promptly removing attached ticks (Corapi, K. M., et al., 2007). Control focuses on reducing tick populations and public education on prevention.

Q Fever

Q fever is a bacterial infection caused by Coxiella burnetii, transmitted to humans through inhalation of contaminated dust from animal birth products, urine, feces, or milk. It causes flu-like symptoms, pneumonia, or hepatitis, and can lead to chronic infection (Woldehiwet, Z., 2004). Q fever impacts livestock health, causing reproductive issues in animals such as sheep, goats, and cattle. Human outbreaks often occur in agricultural settings, highlighting the need for occupational health measures. Prevention includes vaccinating livestock, improving farm hygiene, and educating at-risk populations about the disease (Rahaman, M. R., et al., 2019).

Brucellosis

Brucellosis is a bacterial infection caused by Brucella species, transmitted to humans through direct contact with infected animals or consumption of contaminated animal products (Seleem, M. N., et al., 2010). It causes fever, joint pain, and fatigue, and can become chronic if untreated (Franco, M. P., et al., 2007). Brucellosis significantly impacts livestock, causing reproductive issues and economic losses. Human cases often occur in occupational settings such as farming and veterinary work. Prevention includes vaccinating animals, pasteurizing dairy products, and using protective equipment when handling animals.

Leptospirosis

Leptospirosis is a bacterial infection caused by Leptospira species, transmitted to humans through contact with water contaminated by the urine of infected animals (Bharti, A. R., et al., 2003). It causes flu-like symptoms, jaundice, or severe complications like kidney or liver failure. Leptospirosis affects both humans and animals, particularly in tropical regions with heavy rainfall. Control measures focus on rodent control, avoiding contact with contaminated water, and educating the public about preventive measures.

Anthrax

Anthrax is a bacterial infection caused by Bacillus anthracis, affecting humans and animals through contact with spores in contaminated soil, animal products, or inhalation (Goel, A. K. 2015). It causes cutaneous, inhalational, or gastrointestinal disease, with inhalational anthrax being the most severe. Anthrax outbreaks in livestock can lead to significant economic losses and pose risks to human health. Prevention includes vaccinating livestock, proper disposal of animal carcasses, and educating at-risk populations.

Toxoplasmosis

Toxoplasmosis is a parasitic infection caused by Toxoplasma gondii, transmitted to humans through undercooked meat, contaminated food or water, or contact with cat feces (Jiménez-Coello, et al., 2012). It causes flu-like symptoms but can lead to severe complications in immunocompromised individuals or congenital infections. Toxoplasmosis impacts human health, particularly in pregnant women and those with weakened immune systems. Control measures include cooking meat thoroughly, practicing good hygiene, and reducing cat exposure to infection (Sukthana, Y. 2006).

Plague (Yersinia pestis)

Plague is a bacterial infection caused by Yersinia pestis, transmitted to humans through flea bites or contact with infected animals (Barbieri, R., et al., 2020). It causes bubonic, septicemic, or pneumonic plague, with high mortality rates if untreated. Plague outbreaks historically caused significant human mortality and social disruption. The disease also impacts wildlife, particularly rodents and their predators. Control measures include reducing rodent populations, using insect repellent, and early treatment with antibiotics.

Bovine Tuberculosis (Mycobacterium bovis)

Bovine tuberculosis is a bacterial infection caused by Mycobacterium bovis, affecting cattle and other animals, and transmissible to humans through unpasteurized milk or direct contact (Olea-Popelka, F., et al., 2017). It causes chronic respiratory disease in animals and humans, leading to economic losses in the livestock industry and public health concerns. Control measures include testing and culling infected animals, pasteurizing milk, and improving farm biosecurity.

Salmonellosis

Salmonellosis is a bacterial infection caused by Salmonella species, transmitted to humans through contaminated food, water, or contact with infected animals (Waltman, W. D., et al., 2008). It causes gastrointestinal illness, with symptoms like diarrhea, fever, and abdominal cramps. Salmonellosis is a significant public health concern due to foodborne outbreaks and can also affect livestock, leading to economic losses. Prevention includes proper food handling, cooking, and hygiene practices.

Campylobacteriosis

Campylobacteriosis is a bacterial infection caused by Campylobacter species, transmitted to humans through contaminated food, water, or contact with infected animals (Shane, S. M., 2019). It causes gastrointestinal illness, with symptoms like diarrhea, fever, and abdominal pain. Campylobacteriosis is a leading cause of foodborne illness and can impact livestock, particularly poultry. Prevention includes proper food handling, cooking, and hygiene practices.

Chagas Disease (Trypanosoma cruzi)

Chagas disease is a parasitic infection caused by Trypanosoma cruzi, transmitted to humans through the bite of infected triatomine bugs or contaminated food (Pérez-Molina, J. A., & Molina, I., 2018). It causes acute and chronic phases, with potential severe complications like heart disease. Chagas disease significantly impacts human health in Latin America and affects various animal species. Control measures focus on reducing insect vectors, improving housing conditions, and screening blood donations.

Rocky Mountain Spotted Fever

Rocky Mountain spotted fever (RMSF) is a bacterial infection caused by Rickettsia rickettsii, transmitted to humans through tick bites (Dantas-Torres, F., 2007). It causes fever, rash, and potentially severe complications like organ failure. RMSF is a significant public health concern in the Americas, requiring prompt treatment with antibiotics. Prevention includes tick control, using insect repellent, and public education on tick-bite prevention.

Transmission Dynamics

Understanding the transmission dynamics of zoonotic diseases is crucial for developing effective prevention and control strategies. Zoonotic diseases can be transmitted through various modes, including direct contact, indirect transmission via contaminated environments or objects, and vector-borne routes. Additionally, reservoir hosts and amplification factors play significant roles in the perpetuation and spread of these diseases (Owen, J. C., et al., 2021). This section explores these aspects in detail.

Direct Transmission

Direct transmission occurs when the infectious agent is transferred from an infected animal to a human through direct contact. This can happen via bites, scratches, or other forms of physical interaction with the infected animal (Rahman, M. T., et al., 2020). Some notable examples include:

Rabies: Transmitted primarily through bites or scratches from infected animals such as dogs, bats, and wild carnivores.

Anthrax: Can be contracted by handling infected animals or animal products, leading to cutaneous, inhalational, or gastrointestinal anthrax.

Brucellosis: Spread through direct contact with infected livestock or consumption of unpasteurized dairy products (Figure 4).

Figure 4; Direct Transmission of Brucella by Consumption of raw dairy milk from affected animal.

Direct transmission often results in a higher risk of infection due to the immediate transfer of the pathogen, which may not be influenced by environmental factors (Estrada-Peña, A., et al., 2014).

Indirect Transmission

Indirect transmission involves the transfer of pathogens through an intermediate object or environment (Loh, E. H., et al., 2015). This can include:

Fomites: Inanimate objects that become contaminated with infectious agents, such as clothing, equipment, or surfaces (Fong, I. W., & Fong, I. W. 2017). For instance, the bacteria causing anthrax or the virus responsible for foot-and-mouth disease can be transmitted via contaminated equipment or footwear.

Airborne Transmission: Pathogens that can be aerosolized and inhaled by humans. An example is the Q fever bacterium (Coxiella burnetii), which can become airborne from contaminated animal birth products and be inhaled by humans (Goodwin, R., et al., 2012).

Indirect transmission often allows pathogens to spread over larger areas and through diverse routes, making control efforts more challenging.

Vector-Borne Transmission

Vector-borne transmission occurs when an infectious agent is transmitted to humans by vectors such as mosquitoes, ticks, or fleas (Khan, M. A. H. N. A., 2015). This mode of transmission often involves complex life cycles and multiple hosts. Key examples include:

Lyme Disease: Transmitted by Ixodes ticks, which acquire the Borrelia burgdorferi bacteria from infected wildlife such as deer and rodents.

Plague: Caused by Yersinia pestis, transmitted to humans through the bites of infected fleas that have fed on infected rodents.

West Nile Virus: Spread by mosquitoes that become infected after biting infected birds and then transmit the virus to humans and other animals (Figure 5).

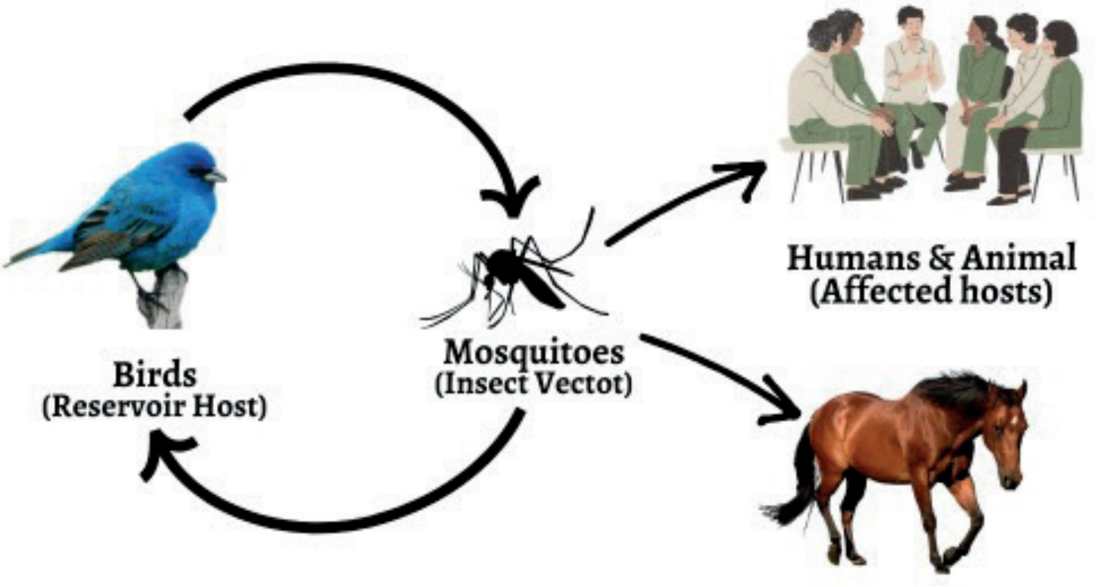

Figure 5; West Nile Virus Transmission Cycle.

Vector-borne transmission can lead to widespread outbreaks, especially in regions where vectors are prevalent and difficult to control.

Reservoir Hosts and Amplification Factors

Reservoir Hosts

Reservoir hosts are animal species that harbor infectious agents without succumbing to the disease themselves. They play a crucial role in maintaining and amplifying zoonotic pathogens in the environment (Owen, J. C., et al., 2021). Important examples include:

Bats: Serve as reservoir hosts for several zoonotic viruses, including rabies, Hendra, Nipah, and various coronaviruses (e.g., SARS-CoV, MERS-CoV).

Rodents: Act as reservoirs for hantaviruses, plague bacteria (Yersinia pestis), and Leptospira spp., which cause leptospirosis.

Birds: Serve as reservoirs for avian influenza viruses and West Nile virus, with migratory species playing a significant role in the global spread of these pathogens.

Reservoir hosts often do not exhibit symptoms of the disease, allowing them to spread pathogens silently within their populations and to other species, including humans.

Amplification Factors

Amplification factors are conditions or events that increase the transmission potential of zoonotic pathogens. These factors can be ecological, environmental, or human-induced. Key amplification factors include:

Environmental Changes: Deforestation, urbanization, and agricultural expansion can disrupt natural habitats and bring humans into closer contact with wildlife, increasing the risk of zoonotic disease transmission. For example, deforestation in the Amazon has been linked to increased malaria transmission due to the creation of suitable breeding sites for mosquitoes.

Climate Change: Alters the distribution and behavior of vectors and reservoir hosts. Warmer temperatures can expand the range of mosquitoes and ticks, leading to increased transmission of diseases like dengue fever, Lyme disease, and West Nile virus.

Human Activities: Intensive farming, wildlife trade, and global travel can facilitate the spread of zoonotic diseases (Esposito, M. M., et al., 2023). Intensive livestock farming can promote the emergence of diseases like avian influenza and swine flu due to high animal densities and close human-animal interactions. Wildlife trade and consumption can lead to the transmission of diseases such as SARS and Ebola.

Case Study: Ebola Virus

The Ebola virus provides a compelling example of how reservoir hosts and amplification factors interplay to influence zoonotic disease transmission. Bats are believed to be the natural reservoir for Ebola, with the virus occasionally spilling over to other wildlife species such as primates and antelope, and subsequently to humans (Malvy, D., et al., 2019). Outbreaks often occur in remote, forested regions where people hunt and consume bush meat, bringing them into direct contact with infected animals.

During the 2014-2016 West Africa Ebola outbreak, several amplification factors contributed to the unprecedented scale of the epidemic. These included:

Human Mobility: Movement of people between rural areas and densely populated urban centers facilitated the rapid spread of the virus.

Healthcare Practices: Lack of adequate infection control measures in healthcare settings led to nosocomial transmission among patients and healthcare workers.

Cultural Practices: Traditional burial practices involving close contact with the deceased facilitated further transmission.

Efforts to control the outbreak included improving infection control in healthcare settings, promoting safe burial practices, and enhancing surveillance and contact tracing. The development and deployment of experimental vaccines also played a crucial role in containing the epidemic.

Case Study: Avian Influenza

Avian influenza, particularly the highly pathogenic avian influenza (HPAI) strains like H5N1 and H7N9, illustrates the role of birds as reservoir hosts and the impact of amplification factors on disease transmission (Alexander, D. J., 2007). Wild birds, especially waterfowl, are natural reservoirs for avian influenza viruses, often carrying the viruses without showing symptoms. These viruses can be transmitted to domestic poultry, leading to outbreaks that can devastate poultry industries and pose risks to human health.

Key amplification factors for avian influenza include:

Poultry Farming Practices: High-density poultry farming increases the risk of virus transmission among birds and facilitates the emergence of new, potentially more virulent strains.

Live Bird Markets: Common in many parts of Asia, live bird markets bring together birds from various sources, creating opportunities for virus transmission and re-assortment.

Migratory Birds: Migratory patterns of wild birds contribute to the global spread of avian influenza viruses, with infected birds carrying the viruses across continents (Global Consortium for H5N8 and Related Influenza Viruses., 2016).

Control measures for avian influenza involve a combination of surveillance, culling infected or exposed poultry, vaccination, and biosecurity practices to prevent the spread of the virus. Public health measures also include monitoring human cases and preparing for potential pandemics.

The transmission dynamics of zoonotic diseases are complex and multifaceted, involving direct, indirect, and vector-borne routes. Reservoir hosts play a critical role in maintaining and amplifying zoonotic pathogens, while various environmental, ecological, and human-induced factors influence the spread of these diseases. Understanding these dynamics is essential for developing effective prevention and control strategies to protect both human and animal health. Through coordinated efforts across veterinary, medical, and environmental sectors, it is possible to mitigate the risks associated with zoonotic diseases and prevent future outbreaks.

One Health Approach

The One Health approach is an integrated strategy for managing zoonotic diseases that acknowledges the interconnectedness of human, animal, and environmental health (Mackenzie, J. S., & Jeggo, M. 2019).. This concept recognizes that the health of people is closely linked to the health of animals and our shared environment. The One Health approach is particularly relevant for zoonotic diseases, which are infectious diseases that can be transmitted between animals and humans. By promoting a holistic and interdisciplinary approach, One Health aims to enhance disease surveillance, prevention, and control efforts, ultimately improving health outcomes across all species (Cunningham, A. A., et al., 2017). The One Health concept has gained prominence in recent years due to several factors, including the increasing frequency of zoonotic disease outbreaks, the emergence of new pathogens, and the recognition of the limitations of traditional, siloed approaches to health. The One Health approach is grounded in several key principles:

1. **Interdisciplinary Collaboration:** One Health fosters collaboration among various disciplines, including veterinary medicine, human medicine, environmental science, epidemiology, and public health. This collaborative framework ensures that knowledge and expertise from different fields are integrated to address complex health issues effectively.

2. **Surveillance and Early Detection:** One Health emphasizes the importance of integrated surveillance systems that monitor disease trends in humans, animals, and the environment. Early detection of zoonotic disease outbreaks in animals can serve as a warning system for potential human health threats, enabling prompt and coordinated responses.

3. **Prevention and Control:** The One Health approach advocates for comprehensive prevention and control measures that consider the health of animals, humans, and ecosystems. This includes vaccination programs, biosecurity measures, public health interventions, and environmental management practices.

4. **Research and Innovation:** One Health promotes research that bridges the gaps between human, animal, and environmental health. This includes studies on pathogen transmission dynamics, the development of new diagnostic tools, and the evaluation of interventions that can reduce the risk of zoonotic disease transmission.

5. **Policy and Governance:** Effective implementation of One Health requires supportive policies and governance structures that facilitate cross-sectoral collaboration and resource allocation. Governments, international organizations, and stakeholders must work together to create frameworks that support One Health initiatives.

Collaborative Efforts between Veterinary, Medical, and Environmental Professionals

Collaboration is at the heart of the One Health approach, bringing together professionals from diverse fields to tackle zoonotic diseases. These collaborative efforts are essential for addressing the multifaceted nature of zoonotic disease threats and ensuring comprehensive and effective responses.

Veterinary Professionals

Veterinarians play a crucial role in the One Health approach by monitoring and managing animal health, which is often the first line of defense against zoonotic diseases (Gibbs, S. E., & Gibbs, E. P. J., 2013). Their responsibilities include:

- Conducting routine health checks and vaccinations for domestic and livestock animals.
- Implementing biosecurity measures to prevent disease outbreaks in animal populations.
- Investigating and responding to disease outbreaks in animals, which can provide early warnings for potential human health threats.
- Educating farmers, pet owners, and the public about zoonotic disease risks and prevention strategies.

Medical Professionals

Medical professionals contribute to the One Health approach by focusing on human health and ensuring that zoonotic diseases are diagnosed, treated, and managed effectively in human populations (Pal, M., et al., 2014). Their roles include:

- Conducting epidemiological investigations to trace the source and spread of zoonotic diseases in humans.
- Developing and administering vaccines and treatments for zoonotic infections.
- Collaborating with veterinarians and environmental scientists to identify and mitigate zoonotic disease risks.
- Educating patients and the public about zoonotic diseases, including prevention and control measures.

Environmental Professionals

Environmental scientists and professionals play a vital role in understanding and managing the ecological factors that influence zoonotic disease transmission (Pal, M., et al., 2014). Their contributions include:

- Monitoring wildlife populations and their interactions with domestic animals and humans.
- Studying the impact of environmental changes, such as deforestation and climate change, on the emergence and spread of zoonotic diseases.
- Implementing habitat management and conservation strategies to reduce the risk of zoonotic disease transmission.
- Advising on environmental policies and practices that promote ecosystem health and resilience.

Collaborative Initiatives

Several collaborative initiatives exemplify the One Health approach in action (Vicente, C. R., et al., 2021).

Integrated Surveillance Systems: These systems involve the collection and analysis of health data from human, animal, and environmental sources. By sharing information across sectors, integrated surveillance systems can detect zoonotic disease outbreaks more quickly and coordinate responses more effectively.

Joint Research Programs: Multidisciplinary research programs bring together experts from different fields to study zoonotic diseases (Vicente, C. R., et al. 2021). These programs can lead to the development of new diagnostic tools, vaccines, and intervention strategies that address the complex interactions between humans, animals, and the environment.

Cross-Sectoral Training and Education: Training programs that educate professionals about the principles and practices of One Health can foster a culture of collaboration and improve the capacity to respond to zoonotic disease threats (Ahmed, T., et al., 2023). These programs often involve joint workshops, seminars, and field exercises.

The One Health approach is a powerful framework for managing zoonotic diseases, emphasizing the interconnectedness of human, animal, and environmental health. By fostering interdisciplinary collaboration, enhancing surveillance and early detection, and promoting comprehensive prevention and control measures, One Health can improve health outcomes across all species. Collaborative efforts between veterinary, medical, and environmental professionals are essential for the successful implementation of One Health, ensuring that zoonotic diseases are addressed holistically and effectively.

Prevention and Control Strategies

Surveillance and Early Detection

Surveillance and early detection are critical components of managing and controlling zoonotic diseases. Effective surveillance systems aim to monitor disease trends, identify new and emerging pathogens, and provide timely information for public health interventions (Sharan, M., et al., 2023). These systems involve a coordinated approach that includes both passive and active surveillance mechanisms (Pimentel, L. C., & Taylor, E. V., 2014).

Passive Surveillance relies on the routine reporting of cases by healthcare providers, laboratories, and veterinarians. This type of surveillance is essential for tracking the incidence and prevalence of known zoonotic diseases and can highlight unusual increases in disease activity that may signal an outbreak.

Active Surveillance, on the other hand, involves proactive efforts to search for and identify cases of zoonotic diseases. This can include field investigations, targeted surveys, and the use of advanced diagnostic tools to detect pathogens in animal and human populations. Active surveillance is particularly important for detecting emerging diseases and monitoring wildlife reservoirs that may harbor zoonotic pathogens.

Integrated Surveillance Systems combine data from human health, animal health, and environmental monitoring to provide a comprehensive picture of zoonotic disease dynamics (Zinsstag, J., et al., 2020). These systems facilitate the early detection of outbreaks by enabling the sharing of information across sectors and geographic regions. Examples include the Global Early Warning System for Major Animal Diseases (GLEWS) and the One Health Surveillance system, which integrate data from various sources to enhance situational awareness and guide response efforts.

Vaccination Programs for Animals and Humans

Vaccination is one of the most effective tools for preventing zoonotic diseases. Vaccination programs can significantly reduce the incidence of zoonotic diseases in both animals and humans, thereby breaking the transmission cycle and protecting public health.

Animal Vaccination programs focus on immunizing livestock, pets, and wildlife against key zoonotic pathogens (Carpenter, A., et al., 2022). For example, rabies vaccination campaigns in domestic dogs have been highly successful in reducing human cases of rabies in many parts of the world. Similarly, vaccination of poultry against avian influenza and cattle against brucellosis and anthrax can prevent the spread of these diseases to humans.

Human Vaccination programs are essential for protecting people at high risk of exposure to zoonotic diseases. This includes vaccination against diseases such as rabies, which is critical for individuals who work closely with animals, such as veterinarians, wildlife handlers, and laboratory personnel (Shiferaw, M. L., et al., 2017). In regions where zoonotic diseases are endemic, vaccination programs can be targeted at vulnerable populations to prevent outbreaks. For example, the human papillomavirus (HPV) vaccine helps reduce the risk of zoonotic strains of the virus that may contribute to cancer development.

Combined Vaccination Strategies that involve both animals and humans are particularly effective in managing zoonotic diseases. These strategies often form part of One Health initiatives, where coordinated efforts are made to vaccinate animals and humans in parallel. This approach not only protects individual species but also contributes to the overall reduction of zoonotic disease transmission.

Hygiene and Biosecurity Measures

Maintaining high standards of hygiene and implementing biosecurity measures are crucial for preventing the spread of zoonotic diseases (Tayib, G. A., 2023). These practices are essential at all levels, from individual hygiene to institutional biosecurity protocols.

Personal Hygiene practices, such as regular hand washing with soap and water, are fundamental in preventing zoonotic infections (Cediel, N., et al., 2013). Individuals who handle animals or animal products should take additional precautions, such as wearing protective clothing and using disinfectants to clean equipment and surfaces.

Institutional Hygiene measures are necessary in settings such as farms, abattoirs, and markets where animals are kept or traded. These measures include regular cleaning and disinfection of facilities, proper waste disposal, and the provision of handwashing stations for workers and visitors. Ensuring that animal housing areas are kept clean and free of pests can also reduce the risk of zoonotic disease transmission.

Biosecurity Measures involve practices designed to prevent the introduction and spread of infectious diseases within animal populations. On farms, biosecurity measures include controlling access to the premises, ensuring that new animals are quarantined before mixing with the herd, and implementing protocols for the movement of animals and equipment ((Tayib, G. A., 2023). Regular health monitoring and vaccination of livestock are also key components of biosecurity.

Wildlife Biosecurity is important for preventing zoonotic diseases that originate in wild animals. Measures such as habitat management, controlling wildlife access to human settlements, and monitoring wildlife health can help reduce the risk of zoonotic pathogens spilling over into human populations (Artois, M., 2011). Sustainable control of zoonotic pathogens in wildlife: how to be fair to wild animals?. Revue Scientifique et Technique-OIE, 30(3), 733..

Food Safety Practices are critical in preventing zoonotic diseases transmitted through contaminated food. These practices include proper handling, cooking, and storage of food products, particularly those of animal origin. Implementing food safety regulations and conducting regular inspections can help ensure that food products are safe for consumption and free from zoonotic pathogens (Latif, M., et al., 2023).

The prevention and control of zoonotic diseases require a multifaceted approach that includes surveillance and early detection, vaccination programs for both animals and humans, and stringent hygiene and biosecurity measures. Integrated surveillance systems enable the timely identification of outbreaks, while vaccination programs break the transmission cycle of zoonotic pathogens. Hygiene and biosecurity measures at both personal and institutional levels further reduce the risk of zoonotic disease transmission. By implementing these strategies in a coordinated manner, it is possible to significantly mitigate the impact of zoonotic diseases on public health, agriculture, and the environment.

Challenges and Future Directions

Emerging Zoonotic Diseases and Antimicrobial Resistance

One of the most pressing challenges in the field of zoonotic diseases is the continual emergence of new pathogens. Emerging zoonotic diseases, such as the novel coronavirus (SARS-CoV-2), which caused the COVID-19 pandemic, highlight the profound impact these diseases can have on global public health, economies, and societies. Factors contributing to the emergence of zoonotic diseases include increased human-wildlife interaction, habitat destruction, urbanization, and global travel and trade. These factors create opportunities for pathogens to jump from animals to humans, leading to new outbreaks.

The rise of antimicrobial resistance (AMR) further complicates the management of zoonotic diseases. AMR occurs when microorganisms develop the ability to defeat the drugs designed to kill them, making infections harder to treat and increasing the risk of disease spread, severe illness, and death ((Trott, D. J., et al., 2018). The misuse and overuse of antibiotics in both human medicine and animal agriculture are major drivers of AMR. In livestock, antibiotics are often used not only for treating infections but also for growth promotion and disease prevention, contributing to the development of resistant strains that can be transmitted to humans through direct contact or the food chain.

Combatting AMR requires a multifaceted approach. Strategies include:

1. **Responsible Use of Antibiotics:** Implementing stewardship programs to ensure antibiotics are used judiciously in both human and veterinary medicine.
2. **Surveillance:** Enhancing monitoring systems to track the prevalence of resistant strains in humans, animals, and the environment.
3. **Research and Development:** Investing in the development of new antibiotics, alternative therapies, and rapid diagnostic tools.
4. **Public Awareness:** Educating healthcare professionals, farmers, and the general public about the importance of responsible antibiotic use and the dangers of AMR.

Implications of Climate Change on Zoonotic Disease Patterns

Climate change is another significant factor influencing the patterns and dynamics of zoonotic diseases. Changes in temperature, precipitation, and extreme weather events can alter the habitats and behaviors of wildlife, vectors (such as mosquitoes and ticks), and pathogens, thereby affecting the transmission dynamics of zoonotic diseases (Estrada-Peña, A., et al., 2014).

1. **Geographic Range Expansion:** As temperatures rise, many vector species are expanding their geographic ranges into previously temperate regions. For example, the spread of Aedes mosquitoes, which transmit diseases like dengue, chikungunya, and Zika virus, is linked to warming climates. Similarly, the range of ticks that carry Lyme disease is expanding, leading to increased incidence in new areas.
2. **Seasonality and Transmission Cycles:** Climate change can also affect the seasonality of

zoonotic diseases. Warmer temperatures and altered rainfall patterns can extend the breeding season for vectors, increasing the duration and intensity of disease transmission periods. For instance, changes in the monsoon patterns in Asia can influence the transmission of diseases like Japanese encephalitis and leptospirosis.

3. **Impact on Wildlife Populations:** Climate change can stress wildlife populations by altering their habitats and food sources, leading to increased interaction with human populations as animals migrate or seek new resources. This increased contact heightens the risk of zoonotic spillover events. For example, deforestation and habitat fragmentation can bring humans into closer contact with bats, which are reservoirs for several zoonotic viruses, including Ebola and coronaviruses.
4. **Environmental Changes:** Environmental disruptions, such as flooding and drought, can influence the spread of zoonotic diseases. Flooding can lead to outbreaks of waterborne diseases like leptospirosis, while drought can concentrate animals around limited water sources, increasing the risk of disease transmission.

Future Directions

Addressing the challenges posed by emerging zoonotic diseases, AMR, and climate change requires a proactive and integrated approach that spans multiple disciplines and sectors.

1. **One Health Approach:** Strengthening the One Health framework is critical. This approach emphasizes the interconnectedness of human, animal, and environmental health and promotes collaborative efforts across sectors to prevent and control zoonotic diseases. Enhanced communication and coordination between public health, veterinary, and environmental agencies can lead to more effective surveillance, risk assessment, and response strategies.
2. **Enhanced Surveillance and Monitoring:** Investing in robust and integrated surveillance systems is essential for early detection and rapid response to emerging zoonotic threats. This includes utilizing advanced technologies such as genomic sequencing, remote sensing, and data analytics to monitor and predict disease outbreaks.
3. **Research and Innovation:** Continued research into the ecology, epidemiology, and transmission dynamics of zoonotic diseases is vital. Innovations in diagnostic tools, vaccines, and therapeutic interventions can provide new means to combat zoonotic pathogens. Additionally, understanding the impact of climate change on disease patterns can inform adaptive strategies to mitigate risks.
4. **Policy and Regulation:** Implementing and enforcing policies that address the drivers of zoonotic disease emergence, such as wildlife trade and habitat destruction, is crucial. Strengthening regulations around the use of antibiotics in agriculture can help combat AMR. International cooperation and agreements are necessary to tackle these global challenges effectively.
5. **Education and Public Engagement:** Raising awareness among the public, healthcare providers, and policymakers about the importance of zoonotic disease prevention and the impact of AMR and climate change is essential. Education campaigns can promote behavioral changes and support for sustainable practices that reduce the risk of zoonotic disease transmission.

In conclusion, addressing the complex challenges posed by zoonotic diseases, antimicrobial resistance, and climate change requires a comprehensive and collaborative approach. By integrating efforts across disciplines and sectors, we can enhance our capacity to prevent, detect, and respond to these threats, safeguarding public health and ensuring a resilient future.

Notable Outbreaks and Their Impact on Public Health Policies

Ebola Virus Outbreak (2014-2016)

The Ebola virus outbreak in West Africa from 2014 to 2016 was one of the most severe in history, with over 28,000 cases and more than 11,000 deaths (Bell, B. P., 2016). The outbreak exposed significant weaknesses in global health systems, including delays in outbreak detection and response, insufficient healthcare infrastructure, and a lack of coordination among international agencies. The World Health Organization (WHO) and other health bodies have since implemented reforms to improve epidemic preparedness and response. This includes the establishment of the WHO's Health Emergencies Programme, designed to provide rapid support during outbreaks and the development of the Coalition for Epidemic Preparedness Innovations (CEPI) to accelerate the development of vaccines against emerging infectious diseases (Gouglas, D., et al., 2019).

H1N1 Influenza Pandemic (2009)

The H1N1 influenza pandemic, commonly known as swine flu, emerged in 2009 and spread rapidly across the globe, infecting people and causing about 40000 deaths (Osztovits, J., 2009). The pandemic highlighted the need for rapid vaccine development and distribution, effective communication strategies, and coordinated global responses. In response, many countries revised their pandemic preparedness plans, emphasizing the importance of surveillance, stockpiling antiviral medications, and ensuring the availability of critical medical supplies. The experience also underscored the necessity of transparent communication to manage public fear and misinformation.

COVID-19 Pandemic (2019-2022)

The COVID-19 pandemic, caused by the novel coronavirus SARS-CoV-2, has had a profound impact on global health policies. With over 600 million confirmed cases and more than 6 million deaths worldwide, the pandemic has led to unprecedented public health measures, including lockdowns, travel restrictions, and widespread vaccination campaigns. The pandemic has accelerated the adoption of telemedicine, highlighted the importance of robust healthcare systems, and spurred significant investment in vaccine research and development. It has also emphasized the critical need for international cooperation and the One Health approach to prevent future zoonotic spillovers.

Success Stories in Zoonotic Disease Control

Rabies Control in Latin America

Rabies, a fatal viral disease primarily transmitted through dog bites, has seen significant control efforts in Latin America. Mass dog vaccination campaigns, public awareness programs, and improved access to post-exposure prophylaxis (PEP) for humans have dramatically reduced the incidence of rabies in the region. Countries like Mexico and Brazil have implemented national rabies control programs that include regular vaccination drives, stray dog population management, and community education (Ciotti, M., et al., 2020). As a result, many countries in Latin America are on the path to eliminating human rabies transmitted by dogs, showcasing the effectiveness of sustained and coordinated control efforts.

Eradication of Rinderpest

Rinderpest, a highly contagious viral disease affecting cattle and other cloven-hoofed animals, was officially declared eradicated in 2011, marking a significant milestone in veterinary and public health. The global eradication campaign, led by the Food and Agriculture Organization (FAO) and the World Organisation for Animal Health (OIE), involved widespread vaccination, surveillance, and prompt reporting of outbreaks (Roeder, P., et al., 2013). The successful eradication of rinderpest has had profound economic benefits for livestock-dependent communities and demonstrates the potential for international collaboration in disease control.

Control of Nipah Virus in Malaysia

Nipah virus, a zoonotic pathogen with a high fatality rate, first emerged in Malaysia in Ciotti, M.,.causing severe disease in humans and pigs. The outbreak was linked to close contact between pigs and fruit bats, the natural reservoir of the virus. The Malaysian government implemented rigorous control measures, including culling infected pigs, banning the movement of pigs from affected areas, and educating farmers about the risks of bat exposure (Shariff, M., 2019). These efforts successfully contained the outbreak, and continuous surveillance and improved farm management practices have prevented subsequent outbreaks. This case highlights the importance of rapid response and the integration of veterinary and public health measures in controlling zoonotic diseases.

The case studies of notable outbreaks and success stories in zoonotic disease control illustrate the complex interplay between human and animal health and the critical need for coordinated efforts across disciplines. The impact of outbreaks such as Ebola, H1N1, and COVID-19 on public health policies underscores the importance of preparedness, rapid response, and international cooperation. Success stories like the control of rabies, the eradication of rinderpest, and the management of Nipah virus demonstrate that with sustained efforts and collaborative approaches, significant progress can be made in controlling and preventing zoonotic diseases. Continued investment in research, surveillance, and public health infrastructure is essential to address the evolving challenges posed by zoonotic diseases and to protect global health.

Summary

In this chapter, we have explored the multifaceted and critical issue of zoonotic diseases and their profound impact on public health, agriculture, and the environment. We began by defining zoonotic diseases and discussing their significance in the context of global health. The historical perspective provided insights into early observations, significant epidemics, and the scientific advancements that have shaped our current understanding of zoonoses. The epidemiological section highlighted the global prevalence and distribution of zoonotic diseases, emphasizing the various factors that influence their spread, including human behavior, environmental changes, and animal interactions.

We then delved into major zoonotic diseases such as rabies, avian influenza, and Lyme disease, examining their impact on both human and animal populations. Understanding the transmission dynamics, including direct, indirect, and vector-borne modes, as well as the role of reservoir hosts, is crucial for developing effective control strategies. The One Health approach was emphasized, showcasing the importance of interdisciplinary collaboration among veterinary, medical, and environmental professionals in managing zoonotic diseases. Prevention and control strategies, such as surveillance, vaccination programs, and hygiene measures, were discussed in detail, highlighting their role in mitigating the risks associated with zoonotic diseases. The chapter also addressed the challenges posed by emerging diseases and antimicrobial resistance, as well as the implications of climate change on disease patterns.

Case studies of notable outbreaks, such as Ebola, H1N1, and COVID-19, illustrated the impact of zoonotic diseases on public health policies and the success stories in disease control, such as the eradication of rinderpest and the control of rabies in Latin America, underscored the importance of sustained and coordinated efforts. The ongoing threat of zoonotic diseases necessitates continuous research, surveillance, and international collaboration. By embracing a One Health approach and leveraging advances in science and technology, we can better understand, prevent, and control zoonotic diseases, ultimately safeguarding the health of both humans and animals. The lessons learned from past outbreaks and the success stories in disease management serve as valuable guides for future efforts in combating these complex and evolving threats.

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About the Author

Muhammad RAMEEZ received his Doctor of Veterinary Medicine (DVM) from the University of Veterinary and Animal Sciences, Lahore, Pakistan. His research interests include zoonotic diseases, public health, antimicrobial resistance, and disease prevention in animals. He has authored several articles and a book chapter in the field of veterinary medicine and public health. Muhammad has actively contributed to public awareness campaigns, particularly related to rabies prevention and vaccination in companion animals. He is also involved in advocacy for health systems strengthening and resilience in developing countries.

E-mail mrameez953@gmail.com ORCID 0009-0008-4822-362

Dr. Aman Ullah Khan, a Ph.D. holder from Freie University Berlin, Germany, serves as a dedicated Lecturer in the Department of Microbiology at CVAS, Jhang, UVAS, Lahore, accumulating 13 years of teaching and research experience. With over 40 publications in high-impact journals and three authored book chapters, his expertise spans zoonotic pathogens' surveillance, molecular characterization, and combating antimicrobial resistance. Having initiated his career in 2011, Dr. Khan's international stint at Friedrich-Loeffler-Institut, Germany, focused on Brucellosis. Actively participating in 50+ conferences and supervising postgraduate students, he aspires to establish advanced diagnostic methods for zoonotic diseases, contributing to Microbiology and Public Health.

E-mail amanullah.khan@uvas.edu.pk ORCID 0000-0002-5616-7833

Dr. Muhammad Farooq

Dr. Muhammad Farooq has been working as Assistant Professor in (Section of Epidemiology and Public health) Department of Clinical Sciences, College of Veterinary & Animal Sciences Jhang, Pakistan since September 2013. He earned DVM from CVAS, Jhang and was awarded Gold Medal (UVAS), Solve-agri Gold medal & cash prize and Prof. Dr. Tufail Muhammad Cash Award. He earned his MPhil in microbiology from UVAS, Lahore. He recently completed his PhD from University of Rennes 1, France in 2019. His area of research is study of host pathogen interactions with reference to hepatitis. He has vast experience of working on mice and cell culture. His other expertise lies in a wide range of multidisciplinary techniques such as Cell Culture, Western Blot, Conventional and Real-time PCR, Gene expression, FACS. He has published various article in international journals. He has written several high impact factor articles and also editor of two international journals.

E-mail muhammad.farooq@uvas.edu.pk ORCID 0000-0002-8771-3219

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MICROORGANISM AND ANIMAL: EXPLORING SYMBIOTIC RELATIONSHIP

Asad Ullah KHARIK

Symbiotic relationships between microorganisms and animals are fundamental to biotechnology, offering a myriad of applications in various industries. This chapter provides an overview of symbiosis, highlighting its historical context and significance in biotechnological processes. It explores the microbial diversity involved in symbiotic relationships, emphasizing the role of bacteria, fungi, and protists in biotechnological applications. The chapter also discusses symbiosis in biotechnological processes, including microbial fermentation, bioremediation, and biopharmaceutical production. Furthermore, it examines the engineering of symbiotic relationships through genetic manipulation and synthetic biology, addressing ethical considerations and challenges. Case studies illustrate successful symbiotic relationships in biotechnology, showcasing their impact on industries. The chapter discusses the environmental and economic implications of symbiotic biotechnology, highlighting its sustainability and potential for bio-based industries. It concludes with a discussion on future directions and emerging trends, emphasizing the importance of understanding and harnessing symbiotic relationships in shaping the future of biotechnology.

Introduction

The topic of animal health and productivity is vast and diverse, including everything from illness prevention and nutrition to selective breeding and efficient management techniques. However, a secret world—a tiny domain teeming with life and deep influence—underlies the production and well-being of animals. With their animal hosts, microorganisms, the unseen builders of the natural order, create complex and often necessary connections that influence the very food we consume and have an effect on agricultural systems (LeBlanc, Lissemore, Kelton, Duffield, & Leslie, 2006).

The term "living together," which comes from the Greek "symbiosis," refers to a wide range of interactions that occur between various types of organisms. Symbiosis is the foundation of many biological processes, ranging from mutualistic partnerships where both parties gain (mutualism) to parasitic connections where one-party gains at the cost of the other. The complex network of mutualistic interactions has the most revolutionary potential when it comes to animal health and output (Paracer & Ahmadjian, 2000).

Bees carry out a vital task as they buzz from flower to blossom: pollination. Plant reproduction relies on this exchange to produce fruits, seeds, and the next generation of blooming plants. The bees get delicious nectar and protein-rich pollen in exchange, which provides vital nutrition for their colonies. It's a prime illustration of symbiosis, in which both sides get concrete advantages and support the growth of their mutual environment (Kevan & Phillips, 2001).

However, symbiosis goes well beyond these apparent alliances. Consider the partnership that exists between ants and acacia plants. The acacia's delicious nectar and unique dwelling structures attract the ants, who then turn into ferocious protectors of their home plant. To ensure the acacia's continuous growth and survival, they even drive away rival plants and fight off herbivorous insects. The complex interdependence that results from symbiotic partnerships serve as a reminder of their enormous ecological importance (Richardson, Allsopp, D'ANTONIO, Milton, & Rejmánek, 2000).

Much closer to home, many symbiotic microorganisms live within our own bodies. There are many bacteria, fungi, and viruses in our skin, respiratory system, and, most importantly, digestive system. The microbiome, an internal ecology, is known to perform a startling array of functions in our overall health and wellbeing. Our immune systems are trained to distinguish between friends and foes by gut microbes, which also assist in the breakdown of complex foods and the synthesis of vital vitamins. Disruptions in this complex community have been associated with problems that impact our emotions and mental health as well as ailments including allergies and inflammatory bowel disorders (Wilson, 2005).

The productivity and general health of the animals we raise for food are governed by the same laws that govern human health. Cattle, sheep, and goats are examples of ruminant animals that have an amazing digestive system made up of many stomachs (Hofmann, 1989). A variety of microorganisms, including bacteria, protozoa, archaea, and fungus, participate in a symphony of metabolic activities inside the biggest of these, the rumen. The hard cellulose plant matter that makes up the ruminant's diet is broken down by these microorganisms, generating volatile fatty acids that the host animal consumes and uses as its main energy source. The foundation of ruminant nutrition is this collaboration, which allows the animals to flourish on normally indigestible grasses and forages (Van Soest, 1994).

Considerable promise for real-world applications exists in the research of symbiotic interactions in the context of animal health and productivity. Probiotics, which are living microorganisms that benefit their host when given in the right doses, may be used to alter the delicate balance of our internal microbiomeAs well as for pharmacological use, probiotics are also being researched in veterinary medicine for enhancing the effectivity of the animals' immune system and for promoting a healthier digestive system which can eventually lower the need for antibiotics that are administrated during animal-raising. (Johnson, Graham, & Smith, 1997).

Advancing beyond the practically endowed probiotics, new methods of disease prevention in animals might be opened through deepening our knowledge on symbiosis. The studies show that specific symbiotic kinds of bacteria become interact with inflammatory procedures, enhance the host defense mechanism against pathogenic invaders and even educate the immune system. Using such integrated relationships strategically may induce revolutionary improvements in the notion of animal health management and disease prevention. Ranging from farming that is symbiotic, symbiotic principles enter the sphere of sustainable agriculture that battle some of the most grave environmental issues currently faced by us. (Holmgren, 2020). The production of biofuels is in a great deal possible as they the decomposition of cellulose requires a lot energy and is highly notoriously. Research will be carried out on how the microscopic organisms living symbiotically in the intestines of animals like the termites are able to break down plant materials and wood with ease and thereafter devise a bioreactor that will function very well. Therefore, such inventions are necessary part of the diversification of the energy production, of lessening its environmental impact, and of development of a hybrid renewable fuel created of agricultural waste streams. (Cherubini, 2010).

In addition to that, the cattle feeding and nutrition are made symbiotic. The microbiome of the rumen, which is very complex, is targeted by the researchers because it influences feed efficiency, causes methane emissions—a major greenhouse gas, and later on it determines the performance of the animals. These development could be the solution to beef production efficiency and sustainability at the same time which would reduce the global food insecurity. (Godfray & Garnett, 2014).

However, what needs to also be kept in mind is that we still have limited knowledge in the essence of microbe-animal symbiosis which is quite a large and complex realm. While the present alliances make their contribution to development, some are still beyond sight and not so understood that their benefits are not even realized yet. We churn out new processes for creating industrial products, agriculture, and animal health on the basis of every link that we identify and existing mechanism that we identify. On the same theme, recent articles reveal that the bacteria of some insects digest plastic by symbiosis and, hence, could be key agents in the degradation of synthetic substances on land and in the oceans. (Doz & Hamel, 1998). Could this information be used to create innovative bioremediation techniques to address the expanding issue of plastic pollution?

There are many opportunities inside these covert alliances.

It is important to take a comprehensive approach as we explore symbiosis in more detail. The intricate balance of these interactions is sometimes influenced by a variety of events, making them seldom straightforward or predictable. The long-term effects of any treatments intended to modify symbiotic systems must be carefully taken into account. In addition, ethical issues must come first, giving animal welfare and the correct use of biotechnology first priority (Thompson, 1994).

Science, scientific curiosity, and the desire for a more sustainable and healthier future for people and animals alike drive the study of animal-microbe symbiosis. It's an area that encourages cooperation amongst veterinarians, ecologists, microbiologists, and engineers since it blurs the limits between conventional specialties (Bud, 1994). With each step forward, we unveil new layers of complexity and awe-inspiring potential, leading us towards solutions to real-world problems and a deeper understanding of the interconnected web of life. This field is not merely about advancing knowledge; it holds the key to shaping a better, more harmonious future where humans, animals, and the ecosystems we all depend upon thrive in unison (Kimmerer, 2013).

Symbiotic Relationships

Symbiotic relationships are of great importance in the context of nutrient cycling and ecosystem stability. Bacteria in the root nodules of leguminous plants fix nitrogen, which is to say they convert atmospheric nitrogen to a form usable by plants. This is useful both to the bacteria and the plant. In the gut micro-biome of animals, symbiotic relationships are critical to digestion, immune system development, and protection from pathogens (DeAngelis, 2012).

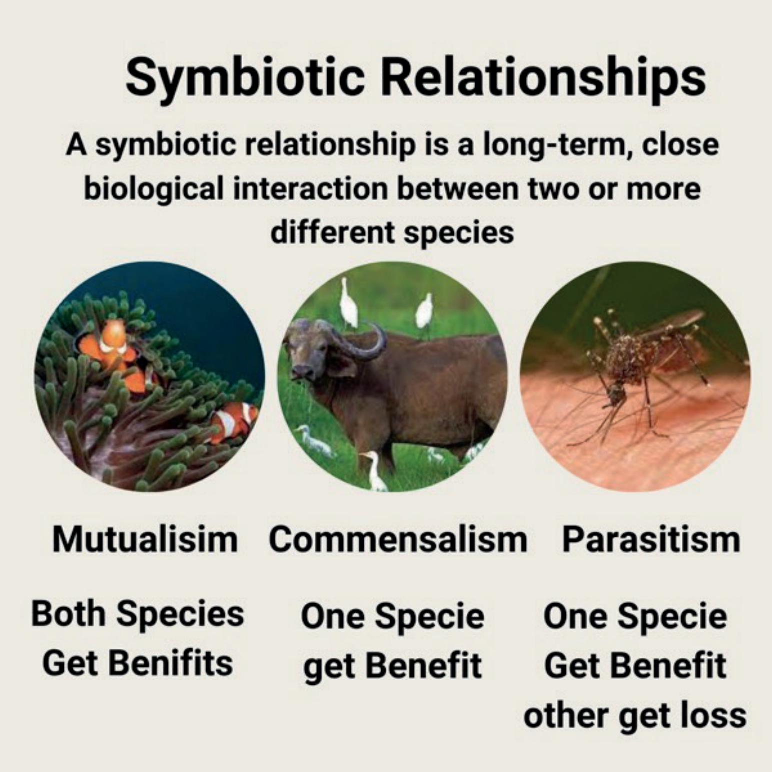

Figure 1. Symbiotic Relationship and its types

Biotechnological Applications

An understanding of symbiotic relationships has led to several highly successful biotechnological applications. In agriculture, the use of symbiotic nitrogen-fixing bacteria as biofertilizers has allowed the reduction of synthetic fertilizer use thereby lowering both cost and environmental impact. In human medicine, a similar strategy is now quite widely employed in that probiotics (food with live beneficial microorganisms) are now commonly used to restore microbial balance in the gut and as a treatment for a variety of digestive disorders (Ramanan, Kim, Cho, Oh, & Kim, 2016).

Table 1: Biotechnological Applications of Animal-Microorganism Symbiosis

Field	**Symbiotic Relationship**	**Animal/ Human**	**Microorganism**	**Application**	**References**
Animal Health	Mutualism: Gut Microbiome	Animal	Beneficial gut bacteria (ex: Lactobacillus, Bifidobacterium)	Probiotics (improves digestion, potential broader health impacts)	(Sender et al., 2016)
Animal Health	Commensalism: Skin Microbiome	Animal	Various skin bacteria and fungi	Support for healthy skin, protection against pathogens	(Grice, 2023)
Animal Health	Mutualism: Ruminant Digestion	Ruminants (cattle, sheep, goats)	Rumen bacteria, fungi, protozoa	Improved digestion of plant material, nutrient extraction	(Hobson & Stewart, 1997)
Environmental	Mutualism/ Commensalism: Bioremediation	Animals (various)	Microbes capable of degrading pollutants	Breakdown of contaminants in animal waste, contaminated sites	(Van Hamme et al., 2003)
Food Production	Mutualism: Fermentation	Animals	Bacteria and yeasts (ex: Lactobacillus in yogurt, Saccharomyces in bread)	Food preservation, flavor development, creation of fermented products	(Steinkraus, 2002)

Challenges and Future Directions

Despite its potential benefits, leveraging the power of symbiotic relationships in biotechnology has its challenges. One such challenge is their inherent complexity, necessitating an interdisciplinary approach for its comprehensive comprehension and application. Future research should aim to explore new symbiotic relationships, reveal the underlying mechanisms of those that are already established, and thereby deliver innovative biotechnological solutions across these relationships (Davis & Eisenhardt, 2011).

The Role of Microorganisms in Animal Health

Microorganisms are the main players in the health and welfare of animals. The microbiota is made up of the microorganisms-fungi, the bacteria, archaea, viruses and protozoa. Good of organisms such as bacteria, archaea, and fungi and others make up the microbiome in the skin, gastrointestinal tract, and reproductive. Plats of the organs is considered to be of very high impact to the animal health levels. The role of the microflora in digestion, immune system formation, and gets rid of the pathogens is known by now. Based on facts, and there is a demanding need to find out what an organic matter has and how the process of decomposition takes place. Which is not only directed to better animal health but also to advance biotechnological usage (Hoffmann, Proctor, Surette, & Suchodolski, 2016).

Composition of the Microbiota

The microbiota includes a wide variety of microorganisms: bacteria, archaea, fungi and virus. They are species that form very complex microbial ecosystems which each one of them has a particular profile. It includes the characteristics of the animal species, its diet and its habitat. In the gut of mammals, the gastrointestinal tract (GIT) is a passage where they digest material orally. Bacteria were even in the majority and this was mainly the corresponding detection of the dominants. Bacteroidetes and Firmicutes reported in Xu et al. Study implied that these microorganisms exist. Hence the yet unknown varieties of organisms are in the habitats and living under such circumstances and biotypes. Where led to digestion and performance of some nutrients' functions sensors and peaks (Gomaa, 2020).

Functions of the Microbiota

The host's microbiota fulfils lots of vital roles which are accountable for the animal's fitness. For example, the microbiota performs digestive purposes, which are degrading complex carbohydrates and proteins hence the host cannot produce in facet. Besides, the microbiota contributes to the early immune system shaping through the time of its development. Educating the immune system to choose between harmful pathogen and actual wellbeing microorganisms (Zmora, Suez, & Elinav, 2019).

Impact of Microbiota Imbalance

Imbalances in the microbiota, called dysbiosis, can have profound impacts on animal health. Dysbiosis may arise due to factors such as antibiotic treatments, diet changes, or stress, and can cause disorders of digestion, immune system function, and increased susceptibility to infections. Understanding and managing dysbiosis is a crucial endeavor in maintaining animal health and harnessing the full potential of biotechnological applications (Carding, Verbeke, Vipond, Corfe, & Owen, 2015).

Future Directions in Microbiota Research

Future research on the microbiota should be directed toward uncovering the mechanisms that mediate microbe-animal associations and studying the many ways microbiotas impact animal physiology and behavior. In order to provide the greatest benefits before, during, and after birth, strategies must be developed to purposely manipulate microbiotas to enhance animal health and production outcomes (Hong, Shang, Sun, Tang, & Wang, 2023).

Biotechnological Applications of Animal-Microorganism Symbiosis

The potential of the symbiotic relationships between animals and microorganisms in biotechnology has been recognized for a long time. From improving animal health and nutrition to enhancing environmental sustainability, there have been a wide range of applications. Thus, many authors have described and interpreted the main biotechnological applications of animal-microorganism symbioses and their implications. This chapter is devoted to explore some of these applications and suggest some others not always sufficiently investigated by the scientific community yet (McFall-Ngai et al., 2013).

Probiotics in Animal Nutrition

Probiotics, micro-organisms capable of fulfilling functional roles and administered in adequate quantities, capable of providing either a protective or beneficial effect. Common reasons that can motivate pet owners to switch to the raw food diet has to do with general health benefits to the host, which is currently the most emphasized area in animal nutrition. They have been used to increased feed nutrient assimilation, and boosted immune response, the effect of which is to increase the quality and yield of the product. Play a huge role as well as in prevention of gastrointestinal illnesses. Slowly but steadily, these disorders will be reduced to a minimum level. Favorably for the most frequent case. For protection of human health pro-bio-microbial Biodegradation is found in Environmental clean-up around the world (Macpherson, 2005).

Lactobacilli are a key group of bacteria found in many probiotic supplements, playing a crucial role in promoting health in both humans and animals. They are naturally present in the gut, where they contribute to a balanced microbiome and support various bodily functions. Lactobacilli-based probiotics are often used in poultry farming to boost intestinal health and increase production. For example, supplementing broiler chicken diets with Lactobacillus acidophilus and Lactobacillus casei dramatically enhanced growth performance, feed efficiency, and gut architecture. This shows that lactobacilli may play an important role in improving poultry productivity and health {Jha, 2020 #2}.

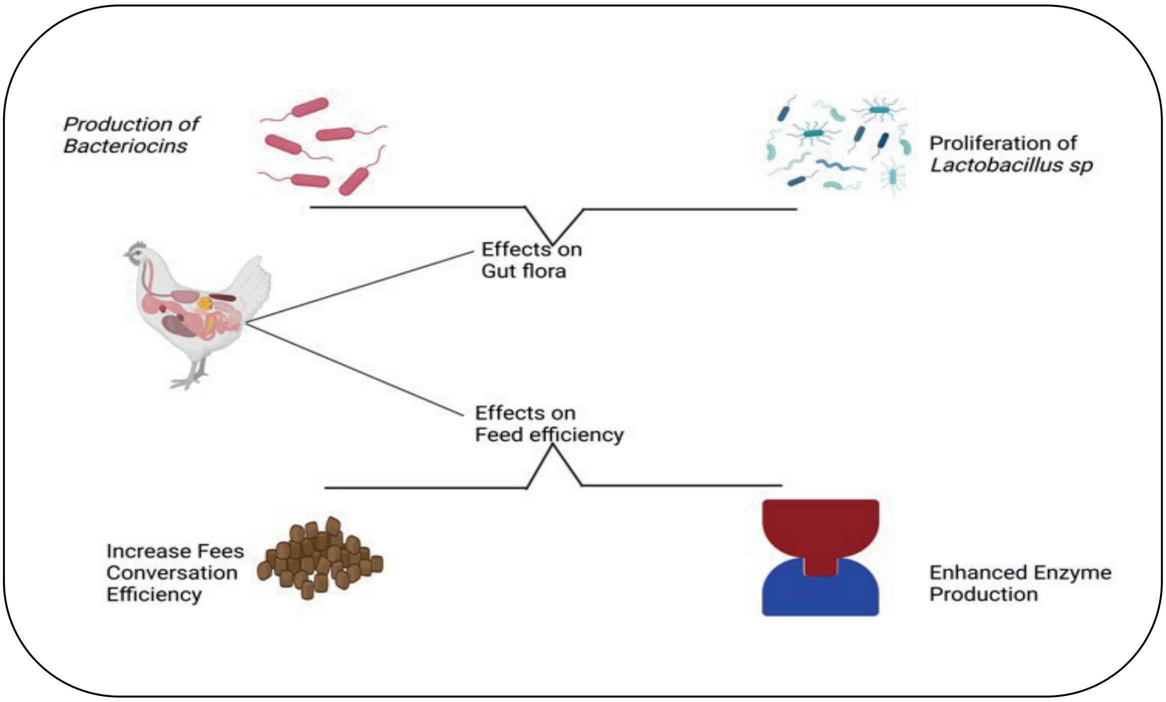

Figure 2. Role of lactobacillus sp in improving poultry productivity and health

Microbial Biodegradation

Microbial transformations are major forces in the process of cleaning up the environment. Microorganisms and microbial communities responsible for rendering pollutants into less hazardous forms are being decisive elements substances. This practice is referred to as biodegradation and is commonly employed in wastewater treatment, fermentation of organic waste into biogas, and recycling of end-of-life products. The role of plants in accumulation of organic pollutants in soil and contaminated sites cleaning. Sustainable management of livestock waste relying on the synergies between the livestock and the microorganisms can enhance the value of the waste from the earth nutrient perspective biodegradation process (Cunningham, Anderson, Schwab, & Hsu, 1996).

Microbial Diversity for Animal Health and Production

The expression “microbial diversity” means the variety of microbes in a specific environment. Revealing this microbial diversity in the area of animal health and production involves the application of such a wide range of microbes as weapons against pathogens and growth promotion. Maximizing energy conversion efficiency and reducing environmental concerns. The importance of such microbial diversity and the biotechnology application are both discussed in this chapter.

Importance of Microbial Diversity

The significance of microbial diversity in the conservation of ecosystem stability and dynamics is unquestionable. In animal systems microbes have a diversity across the gut, skin and some other body parts. The rest of body sites also has huge impact on metabolism and digestion and the growth and the activity of the immune defense, the protection against pathogens. Understanding and preserving microbial as well, sustainability of agriculture and for animal production involve diversity (Bull, Ward, & Goodfellow, 2000).

Animal Health Applications

Utilizing the diversity of microbes will lead to the discovery of novel and better solutions. Methods of developing new probiotics, prebiotics and symbiotic, which improve animal health. Such products are intended to ensure animal health which is a reflection of positive benefits for the consumers as well. Consumer by enhancing nutrient absorption and defending immune functions, and concurrently, lowering the risk of gastrointestinal disorders in animals. Animals will become healthier and thinner, so they will no longer need antibiotics (Woo, Lau, Teng, Tse, & Yuen, 2008).

Applications in Production Efficiency

Microbial diversity can also be deployed to boost the efficiency of feed and animal production. For instance, microbial enzymes can be employed to break down complex feed components into their simpler, more digestible forms, which can in turn improve feed efficiency and nutrient utilization. Moreover, microbial fermentation processes can be used to make a diverse range of valuable products ranging from biofuels to enzymes to products of chemical synthesis, from an almost equally diverse range of waste materials generated during agriculture (Adeola & Cowieson, 2011).

Future Directions in Harnessing Microbial Diversity

The detection of unknown biochemical pathways suggests that the microbial species themselves may also have great potential for application to animal health and production. Collaboration among researchers, industry, and policy makers will be essential for the proper stewardship of microbial diversity in biotechnology. Advances in metagenomics and other molecular methods are revealing a rich resource of functional activities not yet encoded in the genomes of known bacteria. Future work will be focused on the isolation of new species to test in animal-production systems and the culture-independent discovery of genes and gene families with clearly defined roles in supporting animal life (Franzosa et al., 2015).

The Impact of Microorganisms on Animal Behavior

Microorganisms play a major role in shaping the behavior of animals. They influence a variety of behaviors including feeding, social interactions, and mate preferences by mechanisms, which are explored in this chapter, with impacts for biotechnology.

Influence on Feeding Behavior

The gut microbes can affect the feeding behavior by mediating the release of neurotransmitters as well as hormones that regulate appetite. For instance, some short chain fatty acids (SCFA) that are generated by certain strains of gut microorganisms evoke the production of satiety hormones that eventually halt the food intake (Van de Wouw, Schellekens, Dinan, & Cryan, 2017).

Impact on Mating Preferences

Microorganisms also can make an animal's choice of mate recognizable. In one experiment, the author demonstrated that microbial community changes in the gut were followed by dramatic changes in steroid hormone production by the liver resulting in altered pheromone or other signaling molecules that might suggest reproductive status. Such an alteration in behavior will influence reproduction success and population dynamics too (McFall-Ngai et al., 2013).

Biotechnological Implications

The process of coming to realize the impact of microorganisms on animal behavior was not just a fun scientific observation. Fundamental biotechnological considerations are also there.

Such an example could be the altering of the intestinal microbes which could change the feeding behavior of livestock so as to make it more efficient and less harmful to the environment. In addition to this, learning about how microbes are important for social interactions provides clues on the ways in which stress levels can be lowered and welfare status can be enhanced in domesticated animals (Broom, Johnson, & Broom, 1993).

Appropriate Illustrations on Symbiosis in Biotechnology

Case study brings valuable knowledge concerning how symbiosis can be potentially used for practical applications in biotechnology. This section will concentrate on a few of the instances of symbiosis that have been combined to tackle the main agriculture, medicine, and ecology challenges.

Example; Rhizobium-Legume Symbiosis

One of the most well-known examples of symbiosis in agriculture is the association between rhizobium bacteria and leguminous plants. Rhizobium bacteria infect the roots of legume plants (e.g., soybean or alfalfa) and form nodules, where they fix atmospheric nitrogen into a form that can be taken up by the plant and used for growth. The relationship is thought to supply 15–20% of non-symbiotic N2 and reduces the demand for synthetic nitrogenous fertilizer in agricultural plantings, thereby reducing its associated environmental footprint and cost (Gage, 2004).

Challenges and Ethical Considerations in Harnessing Symbiotic Relationships

While symbiotic relationships present numerous opportunities in biotechnology, there are also significant challenges and associated ethical considerations. In this chapter, the essence of some of the main issues as well as ethical aspects of opting to engage in this kind of symbiotic relations have been discussed.

Environmental Impact

The main obstacle and the ethical issue of such big science project is the consequences for nature when such technologies are used in real life, as there is a probability of negative environmental impact. Altering microbial communities. In what of non-native microorganisms are added by the ecosystem, it is then very impossible to know what the consequences might be of that interaction. These transformations can put at risk ecological equilibrium, with so many long-term effects that may turn to be unpredictable. It is paramount that all the possible dangers and chances brought by these associations is examined under close scrutiny (Folke, 2006).

Antibiotic Resistance

Bacteria facing antibiotics develop resistance to them is an innate process that is, however, quickened due to their panting as a drug in the farm animals as well as in human and veterinary medicine. Furthermore, the microbes used by biotechnology to improve plant development could also contain many complicated genes that may modify the resistance against antibiotics. It is a must that the drug resistant mutants should not be able to share their pathways with the single cell organisms or above the level organisms (Sassetti, Boyd, & Rubin, 2003).

Ethical Considerations

Additionally, the ethical aspects of the employment of symbiotic relationships in biotechnology end up with the need for considering the issues resulting from the animals involved in experiments just as the ones showing the benefits and consequences of the usage of genetically modified micro-organisms in the production of food. Not only is it important for research or applications to follow ethical rules, but it is also crucial for them to build ethical standards by themselves (Beever & Kemp, 2000)

Regulatory Frameworks

At the same time, it is essential to create regulatory frameworks that foster the use of symbiotic relationships in biotechnology while also protecting the health of humans, animal welfare, and the environment. Thus, creating effective regulatory frameworks will require the cooperation and input of policymakers, scientists, and other stakeholders.

Addressing these challenges and ethical considerations will be essential for harnessing the full potential of symbiotic relationships in biotechnology. It will be crucial to continue efforts to Develop sustainable practices that encourage the use of symbiotic relationships in biotechnology, minimize risks to human health, animal welfare, and the environment (e.g., by ensuring that only safe, well-tested symbiotic relationships are used) and employ them in a way that respects human rights and is beneficial to society and the environment (Peixoto et al., 2022).

Future Prospects: Emerging Technologies in Symbiotic Relationships

As technology continues to advance, increased opportunities are emerging to exploit symbiotic relationships for both basic and biotechnology applications. This chapter will survey some of the emerging technologies that are poised revolutionize the field of symbiosis and their biotechnology applications.

Microbiome Engineering

Microbiome engineering involves the deliberate modulation of microbial communities to achieve specific, desired outcomes. This may involve the development of custom probiotics/prebiotics that can be used to improve production efficiency in agriculture, or to treat specific health conditions. By modulating microbial communities, it may be possible to optimize the symbiotic relationships that exist among members in the community (Frey-Klett et al., 2011).

Synthetic biology

SFA researchers are intrigued by the potential of synthetic biology to engineer beneficial symbionts. Synthetic biology is a rapidly growing field that focuses on the design and construction of new biological parts, devices, and systems. In the context of symbiosis, synthetic biology can be used to engineer microorganisms with enhanced functional capabilities; for example, enhanced nutrient uptake or the production of valuable compounds. These engineered microorganisms could enable new approaches to enhance agricultural productivity, develop novel therapeutics, or cleanup environmental pollutants (Andrianantoandro, Basu, Karig, & Weiss, 2006).

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About the Author

Mr. Asad Ullah KHARIK, currently he is doing M.Phil in Biotechnology from Institute of Biological and Chemical Sciences, The Islamia University of Bahawalpur Pakistan. His research focus is on green synthesis & application of particles. He has written a few book chapters.

E-mail: asadullahkharik@gmail.com, ORCID: 0009-0001-8092-4267

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IMPACT OF PREBIOTICS, PROBIOTICS, NUTRACEUTICALS, GREEN NANOPARTICLES AND NANO-EMULSIONS ON ANIMAL HEALTH

Muhammad SAFDAR

Tanveer NASIR

Muhammad Mazhar AYAZ

Abdul REHMAN

Tariq ABBAS

Yasmeen JUNEJO

Safdar IMRAN

Mehmet OZASLAN

1. Introduction

The prebiotics, probiotics, nutraceuticals and green nanoparticles play critical role to enhance animal health because these products have ability to influence gut microbiota (Lazar et al., 2022). They improve immune function and provide therapeutic benefits against several diseases such as gastrointestinal disorders, respiratory infections, metabolic disorders, immune-mediated diseases, parasitic infestations, reproductive disorders and neurological disorders (R. Mishra et al., 2023).

Prebiotics are non-digestible food components and typically fibers that beneficially affect the host by selectively stimulating the growth or activity of beneficial bacteria in the gut (Slavin, 2013). These prebiotics promote a healthy gut microbiome. For example, common prebiotics include insulin, fructo-oligosaccharides (FOS), and galacto-oligosaccharides (GOS), found in foods like garlic, onions, bananas and whole grains(Davani-Davari et al., 2019). Therefore, they may improve digestion that enhance the immune system and contribute to gut health (Cummings et al., 2004). Moreover, they enhance digestive health and nutrient absorption. They help to improve immune function that reduce the risk of infections. Additionally, they selectively stimulate the growth of beneficial microbes and contribute to gut health that is associated to improve energy metabolism and reduced inflammation. For instance, incorporating prebiotics into animal diets may lead to healthier and more resilient animals (Gaggìa et al., 2010).

Probiotics are live microorganisms that assist to balance the gut microbiota and boost the immune system (Anadón et al., 2019). Therefore, they improve intestinal health by promoting beneficial bacteria and reducing harmful pathogens that maintain a balanced gut environment (Mitsuoka, 2000). This balance is essential for preventing and managing gastrointestinal diseases and persevering complete metabolic health (De Filippis et al., 2020). Importantly, probiotics work synergistically with prebiotics to enhance their beneficial effects (Wasilewski et al., 2015). They are playing a crucial role in maintaining gut health and supporting the immune system

Nutraceuticals are products derived from food sources that provide additional health benefits beyond basic nutritional value (El Sohaimy, 2012). The term is a combination of "nutrition" and "pharmaceutical." They include dietary supplements, functional foods and herbal products that help in the prevention and treatment of diseases or support cumulative animal health (Vaidya & Forman, 2010). The term is a combination of "nutrition" and "pharmaceutical (Georgiou et al., 2011)." They include dietary supplements, functional foods and herbal products that help in the prevention and treatment of diseases or support cumulative animal health (Hampton et al., 2015). For example, antioxidants are gaining attention for their potential to improve animal health (Ponnampalam et al., 2022). In addition, they help to boost immunity that reduce inflammation and prevent various diseases offering a natural approach to health management (Iddir et al., 2020).

Green nanoparticles are nanoscale particles that are synthesized using environmentally controlled methods that are involved with natural resources such as plants, bacteria, fungi, or other biological entities (Bahrulolum et al., 2021). These are being synthesized by using plant extracts or other biological methods emerging as promising agents in animal health (Das et al., 2017). They have antimicrobial properties and ability to enhance drug delivery makes them valuable for managing infections and improving therapeutic outcomes (Ho et al., 2019).

Nano-emulsions are fine, stable mixtures of two immiscible liquids (like oil and water) where tiny droplets of one liquid are dispersed within the other (Anton & Vandamme, 2011). These droplets are usually in the nanometer size range (20-200 nanometers) (Fang et al., 2006). They are widely used in various industries including pharmaceuticals, cosmetics, food, and agriculture (Morin-Crini et al., 2019). Moreover, nano emulsions play a significant role in enhancing animal health by improving the delivery of nutrients, drugs and vaccines (Abd El-Hack et al., 2022). Additionally, nano-emulsions protect sensitive compounds from degradation in the digestive system that lead to therapeutic effects (Li et al., 2021). These offer a controlled release mechanism that reducing the frequency of administration and improving animal health (Hennessy, 1997).

These bioactive compounds contribute to improved gut health, immune function, and in animal health (Santos et al., 2022). Therefore, the significant impact of prebiotics, probiotics, nutraceuticals, green nanoparticles and nano-emulsions are associated with animal health (Santos et al., 2022). The integration of green nanoparticles and nano-emulsions further optimizes the delivery and efficacy of these compounds (Hendawy, 2021). Furthermore, these advancements may offer promising strategies for promoting animal health and reducing the reliance on traditional antibiotics.

2. Impact of Prebiotics on Animal Health

Prebiotics positively influence gut health to alter the gut microbiota (Lin et al., 2014). In a study, Atlantic salmon were offered a diet supplemented with prebiotics such as fructo-oligosaccharides (FOS) and galactose-oligosaccharides (GOS) that affected gut histology and microbiota diversity. The fish were fed with these prebiotics that exhibited changes in the composition and diversity of gut bacteria that are crucial for nutrient absorption and immune response(Dawood, 2021). But it will not puta significant impact on gut histological parameters (Louis et al., 2016) . It suggests that the benefits of prebiotics should be more related to micro biota modulation than structural changes in gut tissue (Louis et al., 2016).

In several studies, it is indicated that prebiotics improve immune function in animals to stimulate the production of short-chain fatty acids (SCFAs) through fermentation in the gut (Peng et al., 2022). For example, SCFAs butyrate are known to have anti-inflammatory properties and enhance gut barrier function that reducing the risk of infections (Bach Knudsen et al., 2018). The benefits of prebiotics are not limited to a specific species such as poultry, swine, ruminants and aquaculture that showed consistent improvements in growth, gut health and immune responses (Anadón et al., 2019).

The significant role of prebiotics in improves animal health to positively influence gut microbiota (Samal & Behura, 2015). They act as non-digestible fibers that stimulate the growth of beneficial bacteria in the gastrointestinal tract (Montagne et al., 2003). These substances promote better digestion, nutrient absorption and immune system functioning in animals that lead to improve growth rates and productivity (Celi et al., 2017). Furthermore, they have been shown to reduce the prevalence of harmful pathogens in the gut (Pickard et al., 2017).The health benefits of prebiotics particularly prominent in livestock (Uyeno et al., 2015). They are integrated into feed to enhance the digestive health of poultry, and cattle (Adedokun & Olojede, 2019). Some studies indicated that they improve the intestinal microbiota balance (Blaut, 2015). They enhance feed efficiency and weight gain (Grion et al., 2014). Moreover, they reduce the environmental impact to optimize feed conversion ratios that lowers waste product (Khan et al., 2018). For instance, these effects contribute to more sustainable farming that particularly in large-scale animal health (Kaasschieter et al., 1992). Another key advantage of these prebiotics is to modulate the immune system in animals that help them to resist diseases more effectively(Nawaz et al., 2018). For instance, a study showed that prebiotics enhance the production of anti-inflammatory cytokines while decreasing pro-inflammatory responses (Cristofori et al., 2021). Therefore, it is immunomodulatory function that strengthens the animals natural defense against infections and reduces the need for medical interventions (Provenza & Villalba, 2010).

They are also associated to improve meat tenderness, better milk fat content and more nutrient-rich eggs. The inclusion of prebiotics in animal diets and meets consumer demand for high-quality products and agricultural goals for enhanced productivity. Finally, it is proven that prebiotics influence the quality of animal derive products such as meat, milk and eggs.

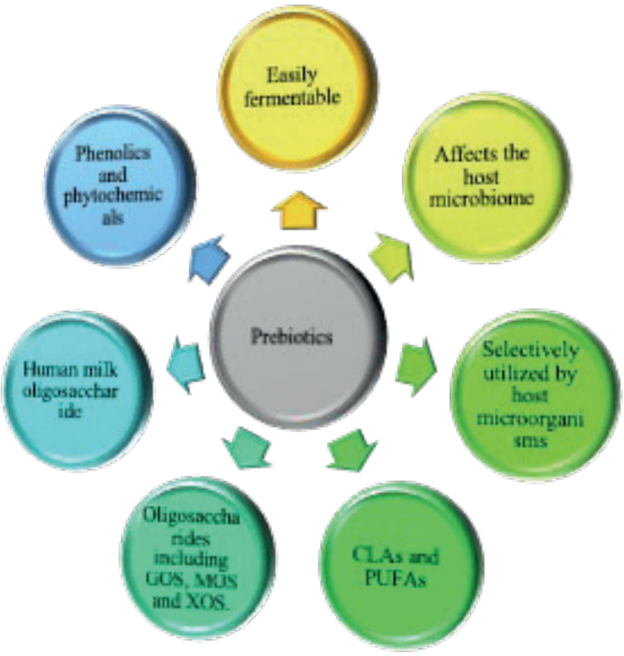

Figure 1. Impact of Prebiotics on Animal Health

3. Impact of Probiotics on Animal Health

Probiotics are getting a great focus due to is roles to improve animal health (Chaucheyras-Durand & Durand, 2010). They are being added into animal nutrition due to their wide-ranging benefits (Wenk, 2000). These live microorganisms (Lactobacillus and Bacillus) provided in adequate amounts that regulate the gastrointestinal microbiota of animals, improving gut health, digestion and nutrient absorption (Leser & Mølbak, 2009). Moreover, the use of probiotics in animals not only enhance productivity but also support their immune systems to promote beneficial bacteria and suppressing harmful pathogens (Dhama et al., 2011).

The major area of probiotic application is in poultry production (Khan & Naz, 2013). The probiotics e.g., Lactobacillus and Bacillus strains have shown promising outcomes (Zhang et al., 2018). Furthermore, some studies have demonstrated that they mitigate the occurrence of necrotic enteritis that is a common disease in broiler chickens (Dahiya et al., 2006). In addition, broilers are supplemented with probiotics that exhibited to improve growth performance, feed conversion ratios and better health (Patel et al., 2015).

In aquaculture, they have similar effects (Weir & Grant, 2005). For example, a study on common carp (Cyprinus Carpio) showed that dietary inclusion of probiotics enhances growth rates, digestive enzyme activity and immune parameters (Jasim et al., 2022). These benefits translated into higher survival rates and more sustainable fish farming practices and contributing to better water quality and disease resistance in aquatic environments (Waite et al., 2014).

The use of probiotics in livestock is also gaining attention as an alternative to antibiotics that have traditionally been used to promote growth and prevent disease (Mingmongkolchai & Panbangred, 2018). Therefore, the particular strains are being used, while they depend on dose rate and timing of administration to influence the animal health (Brown, 1996). Moreover, the stability of probiotics during storage and delivery should be carefully managed to ensure their viability and effectiveness (Terpou et al., 2019). Probiotic supplementation in livestock is associated to improve meat quality that include better texture, flavor and shelf life (Al-Shawi et al., 2020).

For future, it needs more emphasis on identifying more effective probiotic strains and optimizing their use (Mathipa & Thantsha, 2017). The researchers are particularly focused to explore the precise mechanisms that exert actual impacts on animal production (Nardone et al., 2010). It will open new doors for sustainable animal health (Nardone et al., 2010).

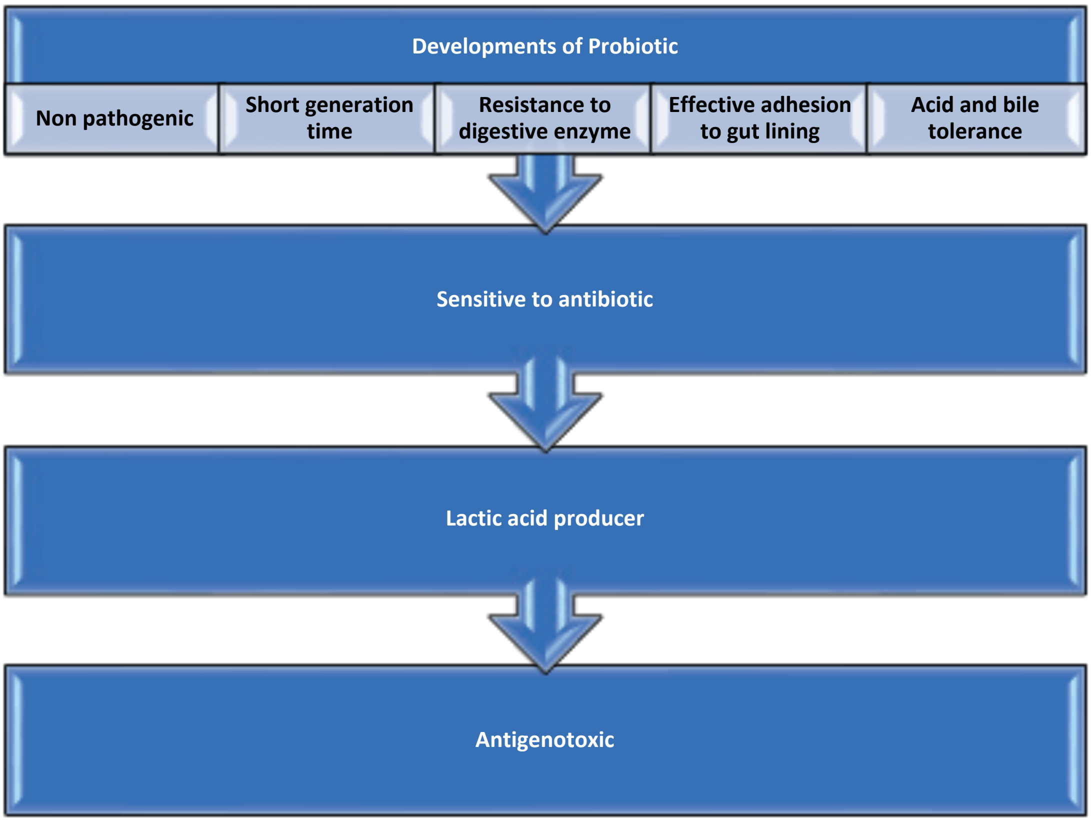

Figure 2. Impact of Probiotics on Animal Health

4. Nutraceuticals: Functional Foods and Their Benefits in Animal Health

Nutraceuticals and functional foods have gained attention in recent years for their profound impact on animal health (Gul et al., 2016). Actually, they are bioactive compounds that derived from natural food sources and offer more than basic nutrition to improving health, preventing diseases and enhancing the immune system (Teodoro, 2019). The concept of One Health - that integrates human, animal and environmental health gains popularity (Humboldt-Dachroeden & Mantovani, 2021). The use of nutraceuticals has seen a surge and particularly in livestock management to optimize productivity and reduce disease incidence (Ballou et al., 2019). They contain omega-3 fatty acids, polyphones and antioxidants that improve metabolic health, reduce oxidative stress and promote animal health.

Another key benefit of nutraceuticals is their ability to mitigate oxidative stress in animals

(Dama et al., 2024). They contain polyphones and arytenoids that help to neutralize free radicals and protect cellular integrity (Stark, 2003). These compounds are often found in functional foods such as fruits, vegetables and plant-based supplements that are incorporated into animal diets to boost their health and productivity (Santos-Buelga et al., 2019). They also hold a significant potential in reducing inflammation in various tissues of animals that lead to a variety of chronic diseases (He et al., 2015). For instance, omega-3 fatty acids, derived from fish oil, flaxseed and other sources that have anti-inflammatory properties to relief from arthritis, dermatitis and inflammatory bowel disease in animals (Balić et al., 2020). These compounds work to modulate different pathways to reduce the production of pro-inflammatory cytokines (Tunon et al., 2009). Therefore, nutraceuticals should be added in animal diets that may enhance the animal health (Gupta & Prakash, 2015).

Moreover, there are still challenges associated with the use of nutraceuticals and functional foods in animal health (Cencic & Chingwaru, 2010). In addition, lack of standardization in clinical trials pose significant barriers to their widespread adoption (Thakkar et al., 2020). Furthermore, we have to prepare guidelines for precise dose and identification of proper interactions with different receptors to work like drugs (Tyson et al., 2020). For instance, without guidelines, nutraceuticals and functional foods may not reach their full potential in animal health (Coppens et al., 2006).

The demand for sustainable animal farming practices to grow nutraceuticals and functional foods are being increase to view a viable alternative to synthetic drugs (El Sohaimy, 2012). Moreover, by enhancing immune function to improve gut health and reducing inflammation, these natural products contribute to welfare of animals (Provenza & Villalba, 2010). Finally, nutraceuticals offer a promising approach to improve animal health (El Sohaimy, 2012). Therefore, their ability to boost immunity, reduce oxidative stress and promote gut health makes them valuable tools in disease prevention and management (Iddir et al., 2020).

Table 1. Nutraceuticals: Functional Foods and Their Benefits in Animal Health

Year	**Developments**	**Benefits in Animal Health**	**References**
2000	Initial Exploration of Nutraceuticals	Vitamins, minerals, and herbal supplements were studied for enhancing general health and performance in animals	(79)
2001	Use of Herbal Supplements	Herbs like garlic and echinacea were explored for their antimicrobial and immune-boosting properties	(80)
2002	Introduction of Functional Foods	Functional foods (e.g., fortified feeds) gained recognition for improving health beyond basic nutrition	(12)
2003	Antioxidants and Immune Function	Antioxidants like Vitamin E were linked to improved immune responses in animals	(81)
2004	Omega-3 Fatty Acids	Omega-3 from fish oil was found to reduce inflammation and support heart health	(82)
2005	Probiotics for Gut Health	Probiotics gained popularity for improving gut microbiota, digestion, and overall health	(83)
2006	Prebiotics Introduced	Prebiotics like FOS were introduced to support the growth of beneficial gut bacteria	(84)
2007	Immune-Boosting Nutraceuticals	Nutraceuticals like zinc and selenium were associated to stronger immune systems in animals	(85)
2008	Functional Foods in Animal Nutrition	Functional foods with specific health benefits (e.g., reducing inflammation) began broader application	(64)

Year	Developments	Benefits in Animal Health	References
2009	Specialized Animal Diets	Functional foods tailored to specific health needs (e.g., joint health, digestion) were developed	(75)
2010	Phytochemicals in Animal Diets	Phytochemicals like flavonoids were explored for their antioxidant and anti-inflammatory effects	(86)
2011	Prebiotics and Probiotics Combined	Symbiotic (prebiotic + probiotic) showed potential for enhanced gut health	(87)
2012	Joint Health Nutraceuticals	Glucosamine and chondroitin showed effectiveness in improving joint health in animals	(88)
2013	Joint Health Nutraceuticals	Glucosamine and chondroitin showed effectiveness in improving joint health in animals	(88)
2014	Probiotics for Growth Performance	Probiotics enhanced growth, feed efficiency, and nutrient absorption in livestock	(89)
2015	Growth of Nutraceuticals	Vitamins, omega-3s, and probiotics gained recognition for improving health and performance in animals	(90)
2016	Functional Foods Defined	Recognition of foods that provide benefits beyond nutrition, such as gut health and immunity	(91)
2017	Probiotics in Livestock	Probiotics were extensively studied for improving gut health and reducing antibiotic use	(92)
2018	Omega-3 and Fish Oil Studies	Omega-3s were shown to improve cardiovascular and cognitive health in animals	(93)
2019	Antioxidants for Immune Support	Antioxidants like selenium were found to reduce oxidative stress and support immune function	(94)
2020	Prebiotics in Animal Diets	Prebiotics like inulin promoted beneficial gut bacteria, improving digestion and nutrient absorption	(95)
2021	Gut Microbiota and Health	Functional foods were linked to better digestion and immune system health through gut microbiota modulation	(96)
2022	Nutraceuticals for Disease Prevention	Curcumin and resveratrol were highlighted for their roles in preventing chronic diseases like arthritis and cancer	(97)
2023	Immunomodulatory Nutraceuticals	Nutraceuticals like beta-glucans and medicinal mushrooms were shown to boost immune systems and reduce infections	(98)

5. Green Nanoparticles: A Novel Approach to Animal Health

Green nanoparticles are increasingly recognized for their sustainable synthesis and beneficial applications in animal health (Bahrulolum et al., 2021). Moreover, traditional nanoparticles that often involve hazardous chemicals (Buzea et al., 2007). They are produced using natural materials such as plant extracts, bacteria and fungi (Shuping & Eloff, 2017). These methods not only reduce environmental toxicity but also offer unique properties due to the natural compounds involved (Atanasov et al., 2021). Therefore, they provide a promising alternative for various applications due to their eco-friendly production processes and potential health benefits (Gayathiri et al., 2022).

Furthermore, synthesis of these particles involves the use of biological materials to replace toxic chemicals traditionally used in nanoparticle production (Pandit et al., 2022). Moreover, common methods include using plant extracts, algae and microorganisms that serve as both reducing and stabilizing agents (Mohamad et al., 2014). For instance, plant-based methods utilize photochemical to reduce metal ions that leading to the formation of nanoparticles with enhanced stability and functionality (Khan et al., 2019). These approaches not only make the process more sustainable but also imparts biological activities to the nanoparticles that tailored by the source (Ahmed et al., 2022).

They have demonstrated significant antimicrobial activity against a variety of pathogens, including bacteria, fungi and viruses (Khezerlou et al., 2018). These nanoparticles, when synthesized using green methods and exhibit potent antimicrobial properties due to their high surface area and reactivity (Sharma et al., 2009). Therefore, nanoparticles may disrupt microbial cell membranes, inhibit enzyme activity and interfere with DNA replication that making them effective agents for controlling infections in animal health (Wang et al., 2017).

Therefore, these particles are being explored for a range of applications that from diagnostics to therapeutic interventions (Yetisgin et al., 2020). For example, these particles may be engineered to deliver drugs directly to target sites within the body that enhancing the efficacy and reducing side effects of treatments (Mishra et al., 2013). Additionally, they are used in imaging and diagnostic tools that their unique properties improve the sensitivity and accuracy of disease detection (Yao et al., 2014). Moreover, it targeted approach promises to enhance the overall quality of animal health by offering more precise and effective treatment options (LeBlanc et al., 2006).

Another major advantage of green nanoparticles is their improved safety and biocompatibility such as compared to those synthesized through conventional methods (Parveen et al., 2016). Therefore, green synthesis methods often produce nanoparticles that are more compatible with biological systems and reducing the risk of toxicity and adverse reactions (Samuel et al., 2022). These particles generally exhibit lower cytotoxicity and are less likely to cause inflammation or allergic reactions in animals (Elsabahy & Wooley, 2013).

The environmental benefits of these particles are substantial that their synthesis typically involves fewer hazardous chemicals and generates less waste compared to traditional methods (Abdelbasir et al., 2020). The use of renewable resources and eco-friendly processes aligns with the principles of green chemistry that promoting sustainability (Akpan et al., 2021). The lower environmental impact of green nanoparticles makes them a viable option for large-scale production and use (Ying et al., 2022).

These particles face several challenges that need to be addressed for broader adoption in animal health (Neethirajan, 2017). Some common issues such as variability in particle size, inconsistent synthesis results and potential stability problems (Soenen et al., 2015). Additionally, there is a need for comprehensive studies to evaluate the long-term effects and interactions of these particles within complex biological systems (Stark, 2011). Moreover, these challenges require further research and optimization to ensure reliable and reproducible result in animal health (Stark, 2011).

These particles in animal health are evolving rapidly with ongoing research focused on addressing current limitations and exploring new possibilities (Neethirajan, 2017). In future studies are expected to enhance synthesis techniques, improve nanoparticle performance and broaden their applications in animal health (Hill & Li, 2017).

Table 2. Green Nanoparticles: A Novel Approach to Animal Health

Year	Focus	Applications in Animal Health	Developments	References
2000	Early Research on Nanoparticles	Investigating basic nanoparticle synthesis methods	Initial studies on nanoparticle synthesis, focusing primarily on chemical methods	(124)
2005	Development of Silver Nanoparticles (AgNPs)	Exploration of AgNPs for antimicrobial properties	Research on silver nanoparticles showed promising results for bacterial and fungal infections in animals	(125)
2010	Rise of Green Nanoparticle Synthesis	Phytochemical synthesis of nanoparticles explored for veterinary use	Plant-based synthesis methods began gaining popularity for their low toxicity and high efficiency	(126)
2015	Drug Delivery Systems	GNPs used for targeted drug delivery in veterinary medicine	Enhanced drug delivery systems using GNPs improved therapeutic outcomes in treating livestock diseases	(127)
2018	Antimicrobial Applications in Livestock	Use of green AgNPs to combat resistant bacterial strains in livestock	Significant advances in combating resistant bacteria using AgNPs, reducing the need for antibiotics	(128)
2020	Sustainability and Environmental Focus	Focus on eco-friendly GNPs to replace harmful chemical treatments	GNPs are used in animal health for sustainable and eco-friendly applications, reducing chemical use	(129)
2021	Veterinary Nanomedicine	Advanced GNP-based solutions for disease diagnosis and treatment	Development of GNPs for diagnostic tools and improved delivery of vaccines in animals	(130)
2023	Green Nanoparticles in Disease Prevention	GNP-based vaccines and biosensors for early detection of diseases	GNPs showed promise in creating more effective and targeted vaccines for livestock and pets	(131)
2024	Emerging Research on Antiparasitic GNPs	Focus on antiparasitic applications of GNPs for improving animal health	Continued research into using GNPs to manage parasitic infections without toxic side effects	(79)

6. Synergistic Effects of Prebiotics, Probiotics, and Nutraceuticals in Animal Health

Recently, these advancements in animal research have increasingly focused on the synergistic effects of prebiotics, probiotics, and nutraceuticals (Bhogoju & Nahashon, 2022). This approach is proving to be highly effective in improving animal health and performance (Berezowski et al., 2019). Therefore, by combining these components, researchers and practitioners are finding enhanced benefits for various species that ranging from livestock to companion animals (Walsh, 2009). Therefore, by combining these components, researchers and practitioners are finding enhanced benefits for various species that ranging from livestock to companion animals (Walsh, 2009).

The synergistic effects of combining prebiotics, probiotics and nutraceuticals have been a focal point of recent research (Walsh, 2009). When used together, these components may enhance each other's effectiveness that leading to more pronounce health benefits (Slavin, 2013). Prebiotics boost the survival and activity of probiotics that resulting in a more stable and balanced gut microbiome (Li et al., 2020). Moreover, nutraceuticals support this balanced microbiome by reducing oxidative stress and inflammation that compromise the efficacy of prebiotics and probiotics (Peng et al., 2020).

Therefore, improvements in growth performance, feed efficiency and disease resistance when prebiotics, probiotics, and nutraceuticals are included in animal diets (Anadón et al., 2019). For instance, the use of a prebiotic-probiotic-nutraceutical combination has been effective in reducing the incidence of gastrointestinal diseases such as colibacillosis and necrotic enteritis in poultry. It integrated to approach also helps in optimizing feed conversion rates and promoting animal health (Celi et al., 2017).

The synergistic effects of prebiotics, probiotics, and nutraceuticals represent a promising frontier in enhancing animal health (Hernandez-Patlan et al., 2023). The integration of these components provides a comprehensive strategy for improving digestive health, boosting immune function and promoting in animal health (Kikusato, 2021). Moreover, research continues to explore and refine these interactions with the aim of optimizing health outcomes and addressing emerging challenges in animal health (Rexroad et al., 2019).

The synergy between prebiotics, probiotics, and nutraceuticals is particularly compelling (Roberfroid, 2000). When used together, these components create a balanced and supportive environment for beneficial gut bacteria and providing direct health benefits through their individual mechanisms (Laparra & Sanz, 2010). For example, prebiotics enhance the survival and efficacy of probiotics that leading to a more robust and stable gut microbiome (Fei et al., 2023). Moreover, nutraceuticals complement this effect by reducing oxidative stress and inflammation that determine the benefits of prebiotics and probiotics (Infusino et al., 2020).

Synergistic interactions between these substances also influence the immune system. Probiotics enhance the gut-associated lymphoid tissue (GALT) function (Sanz & De Palma, 2009). Prebiotics modulate the systemic immune response (Pujari & Banerjee, 2021). This synergy leads to better resistance against infections and reduced inflammation (Hemaiswarya et al., 2008). The combination of prebiotics, probiotics, and nutraceuticals has been shown to improve feed conversion ratios and animal health (Anadón et al., 2019). For instance, probiotics enhance the digestion of nutrients while prebiotics promote a healthy gut microbiota that aids in nutrient utilization (Liao & Nyachoti, 2017). Nutraceuticals such as antioxidants and vitamins support metabolic processes that leading to improve growth rates and productivity in livestock (Alagawany et al., 2021).

7. Challenges and Future Prospects in Integrating Green Nanoparticles in Animal Health

Green nanoparticles (GNPs), synthesized using environmentally friendly methods, have garnered significant attention for their potential applications in animal health. Moreover, these nanoparticles derived from natural sources such as plants or microbes that promise reduced toxicity and environmental impact compared to traditional nanoparticles. Therefore, their integration into practical animal health applications faces many challenges and requires further research and development.

One of the primary challenges in utilizing these particles in animal health is the variability in their synthesis. Moreover, its variability affects their stability and effectiveness. For instance, by standardizing these synthesis processes is crucial to ensure reproducibility and to achieve reliable results in therapeutic applications.

The safety of these particles is of significant concern that they are generally considered less toxic than conventional nanoparticles. Moreover, their interactions with biological systems need thorough evaluation. Furthermore, biocompatibility studies should be conducted to understand potential adverse effects on animal health. For instance, there is a need for comprehensive toxicological assessments to determine safe dosage levels and long-term impacts.

The regulatory landscape for green nanoparticles in animal health is still evolving. Therefore, regulatory agencies require rigorous testing to approve new nanoparticle-based products that may be time-consuming and costly. The lack of standardized guidelines specific to these particles further complicates this process. Therefore, researchers and companies navigate these regulatory requirements to bring GNP-based products to market.

Moreover, effective delivery of nanoparticles to target sites within animals is another challenge. These particles should be designed to achieve optimal biodistribution and targeted delivery to maximize therapeutic efficacy to minimizing side effects. Therefore, developing advanced delivery systems that may ensure precise targeting and controlled release of GNPs remains a critical area of research.

Furthermore, demonstrating the efficacy of these particles in animal health is essential for their acceptance and adoption. There is promising data on their antimicrobial, anti-inflammatory and antioxidant properties that translating these findings into practical treatments requires extensive validation through preclinical and clinical trials. Therefore, ensuring that these particles perform consistently under various conditions is vital for their success.

The cost of producing these particles may be higher than traditional due to the use of natural precursors and complex synthesis processes. Moreover, economic viability is a significant concern that especially for widespread use in animal health. Therefore, researchers and industry stakeholders explore cost-effective production methods and assess the economic feasibility of GNP-based therapies. The integration of these particles in animal health holds considerable promise. Moreover, future research should focus on improving the consistency and performance of GNPs that enhancing their safety profiles and developing regulatory frameworks tailored to their unique properties.

The integration of these particles into animal health represents a promising yet challenging frontier. For instance, addressing issues related to synthesis, safety, regulatory approval, delivery, efficacy and cost will be crucial for the successful adoption of GNPs in this field. Therefore, continued research and innovation will be key to overcome these challenges and realizing the potential benefits of these particles in improving animal health.

8. Summary

Animal health is focused on treating animal diseases or conditions to improve production and performance. Therefore, a holistic approach considers the interconnectedness of various factors affecting animal health, including genetics, environment, nutrition and management practices. For instance, by incorporating insights from fields such as epidemiology, genetics and environmental science that a more comprehensive understanding of animal health challenges may be achieved. Moreover, preventive strategies including vaccination, regular health screenings and proactive management practices that are highlighted as essential components of a holistic approach. The goal is to reduce the incidence of diseases before that they improving animal and reducing the reliance on reactive treatments. Therefore, this proactive stance not only enhances the health of individual animals but also contributes to better herd or flock health Therefore, tailored nutrition plans that address the specific needs of different species, breeds and production stages. Moreover, advances in nutritional science are being applied to develop diets that improve immune function, support growth and reproduction and prevent nutritional deficiencies.

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About the Author

Dr. Muhammad SAFDAR earned his PhD in molecular biology and genetics from Gaziantep University, Turkey. He is a lecturer in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, nutrigenomics, nano-genomics, bioinformatics, biotechnology, and their applications. He has published more than 70 research articles in national and international journals. He has also written many book chapters as well as an edited book. He is an associate editor for international journals.

E-mail msafdar@cuvas.edu.pk , ORCID 0000 0002 3720 2090

Dr. Safdar Imran received his PhD in 2021 from University of Agriculture Faisalabad, Pakistan. He is Assistant Professor of Animal Breeding and Genetics at the Islamia University of Bahawalpur, Pakistan. His research interests include predictive breeding models, Genetic selection, Genomics, reproductive biotechnology and selection and judging of animals for beauty attributes. He has published ten research articles in well-reputed national and international journals. He also has written book chapters.

Email safdar.imran@iub.edu.pk ORCID 0000-0001-5030-2267

Dr. Yasmeen JUNEJO, received her PhD in Analytical Chemistry from Sindh University, Jamshoro, Pakistan and Postdoc from Gaziantep University, Turkey. His main areas of interest are analytical chemistry, nanomedicine, nanostructures, nanobiotechnology and their applications. She is an editor of international journals and also written many books and book chapters as well.

E-mail yasmeen@cuvas.edu.pk, ORCID 0000 0002 3720 3214

Mr. Tanveer Nasir is currently pursuing a BS in Biotechnology at the Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His primary areas of interest include Biotechnology, Molecular Biology, and Genetics. He has contributed three book chapters published in international journals, showcasing his growing expertise in these fields.

Email tanveernasir408@gmail.com ORCID 0009-0008-7232-1053

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IMPACT OF H5N1 INFLUENZA ON DAIRY COWS

Arifa MEHREEN

Muhammad MAJEEBULLAH

Shagufta ABBAS

Muhammad SAFDAR

1. Introduction

The H5N1 flu virus, commonly referred to as avian flu or bird flu, is one of the most threatening diseases to animals and humans worldwide in relation to agriculture and food sector, especially dairy (Duarte et al., 2024). Although the H5N1 strain of the avian influenza virus is mainly reported in birds, its zoonotic nature makes it infect mammals, particularly dairy cows, which has elicited a lot of concern among veterinarian professionals, farmers and researchers. H5N1 threat in dairy cows is complex since it adds multiple issues concerning animal health, milk production and socio-economic situations. H5N1 was first reported in birds in the late twentieth century and has been responsible for several outbreaks fowl resulting in a high mortality in poultry population (Shi et al., 2023). Described as a zoonotic virus, hence one capable of spreading from birds to humans and other animals, the virus has received significant attention from researchers. It is therefore necessary to understand the means through which H5N1 spreads to affect dairy cows. Transmission involves direct contact with infected bird and its excretion feces, feed and water, and other ways like contaminated equipment and through humans(Smith et al., 2020). Wild birds, especially birds that migrate, usually possess the virus and can spread it to other areas ad farms. These numerous pathways of transmission reinforce the importance of sound animal health measures and supervision. Avian flu H5N1 can be devastating to dairy cows, causing illness and potential direct or indirect reduction in production. In particular, affected cows may demonstrate symptoms like respiratory disorders and gastroenteritis as well as severe neurological signs. These symptoms can indeed lead to decreased milk production and poor quality thus being a major concern to most farmers who rear dairy animals. Also, the infection with H5N1 of dairy herds leads to the ban of exports and the decline of consumer confidence, which only increases the losses (Gulati & Juneja, 2023).

Prevention of H5N1 in dairy cows relies heavily on early identification and passive control. The identification of early clinical manifestations alongside testing for the virus assists in quarantine and entails restrictions of the virus transmission. Measures such as supportive therapy for effected animals, implementation of disease control measures and disinfection, as well as the use of vaccines where applicable. The social and economic consequences of H5N1 in dairy populations range extensively. In addition to the direct monetary costs, outbreaks can interfere with local and global dairy production, leading to scarcities and price shifts in food products. The level of psychological disruption is also present in farming societies, which might be forced to slaughter their livestock, and lose jobs (Kappes et al., 2023).

2. Pathways of H5N1 Transmission to Dairy Cows

H5N1 is a virus that is pathogenic mainly to birds but occasionally affects dairy cows through direct and indirect transmission (Graziosi et al., 2024).

Direct Transmission: This occurs through the direct interaction with the bird or their excreta which include feces, saliva and nasal discharge (Ly, 2024). This can be through the cows ingesting the plants that have been contaminated or through the consumption of contaminated water by the animals. It raises the likelihood of transmission specifically where poultry and dairy farming is done in a combined manner as birds and other animals together with farming tools can easily spread the virus. Direct Pathway of H5N1 transmission to dairy cows is shown in the Figure 1.

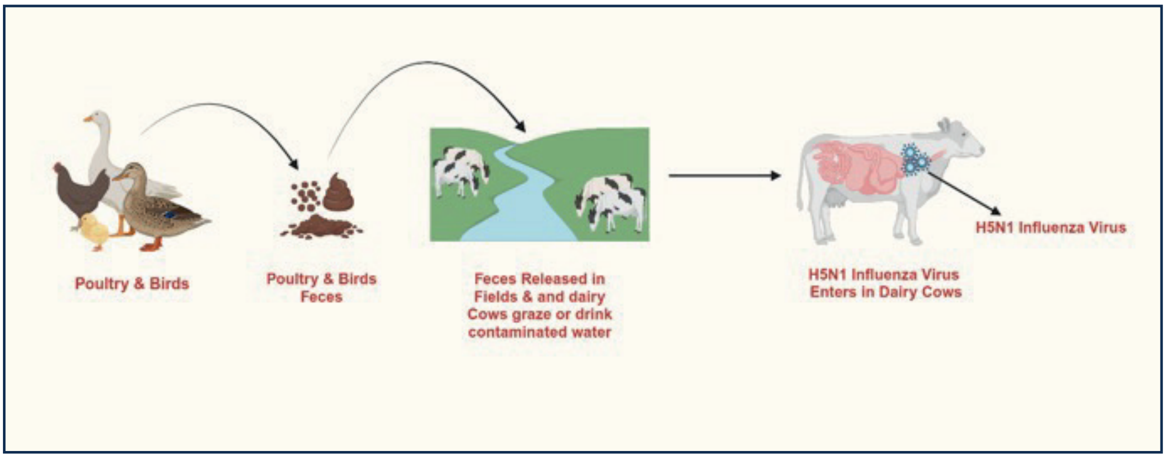

Figure 1 Direct Transmission of H5N1 Transmission to Dairy Cows

Indirect Transmission: It is also passaged by contact with things like tools, cloths, or vehicles bearing the stamp of the virus. This implies that the farm workers, veterinarians and visitors can carry the virus in their belongings from infected poultry farms to dairies. Indirect transmission of H5N1 to dairy cows is shown in Figure 2. It may also be transmitted indirectly through water as the virus can spread on the surface of water after being carried there by dead wild birds (Bauzile et al., 2022).

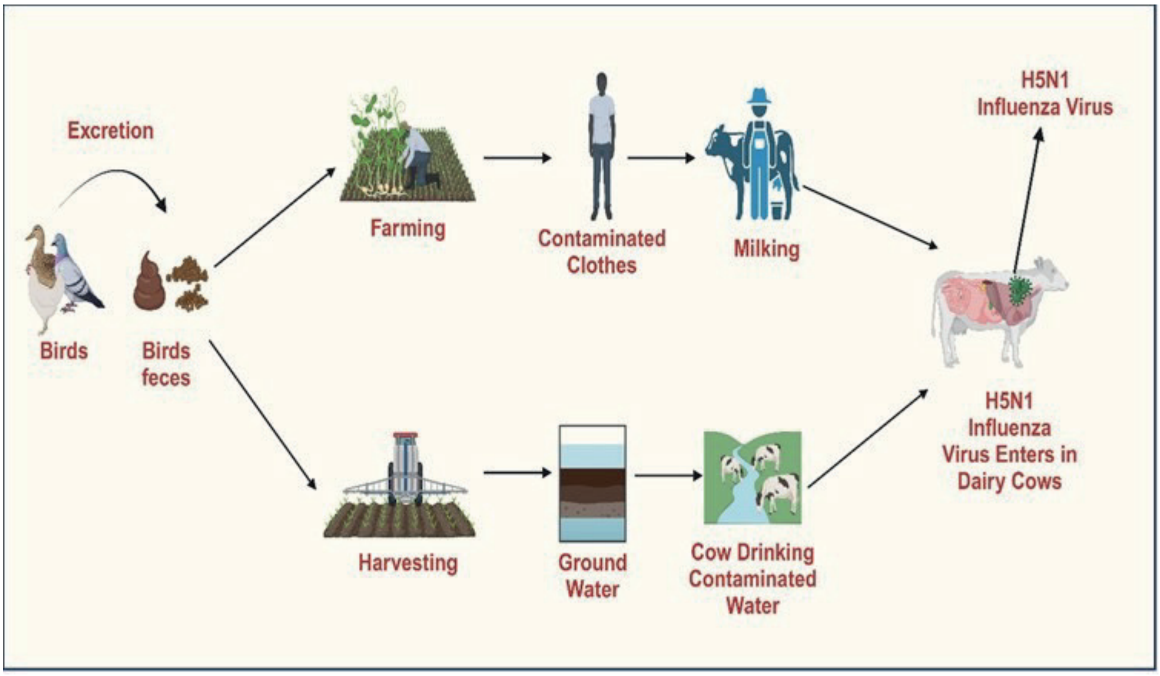

Figure 2 : Indirect Transmission of H5N1 Transmission to Dairy Cows

Airborne Transmission: While considered less probable, H5N1 can also spread through aerosols carrying infectious droplets. Avian influenza viruses are expelled by infected birds as aerosolized particles which can be inhaled by the dairy cows particularly when they are locked or when the houses are inadequately ventilated (Bhalerao et al., 2023).

Human-Mediated Transmission: Humans that are infected with the virus can pass the virus from one human to another, and in the same manner H5N1 can be transmitted from human to other animals. The infected poultry handlers spread the disease to other animals including the dairy cows either through direct contact or through contacting clothes or equipment that has traces of the disease. There is also fear that through the use of vision and voice such items as feed and bedding materials can transmit the virus from one farm to another (Huang et al., 2023).

Wildlife Reservoirs: Wild mosquitoes infected with H5N1 can fly far and spread the virus across regions and possibly to new regions such as the dairy farms (Marrana, 2022).

Contaminated Feed and Water: Feeding and watering are other means through which H5N1 migrates from one poultry house to another since the feed and water sources are also contaminated (Beerens et al., 2021). Virus dissemination is possible through droppings of infected birds and water sources can serve as a vector for the virus. The food and water that is assumed to have been contaminated with H5N1 must always be clean and safe for use.

3. Clinical Manifestations of H5N1 in Dairy Cows

In dairy cows, the clinical signs of H5N1 influenza are unspecific and affect several systems in the body. The initial clinical signs, though often vague, may be fever, anorexia, and nasal discharge. In later stages of the infection, the respiratory signs are characterized by persistent coughing, dyspnea and nasal and ocular discharge (Rosone et al., 2023). Some of the cows may also develop symptoms such as diarrhea and stomach ache. In more serious cases, neurological complications like ataxia, tremor, seizures are observed.

H5N1 also affects the quantity and standard of the milk produced by the animal. Mastitis in cows leads to reduced milk yield and the quality of milk is affected with higher somatic cell counts and can be tampered with by bacterial infection (Yoo et al., 2022). In severe cases, blood or clots can be observed in the milk being secreted by the mammary glands.

Autopsy of affected animals usually shows pathological changes in the lungs, trachea, bronchi, and gastrointestinal systems. In patients with neurological manifestations, neurological lesions may also be seen (Zappulli et al., 2020).

H5N1 infection in dairy cows can be identified through clinical and laboratory examination including PCR to identify H5N1 genetic material. Management mainly consists of supportive measures such as isolation, adequate fluid and electrolyte replacement, nutrition, and antibiotics for secondary bacterial infections. The outcome depends on the extent of the infection as well as the response to treatment.

4. Impact on Milk Production and Quality

H5N1 avian influenza infection in dairy cows leads to a significant decrease in milk production due to several factors: Focal infection, especially common in the form of fever and illness, dehydration, and respiratory troubles are some of the complications (Polley et al., 2022). These it depletes the energy, appetite, and water in the cow, which are all required to produce milk in large quantities. Likewise, (Kim et al., 2010) also consider that H5N1 has an effect on the physical distress of the affected animals, which in turn aids to divert energy from milk production.

Table 1: Impact on Milk Production and Quality

Impact Area	**Observed Effects**	**Underlying Mechanisms**
Animal Health	• Fever, illness, respiratory distress • Increased susceptibility to other diseases	• Direct pathogenic effects of H5N1 virus • Potential for secondary bacterial infections due to weakened immune system • Immunosuppression caused by H5N1 infection
Milk Production	Significant decrease in milk yield	• Focal infection (fever, illness) leading to energy depletion and reduced appetite • Dehydration and respiratory issues further hindering milk synthesis • Physical distress diverting energy from milk production (Kwon et al., 2005)
Milk Quality	Contamination of raw milk	• Presence of H5N1 virus particles or secondary bacterial contamination • Increased somatic cell count (SCC) indicating inflammation or mastitis • Altered fat and protein content due to stress and illness, impacting taste and processing properties
Economic Impact	Reduced profitability of dairy animal production	• Lower revenues due to decreased milk quantity and quality • Increased costs for veterinary services, feed, and potential animal removal • Negative market repercussions due to milk safety concerns, leading to lower milk prices or market restrictions • Long-term economic impacts: decreased returns on dairy farming, potential unsustainability for small farmers due to vaccination, culling, or movement restriction costs (especially with increased H5N1 circulation)

Apart from the raw milk production, H5N1 affects the quality of raw milk since infected cows have contaminated milk as shown in Table 1. The milk also becomes more inclined to exhibit increased somatic cell count (SCC) signifying inflammation or mastitis which hampers the quality of milk making it less preferable for processing. In aggravated cases, the milk may contain the virus particles or secondary bacterial contamination which may be hazardous to the health of consumers. They also lead to stress and illness, which can reduce milk production or increase the fat and protein content, resulting in poorer taste and prospectively and processing properties.

These changes in milk production and quality therefore have a direct impact on the economic profitability of dairy animal production. These are the animal productivity losses and include a decrease in the quantity and quality of milk produced, which may lower revenues while costs for veterinary services, feed and, in some cases, removal of affected animals rise. Furthermore, issues relating to milk safety or quality may have negative repercussions on markets and customers, pushing down milk prices, or even limits access to market by consumers. The more the H5N1 viruses circulate, the greater the potential for long-term economic impacts: the returns on dairy farming can decrease significantly and, for small farmers in particular, may not be sustainable due to costs associated with vaccinations and culling or movement restrictions (Kim et al., 2010).

5. Immune Response to H5N1 Infection

It has been observed that a dairy cow's immune system initiates a complex kind of defense mechanism when it is infected with the H5N1 influenza virus (Alqazlan et al., 2022).

1. Innate Immune Response: This is the first response that the human body deploys in its defense and entails putting up barriers such as mucous membranes and recruitment of cells including macrophages and dendritic cells (Peiris et al., 2009). These cells help in preventing viral replication and also release special chemical substances called cytokines which help in regulating the overall immune response. It also stimulates the inflammation to confine the infections as part of the innate response.

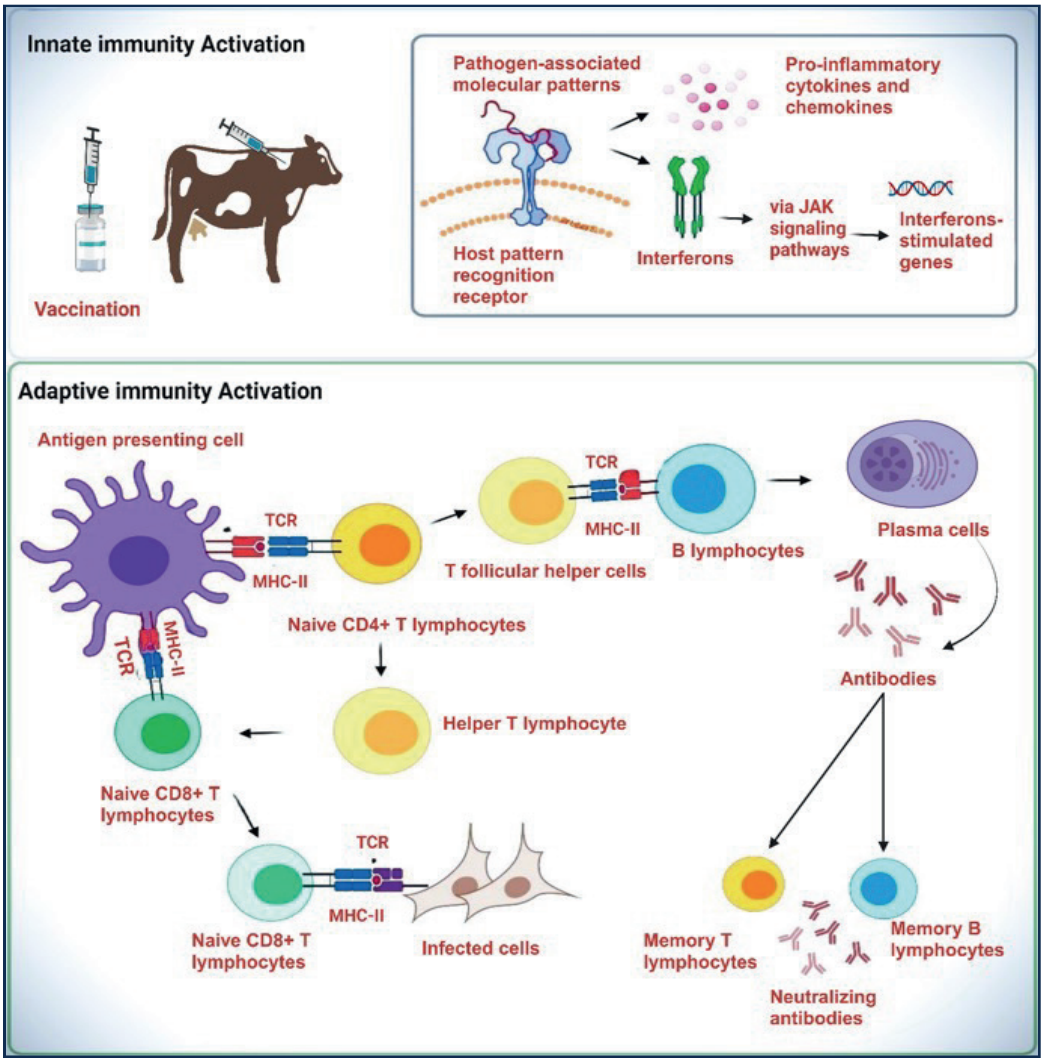

Figure 3: Immune Response and Vaccination Strategies in dairy cows

2. Adaptive Immune Response: This response is more specific and entails the development of antibodies by B lymphocytes cells that can specifically identify and inactivate the H5N1 virus. Many other immune cells are involved in this fight, including specialized T cells: cytotoxic T lymphocytes that are able to find and kill infected cells. Immune Response and Vaccination Strategies in dairy cows are shown in figure 3. Once the pathogens infect the body, immunity cells are created as a memory that lasts and can protect a person in case of subsequent exposure to H5N1 (Lee et al., 2009).

Challenges In Immune Response

1. Antigenic Variation: The H5N1 virus demonstrates high mutation rates and antigenic drifts that alter the virus's surface proteins. This makes escapes the immune system and thus can easily produce new strains that will be very hard for the immune system to combat (Velkov et al., 2013).

2. Immunosuppression: H5N1 has immunosuppressive properties that weaken the immunity of the cow and causes susceptibility to other diseases (Schat & Skinner, 2022).

3. Variable Immune Responses: There are differences from one cow to the next in terms of its immune system and thus it is not the same affected or protected (Trevisi & Minuti, 2018).

Vaccination Strategies

It was found that vaccination remains a very effective option in the prevention and management of H5N1 infections in dairy cows. Strategies such as proper immunization can help increase the level of immunity in a population, limit the virus's circulation, and minimize the consequences of the epidemic (Abdelwhab & Hafez, 2012).

Types of Vaccines

1. Inactivated Vaccines: These consist of inactivated viruses that are able to trigger production of antibodies within the immune system besides not being able to cause an illness.

2. Live Attenuated Vaccines: These employs attenuated live viruses which are very effective in the production of immunity though they pose a slight risk of inflicting illness.

3. Subunit Vaccines: Of these, some contain viral proteins or antigens and are therefore safe but their effectiveness may need to be boosted through the addition of adjuvants.

4. Recombinant Vector Vaccines: These employ non-pathogenic viruses or bacteria which act as vectors to present the H5N1 antigens and elicit persistent immunity.

Vaccination Protocols

Effective vaccination protocols include (Gisbert et al., 2012):

1. Primary Vaccination: The first set of shots to help create immunity against a pathogen or toxin.

2. Booster Shots: A booster that every now and then is required to boost the immune system.

3. Herd Vaccination: This involves vaccinating all the animals within a given population to enhance the levels of immunity within that population.

4. Strategic Vaccination: Focused immunization of the at-risk cattle or areas when there is an epidemic.

Efforts to produce useful H5N1 vaccines that can be deployed for protection of the dairy cows are hampered by the high mutation rate of the virus, safety and efficacy testing, as wells as challenges involved in production and distribution of the vaccines (Okello, 2013).

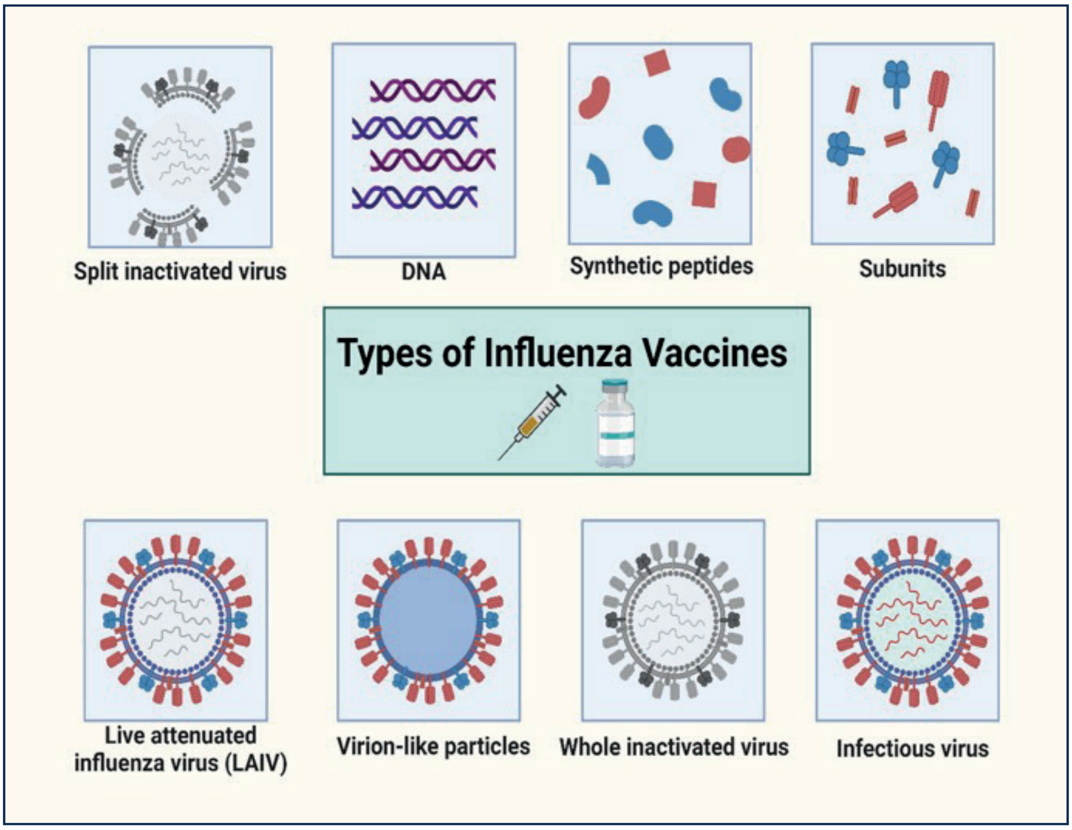

Figure 4: Types of Influenza Vaccines6. Preventive Measures and Biosecurity

The awareness and control of H5N1 avian influenza from entering into and circulating in the dairy cows are essential to the health and productivity of the animals. This demands an integrated approach that accord much consideration to measures aimed at minimization of disease entry and proliferation within and between farms (Authority et al., 2018).

One of the major components of bio security is accommodation and layout of the farm. It was revealed that avoiding exposure of dairy cows to H5N1 sources such as wild birds and other poultry farms was effective in reducing transmission risks within the farm (Gao et al., 2024). This might entail construction of some barriers, housing of various animals separately, and placement of feed and water in appropriate areas.

Another crucial intervention is the necessity to control the access to the farm. Restricting only the management, workers, and vehicles importantly prevents the circulation of contaminated persons and items. It can also be supported by stricter measures enforced at the time of entry and exit into the premises, washing or disinfection of vehicles and footwear (Wireman, 2003).

Survival of H5N1 on equipment, vehicle, and facilities must be minimized through regular cleaning and disinfection. This is even more crucial especially where the input belongs to more than one farm or different personnel. It is important that the standards of cleaning and disinfection should be instituted and practiced so as to enhance the efficiency of these practices.

Measures of quarantine are significant as they help avoid the set in of H5N1 into a dairy population. New animals, animals brought back from shows or markets and those with clinical signs consistent with diseases should be isolated and observed for 7 days before being integrated to the main group. This makes it possible to identify and quarantine people who have possibly been infected with the virus to help curb the outbreak (Yadav et al., 2020).

Another interesting feature of biosecurity is wildlife management. Wild birds are considered as natural hosts of H5N1, especially water birds. Exclusion of wild birds from the farm through use of barriers such as nets, or prevent their approach through using repellants will help minimize contact with the dairy cows. Moreover, feed and water availability should also be safeguarded to prevent contact with wild birds (Feare, 2010).

It is, therefore, very crucial to make sure that feed and water are safe. Proper storage of feed at a safe place and away from birds especially the wild ones that spread H5N1 virus helps avoid contamination (Kelly et al., 2008). The aspects such as water testing and treatment can be a way of eradicating the spread of the virus through water sources.

The other factor that should not be neglected is hygiene of people working on the farms and the tools they use. Treating and ensuring the proper utilization of personal protective gears like boots, coveralls, and gloves when dealing with the H5N1 infected cows or handling objects that may have come into contact with infected cows would help in curbing the spread of the virus from the affected area of the farm to other sections. Cleaning techniques include regular washing of shared equipment such as milking machines, milking tools and utensils after use or when used with infected animals to reduce cross contamination (Organization, 2006).

Determination of H5N1 at an early stage is a crucial step to enable prompt action and prevent its spread. Dairy cows should be checked frequently for clinical symptoms of diseases that could show early signs of an outbreak of the disease, including respiratory distress, low productivity, and weird behavior (Poovorawan et al., 2013). PCR and other diagnostic tests can help detect the presence of the virus in such occurrences and ensure that control measures are taken immediately.

High levels of public awareness are important when it comes to the practice of biosecurity in human societies. The business side of combatting H5N1 includes making sure that all farm personnel undergo and understand biosecurity procedures, disease identification, and emergency response measures. Interaction with colleagues in the field of veterinary medicine, industry associations, and governmental institutions helps to achieve synergy in the fight against diseases.

7. Economic and Social Impacts

Epidemics of H5N1 avian influenza in infected and neighboring dairy farms bring significant social and economic impacts to these farms and the overall dairy farming sector (Proença-Módena et al., 2007).

Economic Impacts

Direct Economic Impact:

- Loss of Milk Production: Milk production is influenced and this in turn influences the amount of money that a farm will generate (Somda et al., 2005).

- Increased Costs: Other costs include veterinary treatment, drugs and improved breeds securities which are costly.

- Culling and Losses: If the animals are infected or have been exposed to the virus, they will be slaughtered; this will cause a loss of money.

Indirect Economic Impact:

- Market Disruptions: Concerns about the purity of milk during epidemic contribute to the economy since it leads to changes in the prices of milk and hitches in selling milk products.

- Supply Chain Challenges: The processors and distributors face a challenge when it comes to attaining and maintaining the right volume of milk supply.

- Long-Term Financial Stability: Any outbreak of the disease puts a very huge cost to the dairy farms, and particularly to small scale farming businesses that can be greatly affected.

Social Implications

• Livelihood Threat: Most of the affected communities rely on dairy farming as their source of income hence, economic loses are against their welfare.

• Community Stress: Measures aimed at controlling and preventing outbreaks may lead to heightened anxiety and stress in farmers and communities that would need friends and resources for mental health.

• Education and Awareness: Knowledge about the H5N1 virus and biosecurity measures is an important component of capacity-building for farmers fighting the disease.

Policy and Governance

• Biosecurity Regulations: Governments have to offer various bio-security features like observation, immunization, and reporting of every disease.

• Financial Support: Assistance in the form of guarantees, subsidies or insurance might help dairy farmers to overcome such an economic blow.

• International Collaboration: Hence, collaboration and cooperation at the international level is important for early detection, follow up action and to prevent virus circulation across the borders.

Future Challenges and Strategies

• Research and Innovation: A lot of money is needed for research if better vaccines, improved diagnostic tools, and ways to contain the disease are to be produced.

• Community Resilience: This would educate, train and provide support networks so that as communities, they would be ready as well as be in a position to handle the effects of the outbreak.

• Adaptive Management: It is thus important to increase the adaptive capacity when dealing with change such as viral mutagenesis in dairy farming systems.

8. Future Directions and Research Needs

Dairy industry towards H5N1 influenza is still under pressure and so further studies and more developments are necessary for better handling of diseases control and preparedness for adverse effects (McLeod, 2010).

Emerging Trends

1. Antigenic Evolution: This is alongside the fact that mutation of the H5N1 virus is not only a one-off occurrence but this has led to the appearance of new strains that affect different species, in this instance, dairy cows, in different ways (Scoones, 2010).

2. Globalization and Trade: Circulation of products and animals across international borders helps in virus spread across borders which makes international cooperation to be very essential (Cartín-Rojas, 2012).

3. One Health Approach: It is due to the social acceptance of the One Health concept in addressing diseases that are realized to have human-animal-environmental interface aspects like zoonotic H5N1 (Zhou & Tanner, 2022).

Research Gaps

1. Vaccine Efficacy: As such, more researches need to be made for purposes of assessing the existing H5N1 vaccines being administered to the dairy cows on various aspects including on the duration of immunity offered and cross protection against other strains.

2. Transmission Dynamics: In the context of such transmission paths, the dynamics of H5N1 within dairy farms and between several farms have to be appreciated so as to come up with a control mechanism.

3. Host Immune Response: Further investigations will be conducted on survival of H5N1 in dairy cow and the objective is to identify immunological markers of protective immunity against avian influenza and facilitate the development of new vaccines.

4. Antiviral Strategies: More detail research on new antiviral drugs and therapy may assist in finding out other therapies applicable in treating the affected cows.

Innovative Approaches

1. Genomic Surveillance: Such awareness of the genetic changes in the virus makes it easy to predict and also develop appropriate vaccines (Gardy & Loman, 2018).

2. Precision Vaccinology: Some suggestions of course, could be improved by stating the particular H5N1 strains for which the vaccine should be developed.

3. Digital Health Solutions: Increased mHealth utilization for reporting diseases and insights collection can improve surveillance and reaction.

Collaborative Initiatives

1. Public-Private Partnerships: COD Promotes: increasing collaboration with federal/state universities, industry and others in the areas of communication, research & grant support, funding and technology transfer.

2. International Cooperation: The studies have it that the schemes which foster dissemination of information, development of capacity among the partners, and collaboration in research enhance the global level of preparedness.

3. Community Engagement: Efforts can therefore be made to ensure that farmers and other members of the communities participate in research and education so as to take up the task of combating diseases.

Future Directions

1. Enhanced Surveillance: Encouraging the application of various surveillance systems to pinpoint and alert the disease and likely occurrences early enough.

2. Capacity Building: The preparedness of diagnostic laboratories, veterinary services, and public health structures that have to be strengthened for increasing the capacities of response.

3. Resilience Building: Increase support from extension agents; educate; also devise contingencies for the dairy farming and financial scenarios in case of an outbreak.

9. Summary

The threat of H5N1 influenza is even higher for dairy cows, as the problem is quite diverse and requires not only local but also systemic solutions to prevent and deal with. They concluded that the virus presents severe economic risks to dairy farming such that milk production lowers, operation costs raise, and the market situation becomes fragile. The disease also has far reaching consequences economic, both for farmers and welfare of rural folks. Vaccination, identification of infected birds promptly, and other matters that pertain bio-security measures are essential to reduce the transmission of H5N1 and hence the impact in the different dairy herds.

Improving global networking and research funding are vital to the creation of better vaccines, diagnostic measures, and ways to address viral diseases. Genomic surveillance precision vaccinology and digital health solutions point to potentially major directions to enhance disease prevention and control. Moreover, preparing the dairy farming communities for disasters and building their capacity to cope with adversity is also an important proactive step. According to the principle of One Health and development of cooperation with the stakeholders it may be speculated that the effectiveness of H5N1 outbreak preventing, detecting and responding would be enhanced and animal health, food security as well as public health globally may be preserved.

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About the Authors

Arifa Mehreen is an Assistant Professor of Zoology at the University of Agriculture Faisalabad (UAF). Her research focuses on antimicrobial properties of natural products, drug formulation and pharmacokinetics, and characterization of bacterial pathogens. She has studied the antimicrobial and toxicological effects of Origanum vulgare, developed a fixed-dose combination drug for cardiovascular disease, and investigated the characteristics of Staphylococcus aureus strains.

E-mail arifa.mehreen@uaf.edu.pk ORCID 0000-0001-5899-8027

Muhammad Majeebullah holds an M.Phil. degree in Zoology from the University of Agriculture Faisalabad (UAF), Pakistan. His research focuses on the effects of nanoparticles on growth, contributing to advancements in this emerging field. Muhammad is dedicated to exploring how nanoparticles can influence biological processes, aiming to uncover new insights and applications.

Email muhammadmajeebullah336@gmail.com ORCID0009-0002-2138-2039

Shagufta Abbas is a Ph.D. scholar at The Women University Multan, Pakistan. Her research is centered on neuroscience, with a keen interest in understanding the complexities of the brain and nervous system. Shagufta is committed to advancing knowledge in this field through her innovative research. Her work aims to contribute significantly to the scientific community.

Email shaguftaabbas6373@gmail.com ORCID 0000-0002-8161-3671

Dr. Muhammad SAFDAR earned his PhD in molecular biology and genetics from Gaziantep University, Turkey. He is a faculty member in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, nutrigenomics, nano-genomics, bioinformatics, biotechnology, and their applications. He has published more than 70 research articles in national and international journals. He has also written many book chapters as well as an edited book. He is an associate editor for international journals.

E-mail msafdar@cuvas.edu.pk , ORCID 0000 0002 3720 2090

Dr. Muhammad SAFDAR earned his PhD in molecular biology and genetics from Gaziantep University, Turkey. He is a lecturer in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, nutrigenomics, nano-genomics, bioinformatics, biotechnology, and their applications. He has published more than 70 research articles in national and international journals. He has also written many book chapters as well as an edited book. He is an associate editor for international journals.

E-mail msafdar@cuvas.edu.pk , ORCID 0000 0002 3720 2090

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LIVESTOCK MANAGEMENT: REPRODUCTIVE AND OTHER HEALTH ISSUES

Sadia Suri KASHIF

Sadaf NAEEM

Pakistan is a state that largely contributes to agricultural activities (production). Among major agricultural activities in Pakistan, raising livestock is very prominent. It largely contributes to the agricultural economy as 55.6 % of the agricultural economy comes from the livestock sector (Khan et al., 2021) which contributes 19.3% of the GDP. Nearly 62 million tons of buffalo and cattle milk as well as 18,751 hides have been provided by livestock annually. Almost 8 million rural farmers with their spouses are engaged in livestock. However, this agricultural sector has recently faced numerous challenges like growing demands for agricultural products as well as an increasing population. To increase productivity, there is a need to implement sustainable alternatives on agricultural lands (Ahmad et al., 2021; Azeem et al., 2022). It was declared that 70% of the population lives in rural areas in Pakistan and is devoid of modern energy facilities. The consumption of livestock waste as an appropriate source of energy is a valuable approach for providing energy to prevailing rural areas that aid in the economic progress of the country (Khan et al., 2021).

Livestock services and products play a crucial role for humans as they supply 33% of protein and 17% of the calories consumed globally (Cheng et al., 2022). Dairy products provide a superior nutrient package like milk which is a robust source of various essential nutrients like calcium, proteins, potassium, etc. (Tricarico et al., 2020). In addition, livestock farming contributes in soil health and ecosystem management via upcycling of resources that are unsuitable for food production, minimizing pesticides and fertilizers (Leroy et al., 2022). Moreover, livestock are frequently kept to acquire transport and power, they also serve as a cultural and financial asset. Livestock production in rural areas on a small scale is highly based on family farming and is crucial to the livelihoods of poor people and their food security. Livestock offers food, income generation and gives quick cash in need of any hazard. Moreover, it has spiritual and cultural value. Small ruminants and poultry are managed by and gives benefits to women directly. In medical science, for improving human health, livestock provides many benefits. Animal models have been used for the advancement of prevention as well as therapeutics in many fields, vaccine production and in various neoplastic, metabolic and genetic disorders (Alders et al., 2021).

Livestock is the sub-area of agriculture; that is, the growth of livestock is directly proportional to agricultural growth. If there is improved agriculture, that corresponds to robust livestock. Ignorance of agriculture can also lead to a reduction in livestock production (Kakar, 2020). Livestock is an integral part of raising GDP having significantly positive effects on economic growth and poverty alleviation. Milk is the most important agricultural product enumerated as Pakistan’s white gold. Globally, Pakistan is ranked among the top five milk-producing countries (Shahzad, 2022). Milk and other animal-produced foods are effective dietary sources of micro and macro-nutrients. Animal-source food demand is highly rising with an estimated 50 % growth in 2030 (Dror & Allen, 2011; van Wagenberg et al., 2017).

POTENTIAL DILEMMAS OF LIVESTOCK

The need for livestock products is rapidly growing, it also faces simultaneously climate change events affecting animal production, like elevated temperatures, changes in precipitation patterns, etc. Such changes influence performance in livestock across many regions. For food security management and sustainability, livestock production systems are already challenged to enhance the production of livestock and minimize environmental effects (Cheng et al., 2022).

In traditional livestock systems, the quality and amount of feed is often inadequate resulting in malnutrition of animals. Additional challenges regarding the production side include insufficient natural resources, lack of infrastructure, disease pressure and limited market access (Tricarico et al., 2020).

Various environmental issues impact the yield, reproduction and health of livestock species. Elevated temperatures potentiate heat stress risk for livestock species. As shown in several studies, heat stress has an impact on various biological processes resulting in high economic consequences. In dairy cattle, it potentiates several issues including a reduction in reproduction and milk production as well as leading to risk of mortality. Moreover, enhanced carbon dioxide levels along with increased temperature due to climate change result in decreased forage quality. This lessened quality is due to the composition of plants influenced by the climatic factors that make it less digestible for livestock. Similarly, an increase in climatic temperature allows vector-borne pathogens to live much longer than they would. This can lead to boosted transmission of disease in livestock (Cartwright et al., 2023).

LIVESTOCK MANAGEMENT SYSTEMS

To understand the livestock management system, we need to have an insight into livestock production systems. A common classification is Agroforestry livestock management and conventional livestock management. Agroforestry is similar to the organic practice of agriculture. Agroforestry is the intentional integration of shrubs and trees into crop and animal farming systems, on the same land, to create environmental, social and economic benefits. It has a multi-functional system of land use described as an agriculture with livestock and trees. It can serve as a sustainable alternative to agricultural practices traditionally. It provides enhanced agrobiodiversity, increased land security and income, more diverse livelihood, sources of water and decreased rainfall dependency. It has a major role in enhancing agricultural yield, improving soil fertility, decreasing soil erosion and in raising income (Ahmad et al., 2021; Ramil Brick et al., 2022).

Conventional system, on the other hand, focuses on technologies to enhance operations and productivity for instance: high-yielding breeds, veterinary health products, modern feeding techniques, fertilizers (synthetic), and pesticides. It was proposed in various studies that agroforestry is a more sustainable system as compared to conventional agricultural systems (Ahmad et al., 2021).

LIVESTOCK HEALTH ISSUES

Worldwide, health issues in animal farming are of utmost concern. The increasing demands of dairy outlets require improved efficiencies and agricultural intensification (McMahon et al., 2015). The environmental factors add to the increased risk factors in the interaction, evolvement, and transmission of bacterial pathogens. Detection, exposure, management, and prevention are the routes to manage the health issues among dairy animals. The disease aspects are complex and have multiple agents to aggravate (Perry et al., 2013). The management solutions, interdisciplinary approaches, and complexity of local bio-systems are used in response (Lorenzo E Hernández-Castellano et al., 2019).

Bacterial Livestock Infections

The pathogenic species (Brucella, Mycobacterium, and Leptospira) cause pandemic bacterial infections in farm animals (dairy producing). This requires proper knowledge and management to minimize the transfer and carriage among such animals, reducing zoonotic risks via contact with infected animal tissues and contaminated environments and food items. However, these days farming practices are connected with zoonotic diseases. Moreover, clinical mastitis in farm (dairy) animals is caused by bacteria Gram-positives (e.g., Staphylococcus, Streptococcus) and Gram-negatives (e.g., Escherichia and Klebsiella). (Lorenzo E Hernández-Castellano et al., 2019; Wall et al., 2016). Bacterial infections require adequate resources and knowledge to create awareness, detection, and implementation of their control. Because it has a range, its transmission and zoonotic potential need methods of prevention, biosecurity, and control for the semi-intensified and local pastoral settings. In the tropics, the management of dairy animals demands added consideration for heat stress; which is a significant risk factor for suspected bacterial infection and its transmission (Lorenzo E. Hernández-Castellano et al., 2019).

Viral livestock Infections

Pakistan's climate offers favorable ground in keeping infectious diseases. Crimean-Congo Hemorrhagic fever (CCHF) or simply Congo Fever is a prevalent disease that produces severe fever outbreaks. It is caused by the Nairo virus, a tick-borne virus (Atim et al., 2022). It was discovered initially in Rawalpindi, in 1976. Thereafter, transmitted to further provinces in the country. It is found in areas where sacrificial animals are found (Masood et al., 2023).

LSD or Lumpy Skin Disease refers to a transboundary re-emerging disease in goats, sheep, buffaloes (outdoor bathwater) and cattle. LSD virus belongs to the Capripoxvirus genus (Azeem et al., 2022). Before January 2022, no case was reported in Pakistan but a sudden outbreak in Sindh occurred. To reduce the extent of disease, vaccination was increased. LPS is characterized by skin nodules followed often by secondary bacterial infection. This disease creates problems for the economy and livestock sector as it may cause skin damage, infertility, mortality, mastitis and reduced milk and meat production. LSD is not contagious to humans and causes no harm to public health (Gibbs, 2021; Imran et al., 2022).

Another potentially zoonotic viral infection affecting poultry is, the avian influenza virus (AIV, the outbreak of which, has been augmented globally, including in Pakistan. Poultry constitutes the largest agricultural subsector in Pakistan as it contributes overall 35% of meat production having a growth rate of 9.1%. It is influenced by a variety of bacterial and viral diseases, predominantly AIVs that instigated high mortality in poultry in the past decade (Channa et al., 2022). It has been observed that Pakistan suffered a heavy loss economically of around 5.4 billion in 2004-2005. Moreover, the outbreaks of AIV have occurred increasingly in past decades. It was reported earlier in studies that AIV can be transmitted to healthy birds from infected ones. The highly pathogenic virus H5N1 can also be transmitted to humans (Channa et al., 2020).

OTHER EMERGING DISEASES AMONG DAIRY ANIMALS IN TROPICS

Health concerns are of utmost importance for dairy animals. Reproduction and productivity are widely affected by diseases specifically in the tropics, for known reasons. However, intensive dairy has evolved at a large scale in other countries, dairy production is still practiced in low-scale farms having both low inputs and outputs. This decreases the chances of production-related diseases. Low input systems affect both quality and quantity. Feed, for instance, contains by-products that have low nutritional value causing deficiencies among farm animals. Moreover, they may have scarce resources for food and water even contaminated with biological and chemically hazardous mycotoxins, pathogens, antimicrobials, and heavy metals. The contamination may contribute to the development of diseases and the promotion of resistance to antimicrobials.

In the tropics, dairy farms often develop low levels of biosecurity and less frequent training possibilities, the animals are likely to be infected with diseases as they limit isolations that make them prone to infectious diseases. However, tropical climate-borne diseases such as East Coast Fever and Nagana (African animal trypanosomiasis) are dependent on climate and environment greatly. Not only environment or climate changes possess infectious diseases in the tropics, low income and scarcity of resources play a pivotal role in the widespread too. The veterinary services, lack of enforcement of regulations and authority, and unregulated pharmaceuticals common in numerous low-income states are the root causes. Limited possibilities for treatment and diagnosis eventually devastate the possibilities of implementing vaccination programs. With little or no knowledge, these farmers cannot prioritize prevention or control over numerous diseases. There are religious or economic restrictions where the fear of animal losses creates havoc on selling infected animals in disease outbreaks, exacerbating the problem (Lorenzo E. Hernández-Castellano et al., 2019).

IMPROVEMENTS IN LIVESTOCK SYSTEM

As animal production and health are critical factors in the agricultural setting, the livestock's health directly impacts their productivity and subsequently the revenue to farmers. In recent years, advancements in technology have contributed to livestock production and health practices. The expansion of the livestock sector offers significant prospects for agricultural development, human nutrition, food security and poverty reduction. Public health and food safety depend on healthy, safe and efficient livestock production. Several techniques are being developed and assessed to increase the agricultural production of different animal species like drug delivery as nano/microsystem; improving animal nutrition by prebiotics, biosorbents, probiotics, or other bioactive substances, precision livestock farming, using genetic improvement methods, disease management by using the vaccines, nutraceuticals or using alternatives to antibiotics, etc. (Hernandez-Patlan et al., 2023). Some of the methods are listed below;

1. Viral Issues Prevention

Various fatal diseases deprive livestock farmers of income and place them at risk of food insecurity. In Pakistan, farmers do not vaccinate their animals regularly against these lethal diseases. Consequently, every third animal suffered, devoiding dairy production. In Pakistan, some livestock diseases still exist that have already been controlled in developed countries. These diseases result in huge economic losses. To avoid these diseases, preventive measures should be taken (Ashfaq et al., 2020).

In Pakistan, the Government advises implementing SOPs (standard operating procedures) prior to the Eid-ul-Azha holidays each year which includes, the use of gloves during sacrificial processes to avoid contact with animal blood. Livestock should be disinfected by anti-tick spray at borders among territories while animal crossing. Public awareness campaigns as a precautionary measure should be done to prevent endemics (Masood et al., 2023). Precautionary measures should be taken while slaughtering and skinning as ticks can bite humans (Ilyas, 2023).

To uplift the economy, Pakistan highly relies on the livestock sector. Lumpy disease is an emerging condition in Pakistan. To prevent this disease, the transport of animals from one to another territory should be stopped. Animals should be vaccinated to prevent this disease (Imran et al., 2022). To treat secondary bacterial infections, good care and antibiotics are recommended (Gibbs, 2021)

2. Optimizing Digitalization with PLF (Precision Livestock Farming)

The penetration of digitalization has been observed nowadays in almost all domains of life; social, political, educational, agricultural, etc. Technology and advanced digitalization tools can help modern farmers enhance their economic contribution, repetitive drudgery of tiring farming tasks and minimize isolated solutions. In livestock setup, digital data is a key factor. The cultural obligations emphasize reducing animal experimentation and even physical contact with animals to reduce outbreaks and promote awareness and welfare. Digitalization technologies are required to be researched and integrated into the trends where novel biometric sensors, blockchain, and big data can be practiced for mutually beneficial livestock management (producers, consumers, and dairy animals) (Neethirajan & Kemp, 2021; Subach & Shmeleva, 2022).

With the increasing population, to meet the needs we must adapt to trends that enhance efficiencies, productivity, quality, and implement improved standards while addressing the common dilemmas related to livestock agriculture. This can be possible with state-of-the-art digital animal agriculture with the PLF techniques mentioned above. Biometric sensors (invasive and non-invasive sensors) monitor each animal's behavior and health in no time and further integrate data for population-level analysis. The real-time data collected is then processed and integrated with a big data analytics system; a statistical algorithm for sorting complex sets of information (data) to provide it to farmers in relevant trending pattern-enhancing decision-making tools. Blockchain (sensor) offers secure transference and traceability of livestock products from farm to table and also aids in monitoring and diagnosing diseases, outbreaks, prevention, calculating potential economic losses, and food-related health pandemics. PLF provides transparent and potential livestock agriculture to the above-stated concerns and entrusts consumers. The new PLF technologies are competitive and excelling but are still in their validation period. However, the next-generation PLF techniques need a proper foundation for prediction and prevention along with providing analytical platforms for precisely analyzed massive data (Neethirajan & Kemp, 2021).

Individual animal continuous data along with suitable analytical procedures may extend animal well-being and enhance production efficiencies. These efficiencies may result in improved livestock reproductive performance and weight, by enhanced precision in diagnosing abnormalities within the herd. Hence, they aid in lessening animal losses and suffering while reducing the administration of prophylactic medication. Sensor technology helps to reduce the repetitive and tedious tasks of laborers by providing flexibility in managing livestock activities. Sensor application reduces labor expenses and monitoring activities (Nyamuryekung'e, 2024).

3. Other Improvements in Livestock Sector

Cows have been manually milked by hand which is time-consuming and requires labor. Robotic machines for milk extraction enable the farmers to reduce physical labor, improve milk production, extract the milk anytime rather than on fixed schedules and keep the milking process hygienic. The sensors in the machine can also detect which cow is ready for milking. The machine can also detect impurities, quality and colour of milk.

Digital feed Monitoring systems allow farmers to inspect and manage the quality of feed and manage the animal feeding pattern. It can also aid in proposing customized diets for each animal based on their body weight, quality of milk and its yield and so enhance productivity and fertility per animal. An Automated traffic management system allows the movement of animals through computerized gates that close and open electronically as there is a risk of injuries to animals during movement (Mishra et al., 2022).

Reproductive Issues Associated with Livestock and Their Management

Poor animal health and diseases are the major risk factors for livestock production in Pakistan. The viability of livestock is determined by their procreative ability, influenced by environmental and genetic factors (Zhang et al., 2020). Successful reproduction is entirely important in food-animal practice to maintain productivity in livestock operations to meet the rising global need for human food (Akbarinejad & Cushman, 2024). Greater reproductive efficiency is crucial for an effective dairy operation and needs an interval for calving which enhances milk production in the herd. Good insemination techniques, good estrus detection, a healthy uterine environment and the quality of semen are the critical criteria of efficient reproductive efficiency (Abunna et al., 2018).

Reproductive performance in livestock is directly impacted by infectious diseases and can be categorized as before, during, and after gestation. Amongst them, Brucellosis is of utmost importance as it may cause miscarriage in the late gestation period or can cause retained placenta, infertility and endometritis in subsequent pregnancies. Regardless of sex, the mature animals are more susceptible to infection. It also contributes to public health concerns and large economic losses throughout the world. The environmental conditions and the management systems could significantly affect the incidence of reproductive disorders (Abunna et al., 2018). Reproductive problems cause huge economic losses to farmers as it can lead to prolonged calving intervals and inter-conception periods, uterine involution, high medication costs and decreased milk production (Arero, 2022).

The occurrence of STDs (sexually transmitted diseases) can be high if an infected male animal is mating with several female animals. These disorders may also spread by improper cleaning of equipment utilized during the process of artificial insemination. Vibriosis is a sexually transmitted disease of livestock, that may cause abortion, other physiological problems and infertility. General infectious diseases, unlike sexually transmitted diseases, are caused by pathogens, bacteria, parasites, viruses, etc. These infectious diseases may infect all animals at the same time in a herd and may result in abortion, infertility and disruptive reproductive cycles. In wild and domestic animals, brucellosis, leptospirosis and tuberculosis can be found that may be transmitted by contact among diseased animals. To prevent diseases, herd-health plans should be focused on avoiding diseases, especially during the early postpartum and prepartum periods, integrating management practices and incorporating a strategy to deal with the diseased animal. Additionally, the thermoregulatory mechanisms and abiotic stress should be managed as they have a pivotal role in the augmentation of reproduction and livestock production (Roy et al., 2020).

Hence, to improve reproduction in livestock, suitable pre and postpartum period treatments should be focused on controlled breeding programs, minimizing post-partum weight loss in livestock and treating repeat breeders and anestrus with appropriate therapy (Mohan, 2015).

The management practices to prevent sexual diseases include limited contact with external animals, sanitation of breeding equipment, use of artificial insemination techniques and implementation of the herd's scheduled vaccination. Vaccination can be more effective if given timely and must be given before breeding season. Other measures to control infection include isolating infected animals for some period, culling from herds and excluding from the breeding programs. The animals infected with reproductive disorders should be given treatment as early as the initial symptoms appear and should be placed under a veterinarian supervision and eliminated subsequently from the herd (Roy et al., 2020).

Table 1: Role of various micronutrients in livestock's reproductive system, (Izquierdo et al., 2019).

Micronutrient	Function	Deficiency Consequences
Vitamin A	Maintenance of reproductive tract integrity and reproduction in both males and females	Cessation of puberty, reduced rates of fertilization, embryonic mortality, reduced sexual desire
Selenium	A cofactor in glutathione per oxidase system, responsible for oxidation of cell membranes including reproductive tract's cell membrane.	Predisposition to reduced fertility, ovarian cysts, placental retention in females and reduced sperm concentration and motility in males
Vitamin E	Maintains and promotes reproductive life	Predisposition of low sperm concentration and sperm malformation in males and placental retention in females.
Zinc	Promotes functioning of various hormones and metabolic enzymes.	Predisposes to proliferation, placental retention and low fertility in females and reduced spermatogenesis in males
Copper	Promotes prostaglandin synthesis and hormones physiological parameters	Predisposes to disorders in estrous cycle, fetal death, placental retention.

Major Reproductive Problems in Livestock

The economic and biological livestock productivity is greatly influenced by reproductive performance (Tolosa et al., 2021). Impaired reproductive functioning results in the failure of an animal to produce its offspring. Reproductive livestock disorders impacting dairy farmer's economy includes dystocia, metritis, retained fetal membrane, prolapse (vaginal and uterine), abortion, anoestrus, repeat breeder, etc. (Verma et al., 2020). Diseases may affect dairy animals by decreasing the reproductive efficiency, reducing milk yield as well as reducing the predicted length of productive life. Reproductive tract diseases are interrelated (Hossein-Zadeh, 2013). These reproductive disorders can be categorized as before (repeat breeding and anestrous), during (dystocia and abortion) and after a gestation (RFM, prolapse and hypocalcemia) (Tolosa et al., 2021).

Table 2: Description of some livestock disorder as adapted (Ghafar et al., 2020)

Constraint	Clinical Signs	Season of Occurrence
Anthrax	Sudden blood oozing from natural orifices and death	Year round
Repeat Breeding	Recurring heat signs, enhanced vaginal discharge	Year round
Anestrus	Frequent vaginal discharge	Year round
Mastitis	Clots, pus and blood in milk, salty taste, fever, swollen udders/ulcers on teats	Year round

Table 3 : Prevalence of reproductive problems in a dairy farm from Sep. 2016 till Sep. 2017 as adapted (Gebremeskel et al., 2019)

Reproductive Problems	No. of cow’s infected (%)
Repeat Breeder	18.6
Abortion	5.81
RFM	6.98
Metritis	4.07
Dystocia	4.65
Vaginal Prolapse	1.16
Anoestrus	4.65

Abortion

Abortion is defined as the abnormal termination of the gestation period. It represents a loss in reproductive efficiency. In livestock, spontaneous abortions represent an underlying problem contributing to inefficiency and reduced herd viability. These causes often may be very difficult to diagnose resulting in frustration for the veterinarians and the dairymen. Numerous causes of abortion in livestock are reported, primarily infectious factors, like Brucella, Mycoplasma bovis, Salmonella Spp., and non-infectious agents including heat, genetics, stress, etc. It was declared that aborted cows were likely to abort in subsequent pregnancies as compared to livestock not ever aborted (Hossein-Zadeh, 2013). It represents a serious livestock threat frequently induced via zoonotic microorganisms. To prevent abortions due to the spread of infectious agents, control programs and effective vaccination strategies must be supported (Zhang et al., 2020).

Retained Fetal Membrane

It is the inability of a livestock to expel fetal membrane within 12 hours of parturition. This retention of fetal membrane results in enhanced postpartum diseases, declined reproductive performance, enhanced culling rates and reduced milk production. The membrane is expelled within 8 hours of parturition and by 12 hours, considered retained. In the US, this disease was reported as the third most affecting health disorder in dairy cows. It was also displayed in several studies that retained placenta produces a significantly negative impact on the yield of milk, weeks after calving (Mahnani et al., 2021; Tucho & Ahmed, 2017). In addition to bacterial and viral infections, nutritional deficiency of vitamins A and E, and selenium are also associated with a high probability of retained placenta (Abdisa, 2018).

Dystocia

Dystocia is linked with fetopelvic imbalance, the inability of the cervix to dilate fully, or congenital defects in animals. It may result in an impaired nervous system of newly newborn at birth or a deceased newborn due to birth injury. Its risk factors include low or high birth weight of newborn, reduced muscle glycogen, mineral imbalance leading to hypocalcemia and lack of antioxidant nutrient levels. Environment and stress can also contribute to dystocia as stress hormones ACTH, cortisol and adrenaline have a pivotal role in the instigation and control of parturition (Jacobson et al., 2020). The consequences associated with dystocia include reduced milk production, decreased reproductive performance, enhanced risk of culling and mortality and increased chances of postpartum diseases (Roche et al., 2023). Dystocia can be relieved by obstetric methods, including fetotomy and cesarean surgery (Weldeyohanes & Fesseha, 2020).

Anoestrus

Anoestrus is the sexual inability to conceive for two months or more. It is associated with inactive ovaries and anovulation. It may be classified as ovulatory, inactive and anovulatory based on ovarian activity. Anoestrus develops due to several interacting factors including physiological, managerial, pathological and nutritional (Abdisa, 2018). Heat stress may also link to hyperprolactinemia, suppressing gonadotropin release and hence altering steroidogenesis and folliculogenesis (Vijayalakshmy et al., 2020).

Treatment for anoestrus could be hormonal and nonhormonal. Non-hormonal herbal treatments include different varieties of plants, as they are enriched with varieties of phytochemicals including minerals and vitamins having estrogenic properties. Plants listed for use in anoestrus include Nigella sativa (Kabir et al., 2001), Asparagus recemosus (satawar) (Pandey et al., 2018), Carica papaya (papaya) (Hitesh et al., 2023), Saracaasoca (ashoka tree) (Rajkumar et al., 2008), Murraya koenigii (curry leaves) (Satheshkumar & Punniamurthy, 2009), Semecarpus anacardium (oriental cashew) (Bechardas, 1992), Leptadenia reticulate (Hitesh et al., 2023).

Hormonal treatments include progesterone and estrogen administration to induce ovulation as exogenous estrogen due to its positive feedback mechanism for LH surge on the pituitary. Exogenous treatment of progesterone imitates the luteal phase of the estrus cycle by a negative feedback mechanism on the pituitary and hypothalamus for the release of LH (Abdisa, 2018). To improve the GnRH effectiveness, the analogue or the hormonal dose can be adjusted (Gallab et al., 2022).

Uterine Prolapse

Uterine prolapse is the exuding out of the uterus through the vulva soon after parturition. This can be due to enhanced intra-abdominal pressure linked with intraabdominal fat, increased pregnant uterus size, pelvic girdle softening, uterine inertia, the extreme force of delivery, lack of exercise, or hypocalcemia (Abdisa, 2018). The treatment protocol includes cleaning the uterus, lifting and replacing of uterus and suturing the vulva (Martin et al., 2023).

Trypanosomiasis

Trypanosomiasis is a life-threatening and common disease. It can lead to immense economic damage by both meat and milk production in livestock. The harmful effects may also extend to humans. It is caused by several trypanosome parasites, the most dangerous Trypanosoma evansi species causes a severe disorder having various pathological manifestations as well as immunosuppressive effects. In Africa, it is among the leading causes of limited livestock production. It causes significant harm to livestock's reproductive aspects resulting from gonads and endocrine damage. T. evansi infection in livestock causes a reduction in reproductive hormones as well as it causes severe morphological changes in sperms due to enhanced oxidative stress and cortisol. It causes failure of complete reproductive functions in extreme cases (Amin et al., 2020). It can be controlled by using trypanocidal drugs therapeutically and prophylactically, targeting the tsetse fly, belonging to four classes: phenanthridine, diamidine, melaminophenyl arsenical and aminoquinalidine (Okello et al., 2021; Venturelli et al., 2022).

Future Recommendations for Improving Livestock in Pakistan

Pakistan's livestock sector possesses a huge potential for the progression of agronomy. Potential opportunities are available for researchers, economists, policymakers and government departments to positively impact the development of Pakistan's livestock sector, thereby contributing to food security, economic growth and poverty alleviation. The following actions to improve livestock are recommended:

Government authorities to conduct training and introduce relevant curricula to aid students learn innovative technologies. These sessions will also be conducted for agricultural consultants and farmers.

- The availability of veterinary doctors should be assured.
- Individualized livestock-based monitoring, traceability and evaluation must be developed.
- Service providers and PLF consultants should be more conscious about the prevailing conditions in Pakistan in order to respond to the needs of the farmers. The relationship of the farmer/consultant should be extended and physically supported to provide practical solutions for training, timely issue resolution and avoidance of impractical technology.
- Studies should be focused on agro-economical Punjab zones, particularly rain-fed areas where the rearing of livestock is a prominent source of living where poverty prevails.
- To develop systems for connecting small farmers to form practical conglomerates so that they can afford investments in innovative technologies and create links to national agencies to establish livestock surveillance.
- Awareness campaigns must be conducted for farm owners to improve livestock management like accurate heat detection, proper feeding, pondering the sire and dam size while using artificial insemination.
- Routine examination of livestock throughout prepartum and postpartum was essential as during this period, there is a higher risk of reproductive problems.
- The dairy animals should be placed in proper hygienic conditions and rescreened regularly to detect any disease.
- Formulations for controlling reproductive problems, awareness about disease transmission and its risk factors should also be focused.

Summary

Pakistan owns the potential to manage its livestock resources, especially its dairy herd, to alleviate poverty and hunger and to stimulate economic growth. Though, the majority of farmers have limited desires for their animals which leads to reduced efficiency, low yield and frequent culling. Moreover, reproductive health problems in livestock lead to high financial loss. All these factors create shortfalls and compromise productivity. There is a need to acquire techniques and trainings from developed industries to optimize and maximize productivity. The presence of high-tech firms, the impact of precision livestock specialists and next-generation education of dairy farmers for using such systems will aid sustain livestock resources as well as make a potentially global impact on economic prosperity and ameliorating food security.

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About the Author

Dr. Sadia Suri Kashif earned her Doctor of Philosophy (PhD) from the Department of Pharmacology, Faculty of Pharmacy and Pharmaceutical Sciences, University of Karachi, Pakistan. She is currently working as an Assistant Professor in the Faculty of Pharmacy and Pharmaceutical Sciences, Ziauddin University, Karachi, Pakistan. Her research focuses on the pharmacological investigation of natural compounds in mental and reproductive disorders.

E-mail: sadia.kashif@zu.edu.pk, ORCID: 0000-0003-0102-2597

Dr. Sadaf Naeem earned her Doctor of Philosophy (PhD) from the Department of Pharmacology, Faculty of Pharmacy and Pharmaceutical Sciences, University of Karachi, Pakistan. She is currently working as Associate Professor, in the Institute of Pharmaceutical Sciences, Jinnah Sindh Medical University, Karachi, Pakistan. She is a pharmacologist with research interests in the fields of pain, depression, fertility, and animal studies models.

E-mail: sadaf.naeem@jsmu.edu.pk, ORCID: 0000-0002-8112-0383

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BIOPHARMING: USING ANIMALS TO PRODUCE HIGH-VALUE PROTEINS AND MEDICINES

Sobia MUSHTAQ

Shumaila ZAIB

Minahil JAVAID

Muhammad SAFDAR

Biopharming, which is also referred to as molecular farming, is the process of producing a variety of pharmaceuticals, such as therapeutic proteins, monoclonal antibodies, and vaccines, using genetically modified plants and animals. These pharmaceuticals are intended to treat inflammatory diseases, cancer, and other serious or devastating illnesses. Animal-derived proteins are a subclass of medications in the medical field. Because these medicinal proteins cannot be chemically manufactured, they are referred to as biopharmaceuticals.

This chapter explains about uses of transgenic animals which are genetically engineered to produce pharmaceutical substances for use in humans. It often involves the insertion of gene constructs derived from humans. For example, genetically modified yeast, bacteria, and animal cell cultures have for some time been used to produce pharmaceutical substances in enclosed bioreactor systems, but are generally not included in the definition of biopharming. Genetic modification of animals to change their nutritional makeup, improve their capacity as models for human diseases and organ transplants, or use them as model systems for DNA microinjection, gene targeting, and cloning has had a profound effect on drug development, human health, and the pharmaceutical industry.

Every recombinant manufacturing system has specific benefits and drawbacks of its own. This chapter looks at the procedures, advancements, and upcoming trends in the manufacture of biopharmaceuticals. Rapid biosystem screening and analysis platform technologies are examined. Techniques for enhancing productivity through integrated and metabolic engineering are also emphasized.

Introduction

Pharming is the combination of pharmaceuticals and farming, often known as biopharming or gene farming. In medicine, proteins extracted from animals represent a significant category of drugs. The term "biopharmaceuticals" refers to the fact that these pharmaceutical proteins cannot be chemically produced. They have been created in genetically modified bacteria, yeast, or animal cell lines or they have been extracted from biological material like donated blood (Abdullah et al., 2008). Recombinant human proteins are now expressed in chicken eggs, milk, and goats.

1. The technology of pharming

Since most organisms are unable to carry out the post-translational changes necessary for the assembly and bioactivity of many complex human proteins, animal pharmaceutics aids in the creation of proteins that are hard to get through other methods. For instance, it might be challenging to control glycosylation, a post-translational modification that adds sugars to proteins in cultivated microbes. It is easier and less expensive to breed more transgenic animals than to build new facilities for the cultivation of bacteria, yeast, or animal cells (Dong DW et al., 2007).

Transgenic animals are frequently used to simulate human situations, especially mice. Researchers studying human developmental and pathological conditions, gene therapy, the genetics of human and animal disease, the assessment of treatment approaches before clinical trials, human and animal disease resistance, toxicological screening for drug and product testing, and the creation of novel products through molecular pharmacology have all found value in using transgenic animals

(Dunn et al., 2005; Pinkert CA. , 2002).

1.1 Recombinant pharmaceutical proteins- Advent of biotechnology

A healthy body produces proteins that aid in normal functioning as well as regulating and mediating metabolic processes. Any form of protein synthesis impairment, including the creation of misfolded or mutant proteins, results in the disruption of the pathway that the protein is responsible for controlling (Gupta et al., 2016). The illness might be one way this shows up. In order to meet the increasing demand, large-scale manufacturing of exogenous proteins is necessary for their supply. The intricate procedure necessitates increased levels of protein production, purification, and processing. For large-scale manufacturing and purification, every product requires a different set of parameters or standards. To create human-derived proteins in bacteria, fungi, insects, or mammals, genetic engineering techniques are applied (Figure 1.1). While using recombinant DNA technology to produce proteins on a wide scale involves a significant investment of time, labor, and resources, it also presents numerous prospects for economic growth (Khan et al., 2016). After reading this chapter, readers should be able to comprehend the fundamentals of recombinant protein creation in a variety of hosts, as well as the benefits and drawbacks of each host system, as well as the properties and production of certain significant growth factors and medicinal substances. Recombinant DNA technology has the following benefits when it comes to protein production:

- It reduces the possibility of an immune response and produces highly active proteins because human genes can be copied and expressed.
- It reduces the possibility of spreading unidentified diseases found in human and animal sources. The therapeutic protein can be generated effectively while being economically viable.

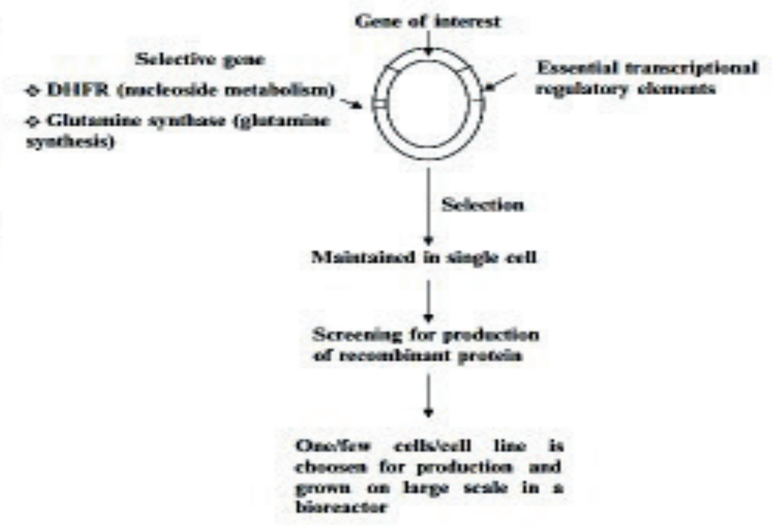

Figure 1.1: The desired gene is cloned using an appropriate vector. The cloned gene contains all the necessary regulatory components needed for transcription in order for its expression.

1.2 Animals as the production platform for recombinant pharmaceuticals

While there are many different host systems available for the synthesis of recombinant proteins, microbial hosts have a number of benefits over alternative systems, including quick, affordable, and efficient production:

1. Simple to use and maintain.
2. Makes use of affordable nutrition sources.
3. Quick development and biomass build-up at high cell densities.

4. A range of potent inducers can be used to modify their expression machinery (Ferrer MN et al., 2009).

In the pharmaceutical sector, the greatest source of innovation at the moment is the recombinant creation of therapeutic proteins against human diseases. The development of novel therapeutic proteins, where transgenesis plays a crucial role, has been propelled by the market's expansion. Because of the transgenic animal platform's low production costs with high productivity and quality recombinant proteins, it presents appealing opportunities. Transgenesis in farm animals typically encounters certain difficulties, mostly because of random transgene integration and control over copy number, despite the fact that numerous ways have developed over the past few decades for the creation of transgenic founders. However, because of its tremendous efficiency and simplicity, the CRISPR/Cas system's recent advancements in gene editing promise to transform the discipline. Additionally, the characterization of bioreactor founders, as well as the expression patterns and protein functions are technical aspects of the process that require regulatory decisions with a focus on biosafety before any given recombinant protein is finally approved for use in animals or humans. The approval of two recombinant proteins produced from the mammary gland for use in clinical and commercial settings has increased interest in finding safer, more effective, and cost-effective methods of creating transgenic founders to fulfill growing global demand for biomedical proteins (Bertolini LR et al., 2016).

1.3 Transgenic construct used for animal pharming

These days, molecular biology is advancing at a pace never seen before. Generically engineering animals is one of them. An animal classified as transgenic is one whose genome has been altered to incorporate genes from a different species or to apply methods to edit animal genome to produce particular features. One can intentionally modify a gene (or genes) to change an animal's traits. The first transgenic animal to be successful was a mouse. A few years later came cattle, sheep, pigs, and rabbits. There are several ways to prepare the foreign genes employed in animal transgenesis. A range of vectors, such as bacterial plasmids, cosmids, and yeast artificial chromosomes, are used to insert the generated gene of interest. The generated vector, which contains the intriguing gene, is delivered into the host cell via a variety of methods, such as heat shock, viruses, the gene gun, electroporation, microinjection, and liposomes. DNA microinjection, retroviruses, stem cells, and cloning can all be used to induce transgenesis in the gonads, sperm, fertilized eggs, and embryos. Currently, fluorescent protein is the most effective transgenic marker available. PCR, ELISA, western and southern blots, and the incorporation of an antibiotic resistance gene all confirm the effectiveness of transgenesis. The most promising technologies in the future will be those that address social and ethical issues (Shakweer et al. 2023).

1.4 Drug Design Models for Human Diseases by Transgenic Animals

The majority of medicine candidates are unable to obtain approval from the US Food and Drug Administration due to challenging nature of preclinical trial and drug development methods. In order to increase chances of success in the process of developing new drugs, effective and forecast methods that can pinpoint high-quality targets must be employed (Sun D et al., 2022). Using affordable and manageable animal models for in vivo research is a useful strategy to solve the challenges faced in the development of innovative drugs and combination therapies.

Transgenic mice are regarded as a valuable resource for studying human illnesses and assessing how treatments work in drug discovery labs. These animals are genetically engineered creatures that have traits similar to those of some human diseases. It provides genetic models of several human diseases, which are essential for understanding illnesses and finding new targets. Since the 1980s, genetic modification has allowed scientists to modify the mouse genome by adding or removing certain genes (National research council, 1993).

The US Food and Drug Administration approved and manufactured ATryn, first drug made from transgenic animals, in less than 20 years after it was developed. This discovery opened the door for the creation of medications made from transgenic animals. Making physiologically safe drugs based on human regulatory proteins is one use for this technology (Hunter, 2019; Bagle et al., 2012). In the upcoming years, a number of issues related to the use of transgenic animals such as ethical questions, legal requirements, and patents will receive more attention. Clinical trials, xenotransplantation, and other fields may benefit from the use of transgenic animals in drug discovery and development (Fung et al., 1997).

1.5 Analysis of transgenic animals

The Food and Drug Administration (FDA) of the United States created rules for the pre-market data submission of prospective goods derived from transgenic sources (FDA, 1995). These standards include, among other things, the need that the integrated transgenic construct's structure and expression pattern be identified in the original animal and proven to be dependable in succeeding generations. To ascertain the composition, copy number, and integration location of every transgene, an analysis of every animal line intended for commercial production is necessary. The inquiry will use Southern hybridization of the genomic DNA to determine the lengths of the various restriction fragments expected from the construct structure. Fluorescence in situ hybridization of spreads of metaphase chromosomes can also be used to identify the chromosomal location or sites of integrated transgenes. Molecular cloning of the integrated transgene and its nearby regions may be required to determine the DNA sequence of the integrated transgenic locus.

Mammalian embryos injected with DNA via microinjection typically integrate the DNA as tandem repeats that are orientated head to tail and typically, but not always, at a single randomly placed locus within the host genome (Smirnov A and Battulin N, 2021). Unlike transgenic loci created by DNA microinjection, those created by random cell transfection need the introduction of selectable marker genes, which usually encode resistance to a common antibiotic like G418, blasticidin, or puromycin. Bacterial gene promoters are omitted from the selectable marker genes in order to prevent potential gene flow from the transgenic animal to prokaryotes. Additionally, site-specific recombination elements, such loxP substrate sites for Cre recombinase, can be placed in front of antibiotic resistance genes to facilitate their eradication. Nevertheless, this can lead to significant deletions in several arrays (Sun et al., 2015).

In most cases, co-injected or co-transfected transgenes integrate at the same locus. Transgenic lines are commonly created from founder animals with large transgene copy numbers because they frequently exhibit the highest levels of expression (Grandjean et al., 2011). However, it has been noted that these lines are susceptible to transgene silence, recombination, and copy loss over several generations. In tandem arrays, transgene copy loss is more common when components are oriented in the opposite direction from one another.

Genes that are incomplete, duplicated, or deleted can result from such unstable arrangements. Because alterations in the translational reading frame might result in the development of shortened and/or abnormal protein species when breaks occur within coding regions, incomplete genes are especially undesirable (Jackson et al., 2018).

1.6 Transgene mRNA expression analysis

Determining tissue specificity of transgene requires characterizing its expression pattern. The main goal of this is to determine whether improper transgenic expression would likely result in any unwarranted negative consequences that would be detrimental to the producing animals (Bandopadhyay R., 2010). To identify temporal or geographical ectopic transgene expression, samples of a wide range of tissue types obtained from transgenic animal necropsy are analyzed using Northern hybridization or reverse transcriptase PCR (RT-PCR). The quantity, position, and type of expression of any ectopic transgene, as well as the protein that is encoded, will determine its importance. To determine the whole spectrum of mRNA species present, transgene mRNA expressed by the relevant tissue has to be thoroughly characterized. To ascertain whether the mRNA is appropriately spliced and maintain its integrity, this is required. Even if they are just minority species, aberrant mRNAs have the ability to encode aberrant proteins that may have serious therapeutic ramifications (Dorn et al., 2011).

1.7 Transgene protein expression analysis

The objectives of transgenic protein analysis are to ascertain whether a protein is completely functional or it degrades in certain situations, such as milk and expression levels are high enough to be economically viable. The next step is to determine how closely the transgenic recombinant protein product matches the original ones and either there are variations that impact immunogenicity, stability, or half-life (Shepelev MV et al., 2018).

In order to do this, significant efforts will be put into the examination of protein products using mass spectroscopy, glycoprotein analysis, peptide mapping, functional testing, and protein sequencing. Evidently, a pharmaceutical product intended for human use must always be of high quality. Protein structure can be impacted by changes in expression levels. For instance, high expression levels may surpass the generating tissue's limited ability for post-translational modification, leading to partially or completely unaltered protein and changed bioactivity. Thus, the amount of variation in protein production among members of a transgenic herd or flock should be minimized (Tikhonov D et al., 2021).

Any transgenic product's evaluation will undoubtedly take into account the purity of the protein production (Shepelev MV et al., 2018). This is crucial in cases when intravenous administration is planned. Producers are responsible for making sure that host animal proteins, DNA, and chemical reagents are removed, as well as for making sure that possible pathogens like viruses, bacteria, and prions are excluded.

2 Protein extraction, purification, and processing

There are well-established basic techniques for the collection and processing of large quantities of milk and eggs. Designing collection methods suitable for the bulk collection of other fluids such as urine or semen has not yet been feasible.

Milk is the sole product of large-scale recombinant protein purification that has been generated thus far. This multi-step system combines industry-standard techniques created for the dairy sector with techniques created for the purification of recombinant proteins produced in cell culture. The application of a given product dictates the amount of purity needed for it. Should the protein be consumed as a nutraceutical, skim milk may be a good option. However, if the product was to be administered intravenously on a regular basis for prolonged periods of time, extraordinarily high levels of purity would be required (Meade HM et al., 1999).

The details of the protein's purification will depend on its composition. The first stages involve removing fat and suspended caseins using techniques including centrifugation, acid precipitation, micro-filtration and chymosin treatment, as the majority of recombinant proteins are found in the whey fraction. A sequence of chromatographic procedures would next be carried out to separate the recombinant protein from leftover milk proteins, whey and other impurities (Nath et al., 2014). The latter steps in the cleanup process might involve heat treatment and ultrafiltration in order to create a pharmaceutical-grade medicinal product. According to current experience, the ultimate yield of purified product can range from 40 to 60% of the quantity found in milk, depending on the protein's makeup and the necessary purification process. Usually, the most loss occurs when the casein is removed. Treatment with chelating drugs that break down casein micelles and release the related recombinant protein may lessen this (Hernandez A and Harte FM., 2009).

Good manufacturing practice (GMP) and standard operating procedures (SOPs) must be followed in the execution of all processes. Manufacturers of transgenic products would maintain sperm banks, much as manufacturers of cell culture products must maintain duplicate banks of cells to guarantee product continuity (Seet et al., 2023).

Animal husbandry: The laws governing the housing of genetically modified animals varied throughout nations. Transgenic animals must have their veterinary health monitored and their consequences from recombinant protein production closely monitored. All animals are typically maintained under some kind of confinement regime, such as in fields that are double-fenced, where each animal is identified by a tag and is closely monitored by an accounting system. It is important to follow the protocols for disposing of garbage and cadavers to guarantee adequate containment. The general animal husbandry regulations of the EU also apply to transgenic flocks or herds (Hallerman et al., 2022).

2.1 Choice of species and site of production

The selection of the appropriate animal species for biopharming is determined by a variety of factors, including the ease of genetic manipulation, reproductive characteristics, protein yield, and ethical considerations. Several species can be used in biopharming, with each offering unique advantages. The most commonly utilized species include goats, cows, rabbits, chickens, and sheep (Table 2.1).

Table 2.1: Species used for protein production

Choice of Species	High-Value Proteins	References
Goat	antithrombin III	Echelard et al., 2009
Cow	human lactoferrin, insulin, and antibodies	Kues & Niemann, 2011
Rabbit	Interleukin-2 and human growth hormone	Zhang et al., 2014
Chicken	human interferon beta	Lillico et al., 2016
Sheep	alpha-1 antitrypsin	Saviano, 2023

2.1.1. Goats: Goats are commonly chosen because of their relatively short gestation period and their ability to produce large quantities of milk containing high-value proteins at relatively high concentrations. For the production of proteins that can be secreted into milk, transgenic goats are perfect. For instance, their milk can include the protein antithrombin III, which has anticoagulant qualities (Echelard et al., 2009). Goat farming is highly popular due to its scalability and ease of milk collection.

2.1.2. Cows: In biopharming, cows are frequently utilized to generate complicated proteins that need for numerous post-translational modifications. Cows are a desirable option for manufacturing milk proteins because of their huge size and great volume of milk output. For instance, human insulin, antibodies, and lactoferrin have all been successfully expressed in the milk of transgenic cows (Kues & Niemann, 2011), providing a scalable and economical production technique.

2.1.3. Rabbits: Compared to larger animals, rabbits have a shorter maturation period and a faster reproductive cycle, which makes them useful for producing transgenic lines more quickly. They work well for manufacturing monoclonal antibodies and high-value proteins in lesser quantities. For example, rabbit milk expresses human growth hormone (HGH) and interleukin-2, suggesting possible uses in biopharmaceutics (Zhang et al., 2014).

2.1.4. Chickens: In order to produce proteins for immunizations and enzyme replacement therapies, hens are kept for their eggs, which provide an efficient and non-invasive source of protein. Eggs are a great biopharmaceutical medium since they are easy to gather and the egg whites have a higher protein content. Transgenic chicken eggs have been shown to produce proteins like human interferon beta (Lillico et al., 2016).

2.1.5. Sheep: Similar to goats, sheep are used to provide milk that is utilized to create proteins like alpha-1 antitrypsin, which is used to treat respiratory ailments. Their ability to produce enormous amounts of milk increases their potential for biopharmaceuticals (Saviano, 2023).

2.2 Site of Production

Protein yield and quality are significantly influenced by the animal's production site (Table 2.2). The main locations are urine, eggs, blood, and milk, each of which has unique benefits and difficulties. (Shakweer et al., 2023).

2.2.1. Milk: The most popular location, milk, has many benefits, such as easy collection and high protein output. Large volumes of milk proteins can be isolated and refined utilizing tried-and-true dairy industry procedures. This method works particularly well for producing therapeutic proteins, such as enzymes, hormones, and antibodies.

Table 2.2: Sites for transgenesis (Shakweer et al., 2023)

Site of Production	Advantages	Challenges
Milk	• easy collection • high protein output • therapeutic proteins including hormones, enzymes, and antibodies.	Refine form
Blood	Effective against naturally occurring bloodstream proteins such clotting factors	complexity of protein extraction and purification along presence of multiple other proteins and cells
Eggs	• high protein concentration • scalable • economical • Producing vaccines and other therapeutic proteins	Extraction of protein in pure form
Urine	Relatively low protein concentration makes the purifying process much simpler	lesser yields

2.2.2. Blood: Producing proteins in the blood is less common because of the complexity of protein extraction and purification as well as the existence of several other proteins and cells. Nevertheless, it functions effectively for naturally occurring bloodstream proteins such clotting factors. The challenge lies in ensuring that the expression of the protein does not adversely affect the animal's health.

2.2.3. Eggs: One effective and non-invasive way to gather proteins is using eggs. The egg white, which has a high protein concentration, can be used to extract proteins. This technique of manufacturing is scalable and economical, ensuring a steady supply of the needed proteins. Producing vaccines and other therapeutic proteins that need precise post-translational modifications is a good use for this technique.

2.2.4. Urine: It has been possible to engineer certain transgenic animals to create proteins in their urine. Relatively low protein concentration in urine is advantageous to this procedure as it makes the purifying process much simpler. Because of the lesser yields in comparison to milk production, it is less common.

Recombinant proteins are being produced using genetically modified animal cells. Transgenic agricultural animals (sheep, pigs, and rabbits) larger than mice (Table 2.3) that release foreign proteins in their milk, blood, and other body fluids have become possible. The β-lactoglobulin gene in sheep was fused with milk protein gene promoters, and the β-lactoglobulin gene was fused with human tissue plasminogen activator (Valender, 1997). Through the use of this method, 100 foreign proteins were secreted into milk in an experimental setting. These included milk with higher casein levels, which are beneficial for making cheese, or milk with specific qualities to fill in demographic gaps, like lactose-free milk for the Asian market, milk without β-lactoglobulin for consumers with allergies, or milk containing human β-lactoferrin protein to protect newborns (Melo et al., 2007). Several of them are clinically examined and found in considerable quantities in the milk of rabbits, sheep, goats, and cows. One of the proteins that helped the clinical condition of infants with Pompe illness was human a-glucosidase, which is produced from rabbit milk. EC superoxide dismutase, fibrinogen, collagen, and spider silk are a few examples of the intricate foreign proteins that the mammary gland may create (Valender, 1997).

Table 2.3: Medicines created against disease using transgenic animals

Diseases	**Target medicines**	**Animal**	**References**
Anti-infection	Alpha-lactalbumin	Cow	Wang et al., 2008
Thrombosis	Human protein C	Pig, Sheep	Peterson et al., 2009
Wound healing	Fibrinogen	Cow, Sheep	Prunkard et al., 1996
Type 1 diabetes	Glutamic acid decarboxylase	Mouse, Goat	Herger et al., 2003
Blood volume maintainance	Human serum albumin (HAS)	Mouse, Cow	Luo et al., 2015
Malaria	msp-1	Mouse	Chen and Zavala, 2012
Cystic fibrosis	CFTR	Sheep, Mouse	Gawenis et al., 2019
Osteoporosis	Human calcitonin	Rabbit	McKee et al., 1998
Arthritic infection	Lactoferrin	Cow	Van Berkel et al., 2002

The efficiency, quality and yield of the proteins produced are all determined by the strategic selection of the species and production site, which is crucial to optimizing the biopharmaceutical process. Various animals such as goats, cows, rabbits, and chickens can provide distinct advantages based on the type of protein and its intended application. Comparably, in order to maximize the production process, great thought must be given to the location of production—whether it milk, blood, or eggs. The potential of biopharming is being further enhanced by advancements in genetic engineering and animal husbandry, paving the way for the production of more efficient and cost-effective high-value proteins and medicines (Fischer et al., 2001).

3 Techniques for creating transgenic animals

Using transgenic animals for protein production is a notable biotechnology breakthrough. Animals whose genomes have been changed to incorporate foreign genes are known as genetically modified organisms, or transgenics (GMOs). These animals can create recombinant proteins, which are useful in agriculture, industry, and medicine. Because transgenic animal technology creates new opportunities for the production of high-value proteins for use in industry, nutrition, and pharmaceuticals, it has completely changed the biotechnology business. Scientists can exploit the biological machinery of animals to generate complex proteins that would be costly or difficult to produce in other ways by introducing foreign genes into their genomes (Spok et al., 2007; Niemann H and Kues WA., 2003).

Many methods for producing transgenic animals have been found in the last few decades. Many sequences have been uncovered as a result of gene sequencing, offering details about genes and promoters that are significant for a wide range of organisms. Proteomics, genomics, and many new reproductive biotechnologies all indicate that transgenic animals can be successfully used in home settings. The methods and processes utilized to create a transgenic animal depend on what purpose the animal will serve. Numerous transgenic animal models have been created to study the functions of genes, act as bioreactors, and serve as prototypes for cutting-edge methods of animal breeding. (Houdebine LM, 2003). Figure 3.1 depicts the main methods used to produce transgenic animals.

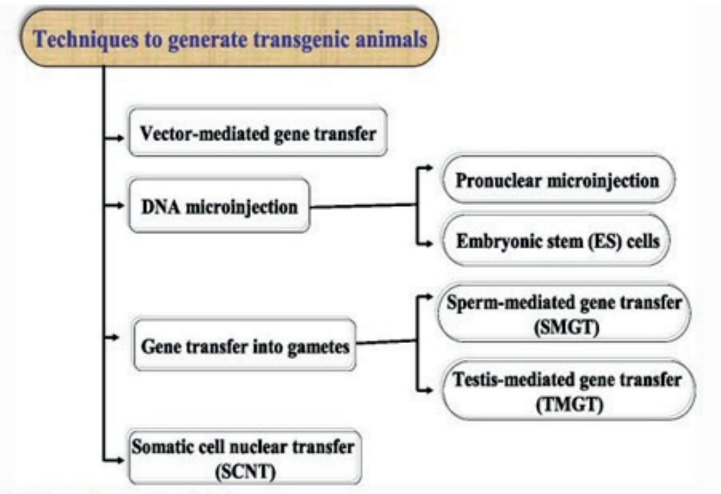

Figure 3.1: Techniques for creating transgenic animals (Shakweer et al., 2023).

3.1 Animal welfare consideration in production phase

Over the years, demand of genetically modified animals for the production of pharmaceuticals, vaccines, antibodies and other such compounds, has been increased rapidly. To get maximum output, large number of animals are reared in relatively small space. Attention is paid on increasing production; whereas little attention is paid towards the wellbeing of animals that damage their physical as well as mental health. However animal welfare awareness has been increased recently due to animal welfare training at colleges and universities (Fridovich et al., 2024).

It is hard to present single definition of animal welfare, interpretation of animal welfare changed with moral view of the concerned person. Generally we can define animal awareness as "how well an animal is coping with the conditions in which it lives" (Sinclair et al., 2022). In simple words animal welfare means to check that animals are not being treated cruelly, or are not given unnecessary pain or suffering. Animal's welfare status is satisfactory if animals are managed with little effort and less expenditure. However, if animal fail to cope with living conditions, animal's welfare status is said to be unsatisfactory. Another way of defining animal's welfare is physical and emotional state of animal due to human behavior. The amount of resources and quality of environment available to an animal is also considered as animal's welfare. Farm animals have feelings as well as emotions, therefore psychological well-being of these animals is very important in order to prevent them from mental trauma (McMillan, 2020). Therefore in order to cope with animal's ability physical and mental suffering should be kept as minimum as possible.

3.1.1 Housing and management

In order to get maximum benefit from animals, proper housing and management is very important. Good management means to provide better housing and proper care to animals so that can grow properly; gain health; reproduce and provides consistent research data. Appropriate housing provides comfort zone to animals where they can move freely and express natural behavior (Faith et al., 2020). They must be provided with clean bedding, enough space for moving and social environment. Many factors need to be considered for appropriate management of animal's housing and suitable living environment. These factors are;

1. First and most important factor is individual's characteristics like species, age, sex, and behavior.
2. It is very important to check animal's ability to live either in groups or singly (Gartland et al., 2022).
3. Design and construction of house is very important factor in managing animal's housing (Singh et al., 2020).
4. Check the availability of supplements to the animals.
5. Proper attention to experimental designs like production process, breeding phase and testing results (Tiwari et al., 2023)
6. Animal manipulation and sensitivity of procedure applied needs to be considered (Steagall et al., 2021).
7. Any hazardous and disease-causing materials need to be checked.
8. Last important factor that needs attention is the duration of holding period (Temple et al., 2020)

While managing animal's housing, attention should be towards maximizing species-specific behavior and reducing stress inducing behavior. Social species should be housed in groups or pairs. In order to achieve desired housing for animal, strategy should be developed by animal care personnel and approved by IACUC. IACUC should take decision after consulting with veterinarian and investigator for animal's wellbeing and consistency with research objectives (Ahn et al., 2022). Then objective assessment should be made to confirm the suitable environment and for animals housing.

3.1.2 Food, Water, Bedding, Sanitation

Animals should be provided adequate non-contaminated and full of nutrients food. Animals should provide foods either on daily basis or as per their requirements. Nutrients requirements of the animals have been provided by National Research Council Committee on Animal Nutrition (2001). By considering their publications, we can check about quality of food, free from all types of contaminants (chemical, microbial and natural toxicants). Water is the most important factor for living bodies. Water acts as the medium for digestion of food, absorption of food and carrying out metabolic activities. Water is also necessary for seat secretion and for removing wastes from body as feces and urine. It acts as major component of body secretions like saliva, milk. It also functions as transportation medium for nutrients, hormones and other chemical messengers. It also assists food in moving through gastrointestinal tract (Saha et al., 2021). Water is also necessary to regulate body temperature through evaporation. A good farmer must make sure the availability of clean water close to the area. Hence, animals should have access to clean drinking water according to their requirements.

Water quality and purity definition changes with locality. If for some particular protocol, highly purified water is required; then water can be purified by various treatments to minimize contaminants. Treatment used for water purification should be given proper attention, as treatment may be suitable for one species and not for other species for example chlorination that is toxic for some species but non-toxic for others (Srivastav et al., 2020).

Cattle are sensitive to taste and odor of water as well as food. If food or water quality is low, they do not take it happily that ultimately lead to decrease in growth as well as production. It will also affect their performance and make them more vulnerable to diseases.

One of the important factor affecting animal's welfare is bedding. Bedding can have effect on experimental data as well. Bedding material should be selected by veterinarian in consideration with investigators. There isn't any ideal bedding for all species, similarly one bedding isn't ideal for species in all conditions (Carter and Lipman 2018). For example, softwood beddings have been recommended for animals but on the other hand use of untreated softwood shavings can effect metabolism of the animal. Similarly Cedar shavings are not recommended because they continuously pass out aromatic hydrocarbons that create cytotoxicity.

Healthy maintenance for animal's welfare includes bedding change, space cleaning and disinfection. Place where animal is living should be clean on regular basis to remove excessive amount of dirt and debris. It should be disinfected to reduce or eliminate the quantity of microorganisms (Carpenter, 2018).

3.1.3 Body Temperature, Ventilation, Light

Homeotherms can survive well in temperature range 36-42ºC. It is very important to maintain animal's body temperature within normal range so that they can grow well. If animals are kept in temperature above or below the ambient temperature, without any shelter, their non-basal metabolic rate increases (Shephard, 2023). However, they can tolerate increased temperature upto a certain limit that defined by their increased metabolic rate. In figure 3.1.1 an increase in metabolic rate of mice is shown when exposed to high temperature.

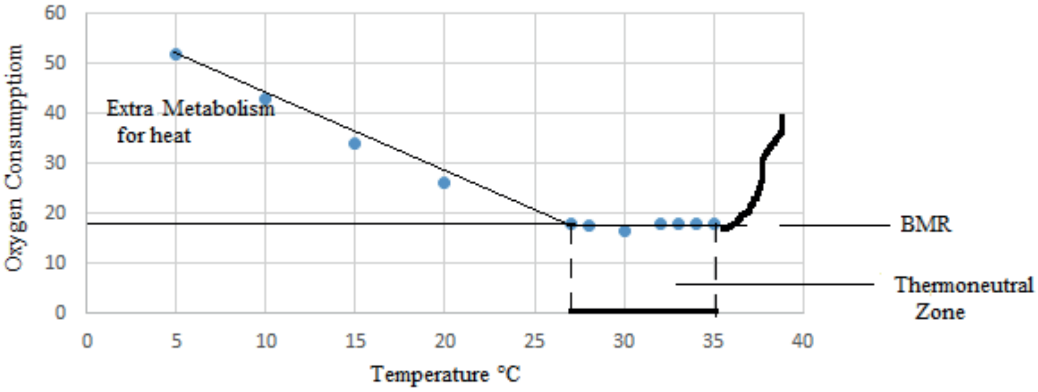

Figure 3.1.1 Increase in metabolic rate of mice when exposed to temperature range outside the ambient temperature. Increased in metabolic rate constrains the limit upto which mice can tolerate the excess temperature (Akin, 2018).

During production phase animals should provide proper ventilation so that maximum product can be achieved from them. Ventilation refers to the provision of adequate amount of oxygen and remove carbon dioxide produced by animal's respiration. Moisture content of room should also be adjusted properly and static pressure differentials should be created between adjoining spaces. Care should also be focused on primary enclosure of animal, as properly ventilation of room does not ensure the adequate supply of ventilation to the animal (Oliveira, 2020).

Light, another factor that needs to be properly managed during production phase of animals as animals can vary their behavior with light intensity. Their physiology and morphology is also affected by the light. Major light contributing factors affecting animal's behavior include inappropriate light duration, increased/decreased light intensity, and quality of the light (Penev et al., 2014). There are several factors that can affect the animal's need for light. These factors include light intensity of light, wavelength of light, animal's body temperature and pigmentation, hormonal condition of the animal, age, sex, species and strain. Animal's room must be monitored regularly by keeping these factors in consideration.

Generally animals produce noise by themselves and noise is also created by animal care activities. Therefore during production phase noise control should be considered an important factor. Noise intensity, frequency, duration and vibration should be in accordance to the tolerance range of the animal (Arcangeli et al., 2022).

3.1.4 Protein Collection

During protein collection form animals they are exposed to several different processes including livestock farming, aquaculture and harvesting. It is ethical, moral and legal responsibility to ensure animal welfare during the protein collection (Hampton et al., 2021). Here are some key points that should be focused while collecting proteins from the animals.

Livestock farming practices should be managed properly to ensure appropriate space for animal growth. Animal should be supplied with adequate amount of nutrition, food, water and oxygen to maximize protein production (McAllister, 2020).

Animals should be treated politely while collecting protein form them. Whether they are harvested for protein, meat or dairy products, they should be treated with care. Workers should use human slaughter methods to reduce the pain and stress to the animals during protein collection. Such types of techniques like stunning before slaughter, should be used that keeps animal unconscious before death (Riaz et al., 2021).

Transporting animals from their development house to processing house is very difficult phase. Animal could have much stress and may be harmed if not manage properly. So while transporting animals, minimize transportation time, arrange comfortable vehicle that must be properly ventilated and handle animal with proper care (Brindle, 2016).

To provide animals with proper healthcare and to protect them from diseases is very crucial step for animal welfare. Animals should be vaccinated regularly, they must be provided with proper veterinary care. Take essential biosecurity measures to prevent the spread of disease in them (Schat, 2014).

While selecting animals for traits like enhanced milk or meat production, balance should be maintained. As breeding animals purely for productivity purpose can lead to several welfare issues like musculoskeletal problems or reduce the power of animal to fight against diseases. Responsible breeding should prioritize the animal welfare and health (Kwon et al., 2014).

Animals should provide opportunities to outdoor space, they should have possibilities to express natural behavior and interact socially. Animal welfare can be improved by allowing them to show their natural behavior and keep them in stress free environment (Sueur and Pele, 2019).

While extracting proteins, workers should follow regulations and standards of the country. By following these standards animals welfare can be guaranteed and their health can be improved (Pejman et al., 2019).

Consumers should be aware about ethically produced protein and demands to get ethically produced protein should be increased. Consumers should choose those proteins that are produced in compliance with ethical standards prioritizing animal welfare (Boer et al., 2022).

In summary animal welfare during production phase is multifaceted approach that involve various approaches that have discussed above. By prioritizing animal welfare, we can get ethically produced and sustainable protein.

3.2 Animal welfare consideration in development phase

A few factors related to animal welfare are taken into account when developing biopharmaceuticals.

- Ensuring that the transgene is expressed only in the desired tissues to avoid harm to the animal
- Selecting animals that are well-suited for biopharming, such as those with high reproductive efficiency
- Implementing human endpoints for animals that develop adverse reactions
- Minimizing animal suffering through proper husbandry and care
- Considering the ethical implications of genetic modification
- Measuring good feeding, good housing, and good health
- Ensuring that animals are handled humanely and do not receive unnecessary constraint throughout the observation

4 Techniques of Creating Transgenic Animals

4.1 Donor animals and foster mothers

Donor animals and foster mothers play crucial roles in biopharming. Both are essential for the successful production of transgenic animals.

Donor animals:

- Provide genetic material (e.g., DNA, sperm, or eggs) for genetic engineering
- Typically males, used for their genetic material to produce transgenic offspring
- Selected based on desirable traits, such as high milk production or specific protein expression

Foster mothers:

- Surrogate mothers that carry and give birth to transgenic offspring
- Provide a nurturing environment for the developing young
- Often used when the genetic mother is unable to carry the pregnancy to term or produce viable offspring

There was a general demand for restrictions on meddling with life after Dolly the sheep was cloned. Dolly was not a typical sheep. In a very real way, she had no father. She began as a cell removed from her biological mother's udder. The nuclear genome of a sheep ovum was removed before this cell was introduced, and it was then altered such that it merged with the ovum's cytoplasm, or "egg-mass," to form an embryo. After the embryo was implanted, the foster mother became pregnant and had a typical pregnancy under strict supervision, giving birth to Dolly as shown in Figure 4.1 (Lassen et al., 2006).

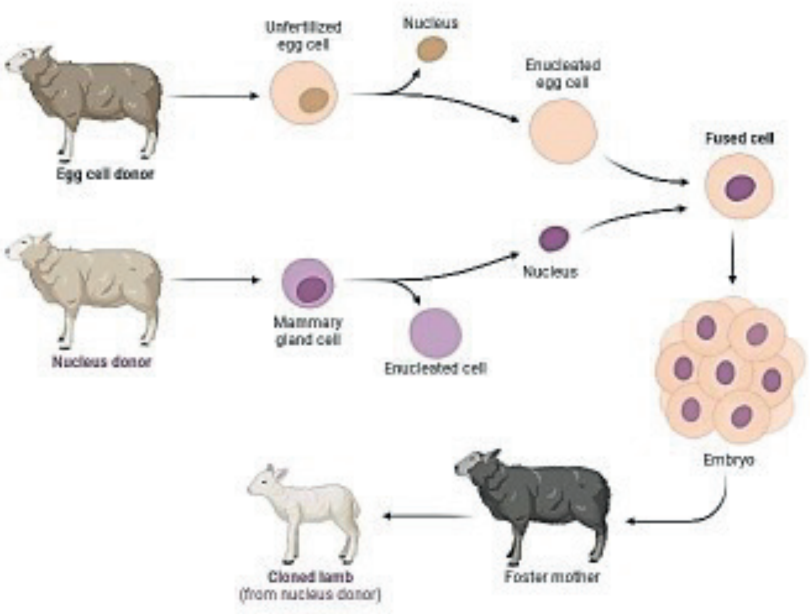

Figure 4.1: Donor animal and foster mother showing by dolly birth using cloning (Shakweer et al., 2023)

4.2 DNA Microinjection

Direct DNA insertion into the pronuclei of fertilized eggs can be referred to as microinjection. This technique is popular because it can target specific genes and has a reasonably high effectiveness. Despite its effectiveness, this method's failure rate is high because DNA integration into the host genome is unpredictable (Wolf et al., 2000). The success rate of this technique varies between species (Pinkert C, 2002). Pollock et al, 1999 explained the production of recombinant proteins now has new options thanks to the capacity to alter animal genomes using microinjection technologies manufacturing human recombinant protein drugs with the intention of using the milk from transgenic farm animals (Figure 4.2).

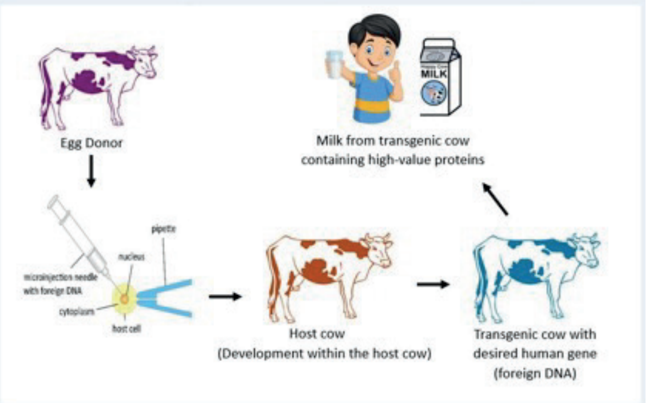

Figure 4.2: Transgenic cow producing high quality milk by DNA Microinjection

4.3 Embryonic stem (ES) cells

The capacity of undifferentiated stem cells to differentiate into other form of cell, including germ and somatic cells, resulting in the creation of an entire organism, is one of their characteristics. It has long been the practice to produce embryonic stem cells in vitro (Yamanaka S, 2020). Homologous recombination is used to introduce the correct DNA sequence into an embryonic stem (ES) cell culture in vitro. ES cells can be transfected with foreign DNA, and clones containing the foreign gene can be produced by using a selective gene. Transgenic chimeric mice could be created using these cells (Figure 4.3).

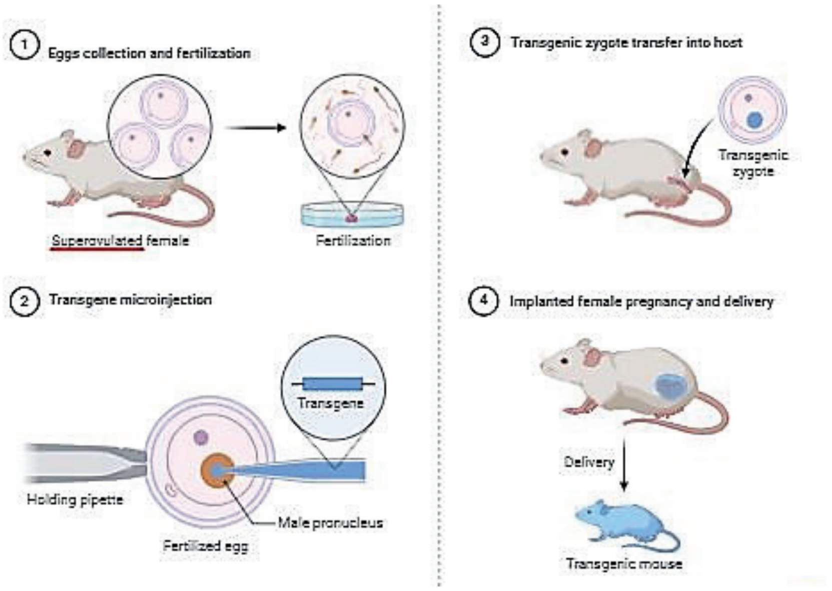

Figure 4.3: DNA microinjection technique using embryonic stem cells.

In these animals, the transgene is mosaic (Kim GB, 2019). When leukemia inhibitory factor (LIF) is added to a culture of stem cells in the lab, the cells remain undifferentiated. ES cells have the ability to differentiate into diverse tissues independently due to the lack of LIF (Figure 4.4).

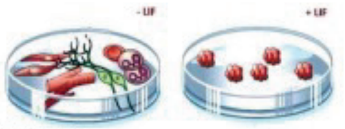

Figure 4.4: In vitro cultured embryonic stem cells (Shakweer et al., 2023).

4.4 Gene transfer into gametes

Sperm mediated gene transfer technique (SMGT) The first indication that foreign DNA might be integrated into untreated sperm was given by Brackett et al., 1971 and Lavitrano et al.1989 for the first time (a) mouse epididymal sperm can spontaneously incorporate plasmid DNA molecules, (b) Through in vitro fertilization techniques with sperm cells that contain plasmids, genetically edited progeny can be produced, (c) Exogenous DNA sequences are expressed in the progenitors (d), and the fertilized ovum incorporates exogenous DNA brought by the sperm as depicted in Figure 4.5 (Catherine et al., 2003; Magnano AR et al., 1998).

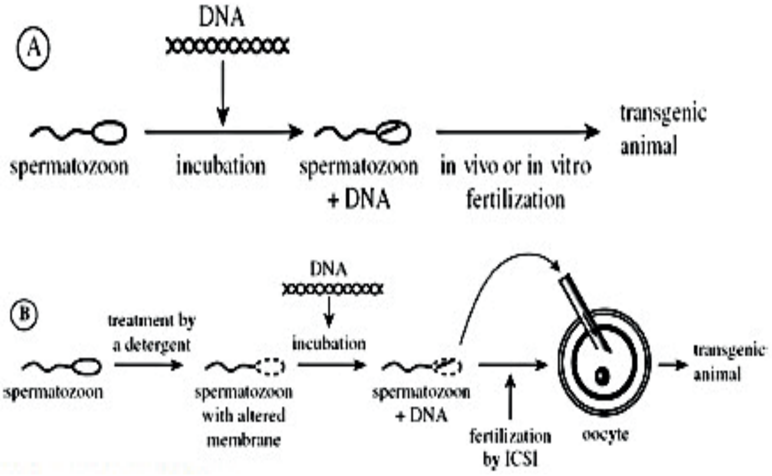

Figure 4.5: Sperm mediated gene transfer technique (Shakweer et al., 2023).

4.5 Somatic Cell Nuclear Transfer (SCNT)

The process known as Somatic Cell Nuclear Transfer (SCNT) involves transferring the nucleus of a genetically altered somatic cell into an enucleated oocyte (egg). Animal cloning is another usage for this technology, which can also be used to generate transgenic animals that express recombinant proteins (Tian XC et al., 2003). This technology gained notoriety with the cloning of Dolly the sheep and allows precise genetic modifications (Figure 4.6).

The process entails moving the nucleus of a somatic cell into the cytoplasm of an enucleated egg, where it will be reprogrammed to form a zygote by components found in the egg's cytoplasm. (BallP J. H and Peters A. R, 2004; Campbell KH, 1996; Wilmut I and Whitelaw CBA, 1994). Mammals require the zygote to be artificially inserted into the uterus of a surrogate mother. (Camara D et al., 2008; Denning C, 2001). Homologous recombination is now the only method available for gene substitution in somatic cells, which are used produce build animals. In sheep, gene inactivation has been accomplished (McCreath KJ, 2000) and pigs (Lai L and Prather RS, 2002). According to findings in cattle, sheep, goats, and pigs, most animals cloned from transfected somatic cells express the transgene (Table 4.1).

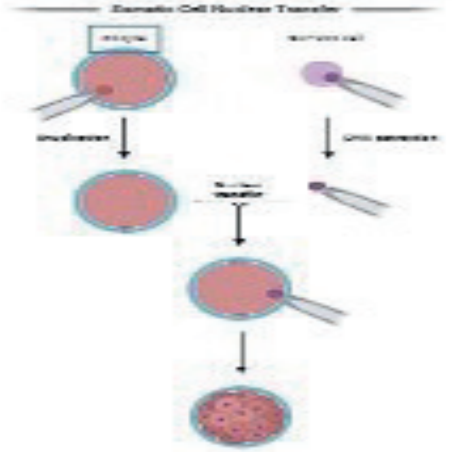

Figure 4.6: Nuclear transfer method using somatic cells

Table 4.1: An analysis of transgenic cattle species and their contribution to the synthesis of protein

Addition/ deletion of Genes	Animal	Performance benefits	References
β and κ casein	Bovine	The expression of casein protein has risen resulting enhanced milk's protein content	Laible G et al., 2016
Intestinal lactase	Bovine	There is less lactose in milk now for lactose intolerant individuals	Marshall A, 1999
Lysostaphin	Bovine	Reduced usage of antibiotics due to resistance to mastitis	Cardoso CV et al., 2019
β-Lactoglobulin	Bovine	Increased growth and disease resistance in calves fed milk along with high levels of protein in the milk resulting less antibiotic use and better health benefits	Sun Z et al., 2018
Growth hormone	Ovine	enhanced feed conversion efficiency, faster rates of lactation (leaner meat), decreased carcass fat content, and increased growth rates	Rexroad et al., 1991

Addition/ deletion of Genes	Animal	Performance benefits	References
Myostatin	Ovine	Myostatin expression was downregulated in sheep, although muscle mass increased (leaner meat)	Hu S et al., 2013
Insulin-like growth factor 1	Porcine	better development rate and less fat content in the carcass	Monaco MH et al., 2005
α-Lactalbumin	Porcine	Health and growth rate of the piglets have both improved	Noble MS et al., 2002

4.6 Retroviral Vectors

Genetic material is inserted into the host genome using retroviral vectors. By integrating with the host DNA, these vectors guarantee consistent gene expression. Transgenic cattle may be produced with this technique, which is especially helpful. Although significant levels of gene expression may be achieved with this approach, the possibility of viral pathogenicity may raise safety concerns (Shakweer et al., 2023).

4.7 CRISPR-Cas9 Gene Editing

The latest advancement in genetic engineering, CRISPR/Cas9 allows for precise editing of the genome by creating targeted double-strand breaks in DNA, thereby facilitating the insertion or deletion of specific genes. This technology has revolutionized genetic engineering, providing a highly efficient and versatile tool for creating transgenic animals. (Javaid D et al., 2022; Adli, 2018).

5 Applications of Transgenic Animals

These include transgenic animals used for outputting proteins;

5.1 Pharmaceutical Proteins

Transgenic Animal Derived Recombinant Proteins for the production of therapeutics, vaccines, and markers on face of crucial public health concerns, recombinant proteins from transgenic animals are mandatory. One example is human antithrombin the, which is produced in goat milk and used to treat blood clotting disorders (Table 5.1).

Therapeutic In some cases, transgenic animals are also used to produce therapeutic proteins, such as insulin, growth hormones, and antibodies. Often these proteins are extracted from animals' milk, blood or urine (Echelard et al., 2009).

Insulin: Originally made from the pancreases of slaughtered animals, insulin is now produced by bacteria and yeast that have been genetically engineered to synthesize human insulin and is no longer obtained from animals four-legged animals.

Antithrombin: The milk of transgenic goats contains antithrombin, which can be used to prevent blood clots occurring in the veins and arteries of patients with hereditary antithrombin deficiency.

Human Growth Hormone (Protein): Produced in transgenic cows and goats, it tends to be more stable and is a cheaper resource as compared to traditional collection.

Table 5.1: Pharmaceutical proteins and their sources (Echelard et al., 2009).

Pharmaceutical Proteins	**Source**
Insulin	the pancreas of slaughtered animal, bacteria, and yeast
Antithrombin	the milk of transgenic goats
Human Growth Hormone	transgenic cows and goats

5.2 Nutritional Proteins

It is possible to design transgenic animals to generate proteins with higher nutritional content, better disease resistance, or faster growth rates. This could lead to more efficient and sustainable farming practices. Additionally, transgenic animals can be used to produce proteins for human and animal nutritional supplements. These proteins can enhance the nutritional value of food.

- Human lactoferrin has been added to the milk produced by transgenic cows, improving the milk's nutritional value and antibacterial capabilities (van Berkel et al., 2002). Transgenic animals could lead to more cost-effective and ecologically sustainable manufacturing methods for industrial enzymes and other proteins (Humphrey et al., 2002).

5.3 Industrial Enzymes

Industrial enzymes, such as those required for food processing or the production of biofuel, can be produced using transgenic animals. These enzymes could be more reasonably priced and environmentally friendly than those produced using more traditional methods. Transgenic animals produce enzymes like phytase, which increase the bioavailability of phosphorus in animal feed (Table 5.2).

5.3.1 Antithrombin-Producing Goats Transgenic goats have undergone genetic modification to generate antithrombin in their milk, which is used to treat patients with antithrombin deficiency (Echelard et al., 2009).

5.3.2 Human Lactoferrin Produced by Cows This milk protein with antimicrobial properties is being produced in transgenic cows to improve baby formula (van Berkel et al., 2002).

5.3.3 Human Lysozyme Produced by Chickens Lysozyme, an antibacterial enzyme produced by transgenic chickens, may be used to treat bacterial infections in humans and other animals (Zhu et al., 2010).

Table 5.2: Role of transgenic animals in protein production

Proteins produced by transgenics	**Benefits**	**References**
Goats Producing Antithrombin	for the purpose of treating individuals who lack antithrombin	(Echelard et al., 2009)
Cows Producing Human Lactoferrin	to enhance infant formula milk with antibacterial qualities	(van Berkel et al., 2002).
Chickens Producing Human Lysozyme	to treat bacterial illnesses in humans and other animals	(Zhu et al., 2010).

6 Ethical and Regulatory Considerations

The ethical and legal issues surrounding the manufacturing of proteins from transgenic animals are numerous. Although regulations vary by country, they all often require thorough testing to ensure safety and efficacy. Animal welfare, possible effects on biodiversity, and the moral ramifications of genetic engineering are examples of ethical issues. The adoption and commercialization of these technologies are also significantly influenced by public perception. (Babale YK and Atoi EN, 2021)

6.1 Ethical Issues

Concerns regarding animal welfare, genetic variety, and environmental effect are raised by the production and application of transgenic animals. Ethical rules and standards need to be thoroughly thought through in order to handle these difficulties.

6.2 Regulatory Framework

Numerous national and international organizations govern the usage and production of transgenic animals. Rules guarantee the items effectiveness and safety as well as the wellbeing of the animals involved (Ormandy EH et al., 2011).

6.3 Public Perception

The advancement and use of this technology may be influenced by how the general public views transgenic animals. To address public concerns and promote acceptance, it is imperative to prioritize transparency, education, and involvement (Einsiedel EF, 2005).

7 Risk assessment of animal pharming

In August 2006, the European Commission unequivocally sanctioned ATryn® as the inaugural animal pharming product intended for human use. ATryn® is presently progressing through phase III clinical trials in the USA. More pharmaceuticals derived from transgenic animals are in advanced stages and are expected to be commercialized soon. These innovative production platforms for pharmaceuticals could potentially impact the environment, posing risks to both animal and human populations. Pharmaceutical production will now occur outside the laboratory, and in some cases, it will be entirely uncontained. Pharming animals may lead to the release of active products into the environment, and GM animals could disperse and impact other ecosystems (Rehbinder et al., 2009)

The new production platforms pose a challenge to current regulations governing traditional pharmaceutical products, GM animals, and animal welfare. The existing legislation pertaining to these matters is intricate, at times overlapping and at others inadequate. Consequently, the implementation of new procedures and regulations is imperative (Ormandy EH et al., 2011). The purpose of the upcoming chapters is to address the adverse environmental consequences associated with pharmaceutical production in genetically modified animals and to offer an overview of the current approaches used to evaluate these effects.

7.1 Biological Risks

7.1.1 Genetic stability and mutation risks

Biological risks in animal pharming mainly concern the genetic stability of the modified organisms. Genetic mutations or unexpected changes can emerge, potentially causing detrimental effects on the animals or the effectiveness of the produced proteins. It takes extensive rigorous testing and observation throughout the animals' lives to guarantee genetic stability (Van Reenen CG and Blokhuis HJ, 1997).

7.1.2 Impact on animal health and welfare

The welfare and well-being of the participating animals pose a serious biological risk. Unintended physiological effects resulting from genetic alterations, leading to suffering or decreased quality of life for the animals. Ethical considerations need careful attention to animal welfare, with techniques in place to alleviate any negative impacts (Clark J and Whitelaw CB, 2003).

7.2 Environmental Risks

The possible effects of genetically modified animals escaping into the environment and being used for pharmaceutical manufacture would depend on a number of things. If they would present an urgent risk of harm, that should be taken into account first. If they were afflicted with an infectious sickness, for example, the circumstances would be the same. Furthermore, if ingested by humans or wildlife, it could have harmful effects. This is unlikely, and the potential for toxicity would be influenced by the bioactivity of the expressed protein, as well as the sites and levels of expressions. Large mammals can be kept from escaping by employing straightforward physical containment techniques like double fence. There will always be a chance of escape because of things like criminal activity, but in houses with barrier features, escapes might be virtually completely avoided. Small mammals, fish, and insects may be easier to get away from and unrecoverable (Nash et al., 2004; Van et al., 2011).

7.2.1 Potential for cross-breeding with wild populations

Environmental risks may arise from the possibility of genetically modified animals mating with wild populations. Such events could result in the unintended dispersion of altered genes into the environment, causing disruption to ecosystems and natural genetic variation. To effectively manage this issue, we must implement strict containment measures, such as physical barriers and regulated breeding environments (Kapuscinski AR and Hallerman EM, 1991).

In the event of animals used for pharming escaping, a crucial consideration is to assess their potential for long-term survival and ability to reproduce in a natural environment without human intervention (Rehbinder E., et al. 2009). For instance, it is highly improbable that domestic sheep and cattle would disappear, survive, and reproduce. It is true that laboratory rabbits and domestic hens are vulnerable to illness and predators . Their phenotype probably cannot compete with other competitors or conspecific wild kinds. Nevertheless, the environment into which the animals escape may have some bearing on the response to this query. The FDA advises neutering transgenic animals in order to lower the possibility of accidental reproduction leading to a non-transgenic population. In the event that animals are able to get out, they could cause environmental disruption and turn into pests.

7.2.2 Ecological impacts and containment strategies

An extensive assessment of the ecological consequences of animal pharming is also necessary. The introduction of genetically modified organisms into the ecosystem could have unforeseen consequences that upset biodiversity and ecological balance. Continuous environmental monitoring and impact evaluations are essential for identifying and reducing these risks (Muir et al., 2002).

7.3 Ethical and Societal Risks

7.3.1 Ethical considerations and public perception

The discussion of animal pharming revolves around ethical concerns. Concerns about the treatment of animals and the naturalness of genetic changes can shape public opinion. Transparent communication of the advantages and disadvantages as well as the moral principles governing the use of animal pharmacology in research and practice are necessary to allay these issues (Kaiser, 2005).

7.3.2 Regulatory and legal challenges

Legal and regulatory obstacles are also important. Regulations pertaining to animal care and genetic alteration differ between nations, therefore it's critical to arbitrate such variations to guarantee public acceptability and compliance (Van der Meer P and Tzotzos GT, 2011).

7.4 Economic Risks

7.4.1 Market volatility and investment risks

Market dynamics and financial risks can have an impact on how profitable animal medicines are. Market volatility can have a financial influence on the manufacture of high-value proteins and pharmaceuticals, and the initial investment costs are sometimes substantial. A thorough cost-benefit analysis is necessary to determine whether animal pharmaceutical projects are financially viable (James, 2000).

7.4.2 Cost vs. benefit analysis in production

Investors and companies must consider the risk that methods employed today will become obsolete due to future technology advancements, necessitating ongoing research and development to stay competitive. Achieving a balance between the potential for significant medical and pharmacological benefits and these financial risks is critical to the success of animal pharmaceutical programs (Kalaitzandonakes et al., 2007).

Conclusion

To sum up, animal pharmaceutics holds considerable promise for the production of valuable proteins and pharmaceuticals. Nevertheless, it is linked to some hazards that require cautious evaluation and handling. A gene encoding a therapeutic protein is inserted into an animal's genome during transgenesis to enable the production of the protein by the animal. This strategy offers a number of advantages including high yields, correct folding, Post-translational modifications and low cost. A few instances of therapeutic proteins created via transgenesis are as follows:

- Insulin (diabetes management)
- Human growth hormone (therapy for growth hormone deficiency)
- Factor VIII (medication for hemophilia A)
- Enzyme replacement therapy (lysosomal storage disease treatment)
- Vaccines made from genetically modified chickens
- Genetically modified goats produce ATryn (antithrombin III)
- Genetically modified rabbits produce Ruconest (C1 esterase inhibitor)
- Sebelipase alfa, or kanuma, grown in genetically modified chickens

These medications are used to treat a variety of uncommon genetic conditions, including lysosomal acid lipase deficiency, hereditary angioedema, and hereditary antithrombin deficiency. Benefits of biopharmaceutics include enhanced productivity, lower expenses, and better-quality products. But it also brings up moral and environmental issues with genetic engineering and animal welfare.

Future Directions

Transgenic animal protein production has substantial advantages for commerce, agriculture, and health, among other areas. But it's crucial to strike a balance between these advantages and moral considerations as well as government regulation. Because of the advances in genetic engineering and biotechnology, there is great potential for the synthesis of transgenic proteins in the future. The manufacture of transgenic animal proteins seems to have a promising future due to advancements in gene editing techniques such as CRISPR/Cas9. Emerging uses include developing complex biopharmaceuticals and improving the nutritional content of animal products. But in order to use this technology effectively, a number of problems must be handled, including ethical quandaries, legal restrictions, and technological limitations.

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About the Author

Dr. Sobia MUSHTAQ received her PhD in 2015 in biochemistry/molecular biology from Quaid-i-Azam University, Islamabad, Pakistan. She is working at University institute of Biochemistry and Biotechnology, Arid Agriculture University, Rawalpindi. Her research interests includes working on molecular mechanisms of diseases especially cardiac disorders and diabetes, nano-particles delivery as drugs to control cardiac disorders and use of microRNAs as therapeutic agents. She has publications in peer-reviewed journals. She also has written many book chapters for BEd course Biology at Allama Iqbal Open University, Islamabad.

E-mail: sobiamushtaq26@gmail.com, ORCID: 0009 0001 2086 8304

Dr. Shumaila ZAIB earned her Doctor of philosophy in Biotechnology from Fatima Jinnah Women University, Rawalpindi Pakistan. She is currently working as Assistant professor in the department of Biotechnology, Faculty of biosciences, International Islamic University Islamabad, Pakistan. Email: shumaila.zaibfju@gmail.com ORCID: 0000-0002-8909-9830

Minahil JAVAID holds a Master's degree in Biochemistry & Molecular Biology. Her research interests focus on human metabolic diseases and the intricate molecular mechanisms that underpin those diseases. She currently serves as the Science Coordinator at Siddeeq Public School, a prestigious institution in the twin cities of Pakistan.

Email: minahiljavaid@gmail.com ORCID: https://orcid.org/0000-0002-4781-4496

Dr. Muhammad SAFDAR earned his PhD in molecular biology and genetics from Gaziantep University, Turkey. He is a lecturer in the Breeding and Genetics department at Cholistan University of Veterinary and Animal Sciences (CUVAS), Bahawalpur, Pakistan. His research interests are molecular genetics and genomics, nutrigenomics, nano-genomics, bioinformatics, biotechnology, and their applications. He has published more than 70 research articles in national and international journals. He has also written many book chapters as well as an edited book. He is an associate editor for international journals.

E-mail: msafdar@cuvas.edu.pk , ORCID: 0000 0002 3720 2090

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VACCINE ADJUVANTS: ENHANCING IMMUNE RESPONSE IN LIVESTOCK VACCINATION

Muhammad Muzammil NAZIR

Asma ASHRAF

Derya Karatas YENI

Vaccines are vital agents in the fight against infectious illnesses in animals. The majority of the components of next-generation veterinary vaccines will be either subunit or inactivated bacteria or viruses. The choice of an appropriate adjuvant that promotes the activation of adaptive immune responses is one of the most crucial phases in the creation of vaccines. The creation of novel and enhanced veterinary vaccine adjuvants that promote the right immunity—such as T cell immunity for intracellular infections and cancer vaccines—is desperately needed. Structure–function relationships that are helpful in the development of novel adjuvants have been established in a number of adjuvants through the identification of chemical groups that interact with particular cell toll-like receptors (innate immunity) or receptors for co-stimulatory ligands (adaptive immunity). Adjuvants are substances, mixtures, or macromolecules that boost non-specific immunity and, when combined with one or more antigens, can modify the nature of the immune response as well as strengthen it. To give the safest stimulation, adjuvants' potential and toxicity must be matched. Based on their main modes of action, adjuvants can be generally classified into two classes: "immunostimulatory adjuvants" and vaccine delivery methods. Vaccine delivery vehicles, such as emulsions, microparticles, ISCOMS, and liposomes, are typically particulate and serve the primary purpose of delivering associated antigens to antigen-presenting cells (APCs). On the other hand, immunostimulatory adjuvants, which activate innate immune system cells, are mostly obtained from pathogens and frequently represent pathogen linked molecular patterns, such as LPS, MPL, and CpG DNA. Adjuvants available on the market and experimental mixtures that focus on mineral salts, emulsions, components produced from bacteria, saponins, and various other immunoactive substances. Furthermore discussed are the various adjuvants' modes of action, instances of adjuvant combinations in a single vaccine formulation, and difficulties encountered during the study and creation of adjuvants for veterinary vaccines. According to certain research, nanoparticles exhibit a remarkably greater capacity for adjuvant action than microparticles. Nanoparticles also work better in targeted antigen delivery because they can more easily pass through biological barriers than nanoadjuvants, which inactively target antigen-presenting cells (APCs) and alter their chemical surface. Adjuvants for immunity work by boosting particular immune responses to vaccinations. Adjuvants, such as copolymer adjuvants, can affect various aspects of immune responses, such as the type of cell-mediated immunity, the frequency of genetic non-responders, and the specificity, titer, duration, memory, class, isotype, and avidity of antibodies. A more sophisticated approach to the study of adjuvants as agents is encouraged. Adjuvants are needed in order to elicit an immunological response from inactivated vaccinations. Whether the immunological response is beneficial, detrimental, or ineffectual depends on the adjuvant or immune enhancer selected.

1. Introduction

One of the best and most affordable methods of preventing a wide range of infectious diseases is vaccination. It seeks to provide persistent protection against infection and elicit an immune response unique to the pathogen (Lee & Nguyen, 2015). Conventional vaccines consisting of live attenuated or inactive pathogens can effectively and long-lastingly stimulate the immune system; however, these vaccines come with a number of safety concerns, such as the potential for partial or full antigen inactivation or mutations that could restore pathogenicity. Subunit vaccinations, on the other hand, are less immunogenic but safer. Thus, adjuvants are required for subunit vaccinations in order to boost immunogenicity (Park et al., 2016). According to Lee and Nguyen (2015), adjuvants are substances that are added to vaccination formulations in order to boost the immunogenicity of antigens. They allow immunization programs to utilize fewer doses of vaccine and facilitate the use of smaller antigen doses (Coffman et al., 2010). Adjuvants also lessen the possibility of vaccines degrading after injection or storage, which contributes to their increased durability. They also affect how quickly, strongly, and long-lasting the immune responses are (Schijns & Lavelle, 2011).

According to (Aucouturier et al., 2001), the best way to keep farm animals safe from infectious disease losses is to vaccinate them widely. Historically, the main components of veterinary vaccinations have been live attenuated pathogens, fully inactivated organisms, or inactivated bacterial toxins (Chroboczek et al., 2014). These methods have generally been effective in the development of vaccines because they induce the production of antibodies that neutralize viruses or bacterial toxins, prevent germs from attaching to cells, or encourage phagocyte absorption of the microbes. Even while veterinary vaccines contain attenuated variants of the disease, there are still worries that these could occasionally return to the virulent form. As an alternative to these vaccines, using killed organisms or sections of them offers a lower level of protection than attenuated forms. Furthermore, it has been generally shown that non-living vaccines are poor at eliciting strong cell-mediated immunity (CMI), especially Th1-specific CMI. Th1 responses are distinguished by the generation of g interferon (IFN), and Th2 responses are mostly based on the cytokine production of T helper cells in mice. Furthermore, Live attenuated vaccines can also infect immunocompromised animals, and many viruses are difficult to cultivate in culture, making the creation of inactivated vaccines impractical. However, live immunizations can trigger the formation of cytotoxic T lymphocytes (CTL) (Bowersock & Martin, 1999).

The 1800s saw the introduction of vaccination, which offered previously unheard-of advantages for veterinary and human medicine. Many illnesses that once plagued humans and animals are now under control or prevented via vaccinations, including poliomyelitis, smallpox, distemper, and parvovirus enteritis. The accomplishments of early vaccine scientists like Pasteur and Jenner are widely acknowledged. Parallel discoveries that increased the effectiveness and, in certain circumstances, even feasibility of vaccination is less frequently reported. In the 1920s, (Ramon, 1925) discovered that horses with injection site abscesses had higher antibody titers after vaccination. Later, he and other researchers found that compounds made of tapioca, agar, lecithin, saponin, and aluminum could all be injected to increase titers (Ramon, 1926) Freund et al. (Freund et al., 1937) developed a very potent mixture of water, mineral oil, and killed mycobacteria in the 1930s. These findings served as the foundation for the creation of adjuvants, which are immune-boosting vaccination additives.

Any material that, an immunologic adjuvant is a substance that is added to a vaccine formulation with the overall purpose of accelerating, prolonging, or enhancing certain immune responses to immunization antigens. The Latin verb adjuvare, which meaning to assist or support, is the root of the English word adjuvant Adjuvant mechanisms of action include extending the biological or immunologic half-life of vaccine antigens, improving antigen delivery to antigen-presenting cells (APCs), facilitating the processing and presentation of antigens by APCs, and inducing the production of immunomodulatory cytokines (Lindblad et al., 1997). By modifying cytokine responses, adjuvant formulations can be produced that encourage the development of T-helper type 1 (Th1) or type 2 (Th2) immune responses to vaccine antigens. The use of new adjuvants in conjunction with human candidate vaccines, such as experimental subunit vaccines against tuberculosis, is now being studied in preclinical and clinical studies (Freund et al., 1937). To aid in the clinical evaluation of novel adjuvants, standardized preclinical adjuvant-safety tests are also being developed. Adjuvants for immunology have been produced and tested throughout the majority of this century. In the mid-1920s, Ramon reported that horses with abscesses established at the site of a diphtheria toxoid injection produced higher antitoxin titers than animals without abscesses. Subsequently, he revealed that abscesses in horses caused by injecting foreign chemicals alongside toxoid also increased their antitoxin responses. Using an alum-precipitated diphtheria toxoid vaccine, Glenny (AT, 1926) showed the adjuvant action of aluminum compounds in 1926. Freund (Freund et al., 1937) created a potent immunologic adjuvant in the middle of the 1930s that was made of a water-in-mineral-oil emulsion and included dead mycobacteria as an extra immunomodulator.

Despite being one of the most powerful adjuvants available, Freund's complete adjuvant (FCA) is extremely reactogenic and therefore unsuitable for use in human vaccines. Nonetheless, Freund's incomplete adjuvant—which is devoid of mycobacteria—was utilized in a UK-licensed influenza vaccination and is currently being tested in multiple HIV vaccines. The adjuvant activity of gram-negative bacteria's endotoxins was originally noted by Arthur Johnson in 1956 (O'HAGAN, 1998). In 1974, Ellouz et al. (Ellouz et al., 1974) discovered that muramyl dipeptide was the smallest adjuvant active component of the mycobacteria in Freund's complete adjuvant. Currently, vaccinations based on aluminum salts are the only immunologic adjuvants used in US-licensed products. Nonetheless, hundreds of artificial and natural substances with adjuvant properties have been found. For several decades, a number of these innovative adjuvants have been developed and evaluated in preclinical settings, with the potential to supplement or replace alum in human vaccinations (Vogel & Powell, 1995). Many new adjuvants have been shown to enhance both antibody and cell-mediated immune responses to vaccination antigens more effectively than alum in animal models. Clinical trials comparing the efficaciousness of different adjuvants have been started, and extensive preclinical testing of innovative immunologic adjuvants has been carried out. "Substances used in combination with a specific antigen that produced a more robust immune response than the antigen alone" was how Ramon (1924) first defined immunological adjuvants. A very large range of materials are covered by this broad concept (Vogel & Powell, 1995). However, the primary adjuvant now approved for human use by the US Food and Drug Administration is based on mineral salts containing aluminum (often referred to as alum), despite rigorous study of a vast variety of alternatives over many years. Although alum has a solid safety record, research comparing the effects on people and animals indicate that it is a weak adjuvant for recombinant protein vaccine-induced antibody production and that it generates a Th2 response as opposed to a Th1 response. Since safety issues have impeded the development of numerous adjuvants since the introduction of Freund's adjuvant and alum more than 50 years ago, toxicity is a critical issue in adjuvant development (Bowersock & Martin, 1999). Although a large number of experimental adjuvants have progressed to animal studies and some have shown great potency, the majority have shown to be too toxic for everyday use. The reactogenicity of the injection site, the adjuvant's removal or biodegradation, and the length of retention at the injection site are some of the key factors that may dictate the usage of these chemicals for veterinary purposes. Adjuvants that cause only minor local and systemic side effects will be approved for use in conventional prophylactic immunization in healthy animals. Adjuvant development also needs to consider practical factors such stability, simplicity of manufacture, cost, and suitability for a variety of vaccines. A few instances of the several adjuvant classes under evaluation for use in human and animal vaccinations against infectious diseases (Bowersock & Martin, 1999).

2. The Discovery of Adjuvants

The finding that an adjuvant added to a vaccine can boost immunity was coincidental, as is the case with many significant medical discoveries. Horses with an abscess at the injection site produced more tetanus and diphtheria anti-sera, according to French veterinarian Gaston Ramon's observations (Di Pasquale et al., 2015). He injected starch, breadcrumbs, or tapioca to create sterile abscesses at the injection site using inactivated toxin, which increased the production of anti-sera. This supported the theory that chemicals that might aggravate the injection site locally might also boost anti-sera yield. Alexander Glenny discovered aluminum salts' immune-boosting qualities about the same time he was conducting research in London with associates. The year 1932 saw the introduction of aluminum as the sole adjuvant in human vaccines, a position it held for about seventy years. Aluminum's immunological mode of action is still not well known, despite its widespread and ongoing use (Marrack et al., 2009). Aluminum adjuvants are appropriate for vaccinations that target pathogens that are mostly eliminated by antibodies since they primarily work to enhance the formation of antibodies. Intracellular pathogen infection has not been successfully prevented by aluminum-adjuvanted vaccinations. Freund's incomplete adjuvant, a mineral oil-in-water emulsion, was another early effort at an adjuvant and was deemed too reactogenic for continuous usage in humans. Adjuvants are currently found in more than 30 licensed vaccinations from various manufacturers and have been used for more than 90 years. Adjuvants are not required for all vaccines. Because they cause a mild infection in recipients and elicit an immune response akin to that caused by infection with wild-type strains, live-attenuated vaccines are effective because they can trigger innate immunity, which in turn triggers adaptive responses that successfully eradicate the pathogen. A heterogeneous blend of different antigens and other pathogen components that function as intrinsic adjuvants have made some inactivated whole-pathogen vaccinations effective. These vaccinations are not appropriate, nevertheless, in situations where the pathogen cannot be cultured in culture or in which the natural infection does not produce lifelong protection (Coffman et al., 2010).

3. Major Types of Adjuvants

There are hundreds of compounds having adjuvant activity that have been discovered since the first adjuvants were discovered in the 1920s. Many of the adjuvants that identified are still in use. The only adjuvants permitted in human immunizations until recently were alum compounds. Animal vaccinations were made with both oil and alum emulsions. Sometimes a powerful adjuvant is needed and inflammation is not a major adverse effect, Freund's incomplete adjuvant (FIA), which is devoid of mycobacteria, is employed. Because of its toxicity, Freund's original emulsion—known as Freund's complete adjuvant, or FCA—was discontinued. Recently, there has been a greater focus on novel adjuvants that have the potential to induce CMI or more powerful immune responses with fewer side effects. There are some vaccines that use proprietary adjuvants, the details of which are not made public (AT, 1926).

4. Role of adjuvants in veterinary vaccine development

Several strategies can be employed with adjuvants to modify antibody avidity, specificity, isotype, or subclass distribution; (1) boost weak antigens' immunogenicity; (2) accelerate and prolong the immune response; (3) activate CTL; (5) encourage the development of mucosal immunity; (6) boost immune responses in immunologically immature or senescent individuals; (7) lower the dose of antigen in the vaccine to lower costs; or (8) help overcome antigen competition in combination vaccines (Freund et al., 1937).

5. Types of Immunologic Adjuvants

Adjuvants for immune function can be categorized based on their sources, modes of action, and chemical or physical characteristics. Examples of adjuvant types being developed and tested for use with human vaccinations are shown in Table 1.

Table 1. Different classes of adjuvants for enhancing immune response to vaccines in animals

Immunostimulatory adjuvants	Cytokines, e.g. lL-2, IL-12, GM-CSF, saponins, (e.g. QS21), MDP derivatives, bacterial DNA (CpG oligos), LPS, MPL and synthetic derivatives, lipopeptides
Mineral salts	Aluminium hy droxide, alum inium phosphate, calcium piosphate
Mucosal adjuvants	Heat-labile enterotoxin (LT). cholera toxin (CT),mutant toxins, e.g. LTK63 and L.TR72. microparticles, polymerised liposomes, chitosan
Lipid particles	Emulsions, eg. Freund's (CFA and IFA), ISA 25. 51, 206, SAF. MES9, liposomes, Virosomes, ISCOMS, cochlecates
Particulate adjuvants	PL. G microparticles, poloxamer particles, vins-like particles

6. Modern Adjuvants

In order to solve the pathogen and population-related problems that 21st-century vaccinations encounter, contemporary adjuvants are being created (Wilson-Welder et al., 2009). Therefore, highly developed adjuvants might be able to aid in the prevention of infectious diseases that are significant worldwide but for which effective vaccines have not yet been developed using conventional technology. Improving pathogen detection and evoking a response akin to the innate immune response is a crucial adjuvant role in mitigating the low immunogenicity of subunit vaccines. Adjuvants, when used properly, can extend the duration and breadth of response that can be obtained using pure sub-unit antigen. Improved immune response has a number of practical implications. For example, adjuvants might allow vaccine doses to include less antigen. There may be a reduction in the number of vaccination doses needed to produce immunity as a result of the enhanced immune response. The combined benefits of dosage reduction and antigen sparing may have a significant impact on enhancing the availability of vaccines worldwide. Additionally, adjuvants can boost immune responses in populations—such as young children, the elderly, and immunocompromised individuals—where vaccination responses are generally lower. The selection of adjuvant(s) can influence the innate immune system's initial signal, which in turn can influence the type of adaptive immunological response that is elicited in response to the delivered antigen. This can lead to the preferential activation of specific T-cell responses. According to results that have been published, the adjuvants AS04 and AS03 have direct effects on innate immune cells and effectors rather than adaptive mechanisms. These are typically localized to the injection site and nearby lymph nodes, and they have a brief duration (Didierlaurent et al., 2009).

Adjuvant systems, or adjuvants with many immune-stimulatory molecules, were the next advancement. The creation of the malaria vaccination by GSK served as the proof-of-concept for adjuvant systems. In the mid-1980s, it was discovered that the recombinant RTS,S antigen, which targets the pre-erythrocytic stage of the malaria parasite life cycle, would be a useful antigen for vaccine development. Pre-clinical and human challenge studies were conducted to examine different combinations of immune-stimulatory substances when the adjuvant aluminum proved unsuccessful. Originally, AS02 was chosen, but as clinical development progressed, it became clear that AS01 might offer more advantages than AS02: In comparison to RTS,S/AS02, RTS,S/AS01 appeared to provide stronger clinical protection and elicit higher levels of cell-mediated immune responses in human challenge trials. Children who have received vaccinations have shown to be protected against malaria infection (Bejon et al., 2008). AS01 is the last candidate malaria vaccine that has been tested in Phase III studies. Hepatitis A vaccinations licensed in the mid-1990s were the first to employ an adjuvant other than aluminum; they use a virosome adjuvant system. The spherical phospholipid layers known as virosomes are contained within the lumen or carry bound influenza antigen on their surface. It is possible to modify the virosome's structure and constituent parts to control how it binds to and interacts with innate immune response effectors, hence influencing the start of subsequent adaptive T-cell and B-cell responses (Moser et al., 2013).

Table 2: Immunologic adjuvant Types

Type of adjuvants	References
Gel-type • Aluminum hydroxide or aluminum phosphate • Caleium phosphate	(AT, 1926) (AT, 1926; Gupta & Siber, 1994)
Synthetic • Nonoie block copolimers • Muramyl pepticde analogues • Pelyphosphazene • Synthetic polynueleoites	(Hunter et al., 1994) (Cohen et al., 1996) (Cohen et al., 1996; Payne et al., 1998) (Harrington et al., 1979)
Particulate • Immunostimulatory complexes (ISCOMs) • Liposomes • Biodegradable microspheres • Saponins 4QS-21	(Putkonen et al., 1994) (Richards et al., 1998) (Men et al., 1996) (Newman et al., 1992)
Cytokines • IL 2 • IL 12 • INF-gama	(Odean et al., 1990) (Nunberg et al., 1989; Odean et al., 1990) (Afonso et al., 1994)
Microbial • DNA CpG motifs • Monophosphoryl lipid A • Cholera toxin • Escherichia coll heat-labile toxin • Pertussis toxin • Muramyl dipeptide	(Afonso et al., 1994; Vogel, 2000) (Schneerson et al., 1991) (Holmgren et al., 1993) (Okahashi et al., 1996) (Okahashi et al., 1996) (Lycke et al., 1992)
Oil-emulsion and emulsifier-based • Freund's incomplete adjuvant • ME59 • SAF	(Dhiman & Khuller, 1997) (Dupuis et al., 1998) (Allison, 1998)

Six additional adjuvants have been added to approved vaccinations in the previous 20 years. Following aluminum, oil-in-water emulsions utilizing oils with higher reactogenicity than Freund's original adjuvant are the adjuvants that are most frequently used. Squalene is a naturally occurring and easily digested oil that is used in a number of oil-in-water emulsions. These emulsions elicit strong cellular and humoral immune responses. Certain adjuvant systems comprise mixtures of adjuvants and are especially engineered to boost T-cell immune responses.

The function of adjuvants in both adaptive and innate immunity The immune system reacts to eliminate an antigen that enters the body. The immune system has two response times: swift and sluggish. The body's initial line of defense is the quickly reacting innate immune system, whereas the slower-acting adaptive immune system offers long-lasting immunological responses (Moser et al., 2013). Innate immunity involves the complement system and phagocytic cells. Antigen-mediated activation of T cells and B lymphocytes with antigen-specific surface receptors starts adaptive immunological responses. Both CD4 T-helper (Th) cells and CD8 cytotoxic T lymphocytes (CTLs) are distinct T cell subtypes. Th cells are further subdivided into Th1 and Th2 cells, which are significant subpopulations (Schwendener, 2014). Innate immune cells carry pattern-recognition receptors, or PRRs, which help identify harmful microorganisms. PRRs are classified into several families, such as retinoic acid-inducible gene-1 (RIG-1) like receptors (RLRs), toll-like receptors (TLRs), nucleotide oligomerization domain (NOD) like receptors (NLRs), and C-type lectin-like receptors (CLRs). Although internal NLRs and RLRs are present, antigen-presenting cells (APCs) have surface TLRs and CLRs. PAMPs, short for pathogen-associated molecular patterns, are molecular patterns that are present in harmful microorganisms such bacteria, viruses, fungi, and parasites (Haghparast et al., 2016). APCs can use PRRs to identify PAMPs before to or during an antigen's endocytosis. Antigens are recognized, processed by APCs, and their peptides are then incorporated onto major histocompatibility complex (MHC) molecules. Th cells can be activated by antigen peptides complexed with MHC class II molecules. This can lead to the induction of humoral immunity (the generation of opsonic and/or neutralizing antibodies by B cells) and/or cellular immunity (CTL responses). MHC class I-complexed antigen peptides can directly activate CD8 T cells, inducing biological responses (Schijns & Lavelle, 2011).

Adjuvants often work by stimulating PRRs found in immune cells to activate the innate immune system. Most immunostimulatory adjuvants function as ligands for PRRs and, by direct enhancement of an activation pathway, result in the release of cytokines. The cytokines, chemokines, and costimulatory substances that prime, expand, and polarize immune responses are encoded by genes that are expressed as a result of receptor-ligand interactions. Thus, because of inflammasomes, elements of injured or dying host cells also support the action of adjuvant. TLR ligands in particular are strong immunomodulators that affect a range of immunological responses. TLRs are capable of identifying several elements found in bacteria and viruses. TLR ligands belong to distinct types that include lipid, protein, and nucleic acid components. Different TLR ligands cause different patterns of gene expression in cells, which illustrates how specific adaptor molecules like MyD88 (myeloid differentiation primary response gene 88) and TRIF (toll/interleukin-1 receptor domain containing adaptor protein producing interferon-b) produce distinct TLR signaling pathways (Akira, 2011).

Conversely, adjuvants have the ability to stimulate humoral immunity, T cell responses, or both in order to elicit adaptive immunological responses. While monophosphoryl lipid A (MPL) stimulates a Th1 response, immune-stimulating complexes (ISCOMs) work by increasing the generation of antibodies and balancing Th1 and Th2 immune responses (Akira, 2011) and cholera toxin (CT) induces a Th2 response. Whereas Th2 cells stimulate humoral responses to neutralize external antigens, Th1 cells use cell-mediated immunity. The creation of innovative adjuvants that can elicit protective CD8 T cell responses is fraught with difficulties. To improve the development of functional CD8 T cells, an antigen and a potential adjuvant should be combined in a way that allows the antigen to enter the MHC class I processing pathway, which will activate dendritic cells (DCs) and produce type-I interferon (IFN) . A class I MHC-restricted CTL response was elicited by ovalbumin given by fusion-active virosomes, as shown by a study by Bungener et al. The significance of virosomes as the best antigen delivery vehicle for eliciting cellular immunity against encapsulated protein antigens was also emphasized (Bungener et al., 2005).

7. Adjuvant Mechanisms of Action

The majority of adjuvants have poorly understood methods of action because vaccination typically sets off a complex chain reaction and makes it difficult to discern the adjuvant's primary effect. On the other hand, mechanical explanations for some adjuvants, especially those that rely on a "delivery" mechanism, become easier to suggest if one accepts the concept of spatial immune reactivity, which states that antigens that do not reach the nearby lymph nodes do not elicit reactions (Zinkernagel et al., 1997). If antigens do not produce reactions when they reach the lymph nodes, then any adjuvant that enhances antigen transport into the cells that migrate to the lymph node may boost the response. As a subgroup, dendritic cells are thought to be the main cells that circulate in peripheral organs and serve as "sentinels," absorbing antigens and delivering them to lymph nodes so that T cells can then be exposed to them. While circulating immature DCs are competent at absorbing antigens, mature DCs are effective at delivering antigens to T lymphocytes. Thus, it is thought that in order to generate robust immune responses, it is necessary to promote antigen uptake into dendritic cells, trafficking to lymph nodes, and dendritic cell maturation. Although macrophages can also be used as APCs, dendritic cells are thought to be the most effective type (Zinkernagel et al., 1997).

Adjuvants have different modes of action, therefore the choice of adjuvant to employ with a particular vaccine depends on the desired immunological response as well as the administration method. The first mechanism of adjuvant action to be identified was the depot effect, which happens when gel-type adjuvants, such as aluminum hydroxide, or emulsion-based adjuvants, such as Freund's incomplete adjuvant, associate with antigen and facilitate antigen transport to the draining lymph node, where immune responses are generated. Adjuvants have different modes of action, therefore the choice of adjuvant to employ with a particular vaccine depends on the desired immunological response as well as the administration method. The first mechanism of adjuvant action to be identified was the depot effect, which happens when gel-type adjuvants, such as aluminum hydroxide, or emulsion-based adjuvants, such as Freund's incomplete adjuvant, associate with antigen and facilitate antigen transport to the draining lymph node, where immune responses are generated. Adjuvants that bind to and form particles with tiny antigens, like synthetic peptides, can enhance the immunogenicity of these antigens, which would otherwise be quickly removed from the injection site and draining lymph nodes. Adjuvants may also work by improving the way that antigens are presented. APCs like macrophages and dendritic cells are impacted by immune adjuvants either directly or indirectly. It has recently been demonstrated that dendritic cells internalize the emulsion-based adjuvant MF59 (Baz et al., 2013). Purified saponins, immunostimulatory complexes, and liposomes are examples of novel adjuvants that have been demonstrated to significantly enhance the induction of CD81 cytotoxic T lymphocyte (CTL) responses restricted by the major histocompatibility complex (MHC) class I when compared to when the same antigen is administered alone or in conjunction with conventional alum adjuvants. By introducing antigen into the cytosol for presentation with MHC class I molecules, these adjuvants have the potential to trigger CTL responses. Membrane-active adjuvants that imitate the presentation of antigens during viral infection or live-attenuated vaccine vaccination may be used to transfer antigens into the cytosol (Paavonen et al., 2009).

When antigen is given alone or with alum, it can avoid endosomal antigen delivery and subsequent processing with MHC class II molecules. Antigen supplied to the cytosol can elicit antibody responses predominantly through presentation to CD41 T helper cells . Adjuvants can facilitate the passage of antigen across endosomal membranes into the cytosol following APC consumption of antigen-adjuvant complexes, hence facilitating cytosolic antigen transport and MHC class I presentation. Particulate adjuvants like liposomes can direct antigen toward macrophages or dendritic cells. Adjuvants have the ability to induce APCs to release cytokines that modulate immunity. Adjuvant-induced cytokines influence lymphocytes to primarily stimulate Th1 or Th2 immunological responses (Ahmed et al., 2011; Kundi, 2007). Adjuvants that induce IFN-g and delayed-type hypersensitivity to promote Th1 immune responses also produce IgG subclasses that fix complement and bind with high affinity to Fc-g-I receptors (e.g., IgG2a in mice and IgG1 in humans). These immunoglobulin subtypes are best suited to mediate the complement-mediated lysis and antibody-dependent cell-mediated cytotoxicity effector pathways.

As adjuvants for vaccines, cytokines such as IL-2, IFN-g, granulocyte-macrophage colony stimulating factor, and IL-12 are being studied (Di Pasquale et al., 2015). The immunomodulatory effects of different immunologic adjuvants may be significantly influenced by IL-12, a cytokine that has only been well studied . According to Jankovic et al. (Fox & Haensler, 2013), adding IL-12 to an alum-adsorbed HIV-1 gp120 vaccination caused mice to produce Th1 cytokines as well as

IgG2 and IgG3 antibody responses; the same vaccine, when IL-12 was not added, produced Th2 cytokines and IgG1 antibody responses. Bacterial toxins having adjuvant effect, such as cholera and pertussis toxins, have been shown to increase the generation of IgA and IgE antibodies because they preferentially stimulate Th2-like responses. Th2-like adjuvants have the potential to improve defenses against mucosal viral transmission by increasing IgA synthesis (Fox & Haensler, 2013).

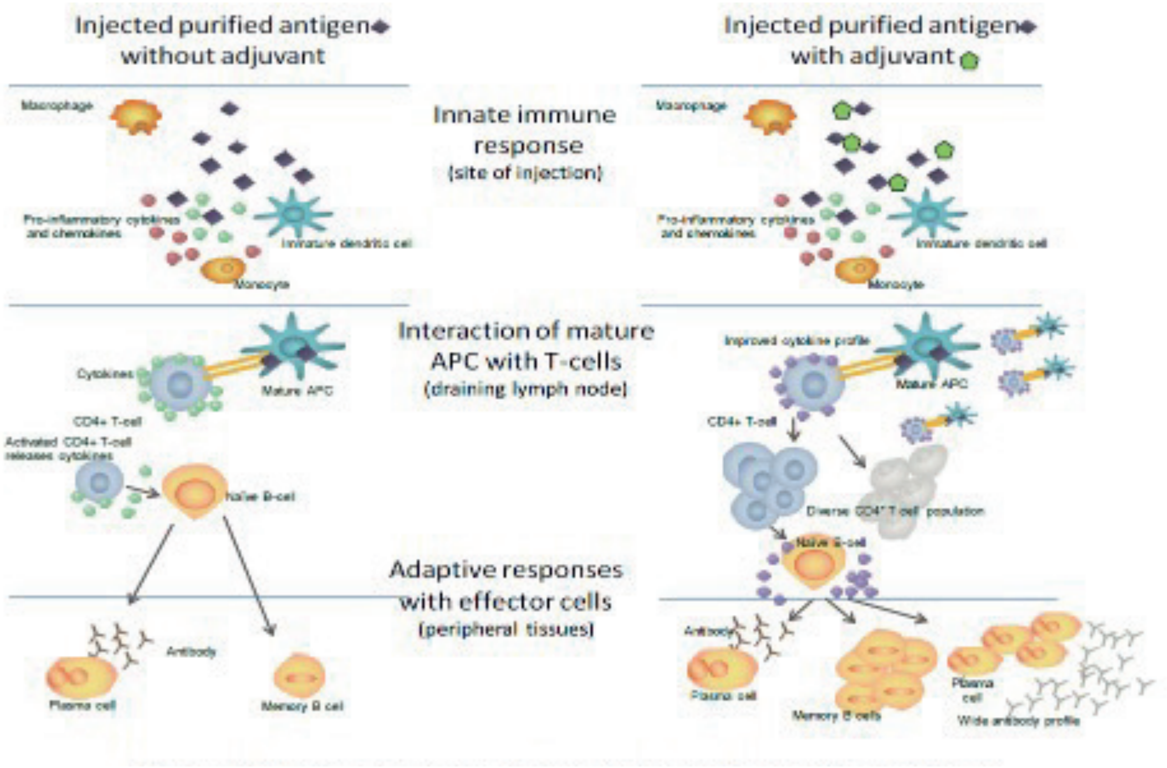

Figure 1: The immune response to vaccination with and without adjuvant (Di Pasquale et al., 2015).

Chemicals, microbiological components, or animal proteins make up the majority of adjuvants. Years of research have left their method of action mostly theoretical. Most seem to work as immunomodulators, to promote antigen stability, or to improve antigen presentation. An adjuvant may function through multiple mechanisms. Adjuvants, for instance, that support the preservation of the antigen's structure can both extend the vaccine's shelf life and enhance its efficacy. This intricate process can be impacted by adjuvants at multiple stages that modify antigen presentation. During an immune response, vaccine antigens need to reach secondary lymphoid tissues, which are usually the lymph nodes. The majority of these antigens are transported to lymph nodes by dendritic cells (Fox & Haensler, 2013). T lymphocytes view epitopes on Major Histocompatibility Complex (MHC) molecules that are processed by these antigen-presenting cells (APCs), B cells, and macrophages. Dendritic cells, macrophages, and B cells also supply additional signals needed to initiate immunization, such as those supplied by the B7 family of molecules. Any adjuvant that improves these cells' capacity to absorb antigens, boosts their production of MHC or costimulatory molecules, or promotes their migration into lymph nodes can boost immunity. Dendritic cells, macrophages, and B cells also supply additional signals needed to initiate immunization, such as those supplied by the B7 family of molecules. Any adjuvant that improves these cells' capacity to absorb antigens, boosts their production of MHC or costimulatory molecules, or promotes their migration into lymph nodes can boost immunity. Adjuvants that trap antigen at the injection site and supply local APCs with it continuously seem to work. The liver's ability to eliminate the antigen may be hampered by this depot effect. Short-term (8–10 days) depots that are adequate to boost immunity can be formed using oil emulsions, such as Freund's adjuvants. Recent developments in microparticle adjuvants have the potential to deliver antigens in pulsed dosages and establish long-term depots lasting 1-6 months. The liver's Kupffer cells may be saturated by other adjuvants.

Adjuvants like these have the potential to enhance the quantity of antigen that reaches APCs by decreasing hepatic absorption of the antigen. Diethyl aminoethyl (DEAE) dextran and high-molecular-weight sulfated dextran are two examples of derivatized polysaccharide adjuvants for which this process has been proposed (Fox & Haensler, 2013).

Adjuvants can enhance the targeting of antigens to APCs. Particulate adjuvants that encourage the development of aggregates, like alum or aluminum salts, make them easier for phagocytosis. By binding to carbohydrate receptors, carbohydrates polymers like mannan or acemannan may be able to direct antigens to APCs. Carrier proteins such as keyhole limpet hemocyanin (KLH), diphtheria or tetanus toxoid, and bovine serum albumin may assist deliver haptens or carbohydrate antigens by recruiting T-helper cells. Additionally, it seems that certain adjuvants direct the antigen into particular APC compartments and affect the CTL response's activation. Interaction with antigens contained in MHC II or MHC I molecules, respectively, triggers T-helper cells and CTL responses. While there is some "cross-presentation" (or crossing of antigens between routes), antigens displayed in MHC II molecules often originate outside of APCs and are taken up by phagocytosis, while antigens shown in MHC I molecules typically originate inside the APC cytoplasm. The majority of adjuvants are capable of efficiently boosting humoral immunity and helper cells. Certain substances, including liposomes, seem to also carry antigens to pathways that result in MHC I molecule presentation and the activation of a CTL response and Cross-presentation might be crucial in some circumstances for producing CTLs.

An further mode of action is immunomodulation. Immunomodulators modify the cytokine network to activate the immune system. Certain adjuvants stimulate the immune system overall and cytokines in particular. Adjuvants typically affect the kind of immunity by raising the levels of specific cytokines and lowering those of other cytokines. Interleukin-2 (IL-2), interferon gamma (INF-g), and IL-12 are cytokines that are linked to Th1 responses in T-helper cells and cell-mediated immunity (CMI). T-helper type 2 (Th2) responses and humoral immunity are linked to IL-4, IL-5, IL-6, IL-13, and potentially IL-10. Adjuvants such as saponins can increase CMI to an antigen that would typically generate just antibodies by altering the balance of these two sets of cytokines. Certain adjuvants that modulate immunity enhance the expression of MHC or costimulatory molecules on antigen-presenting cells (APCs), either by direct means or by inducing cytokines (Fox & Haensler, 2013).

Summary

Several artificial and natural adjuvants can be added to animal immunizations to increase their effectiveness. Some ingredients, such as emulsions, carbomers, cytokines, and polyphosphazenes, have already been included in goods under license, while others, such as aluminum compounds, saponins, and carbomers, are presently being evaluated in experiments. Numerous considerations should be made when selecting or developing adjuvants for animal vaccines, including animal safety, compliance with food safety laws, efficacy in the target animal species, induction of a prompt and durable protective immunity, viability for production scaling up, and, last but not least, cost effectiveness. Even while modern vaccination adjuvants effectively generate humoral or antibody-mediated immunity, cell-mediated immunity is still required for effective defense against many diseases that affect people and animals today, such as tuberculosis and malaria. The available vaccination adjuvants, their effect on eliciting immunological responses, and vaccine adjuvants showing promise in the most current studies are all thoroughly analyzed. Adjuvant vaccines can have a variety of beneficial benefits. These include: (1) increasing the likelihood that vaccinations will reach higher levels of immunogenicity and protective efficacy (e.g., alum for bacterial and viral vaccines); (2) reducing the dose of antigens needed for vaccinations to be effective (e.g., MF59 for influenza vaccines); (3) accelerating and reducing the number of vaccinations needed to achieve effectiveness (e.g., AS04 for hepatitis B vaccine); (4) broadening the repertoire of antibody responses (e.g., MF59 for influenza vaccinations); and (5) modulating the phenotype of T cell responses. The variety of disease targets, small molecule compounds, and patient populations have created an environment that is conducive to the discovery and development of novel adjuvants.

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About the Author

Muhammad Muzammil Nazir[1], Asma Ashraf [1], Derya Karatas Yeni[2]

[1]Department of Zoology, Government College University, Faisalabad 38000, Pakistan;

muzammilnazir51@gmail.com (M.M.N) asmabinm@gmail.com

[2]Department of Microbiology, Veterinary Faculty, University of Necmettin Erbakan, Ereğli,

42310, Konya,Turkey; vhekimderya@hotmail.com (D. K.Y.)

Corresponding author: asmabinm@gmail.com Prof. Dr. Asma Ashraf +92332-6735319

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EMERGING INFECTIOUS DISEASES (EIDS) IN ANIMALS

Shafeeq Ur REHMAN
Muhammad SAFDAR
Faizan ALI
Muhammad Naveed NAWAZ
Minahal FATIMA
Danish RIAZ
Khizar ABBAS
Muhammad EJAZ
Mehmet OZASLAN

Zoonotic diseases in animals also referred to as Emerging Infectious Diseases (EIDs) are proving to be a major threat to health, wildlife, and agriculture. They result in increased morbidity and mortality thus affecting the production of animal products and constitute public health threats because of the zoonotic potential of the diseases in terms of their recent emergence or expansion in area of occurrence. This chapter covers various aspects of EIDs in animals to include the emergence of these diseases, the rates at which new diseases are being discovered, and other related issues. Several studies have however indicated that EIDs are dynamic and complex diseases which will be highlighted in this chapter by evaluating their origins, transmission mechanisms, and the factors that lead to the emergence of the diseases. The increasing occurrence of EIDs is illustrated in the study about wildlife, domestic animals, and changes in the environment to give a view of the zoonotic potential of the diseases as one Health framework. Also, the chapter overviews surveillance approaches, diagnostics, and the need to perform early identification and response to EIDs' effects. Thus, a complex approach should be used to minimize the risks connected with EIDs. Thus, further epidemiological research, and collaboration with practitioners such as veterinarians, and specialists in ecology and other branches of science are crucial for investigating disease processes and finding effective prevention measures. The chapter also focuses on One Health activities that are essential in understanding the interconnection of human, animal, and environmental health.

1. Introduction

Emerging infectious diseases, often known as EIDs, are contagious illnesses that have been identified for the first time in a community or that have been present in the past but are seeing a significant increase in the number of cases or geographic ranges they affect. In other words, these could be novel infections arising from modifications or adaptations in current organisms or established infections that extend to different geographical regions or populations. On the other hand, previously unrecognized infections are emerging in areas undergoing ecological changes, or recurring infections are due to the development of antimicrobial resistance in known agents or failures in public health interventions. The results of the Ninth International Conference on Emerging Infections show that emerging infections account for a minimum of fifteen percent of all human disorders (McArthur, 2019). There is a significant cause for worry over the synergistic communication that occurs between newly developing illnesses and other infectious and non-infectious ailments. An animal receptacle is responsible for the incubation of the organism, which then involves random transmission into human populations. Many newly developing illnesses are zoonotic or synoptic disorders.

Similarly, EID may be transmitted via the air, by vectors, or through food. On the other hand, for an EID to be created, the infectious agent must first be introduced into a population that is susceptible to the illness, and the infectious agent must also be capable of transmitting the disease from one person to another (McArthur, 2019). Infectious illnesses, in contrast to other human diseases, have the capacity to be unexpected and have the potential to cause epidemics affecting the whole world. Additionally, there is the possibility of developing immunity against reinfection despite the fact that they are contagious. Vaccines have the potential to eradicate many diseases, and they may be used to prevent their spread. The conduct of humans and the natural world are interdependent on one another (Fauci & Morens, 2012). The difficulty of EID is related to the influence that they have on people, including pandemics and epidemics, as well as the risks to human health and the stability of the world government (Fauci & Morens, 2012; Morens & Fauci, 2013). It is well known that the emergence of new pathogens is inevitable. However, despite the progress that has been made in the creation of preventative measures, diagnostics, treatments, and vaccinations, the addition of worldwide travel and growing global interdependence has increased the number of challenges that arise when attempting to diagnose and control these illnesses. As emerging illnesses in the current day, the majority of people may relate to the human immunodeficiency virus (HIV) and AIDS, severe respiratory syndrome, and pandemics, such as the H1N1 influenza that occurred in 2009 (Zambon, 2014). Not to mention the profound effect that these illnesses had on the quality of life of those who were affected and their families, the social and economic impact of these diseases was remarkable. It is essential to have a solid understanding of the many types of infectious illnesses. There are three distinct groups of organisms those that are just beginning to emerge, those that have already established themselves and may sometimes reappear, and those that have become endemic in a stable manner (Morens & Fauci, 2013).

Zoonotic illnesses are diseases that are transferred from animals to people by direct contact or through food, drink, or the environment. Zoonotic diseases are responsible for 61% of the infectious organisms that harm humans. The capacity of zoonotic illnesses to spread among people may be broken down into five phases, beginning with the pathogens that are exclusively transmitted between animals and progressing all the way up to the infections that are transmitted to humans (Wolfe et al., 2007). The National Center for Emerging and Zoonotic Infectious Diseases (NCEZID) functions with the purpose of safeguarding individuals from both local and international health hazards. Their coverage encompasses foodborne and waterborne infections, nosocomial infections, antibiotic-resistant infections, lethal diseases like Ebola and anthrax, illnesses affecting immigrants, migrants, refugees, and travellers, zoonotic diseases, and vector-borne diseases transmitted by mosquitoes, ticks, and fleas (Control & Prevention, 2022). The interaction between people, animals, and the environment is a breeding ground for illnesses that have the potential to affect public health as well as the social and economic well-being of the whole world population. Take into consideration the elements that were mentioned before. When people live close to animals and when humans come into touch with animals in new geographical locations, the risk of contracting zoonoses is increased. Some examples are Lyme disease, which is spread by tick bites, and salmonella, which is transferred through contact with hens. The recent occurrences of Salmonella outbreaks in shell eggs, chicken products, raw turkey products, and pet guinea pigs are memorable events (Byrne & Hays, 2021).

Vectors are insects and ticks that feed on blood and are capable of spreading infections from one host to another. These particular illnesses are among the leading causes of death and disease on a worldwide scale. Ticks and mosquitoes are responsible for the transmission of the most frequent illnesses in the United States. These infections include Lyme disease, Rocky Mountain spotted fever, West Nile virus, dengue fever, and Zika virus. In both the United States and across the world, these illnesses are becoming an increasingly severe threat to public health. Both municipal and state health agencies are responsible for monitoring data; nevertheless, there has been a noticeable improvement on a national scale in terms of surveillance, diagnostics, reporting, and vector management, in addition to the introduction of new vaccinations (Rosenberg, 2018).

Due to the existence of the particular vector, EID infections that are transmitted by mosquitoes have the potential to spread locally in the United States. In a similar vein, international travel and immigration have the potential to introduce these illnesses to the United States, where they might potentially be transmitted. The Zika virus, yellow fever, chikungunya virus, and dengue virus are the four viruses that are transmitted by mosquitoes and are considered to be of concern (Table 2) (Rosenberg, 2018).

Table 1: Biological Agents that could present a threat to National Security

Category A	**Category B**	**Category C**
Variola major (smallpox)	*Coxiella burnetti* (Q fever)	Nipah virus
Bacillus anthracis (anthrax)	*Brucella* species (brucellosis)	Hantaviruses
Yersinia pestis (plague)	*Burkholderia mallei* (glanders)	Tick-borne hemorrhagic fever viruses
Clostridium botulinum toxin (botulism)	Alphaviruses	Tick-borne encephalitis viruses
Francisella tularensis (tularaemia)	Venezuelan encephalomyelitis	Yellow fever
Filoviruses	Eastern and Western equine encephalomyelitis	Multidrug-resistant tuberculosis
Ebola hemorrhagic fever	Ricin toxin from *Ricinus communis* (castor beans)	
Marburg hemorrhagic fever	Epsilon toxin of *Clostridium perfringens*	
Arenaviruses	*Staphylococcus enterotoxin* B	
Lassa (Lassa fever)	A subset of list B agents includes pathogens that are food- or waterborne. These pathogens include but are not limited to	
Junin (Argentine hemorrhagic fever) and related viruses	*Salmonella* species	
	Shigella dysenteriae	
	Escherichia coli O157:H7	
	Vibrio cholerae	

2. FACTORS CONTRIBUTING TO EMERGENCE OF OUTBREAKS

From 1940 to 2004, a total of 335 occurrences of Emerging Infectious Diseases (EID) were documented. Approximately 63% of the cases were derived from natural habitats of wild animals, whereas roughly 20% of the cases were transmitted from animal hosts to human hosts by disease-carrying organisms like ticks and mosquitoes (Jones et al., 2008). In the year 2008 and beyond, the discovery of the thrombocytopenia virus and the Middle East respiratory syndrome coronavirus, as well as the unanticipated outbreaks of the Zika virus, yellow fever, and Ebola, caused severe fever. This EID highlights the significance of demographic transitions, global travel and business, and the potential impact of climate change as driving forces (Van Doorn, 2014). The following are examples of biological, social, and environmental factors, all of which are directly connected 1) The modification and adaptability of microorganisms (for example, the genetic drift and shift in influenza A), 2) The susceptibility to infection, 3) The high population density of the human people. The following factors contribute to the spread of infectious diseases Poverty and social inequalities (such as TB); the impact of agricultural development on the environment; the globalization of the food market and manufacturing; environmental pollution; climate change; population expansion, spread in health care institutions, an aging population, international travel, changing and growing vector habitats (higher temperatures may enable mosquitoes and the diseases they carry to spread to new locations), and international travel. Drug resistance is a factor that leads to the reoccurring of microorganisms such as bacteria, viruses, and other microorganisms that evolve throughout time. Influenza, A virus that causes illness and alters its genetic code, is a good illustration of how these factors impact the development of new diseases at the present moment (van Doorn, 2017). Pandemics can arise when these alterations are significant because they provide a challenge to the human immune system. When people live in close proximity to agricultural animals, such as chickens, ducks, and pigs, who are natural hosts of the virus, the likelihood of those humans being infected with the virus and experiencing genetic alterations is enhanced. The avian H5N1 influenza, often known as bird flu, may only be acquired via direct contact with birds that are infected with the illness. Even though this virus is very lethal, it is not capable of spreading from one person to another. This contrasts with the H1N1 influenza virus, which was transmitted from pigs to people. Because of human activities, particularly air travel, this virus was able to spread worldwide in 2009 (McArthur, 2019). HIV serves as an additional illustration of an infectious illness that may be traced back to human actions. It is a widely held belief that the first human infection with HIV occurred in remote parts of Africa and that it was transmitted to humans via intimate contact with chimpanzees, maybe through the act of hunting bushmeat. The medium of air travel was responsible for the spread of the disease from rural areas to international locations. Human actions, such as the use of intravenous drugs, sexual transmission, and the transfer of blood products, happened before the identification of the new illness, which resulted in the fast spread of the disease (McArthur, 2019). Taking into consideration the variations in the environment, take into consideration the tropical sickness known as chikungunya, which was explained before. The mosquito that is responsible for transmitting this virus was initially only found in tropical locations within the vicinity of the Indian Ocean. After an epidemic of this illness occurred in 2007, more than two hundred people living in a town in Italy were affected by it. The subsequent events have resulted in epidemics occurring on every continent. As individuals who offer medical treatment within the context of healthcare systems, it is essential to continue the conversation about the shifting demographics of the population. An increasing number of risk factors for infection and consequent hospitalization are associated with advancing age, which further increases the patient's susceptibility to infection. In this article, the author addresses the newly discovered fungus species Candida auris, which is responsible for outbreaks in healthcare institutions and is linked to high death rates in patients who have underlying comorbidities (KRISTEN, 2018; Petersen et al., 2018).

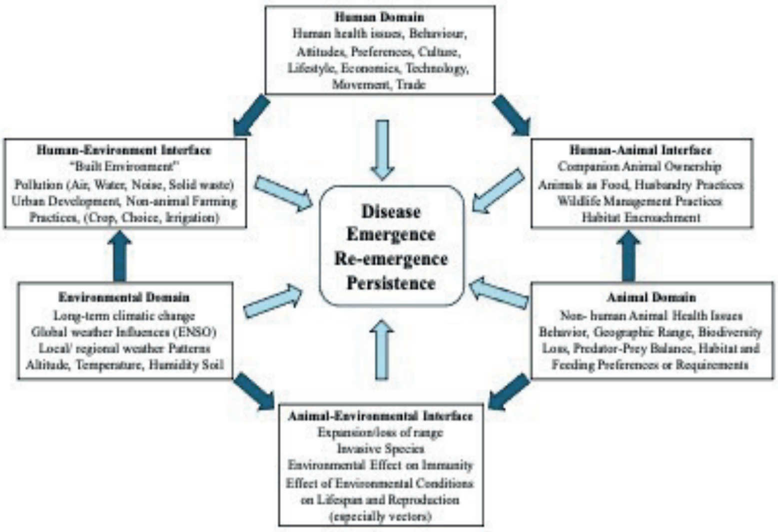

Figure 1: The emergence of infectious diseases: Animal, Human, and Environmental dimensions

The emergence of zoonotic illnesses in human populations and cattle populations may be impacted by a variety of factors, which can be classified into three categories biological, ecological, and socio-economic factors. In one health viewpoint, the interplay of human, animal, and environmental elements in the transmission and development of infectious zoonotic illnesses has been described in Figure 2. This interaction relates to the spread of contagious diseases. On the other hand, these elements are further categorized, and the following is a discussion of the crucial factors that may contribute considerably to the establishment of zoonotic infectious diseases (Usmani et al., 2023).

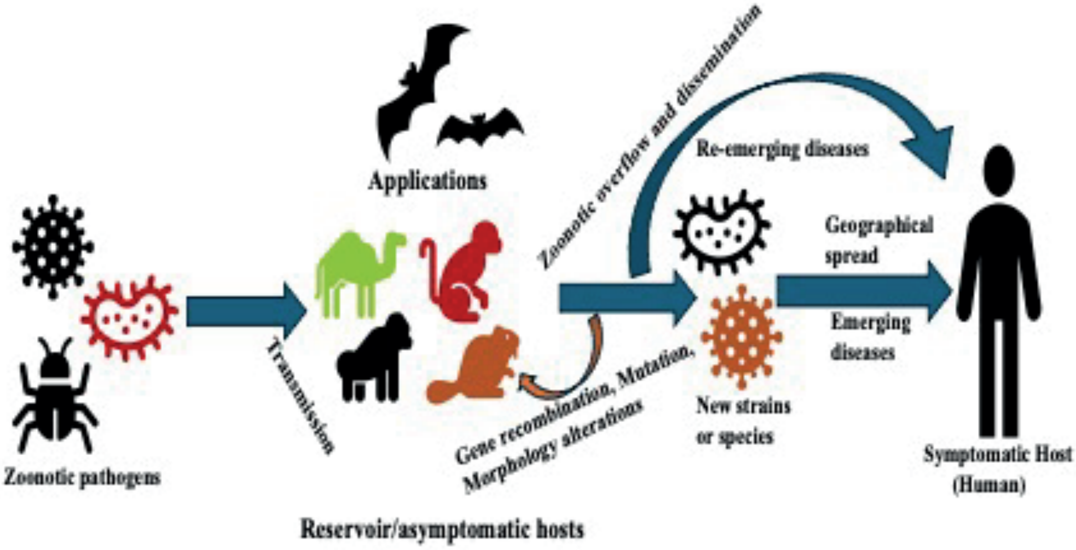

Figure 2: Emergence of infectious disease in animals and transmission to humans

2.1. ECOLOGICAL CHANGES

Habitats have been altered as a result of human-induced changes to ecosystems, such as deforestation, agricultural expansion, and urbanization (Fong & Fong, 2017). These changes have also seen an upsurge in the interaction between human population, livestock and wildlife. Because of such interaction, a concave for spreading zoonotic diseases was created, and consequently, dynamics of diseases and corresponding changes in fragmentation and distribution, as well as the behaviour of humans, livestock, and animals, were created. These changes increased their interactions, as concluded by García-Pena et al. (2016), and escalated the chances of transferring infections across different species from one region to another (García-Peña et al., 2016).

2.2. CLIMATE CHANGE

Climate altering across the world affects vector-borne diseases, that is, those diseases that are transmitted by insects and other carriers and mechanical vectors, including mosquitoes, ticks, and flies, and their biological carriers. Barry et al. (2018) also highlighted this point by explaining that it also led to shifts in the spatial organization of populations of humans, animals, and cattle that heightened the odds that pathogens would be passed between the species (McMahon et al., 2018). It is noteworthy that the frame of climate change influences the distribution and behaviour of zoonotic pathogens and their hosts, including animals and insects like ticks and mosquitoes, transformed and changed as well. The authors Alvi et al. also agree that the hosts and vectors of these pathogens enlarged and shifted to the warmer and more humid temperate areas, which in turn exposed them to novel people and animal communities (Alvi et al., 2020). Due to such a rise in the temperature, contrary conditions that are optimum for the reproduction and sustenance of vectors that spread diseases are enhanced. For instance, elevated temperatures facilitate diseases spread by mosquitoes, such as malaria, dengue fever, and the Zika virus (ZIKV); alterations in atmospheric temperature affect zoonotic pathogens' transmission patterns (Imran et al., 2023). The fact is that epidemics may develop more violently regarding the severity of illness in conditions of high temperature, short incubation time, and high transmission coefficient. This may lead to the spread of diseases at a larger scale and, sometimes, severe cases in terms of the illness. Some of the aspects that are affected by climate change include the host and pathogen's physiological and behavioural characteristics. It remains possible that this will alter the dynamics of the interaction between the host and the pathogen and, subsequently, the patterns of occurrence, morbidity and severity of the diseases (Petersen et al., 2016).

2.3. GENETIC DIVERSITY

The microbes, viruses, and bacteria evolved, resulting from mutations and recombination, creating new strains that would pose an even higher threat than previous ones. Bhatt et al. (2013) also claimed that these newly emerging strains can affect many species, including people and animals, and their severity is higher than before (Bhatt et al., 2013). Also, the genetic stock difference within cattle populations might influence susceptibility to disease. Because of the existence of low genetic diversity resulting from the use of intentional breeds for specific traits, the animals can become prone to specified diseases. The probability of disease occurrence and spread within livestock populations is also enhanced, as explained by (de Thoisy et al., 2014). However, the genetic homogeneity of a population may also make some illnesses more transmissible in the animals from one animal to the other. One virus can reach out to other people in a community within the shortest time possible, which increases the chances of a zoonotic event happening. This is even the case if they're located in populations that show slight variation genetically (Ioos et al., 2014).

2.4. PATHOGEN RESERVOIRS

It is vital to note that there are various viruses which can lead to zoonotic infectious diseases, and the livestock population is a source of these infections. These pathogens can indeed be present in animal populations and pass through the animals without making them sick; nonetheless, they can be transmitted to people and cause infections (Alvi et al., 2023). Animals that are kept in close proximity to one another, shed harmful organisms, and distribute them across the environment are higher sources of diseases to people and their excrement as a result of intensive farming procedures. As a consequence of this, there is a higher probability that viruses will be discharged into the environment, including the possibility that they may infect individuals who come into contact with dirty surfaces, water, or air (Binetruy et al., 2020). There are more than a billion individuals who are afflicted with zoonotic infectious illnesses, and each year, more than sixty percent of mortality is documented in humans as well as domestic or wild animals. Zoonoses are responsible for around seventy-five percent of newly developing infectious illnesses, according to estimates. There is a vast range of vertebrate species, both terrestrial and aquatic, that are capable of transmitting a wide variety of microbial illnesses to humans, either directly or indirectly (Usmani et al., 2022). The enormous spectrum of infectious agents includes a wide variety of microorganisms, such as rickettsiae and mycobacteria, viruses, fungi, parasites (including protozoa, metazoans, and helminths), and prions. These microorganisms are all responsible for the transmission of infectious diseases. Animals have the ability to transmit infectious diseases to humans through various means. These include the transmission of diseases through contaminated food, water, or unwashed hands, as well as through direct contact with animals, whether or not there are bites or scratches. Also, there are communicable diseases, which are transmitted indirectly through vectors like, mosquitoes, sandflies, fleas, and ticks. Besides, there is a likelihood of spillover through environmental exposure to pathogens from animals, for instance, via the breath of dried infected animal faeces (Imran et al., 2023).

2.5. ANTIMICROBIAL RESISTANCE

This is an indication that both the use of antimicrobials in human and animal health and the undue pressure to resist infections eventually lead to the development of infections that are probably harder to treat and manage. This is the same case for human and animal medicinal treatment. Regarding cattle production, the misuse of antibiotics may have a role to play in the emergence of drug-resistant diseases. Antibiotics have to be administered safely and judiciously in the context of veterinary and human medicine operations, which will help delay the creation of antibiotic resistance. The increasing trends in antibiotic resistance and emergency control measures can be determined by constant surveying of antibiotic bacteria resistance in individuals and animals (Mosnier et al., 2020). Such trends may be identified by routine monitoring. Further, the One Health approach collaborates with humans, animals, and the environment, and it is equally a part of recognizing and controlling the development of antibiotic-resistant microorganisms (AMR) in the transition zone between humans, animals, and the environment (Blaizot et al., 2020). Besides, this one-health approach is helping in decreasing the selection pressure for antibiotics in a big way. To this end, we are encouraging the use of organic and sustainable forms of medicinal agents, where it is obvious that we are going to achieve a decrease in the cases of overuse of antibiotics. By so doing, this will be effective in decreasing the rate at which antimicrobial resistance spreads and the general health status of both humans and animals (Mosnier et al., 2020).

2.6. INTENSIVE LIVESTOCK FARMING PRACTICES

A system of rearing animals that involves a large number and fewer species of animals may, in fact, create a situation where diseases would quickly spread among animals being raised for sale. These kinds of systems keep the animals under very high stress, and biosecure measures are compromised, which adversely affects the animals' immunity and production efficiency, as well as raising their susceptibility to diseases. According to Cascio et al., selective breeds are commonly supported within intensive farming since they are characteristically endowed with the right features that enhance production (Cascio et al., 2011). In addition, these animals are often overcrowded and thus provided with minimal space in smaller confined areas. Any factor that stresses an animal, causes overcrowding, poor biosafety, and hygiene could compromise the immune status of animals and hence make them more susceptible to diseases. This is because these conditions increase the chances that animals become ill through diseases and that there are higher chances of zoonotic infections spreading from animals to human beings, and their instances increase. It is also possible for animals to get in touch with various poisons that are present in the byproducts of plants and animals when offered these byproducts. This may lead to the emergence of zoonotic diseases and the introduction of new microbial human and animal pathogens into society (Craddock & Hinchliffe, 2015).

2.7. INADEQUATE DISEASE SURVEILLANCE AND MONITORING SYSTEM

According to Usmani et al. 2022 if no instrument is both rapid and precise for the detection and reporting of evolving infectious diseases, then there is a tendency for the correct diagnosis and proper prevention measures against zoonotic diseases. It may not be instituted early enough, and therefore, the chances that these diseases may spread quickly and widely would be high (Usmani et al., 2022). Early and accurate detection of infection is very crucial to prevent the expansion of such epidemics within a large, granted area. Thus, zoonotic diseases may not be reported or misidentified since there is a lack of diagnostic laboratories, there are few qualified personnel, and the health care system is underdeveloped. The tasks of practical control activities are also frequently hindered daily due to inadequate data on the incidence and dispersion of the disease (Cascio et al., 2011).

2.8. SOCIOECONOMIC FACTORS

Socioeconomic situations are linked with the creation and spread of diseases. They include poverty, this being because many people cannot afford to seek medical help, they cannot easily access medical facilities and poor methods of animal treatment. These may complicate disease surveillance, preventive measures, and timely intercession, hence the spread of illnesses. There are social and external conditions that influence the emergence and dissemination of zoonotic diseases shift of spatial environment, alteration of ecosystems, pathogens' evolution, alteration of farming practices and livestock production systems, anthropogenic pressure such as urbanization, deforestation, and global warming (Cipolla et al., 2015). Eating meats or using animals in some cultural practices and natural cure activities are some of the behavioural patterns that expose people to diseases originating from animals. Some of them include the use of animals in traditional aches and pains medicine. Lack of proper sanitation regimes and hygiene among both people and livestock could likely promote the efficiency of zoonotic infectious diseases and their sustainment in the environment. Also, Poor economy, low nutrient intake, and weak health facilities may play a part in the development and transmission of zoonotic diseases. This means that people with such diseases are likely to have reduced access to medical care reduced, efforts aimed at containing the diseases hampered, and individuals more vulnerable to getting infections (Wood et al., 2016).

2.9. GLOBAL TRADE AND TRAVEL

Infections unknown to the previous generations may find their way to the hitherto unexposed populations through enhanced traffic in persons, animals and animal products across borders. As for the spread of zoonotic diseases, the trade in live animals is especially vulnerable to the phenomenon described. Crossing animals from one country to another, either within the country or across borders step, may also promote disease strain. Referring to de Thoisy et al. (2010) and Hoen et al. (2018) pointed out that the movement of humans associated with the management of livestock, movement of live animals and animals' products may lead to the import of viruses into new areas and increased risk of emergence of diseases (de Thoisy et al., 2010; Hoen et al., 2018).

2.10. CHANGES IN LAND USE AND AGRICULTURE PRACTICES

Wangdi et al. (2015) demonstrated that alterations in land spaying, for instance, areas under cultivation or shifts in grazing practices, affected livestock, wildlife, and people. There is also likely to be increased interaction between livestock and people and animals due to drawing closer to the areas occupied by wildlife or turning over forests to farming (Wangdi et al., 2015). This may enhance the chances of acquiring new diseases in an individual's body system. Most of the animals that are raised are livestock and are usually closely associated with humans, hence making contact easy between humans and animals. Civitello et al. (2015) note that factory farming, for instance, involves rearing large numbers of animals together and hence, different herds get infected easily and concurrently (Civitello et al., 2015).

2.11. WILD ANIMALS AND RE-EMERGING ZOONOSES

Habitat loss, globalization, climate change, the emergence of new diseases, extinction of species, and loss of species diversity can alter the dynamic of one health system. This disturbance may eventually lead to changes in the patterns or presentation of zoonotic diseases that are different from the initial presentations. According to Roux et al. (2013), wild animals, including mammals, reptiles, wild birds, fish, amphibians, and other species, harbour Zoonotic diseases, which are diseases that could be transmitted to man or other different animal species (Roux et al., 2013). This is worrisome because wild animals are assumed to be involved in the genesis or, at the very least, the transmission of zoonotic diseases. Chaisiri et al. (2017) have identified that pathogen type plays a significant role in the patterns of transmission of animal zoonoses and weather factors, including temperature, humidity, and rainfall. These viruses' transmission patterns between birds, livestock, and humans are the determinants of when and if those first appear and if they re-emerge (Chaisiri et al., 2017).

The subsequent elements influence these procedures The possible ways include (1) the increase in the human population rate; (2) consumption of bush meat; (3) increased contact between humans and animals; (4) careless handling and transport of carcasses; (5) wildlife domestication; (6) ease of travelling locally and internationally; and (7) variation in methods of rearing livestock. According to investigations by Zhang, while constructing and recreating novel diseases, human-to-wildlife transmission is relatively standard. Most zoonotic diseases that occur in humans are acquired from wildlife either through contact or indirectly because of the use of vectors. This is so evident with lyssavirus, hantaviruses, the Nipah virus, the WN virus, and the agents that cause leptospirosis and ehrlichiosis, among others. Social transmission is cited as one of the causes of different diseases such as coronavirus the Ebola virus, and HIV is the transmission of the virus from one person to another (Blaizot et al., 2020).

3. Spill-Over and Spill-Back

Infectious agents may spread from reservoir animal populations, which are often farmed animals, to sympatric wildlife via a process known as spill-over. This process is the driving force behind the formation of a wide variety of wildlife EIDs. In the case of endangered species, spill-over poses a particular risk since the presence of infected reservoir hosts might reduce the threshold density of the virus, which can ultimately result in the extinction of the population at the local level. Since the 1960s, there has been a downward trend in the populations of the African wild dog, also known as Lycaon pictus (Bucci et al., 2022). The current population of this species is fewer than 5000 individuals, making it vulnerable to random occurrences such as the spread of illness. As a result, this species is currently considered endangered. In 1991, wild dogs in the Serengeti went extinct, which coincided with the outbreak of epizootic canine distemper in sympatric domestic dogs (Spinage & Spinage, 2012). There have also been cases of rabies that have resulted in the death of wild dogs, and a viral variation that is typical of sympatric domestic dogs has been found in one of these cases. There is a possibility that the appearance and effect of rabies in wild dogs in the Serengeti might be attributed to the geographical expansion of human populations and the subsequent incursion of domestic dog carriers. Spill-over epizootic outbreaks pose a significant risk not only to wild animals but also via the process of reverse spill-over, often known as "spill-back," to sympatric populations of domesticated animals that are vulnerable to the disease (Vicente et al., 2021). The disease known as brucellosis most likely arrived in the United States via cattle. The occurrence of this illness in elk and bison at Yellowstone National Park, which is located in the United States, is regarded to be a possible hazard to domesticated cattle that are grazing inside the park limits. There are also other instances of spill-over illnesses, such as sarcoptic mange in foxes (Europe) and wombats (Australia), as well as bovine TB (an international disease). The latter poses a risk of spreading to domestic cattle and, eventually, to people living in the United States (Daszak et al., 2000).

Table 2: Summary of EIDs with host and factors related to emergence.

Sr. NO	EIDs and class of EID	Pathogen	Host	Factors associated with Emergence
1	Hantavirus pulmonary syndrome 1	Bunyaviruses such as Sin Nombre and other hantavirus strains	Humans, *Peromyscus* spp., and other rodents	ENSO event and human encroachment
2	Cryptosporidiosis 4	*Cryptosporidium Parvum* (protozoan parasite)	Cattle, wild rodents, humans, and other animals	Farming methods, HIV emergence, and interspecies transmission
3	Hendra virus disease 1	Hendra virus (paramyxovirus)	Fruit bat reservoir, humans, and horses	Unknown
4	Marburg virus and Ebola virus hemorrhagic fever 1	Marburg and Ebola	Both nonhuman primates and humans, as well as potential insectivorous or fruit bat reservoirs	Ebola: interaction with infected human or animal corpses or patients; Marburg: transfer of diseased monkeys for laboratory study
5	Canine distemper 3	Canine distemper virus (morbillivirus)	a large variety of carnivores	Spill-over from domesticated dogs
6	Varroasis 2	*Varroa jacobsoni*	Both armed and wild honeybees	Host introduction into the enzootic zone
7	Plague 4	*Yersinia pestis* (bacterium)	Humans and many other mammals, particularly rodents, as hosts	Enzootic foci are remnants of the last panzootic outbreak in
8	Canine parvovirus disease 1	Canine parvovirus	Canids	Evolution of novel strain, contact with domestic dogs
9	Pneumonia	Ophidian paramyxovirus	Snakes	Unknown
10	Sarcoptic mange 2	*Sarcoptes scabiei* (mite)	Mammals	Dispersal of infected wildlife; Domestic dog wildlife interactions
11	Steinhausiosis	*Steinhausia* sp. (protozoan parasite)	*Partula* snails	Unknown
12	Neurotropic velogenic Newcastle disease 2	Newcastle disease Virus (paramyxovirus)	Double-crested cormorants, pelicans, gulls, poultry	Unknown
13	Viral chorioretinitis ÒKangaroo blindness 1	Wallal virus and ossibly Warrego virus; vector-borne orbivirus	Kangaroo spp.	Unknown; possibly weather-related

4. Surveillance and Detection of Emerging Infectious Diseases in Animals

One of the most important aspects of reducing possible risks to public health is the surveillance and detection of EID in animals. A thorough One Health approach is needed due to the intricate relationship of ecosystems, human health, and animal health. In addition to recognizing the reciprocal impact of environmental, animal, and human health, this approach encourages a transdisciplinary, multi-sectoral system for disease surveillance (Asaaga et al., 2022). Effective surveillance is an essential component of rapid disease control, as early detection of emerging occurrences is critical. Whether the disease is present or not will determine the precise goals that should be pursued while formulating and carrying out infectious disease monitoring (Cameron et al., 2014). Species, subpopulations, production systems, or demographic groupings that are more likely to acquire an infection are the focus of risk-based surveillance (Stärk et al., 2006).

4.1. Recent Technological Advancement

New technological developments have greatly improved the ability to detect and monitor infectious diseases in animals. A key instrument in the genomic surveillance of pathogens is whole genome sequencing (WGS). Real-time monitoring and enhanced risk assessment are now possible due to the incorporation of this technology into larger surveillance systems for antimicrobial resistance (AMR) and other diseases (Suminda et al., 2022). Artificial intelligence (AI) and digital tools have also been included in recent surveillance systems to facilitate data sharing, analysis, and acquisition. These technological advancements provide expedited detection of epidemics and accurate estimation of disease propagation. In order to identify errors that can point to the introduction of a novel virus, artificial intelligence (AI) algorithms are able to process enormous volumes of data from a variety of sources, including ecological sensors, veterinary records, and wildlife monitoring (Guo et al., 2023).

4.2. One Health Approach

The One Health concept demonstrates that cross-sectional coordination is essential for surveillance initiatives. This strategy is being used more and more in projects to improve data exchange and standardize practices across various industries, such as environmental agencies, veterinary services, and public health (Bidaisee & Macpherson, 2014). Efficient surveillance systems for One Health enable prompt actions to avert extensive epidemics by facilitating the early detection of zoonotic infections (Singh et al., 2024). The recent identification of avian influenza subtypes like H5N6 and H9N2 in China highlights the ongoing threat posed by zoonotic influenza viruses. When these viruses develop mutations that allow for human-to-human transmission, they have the potential to increase human morbidity and mortality [50] seriously. Further evidence of the crucial requirement for ongoing surveillance and prompt action has come from anthrax outbreaks in African nations like Zambia and Uganda. To effectively manage and restrict such outbreaks, the unrestricted movement of humans and animals between regions requires a coordinated response (Nalishuwa et al., 2024).

Different regions have varying capacities for surveillance, which is one of the main challenges. The infrastructure and funding required for deploying cutting-edge surveillance systems are frequently lacking in developing countries (Buckee et al., 2018). Enhancing laboratory facilities, training staff in contemporary surveillance strategies, and building local capacities all require funding as well as assistance from overseas. It is crucial to manage the ethical implications of data sharing properly. For the betterment of world health, sharing surveillance data is essential, but it must be done in a way that respects individual privacy and adheres to moral principles (Kalkman et al., 2019). The protection of the world's health depends on surveillance and identification of newly emerging infectious diseases in animals. We can improve our capacity to identify and counter these threats by utilizing innovative technology, implementing a One Health strategy, and resolving issues with data exchange and capacity (McArthur, 2019).

5.. Prevention and Control Strategies for Emerging Infectious Diseases in Animals

Protecting the health of animals and the general public requires effective prevention and control measures for newly emerging infectious diseases in animals. Significant strategies include immunization and vaccination campaigns, as well as biosafety procedures and quarantine restrictions.

5.1. Vaccination and Immunization Programs

One of the main preventive strategies is vaccination, which drastically decreases the prevalence and spread of infectious diseases among the populations of animals. These measures limit disease incidence and prevent transfer to humans by increasing immunity within animals. Recombinant and mRNA vaccines, among other recent developments in vaccine manufacturing, provide higher efficacy and flexibility towards emerging infections (Maruggi et al., 2019).

5.1.1. Vaccine Development

The management of diseases affecting poultry and animals depends on widespread immunization campaigns. Fast immunization of large populations is the goal of mass vaccination campaigns, which help to limit the spread of disease and develop herd immunity (Trovato et al., 2020).

Cattle vaccination initiatives against foot-and-mouth disease have contributed to the restoration of trade and economic stability by preventing widespread outbreaks. Strategies for immunizing poultry against avian influenza have also proven crucial in preventing outbreaks and reducing financial losses (He & Kam, 2024).

5.1.2. Vaccination Campaigns

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5.1.3. Booster Programs

Maintaining immunization requires both the establishment of booster programs and ongoing evaluations of vaccine efficacy. Based on surveillance data, booster vaccinations are recommended when new pathogen strains appear in areas with high disease stress (Endale et al., 2022). It is ensured that animal populations are safeguarded against ever-changing threats by routinely updating vaccination methods based on surveillance results.

5.2. Quarantine Measures and Biosafety Protocols

Biosafety procedures and quarantine regulations are essential for managing and preventing the spread of infectious diseases in animals. These measures emphasize controlling animal movement, keeping high standards of hygiene, and isolating afflicted animals in order to prevent the spread of disease (Collett et al., 2020).

5.2.1. Quarantine Measures

Limiting the spread of new EIDs in animals requires the implementation of quarantine measures, which include isolating and restricting animal mobility. In order to prevent the spread of zoonotic diseases to humans and to prevent outbreaks, quarantine is a crucial part of biosecurity approaches (Yadav et al., 2020). It is particularly essential to isolate affected animals in cases of diseases like foot-and-mouth disease, African swine fever, and avian influenza that have high rates of transmission or severe effects on animal health. Disease outbreaks result from high economic losses due to a decrease in productivity, trade restrictions and the expenses of managing and eliminating diseases (Baker et al., 2022).

5.2.2. Quarantine Implementation

1. The first step of quarantine measures is quick detection and isolation of affected animals through veterinary examinations and diagnostic testing.
2. To stop the spread of contagious diseases, movement limitations must be established. Limiting the movement of animals, animal products, and potentially contaminated items like feed, tools, and automobiles is also included (Collett et al., 2020).
3. Controlled entry and exit points facilitate the management and observation of animal and human activity within quarantine areas.
4. It is essential to conduct ongoing surveillance and monitoring of animals under quarantine in order to monitor the disease's progression and determine whether the quarantine is effective (Li et al., 2021).

Quarantine buildings, testing labs, and skilled staff are some of the necessary infrastructure and resources needed for an effective quarantine. The implementation and maintenance of efficient quarantine measures can be complex in many areas, particularly in poor nations, due to a lack of resources (Benjamin et al., 2006). To ensure compliance, farmers, veterinarians, and animal handlers must be made aware of the significance of quarantine, and regulations must be enforced by inspections and fines (Otte et al., 2004).

5.2.3. Biosafety Protocols

The entry and transmission of infectious diseases within animal populations, as well as from animals to people, are prevented by the implementation of biosafety standards. High standards of hygiene, containment, and biosecurity in animal husbandry and associated operations are ensured by these protocols, which include a broad range of procedures (Neumann, 2012). One essential component of biosafety is the use of personal protective equipment (PPE) by individuals who work with animals. PPE acts as a defense against infections and includes items like gloves, masks, and coveralls (Singh et al., 2020). Biosafety relies on efficient waste management procedures. This concerns the secure disposal of animal carcasses, waste materials, and other possibly infected items. In order to stop infections from waste products from spreading to other animals or the environment, proper disposal techniques like deep burial or incineration are used (Gwyther et al., 2011). In order to prevent infections from entering the food chain, biosafety precautions are also applied throughout the handling and processing of animal products.

6. One Health Approach: Future Directions in Research and Management of Emerging Infectious Diseases in Animals

Animal-borne emerging infectious diseases (EIDs) pose a severe risk to biodiversity, economy, and public health. In order to deal with these issues, the One Health approach—which acknowledges the interdependence of environmental, animal, and human health—is essential (Aiyar & Pingali, 2020). At the cross-section of humans, animals, and the environment, this comprehensive framework fosters multidisciplinary cooperation and integrative approaches for the prevention, detection, and response to infectious disease risks. Through the perspective of the One Health concept, this thorough review examines the future paths in research and management of EIDs in animals, emphasizing crucial issues, including monitoring, diagnostics, immunization, antibiotic resistance, and policy development (Matias, 2024).

6.1. Surveillance and Early Detection

Establishing robust monitoring systems is essential to controlling EIDs in animals. The creation and deployment of resilient, real-time monitoring networks that incorporate data from several sources, such as the veterinary, medical, and environmental domains, must be given top priority in the future of One Health research (Morse et al., 2012). Technological innovations like bioinformatics and genetic sequencing have hitherto unseen possibilities to improve pathogen monitoring and detection. Effective measures are made possible by the swift detection of infections and their routes of transmission made possible by genomic epidemiology (Wolking & Mazet, 2022). Furthermore, surveillance systems that use artificial intelligence (AI) and machine learning (ML) can better predict disease outbreaks. These technologies enable preemptive actions by identifying trends and risk factors linked to EIDs through the analysis of massive databases. In order to improve these models' precision and dependability in forecasting epidemics and directing resource distribution, research should concentrate on enhancing them (Redding et al., 2019)..

6.2. Innovative Diagnostics

Effective therapy of EIDs in animals depends on prompt and precise diagnosis. The creation of quick, affordable, and user-friendly point-of-care diagnostic instruments needs to be the top priority for future research (Parida et al., 2008). Pathogen detection has been transformed by molecular methods such as loop-mediated isothermal amplification (LAMP) and polymerase chain reaction (PCR). Nonetheless, further innovation is required to create multiplex diagnostic systems that can identify many diseases at once (Venkatesan et al., 2022). Biosensors and microfluidic devices are examples of nanotechnology-based diagnostics that show potential for improving diagnostic performance. These methods allow for the identification of low pathogen loads in a variety of samples due to their great sensitivity and specificity (Sulaiman, 2024). Furthermore, the application of metagenomic techniques can offer a comprehensive understanding of the microbial communities connected to EIDs, assisting in the identification of new diseases and comprehension of their ecology (Hasan, 2013).

6.3. Vaccination Strategies

One of the most valuable methods for managing and preventing transmissible diseases is vaccination. Research on One Health should concentrate on creating new vaccines that are effective, reliable, and capable of offering protection across a wide range of conditions in the future. Reverse and structural vaccinology are two advances in vaccine science that make it possible to create vaccinations that target conserved epitopes in a variety of pathogen strains (Plotkin & Plotkin, 2011). Novel vaccine methods for delivery, such as DNA/RNA vaccines and vaccinations based on nanoparticles, should also be investigated in research because they have demonstrated potential in recent trials (Stefanetti et al., 2022). These systems have the potential to improve vaccination immunogenicity, stability, and administration simplicity. Moreover, vaccination campaigns can be streamlined by the creation of multivalent vaccines, which offer simultaneous protection against several infections, especially in environments with limited resources (Khan et al., 2024).

6.4. Addressing Antimicrobial Resistance

Animal EID control is seriously threatened by AMR. The establishment and dissemination of resistant infections are facilitated by the overuse and abuse of antibiotics in veterinary practice. In order to counteract AMR, future research should concentrate on comprehending the mechanisms of resistance and developing substitute tactics (Laxminarayan et al., 2016). The creation of new antimicrobial agents that can target resistant bacteria, such as bacteriophages, antimicrobial peptides, and phytochemicals, is one potential strategy (Wright, 2010). Additionally, one possible tactic to lessen dependency on antibiotics is the use of probiotics and prebiotics to modify the gut microbiota and improve host immunity. Along with developing mitigation plans, research should examine how environmental issues like pollution and climate change contribute to the spread of

AMR (Baquero et al., 2021).

6.5. Integrative Policy Development

Extensive regulations that take into account the health of people, animals, and the environment are necessary for the efficient management of EIDs in animals. The development of evidence-based policies that support One Health concepts locally, nationally, and worldwide should be the main emphasis of future study. This entails fortifying the legal frameworks governing immunization, antibiotic usage, diagnostics, and disease surveillance (Zinsstag et al., 2011). The effective execution of One Health programs necessitates cooperation among stakeholders, including government agencies, non-governmental organizations, academia, and the commercial sector (Gebreyes et al., 2014). One Health task groups and committees are examples of methods that should be investigated in research to improve collaboration and involvement among stakeholders. Furthermore, specialist skill sets and knowledge may be enhanced via capacity-building efforts, including training courses and workshops for those working on One Health projects (Adnyana, 2024).

6.6. Environmental and Ecological Considerations

The wellness of ecosystems is intrinsically related to the health of humans and animals. The natural course of infectious illnesses can be altered by habitat degradation, loss of biodiversity, and changes in the climate, which can promote the formation and spread of EIDs. Future studies should concentrate on comprehending the environmental causes of EIDs and creating plans to lessen their effects (Patz et al., 2004). Techniques for remote sensing and ecological simulation can offer critical new perspectives on the connection between disease progression and changes in the environment. These resources can be used to pinpoint high-risk locations and direct focused efforts (Altizer et al., 2013). Furthermore, conservation initiatives like wildlife preservation and habitat restoration can lower the chance of pathogens spreading from animals to people. The function of ecosystem services, such as pollination and water purification, in preserving health and resistance to EIDs should also be investigated in research (Ostfeld et al., 2020).

6.7. Interdisciplinary Education and Training

A multidisciplinary workforce is necessary for the One Health concept to be implemented successfully. Future studies should concentrate on creating curricula that support practitioners in veterinary medicine, public health, environmental science, and allied professions in acquiring One Health competencies. These courses ought to stress the value of teamwork and include hands-on instruction in AMR management, monitoring, diagnosis, and immunization (Steele, 2021). Additionally, studies should look into cutting-edge approaches to One Health education delivery, such as virtual simulations, online courses, and multidisciplinary workshops. These methods can improve accessibility and involvement, especially in environments with limited resources (Rüegg et al., 2018). Future One Health professionals might benefit from excellent practical experience and cooperation opportunities offered by mentoring programs and cross-disciplinary internships.

6.8. Global Collaboration and Data Sharing

Global cooperation, along with data exchange, is necessary due to the worldwide nature of EIDs. The development of frameworks and platforms that enable the cross-border flow of resources and information should be the main emphasis of future studies (Mackenzie et al., 2013). Creating international databases for pathogen genomes, surveillance information, and trends of antibiotic resistance are some examples of this (Jones & Jeffery, 2023). Coordination and the exchange of best practices may be significantly aided by cooperative organizations like the One Health Global Network and the Global Health Security Agenda (Mazet et al., 2009). Methods to improve the efficiency of these systems, such as regulated data-gathering methods and information exchange between systems, should be the subject of future research. Furthermore, current information collecting, processing, and transmission can be improved through the application of technological advances like cloud computing and mobile health (mHealth) apps (Berrian et al., 2020).

The One Health strategy provides a thorough framework for handling the intricate problems brought on by newly developing transmissible diseases in animals. Exploration and management efforts should be given high priority to developing cutting-edge instruments for surveillance and diagnosis, creative immunization plans, and other tactics to fight antibiotic resistance in the future. A sustainable One Health plan must include multidisciplinary education, global collaboration, ecological and environmental issues, and integrative policy creation. The international community can protect the well-being of people, animals, and ecosystems by adopting these prospects for the future and strengthening its ability to avoid, recognize, and react to EIDs.

7. Summary

Emerging infectious diseases (EIDs) are contagious illnesses that have been identified or present in the past but are increasing in cases or geographic ranges. Vaccines have the potential to eradicate many diseases and prevent their spread. The interdependence of humans and the natural world is crucial in addressing EIDs, which can have significant impacts on people's health, social, and economic well-being. Factors contributing to the emergence of EIDs include demographic transitions, global travel, business, and climate change. Antimicrobial resistance (AMR) poses a significant threat to animal EID control, and future research should focus on understanding resistance mechanisms and developing alternative tactics. Intensive livestock farming practices can lead to the spread of diseases among animals, as they expose them to high stress, compromised biosecurity measures, and poor biosafety. This can compromise the immune status of animals, increasing their susceptibility to diseases. Inadequate disease surveillance and monitoring systems can also contribute to the spread of diseases. Socioeconomic factors like poverty, poor animal treatment methods, and poor economic conditions can complicate disease surveillance and preventive measures. Global trade and travel can also contribute to the spread of diseases. Changes in land use and agriculture practices can affect livestock, wildlife, and people, increasing the risk of acquiring new diseases. Wild animals, including mammals, reptiles, birds, fish, amphibians, and other species, harbor zoonotic diseases that can be transmitted to humans or other animal species. A sustainable One Health plan should include multidisciplinary education, global collaboration, ecological and environmental issues, and integrative policy creation. Technological advancements have improved the detection and monitoring of infectious diseases in animals, with whole genome sequencing (WGS) and artificial intelligence (AI) playing key roles in genomic surveillance. The One Health approach emphasizes cross-sectional coordination for surveillance initiatives, enabling prompt actions to prevent extensive epidemics. However, developing countries often lack the infrastructure and funding to deploy advanced surveillance systems.

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About the Authors

Shafeeq Ur Rehman earned his Bachelor in Applied microbiology from Cholistan University of Veterinary and Animal Sciences (CUVAS) Bahawalpur Pakistan. Currently he is pursuing M. phil in Microbiology from Cholistan University of Veterinary and Animal Sciences (CUVAS) Bahawalpur Pakistan. He is also working as research assistant in a project titled as “Robust Molecular Detection of Silent Circulation of FMD and PPR Viruses in Cholistan as a Model for Disease-Free Zone”. His research interest is in FMD and PPR Viruses, Mucosal Immunity, Virology, Molecular cell biology, Cell culture, Microbial genetics and CRISPR case tools for combating viral diseases. He has published 7 articles and many book chapters in national and international journals.

Email: shafeequrrehmanbhutta@gmail.com ORCID: 0000-0003-3571-8226

Faizan Ali is doing BS Applied Microbiology from Cholistan university of veterinary and animal sciences (CUVAS) Bahawalpur Pakistan. His research interests are cell culture techniques, virology, genetics and molecular cell biology.

Email: faizansarwarali@gmail.com ORCID: 0009-0008-1066-7446

Minahal Fatima and She is doing M.Phil in Zoology, Wildlife and Fisheries from University of Agriculture, Fasilabad, Pakistan. Her research interest includes fish survival via changing the environmental factor. Not only the fish survive it also counts the progeny's survival. She has only one paper in International Journal and 12 Chapters in national and international Journals.

Email: fatimaabdulhameed08@gmail.com ORCID: 0009-0003-4387-6854

Khizar Abbas earned Bachelor in Applied microbiology from Cholistan university of veterinary and animal sciences (CUVAS) Bahawalpur Pakistan. Currently he is doing M.phil in Microbiology from Cholistan university of veterinary and animals sciences (CUVAS) Bahawalpur Pakistan. His research interest in Microbial genetics, Virology, Molecular biology and Biotechnology.

Email: khizarabbas2395@gmail.com ORCID:0009-0005-9044-1161

Dr. Danish Riaz received his PhD (Zoology) in 2018 from Government College University Faisalabad, Pakistan. He is serving as Assistant Professor of Zoology at the Department of Zoology, Division Science and Technology, University of Education Lahore Pakistan. His research interests include Biological Science with a specialization of animal biotechnology and Fisheries. He has published over 34 research articles in well-reputed national and international journals. He also has written book chapters.

Email: danish.riaz@ue.edu.pk ORCID-0000-0002-6137-8993

Muhammad Ejaz earned Bachelor’s in applied microbiology from Cholistan university of veterinary and animal sciences (CUVAS) Bahawalpur Pakistan. His research interest in Microbial genetics, Molecular biology, and food quality and its application.

Email: ijazrasheed334@gmail.com ORCID: 0009-0006-1709-6653

Muhammad Naveed Nawaz did his Bachelor's degree in Applied Microbiology from Cholistan University of Veterinary and Animal Sciences, Bahawalpur. Now, he is doing his Master's degree at China University of Geosciences, Wuhan, China. His research interests include emerging infectious diseases, antimicrobial resistance, public health, environmental microbiology, microbial ecology, bioremediation and biodegradation. He has published few articles in reputed international journals and has also written some book chapters. Email: muhammadnaveednawaz4@gmail.com ORCID: 0000-0002-2479-6547

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MICROORGANISMS AND ANIMALS: EXPLORING SYMBIOTIC RELATIONSHIPS IN BIOTECHNOLOGY

Saba SABA

Mohsin Tassawar CHEEMA

Momena HABIB

Naila NOUREEN

Adeela NAEEM

Memoona SIDDIQUA

Fakhr-Un-NISA

Abid HUSSAIN

Symbiosis is a close relationship between two biological species. This chapter explores the vital symbiotic relationships between animals and microorganisms, which are crucial for various physiological processes such as digestion, immunity and nutrient synthesis. Different forms of symbiosis, including mutualism, commensalism, and parasitism and their significance in biotechnology is described here. The importance of symbiosis in maintaining livestock health and productivity and its implications for biotechnology are highlighted. The chapter further explores diverse range of symbiotic relationships, including mutualistic relationships that benefit both parties, commensal relationships that benefit one party, and parasitic relationships that harm the host. Moreover, the mechanisms of formation and maintenance of these relationships and their impact on health and disease is discussed here. The importance of symbiotic relationships in developing antibiotic resistance and their potential in biotechnology is explored. Recent advances in synthetic biology have led to the development of advanced microbiome supporters and live biological therapeutics with improved assets. These products have the potential to revolutionize the field of biotechnology. Advances in transcriptomics, genome sequencing, and metagenomics have opened new avenues for studying symbiosis, enabling cross-species comparisons of bacterial evolution and host integration stages. These advances have also led to a better understanding of the mechanisms of symbiosis and its potential applications. Finally, the chapter explores future directions and emerging trends in symbiosis research, highlighting its potential for advancing livestock health and productivity.

1. Introduction

1.1. Definition and Types of Symbiosis

Symbiosis is defined as any close and long time biological relationship between two or more biological species (Wiesmann, Wang, Zhang, Liu, & Haney, 2023). Ruminant microorganisms and cattle have a symbiotic interaction. Microorganisms in the rumen help cattle digest plant cellulose. Microbes get home and nutrients, and cattle profit from the breakdown of complex plant components into absorbable nutrients, demonstrating mutualism. This connection is required for effective digestion in ruminants (X. Chen et al., 2022). Symbiotic relationships can be of various types such as

- **Mutualism:** If both organisms mutually benefit, it is called mutualism. This type of relationship can be seen in the rumen of cattle, where various microorganisms (bacteria, protozoa, and fungi) help digest cellulose from plant material. The microbes gain a habitat and nutrients, while the cattle benefit from the breakdown of complex plant materials converted to volatile fatty acids, that are used and absorbed for energy (Yang, Zhang, &

El-Mahallawy, 2024).

- **Commensalism:** If one organism is benefited and another organism is not harmed and benefited it is then called as commensalism. Cattle egrets frequently accompany animals, including cattle, buffalo, and horses. As these enormous creatures walk through grassy regions, they disrupt insects on the ground, making it simpler for egrets to catch and consume. The egrets benefit from having easy access to food without causing injury or serious damage to the animals they follow(Y. E. Chen, Fischbach, & Belkaid, 2018).
- **Parasitism:** When one organism is benefited and another organism is harmed it is known as parasitism(Ichihashi et al., 2020)Liver flukes are parasitic flatworms that infect the livers of animals including sheep, cattle, and goats. They induce liver tissue damages, resulting in lowered production, weight loss, and, in severe cases, it causes death. Livestock become sick after consuming water plants polluted with fluke larvae, showing a crucial parasitic link that affects livestock health and agriculture(Gunturu, Yegireddy, Mannem, Mekapogu, & Tollamadugu, 2019).

1.2. Importance of Symbiosis in Biotechnology

Symbiotic relationships are crucial in livestock farming, significantly enhancing animal health and productivity. These interactions, which include mutualistic, commensal, and sometimes parasitic relationships, are vital for nutrient absorption, disease resistance, and overall well-being. To break down complex plant elements like cellulose, ruminants like cows and sheep rely on a symbiotic connection with a wide variety of bacteria in their rumen. These microorganisms, comprising of fungi, bacteria, and protozoa ferment ingested food, converting it into volatile fatty acids, which serve as the primary energy source for the host. This mutualistic interaction enhances nutrient absorption efficiency and overall livestock productivity (Arshad et al., 2021).

Probiotic supplementation in livestock diets introduces beneficial bacteria that improve gut health, enhance digestion, and increase feed efficiency. This results in better growth rates, improved feed conversion ratios, and higher overall productivity (Bhogoju & Nahashon, 2022). Prebiotics, on the other hand, stimulate the maturation of beneficial gut bacteria, further promoting a healthy gut environment (Cangiano, Yohe, Steele, & Renaud, 2020). The presence of a balanced microbiota can help reduce stress in livestock by maintaining gut health and preventing dysbiosis (microbial imbalance). Reduced stress levels contribute to better animal welfare, which is closely linked to productivity and health (Ozbayram, Kleinsteuber, & Nikolausz, 2020).

1.3. Historical Perspective and Current Trends

The study of symbiotic relationships in livestock has a rich history. In the late 19th and early 20th centuries, scientists discovered the presence of microorganisms in the rumen of cattle and sheep, establishing the foundation for microbial ecology. Mid-20th century advancements, provided by Robert Hungate, allowed for culturing and understanding specific rumen bacteria (Pidcock, 2022). The modern era with molecular and genomic techniques, has fostered insights into microbial diversity and functions in livestock, enhancing our understanding of nutrient absorption and disease resistance (Ozbayram et al., 2020).

Recent and current modifications in research have been moved to practical applications of symbiotic relationship of livestock production. Probiotic and prebiotic supplements are being formulated to optimize gut health, enhance feed efficiency, and boost immunity in livestock (Ozbayram et al., 2020). Concurrently, research is investigating microbiota manipulation to ease methane emissions from ruminants, promoting more sustainable livestock farming practices (Hesham et al., 2021). These interventions aim to improve overall livestock productivity while addressing environmental impacts associated with animal agriculture

a. Emerging drug resistance is another challenge worldwide that is decreasing the efficacy of antibiotics in livestock, and it is a food chain that is polluting every single species. In this case, scientists are working on a symbiotic relationship between microbes and livestock which can enhance the productivity of livestock by overcoming antibiotic resistance in them. The symbiotic relationships concerns with bacteria and fungi can be an area that remains widely unknown for the discovery and development of new antibiotics (Gogineni, Chen, Hanna, Mayasari, & Hamann, 2020).

b. Synthetic biology and engineered symbioses, microbiome research, bio-remediation and bioenergy, co-culture systems are the recent trends in biotechnology (Lv et al., 2021).

c. The roles that microbiomes play in biotechnological applications are crucial for maintaining the health of humans, animals, plants, and the environment. Given microbiomes are found in a wide variety of natural and artificial environments, including those of people, plants, soils, sediments, and livestock animals.

d. Applications of microbiome, including various aspects such as biofertilizers, biocontrol agents, and pre- and probiotic food supplements are expected to provide valuable contributions to combat major societal challenges, such as zero hunger. They are being used to reverse biodiversity loss and global climate change (Bhogoju & Nahashon, 2022).

2. Microorganisms and Animals: An Overview

2.1. Microbial Diversity in Animal Hosts

The microbiome, which is an essential component of animal physiology and aids in the preservation of species, need to be enhanced and added to the database of future management techniques (Dallas & Warne, 2023). Any microbes that live in and on the host animal, including their genomes and extrachromosomal components, as well as their interactions with the skin, vaginal environment, and gastrointestinal tract (GIT), are collectively referred to as the "microbiota" (Xu et al., 2021). These two terms “microbiota” and “microbiome” are often used reciprocally. Organisms that have gut microbiota exist outside the mucosal layer and are essential for robust the host immunity and facilitating the link between the gut and brain (Xu et al., 2021). The GIT comprises the dense amount and largest diversity of microorganisms (Khan et al., 2023).

A community of commensal, symbiotic, and pathogenic microorganisms that live in the mammalian gut, such as bacteria, viruses, parasites, fungi, archaea, and protists, is referred to as the GIT microbiota (Jwher & Ezzulddin, 2022). Such kind of mammalian gastrointestinal tract is believed to have approximately 1014 bacteria consisting of 500–1000 unique species, which form a symbiotic relationship with the host. The microbiota that live on an organism are involved in digestion, the use of nutrients, the elimination of toxins, the fight against pathogens, also includes the modulation of the immunological and endocrine systems (Patil, Gooneratne, & Ju, 2020). There is a clear link between rumen bacteria and the digestion of cellulose and hemicellulose. A significant amount of research has been done on the fundamental laws guiding the cellulolytic bacteria *Butyrivibrio fibrisolvens* and *Ruminococcus flavefaciens*. The most prevalent bacterial families in the rumen were *Bacteroidales, Clostridiales, Butyrivibrio, Ruminococcus,* and *Prevotella* (X. Chen et al., 2022).

It is well known that microbiota is essential to the GIT of both ruminant and non-ruminant animals. Ruminal microbial organisms are essential to the nutrition and nutrient synthesis necessary for the growth and productivity of dairy animals (Gunturu et al., 2019). Animals and microorganisms have complex interactions that can be mutually beneficial (mutualism), neutral (commensalism), or even harmful (parasitism). Microbes act as a biological factor that regulates microbiota of the gastrointestinal tract coupled with the betterment of reaction with the environment and to make a strong impression of immunity response (Jwher & Ezzulddin, 2022).

Homo sapiens are vital symbiotic organisms. In GIT/gastrointestinal tract, bacteria constitute most of the microbial population. The Bacteroidaceae family contains at least 500 different species of bacteria, including *Clostridium, Lactobacillus, Eubacterium, Bifidobacterium,* and *Braceroids*. These bacterial species generally crossover with the GIT and exist amicably with the intestinal mucosa. The composition and abundance of this microbiota are determined by the physiological resources of the various GIT sections, and they are also influenced by a range of autogenous and allogeneic factors. Therefore, the microbial population supports cellular homeostasis, assists in nutritional utilization and digestion, and creates vitamins, enzymes, and other nutrients that are lacking in diets by acting as a protective barrier with antibacterial, antioxidant, and immunological characteristics (Melara et al., 2022).

In the United States, the deer tick *Ixodes scapularis*, is responsible to transmit an array of pathogens, including viruses like Powassan and the bacterium that causes Lyme borreliosis. It also carries the protozoan agent that causes babesiosis. But a variety of other microbes have also changed the symbiotic connections with this type of tick, and it seems likely that several of such microorganisms have developed methods to affect both their tick host and each other at the same time (Tsao, Hamer, Han, Sidge, & Hickling, 2021).

2.2. Types of Microbial Symbionts

Microbial symbionts' relationships with their hosts and each other can be compared to that of passengers sharing a ride. They may or may not interact directly; one may pay for the ride or the other may ride at another person's expense; they may be amicable, indifferent, or antagonistic; they may sit next to each other or keep apart to use different parts of the car; and they may exist in different places or remain there for an extended amount of time (Stewart & Bloom, 2020). Examples of these ride-sharing-like symbiotic connections, for instance, between microbiota and arthropods have been well-documented. Examples of beneficial interactions are the two bacterial endosymbionts of the glassy-winged sharpshooter (Homalodisca coagulata), which synthesize different essential metabolites for the host and possibly for each other, and the gut commensal bacteria of an Aedes aegypti mosquito that promotes arboviral infection by altering the gut epithelial layer (Wu et al., 2019). An example of a symbiotic interaction in arthropods includes the inhibition of Plasmodium falciparum growth within the midgut of Anopheles gambiae mosquitos resulting from the initiation of reactive oxygen species produced by an endogenous Enterobacter strain.

Presumably, a multitude of symbiotic protozoa are hosted by most metazoa. These symbionts reside in the gut lumen, on ciliated epithelia like the exoskeletons of crustaceans and the gills of aquatic creatures, and on body surfaces. Some of them also exist extracellular or intracellular, in different tissues and organs. On the other hand, it is likely that symbionts are descended from free-living species that changed to live in the unique environments that animals make up, and these evolutionary processes are currently occurring. As a result, it is difficult to distinguish between symbiotic and free-living protozoa. Several organisms from the genera Acanthamoeba and Naegleria are well-known examples. These species are freshwater amoebae that live freely. However, isolated cells may occasionally infect people, resulting in deadly diseases (Visvesvara et al. 2007).

It is commonly known that the pig gut microbiota is crucial for maintaining metabolic homeostasis and for carrying out several other physiological, neurological, and immune processes, including pathogen defense and the digestion of food that pig would not otherwise be able to digest. The hallmark of optimal health is a diverse gut microbial ecology or balanced microbiota; nevertheless, alterations in the composition of microbes, both in terms of quantity and quality, can lead to the emergence of a wide range of illnesses. On the other hand, conditions brought on by stress or other variables have been demonstrated to damage the microbiome (Patil et al., 2020). The main prokaryotic symbiont of I. scapularis is Rickettsia buchneri, which has a different relationship to the tick than B. burgdorferi. It seems to be an obligatory intracellular bacterium that may colonize a variety of organs, such as the ovaries, midgut tissues, and salivary glands (Stewart & Bloom, 2020). The difference between eukaryotic and prokaryotic symbionts is described here in Table 1.

Table :1 Difference between eukaryotic and prokaryotic symbionts(Skipper, 2005)

Properties	Eukaryotic symbionts	Prokaryotic symbionts
Cell structure	Complex cell structure with membrane-bound organelles	Simple cell structure without membrane-bound organelles
Genetic material	DNA enclosed within a nucleus	DNA is free-floating within the cell, not enclosed in a nucleus
Size	Generally larger (10-100 micrometers)	Generally smaller (1-5 micrometers)
Reproduction	Sexual and asexual reproduction through mitosis and meiosis	Asexual reproduction through binary fission
Examples	Protozoa in the rumen of cattle that aid in breaking down complex carbohydrates	Gut bacteria (e.g., Lactobacillus species) that assist in nutrient absorption and pathogen resistance, Rumen bacteria (e.g., Fibrobacter succinogenes, Ruminococcus albus) that help in cellulose digestion.

3. Diversity of symbiotic Relationship

When organisms from two distinct species coexist for a considerable amount of time, this is known as symbiosis (Hom & Penn, 2021). Symbionts are the organisms that participate in symbiosis. Microbial symbiosis refers to the various forms of symbiosis in which a microbe is involved e.g., mutualism, commensalism etc. (Wiesmann et al., 2023) . Numerous animals that are thought to be nonpathogenic exhibit microbial symbiosis, and plenty of bacteria have evolved to live and colonize in biological systems (Hom & Penn, 2021).

3.1. Mutualistic symbionts

Animal fluids, cells, surfaces, cavities, and notably their guts are home to a wide variety of microorganisms, in which at least 15% to 20% of all insects have symbiotic relationships with bacteria (Hom & Penn, 2021). The bacterial Symbionts have emerged throughout the last ten years. The efficiency and health of ruminants is influenced by the mutualistic relationship between the microorganisms living in their gastrointestinal tracts (GITs) and the host (Schluter & Foster, 2012). The immune system of the host and the GIT microbiota interact to affect not just the GIT but also other tracts in the body. Microorganisms perform various functions in detoxifying harmful substances present in feed, thereby lowering the risk of toxin-related diseases in livestock (Xu et al., 2021).

a) Commensal symbionts

The commensal microbiota improves animal health in several ways, including by aiding in the digestion of plant fiber that would normally be indigestible. Besides that, it supplies the host with building blocks such as carbohydrates, peptides, and lipids, plus minerals and energy sources like volatile fatty acids. It also modifies the immune system by producing cytokines and antibodies (Sanjorjo, Tseten, Kang, Kwon, & Kim, 2023). Pathogens and immune cells are physically separated by the microbiota, which also competes with them for resources and adhesion sites (Leijon, Atkins, Waller, & Artursson, 2021). Furthermore, these microorganisms stop the growth of harmful substances by generating antimicrobial agents. It includes organic acids, hydrogen peroxide, bacteriocins, and biosurfactants (Yang et al., 2024).

Throughout these organs, the distribution changes according to the factors associated with the host and unique physiochemical characteristics of the colonization site, ruminants, like cattle, sheep, and goats, depend on their gut flora for proper digestion and nutritional absorption as well as general health (Xu et al., 2021). The rumen, the main stomach chamber in ruminants, is home to these microorganisms, which are mostly bacteria, archaea, protozoa, and fungus as summarized in Table 2 (Sanjorjo et al., 2023). They aid in the digestion of complex plant elements like cellulose and hemicellulose, which the animals are unable to digest on their own (X. Chen et al., 2022).

A case study in which one of the important cellulolytic bacterium found in the rumen of many ruminants is Fibrobacter succinogenes (Fakih et al., 2023). One of the main components of cell walls in plants, cellulose, is broken down by this bacterium into simpler sugars that the host can ingest and use as fuel. This relationship is a prime example of commensal symbiosis, in which the ruminant gains in better nutrient absorption and fiber digestion, and the bacteria benefits from a consistent environment and supply of nutrients. Research shows that F. succinogenes colonizes the rumen after birth, establishing a stable population that resides in animals for a lifetime. It produces cellulolytic enzymes that efficiently degrade cellulose into fermentable sugar (Al-Shawi et al., 2020). The significance of this commensal connection is demonstrated by the improved growth rates and conversion of feed efficiency of ruminants with a healthy population of F. succinogenes (Swift et al., 2021).

b) Parasitic symbionts

A relationship in which one organism, the parasite, benefits at the burden of the other, the host, is known as a parasitic symbiosis. Because it depends on the host for resources like nutrition, the parasite frequently causes varying degrees of damage to the host (Ichihashi et al., 2020). For example, ticks on mammals feeding on their blood such as deer dogs and humans, fleas fees on human blood and cause allergic reactions. They can be the source of various diseases e.g., Lime disease parasitic symbionts include plasmodium in humans causing malaria, liver flukes in sheep and cattle. Numerous pathogenic microorganisms can cause diarrhea, viruses (such as bovine viral diarrhea and ovine rota-virus), bacteria (for instance Salmonella enteritidis and E. coli K99/O157), and parasites such as Cryptosporidium sp. and Coccidium sp. (Tsao et al., 2021). Slow weight increase in sheep and beef cattle due to respiratory diseases can result in significant financial losses for producers of lamb and beef (Yang et al., 2024).

Table:2 Composition of rumen gut microbiota (Jwher & Ezzulddin, 2022; Sanjorjo et al., 2023)

Type of Microbiota	Examples
Bacteria	*Fibrobacter succinogenes, Ruminococcus flavefacien, Ruminococcus albus, Butyrivibrio fibrisolvens,Prevotella ruminicola Bacteroides, Methanobrevibacter ruminantium, Selenomonas ruminantium*
Archea	*Methanobrevibacter ruminantium, Methanosarcina barkeri, Methanobacterium formicicum, Methanomicrobium mobile*
Protozoa	*Entodinium, Epidinium, Diplodinium, Isotricha*
Fungi	*Neocallimastix frontalis, priomyces, Orpinomyces, Anaeromyces*

Body cavities, epidermis mucosa, respiratory, gastrointestinal, and urogenital tracts are all colonized by microbial populations as shown in the cattle microbiome (Hobson & Stewart, 1988). Throughout these organs, the distribution changes according to the host factors and unique characteristics of the colonization site of different animals such as ruminants, like cattle, sheep, and goats, depend on their gut flora for proper digestion and nutritional absorption as well as general health (Xu et al., 2021). They help in the digestion of complex plant elements like cellulose and hemicellulose, which the animals are unable to digest on their own (X. Chen et al., 2022).

4. Habitat and Transmission of Microorganisms within Animals

4.1. Environmental and Host Factors Influencing Microbial Colonization

An imbalance in the microbiome, known as dysbiosis, is marked by a disruption in the balance of microorganisms, leading to a decrease in diversity, an overgrowth of harmful pathogens, a decline in beneficial commensals, and changes in metabolic function. This imbalance is directly linked to the progression of chronic inflammatory and metabolic diseases, as well as an enhance risk of infections (Frank et al., 2007; Turnbaugh et al., 2006). Difference in the composition of various microorganisms between and within host species is caused by multiple factors that can be lifestyle, age, geography nutrition, and life events (such as antibiotic treatments and stress) (Cammack, Austin, Lamberson, Conant, & Cunningham, 2018; Spor, Koren, & Ley, 2011; Taschuk & Griebel, 2012).

Host phylogeny significantly influences microbiome composition, with trends in core microbiota largely restricted to specific host phylogenetic clades (Ley et al., 2008). While some animals rely on endosymbionts for survival, others have minimal evidence of a core microbiome (D Ainsworth et al., 2015). Most animals fall in between, with a core microbiome that provides benefits but is shaped by dietary variation, social groups, and environmental exposures, leading to inter-individual microbiome variation within a species (R. K. Singh et al., 2017).

Host genetics significantly influence the microbiome composition, influencing host characteristics like immunology, metabolism, and morphology. Understanding host genes and metabolic pathways helps understand physiological processes and evolutionary forces acting on the host and microbiome (Ryu & Davenport, 2022). Because different microbial species have been a greater part of metabolic enzymes encoded in their genomes, enabling them to metabolize varied substrates to support growth, diet plays a major role among these parameters (Scott, Gratz, Sheridan, Flint, & Duncan, 2013). Seasonal variations in diet or other environmental stressors (drought, habitat fragmentation, etc.) might modify the taxonomic composition of the gut microbiota or the expression of metabolic genes within the same species. Certain Bacteroides members, for instance, can change the production of enzymes that break down carbohydrates based on the availability of complicated plant-derived substrates as opposed to endogenous host substrates like mucins (McNulty et al., 2013). The exposed living environment, including temperature, humidity, location, and herd management, significantly influences the symbiotic relationship of rumen microbiota and host (K. Liu et al., 2021). Changes in host living conditions cause microbial genomes in the gastrointestinal tract to shift, affecting the gut microbiomes of different hosts (K. Liu et al., 2021).

4.2. Vertical and Horizontal Transmission Mechanisms

Research on the different microbiomes has surged for the last 15 years, driven by growing interest in its link to health and disease, and technological advancements. The impact of collaborative efforts like the Human Microbiome Project and Earth Microbiome Project have further accelerated this field of study (Ghosh & Pramanik, 2021; Gilbert, Jansson, & Knight, 2014). Unlike animals and plants, which pass on their genomes to their offspring through a standard and well-understood process, microbiomes are inherited and shared through various unconventional methods, including both vertical (from parent to offspring) and horizontal (between individuals) transmission pathways (Rosenberg & Zilber-Rosenberg, 2021). Horizontal transmission originates from the environment, while vertical transmission involves the migration of microbiota from parent to child without interacting with environmental bacteria (Rosenberg & Zilber-Rosenberg, 2021).

Although horizontal gene transfer is difficult to classify as an ecological interaction, it may be advantageous to both parties and fall under the umbrella of cooperation. The well-known instance is when antibiotics are used in a medium containing multiple microbial taxa, and most bacteria are first sensitive to a substance they have never encountered before. Antibiotic-resistant mutants will spread widely. Lastly, susceptible cells from the same taxon or from a different taxon may receive the DNA fragment that confers antibiotic resistance (Moënne-Loccoz, Mavingui, Combes, Normand, & Steinberg, 2015).

Pregnancy, nursing, and birthing all include the critical process of microbe transmission from mother to child. The mother's gut microorganisms are extremely important in determining how the offspring's immunity and metabolic functions develop (S. Liu, Zhang, & Ma, 2023). During pregnancy, the mother's gut microbes change and prepare for vertical transmission, and short chain consisting of fatty acids produced by these microbes promotes the growth and development of the neonatal immune system (S. Liu et al., 2023). After birth, the mother's microbes transmit to the baby through breast milk, influencing the development of their immune system. Immune cells and blood flow mediate the microorganisms' migration from the gut of the mother to the baby and mammary gland, enabling the beneficial flora to be passed on to the future generation as described in Figure 1 (S. Liu et al., 2023). This process is essential for the maturation of the offspring's immune system and has a long-term impact on their health and disease susceptibility (S. Liu et al., 2023)

4.3. Role of Animal Behavior in Microbial Dispersal

Animals' bacterial communities can be influenced by their social structure and behavior, either through shared habitats or direct physical contact. The genetic composition of the microbiota may change because of these social processes, which may have an impact on the services that microbiomes offer to their hosts. The microbiome can influence host social behavior. Microbial communities can convey a great deal of information about animals because of their metabolism, which can release volatile compounds that are detectable by animals, and because bacterial communities can change depending on the characteristics of their hosts. Their hosts may even appropriate this function for social signaling. Additionally, microorganisms have the unique characteristic to actively "hack" the host nervous system to enhance microbial transmission, essentially altering host behavior for their fitness.

Microbes spread socially through grooming, feeding, mouth-to-mouth interactions, and coprophagy, offering health benefits to hosts. Gut bacteria from social interactions reduce honeybee vulnerability to parasites like *Lotmaria passim* and *Crithidia bombi* while solitary bees lack these gut microbes causing more severe impacts.

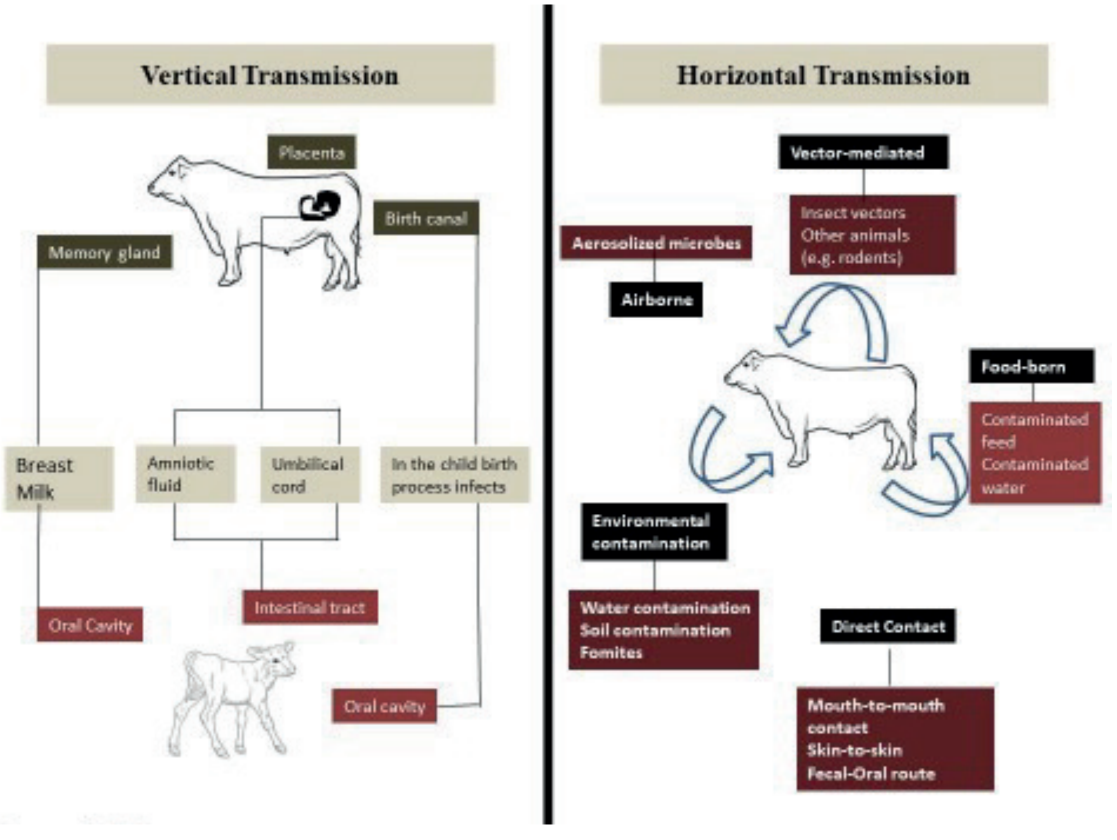


Figure 1; Diagram showing pathways of microbial transmission (vertical and horizontal) in livestock. On the left side in figure vertical transmission modes are given. On the right side horizontal transmission modes are given. Microbial transmission in livestock v in vertical transmission happens via placenta, memory glands & birth canal while in horizontal transmission transfer can be from aerosolized, vector mediated, food borne, environmental contamination and can be via direct contact.

5. Role of Microbe-Animal Symbiosis in Health and Disease

5.1. Disease Tolerance and Immune Modulation:

The formation of the gastrointestinal tract (GIT) microbial community is essential for activating and regulating a calf's immune system in its early life stages (Gomez, Galvão, Rodriguez-Lecompte, & Costa, 2019). Previous studies have indicated that the hindgut is vital for immune system development in animals with single-chambered stomachs (Mulder et al., 2011). Current research shows that the microbial population that resides in the hindgut portion of animal gut, is equally important for the proper development of a calf's immune system (Malmuthuge & Guan, 2017), and this immune system imposes an impact on GIT health of calf by affecting digestion and energy production. The immune system engages with the microbiota via the immunoregulatory pathway, that impact the production of cytokines and cytokinetic reactions as well as prostaglandin E2 (Feng, Chen, & Wang, 2018). These interactions subsequently influence brain function (Das & Ranjan, 2020). The main role of the microbiota-gut-brain-axis (MGBA) in the modulation of host health has been extensively studied in humans as well as in animals. This bidirectional conversation can be influenced by infections in the gastrointestinal tract (GIT) microbiota, which can negatively impact the brain function and increase sickness behavior in animals, or by a healthy GIT microbiota, which can enhance brain function. Germ free animals studies reveals a significant factor about inclusion of probiotics and prebiotics leads to behavioral changes (Kraimi et al., 2019).

Livestock production often involves unavoidable stressors like weaning and transportation. Studies have shown that transportation stress increase level of some pro-inflammatory cytokines, hormones including adrenocorticotropic (ACTH) and cortisol (Li et al., 2019). Additionally, an abundance of ruminal Lactobacillus has been found to correlate positively with interleukins (IL-6 and IL-4). The addition of prebiotics and probiotics in ruminant diets can help prevent HPA axis signaling, which reduces anxiety. Research on dairy calves indicates that before weaning, a multispecies probiotic supplement improves growth, decreases diarrheal occurrence, changes the fecal microbiota (raising Bifidobacterium, Lactobacillus, Collinsella, and Saccharomyces), and lowers serum IgA, IgG, and IgM concentrations (Y. Wu et al., 2021). Overall, the GIT microbiota significantly affects animal behavior and health by directly influencing the immune system (Han et al., 2017).

5.2. Detoxification and Metabolic Cooperation:

It has been demonstrated that microbes possessing certain metabolic capacities can exist in the natural world. It is probable that bacteria that degrade toxins eaten by herbivores are widespread among herbivorous species (Hammer & Bowers, 2015). Strong selection pressure for breakdown capacity should be applied to microorganisms in high toxin abundance local habitats, such as those around toxin-producing plants (Stapleton, Kohl, & Dearing, 2022). Moreover, because of horizontal gene transfer and quick generation rates, detoxifying capacity should proliferate quickly among microbial communities. Additionally, microbes have the benefit of catalyzing a wide variety of reactions that are not yet understood in herbivores including vertebrates and invertebrates. Examples of these reactions include those catalyzed by isothiocyanate hydrolase and catechol dioxygenases (Wadke, Kandasamy, Vogel, & Lah, 2016). Furthermore, microorganisms generate laccases, which are incapable of carrying out phenolic detoxification in animals while vertebrate herbivores lack these enzymes (De Fine Licht et al., 2013).

5.3. Microbiome Dysbiosis and Disease Development:

Disturbances in the delicate equilibrium of the microbiological consortium during ailment instances triggers dysbiosis, which can result in the emergence or disappearance of distinct microbial species (Wilkins, Monga, & Miller, 2019). Dysbiosis can cause or worsen various disease phenotypes in cattle, such as Johne's disease, uterine infections, and metabolic disorders like ruminant acidosis (Derakhshani et al., 2016; Jeon et al., 2016).

When intramammary infections occur, mastitis is characterized by an inflammatory reaction that compromises the physical barrier of the mammary glands (Abebe, Hatiya, Abera, Megersa, & Asmare, 2016). It is categorized into clinical and subclinical forms based on disease severity. Subclinical mastitis has no symptoms despite the presence of infections, whereas clinical mastitis exhibits noticeable alterations in the milk and udder (A. Ashraf & Imran, 2018). Usually, a variety of bacterial species are the etiological agents of mastitis. Major pathogens include *Mycoplasma sp., Escherichia coli, Streptococcus dysgalactiae, Staphylococcus aureus,* and *Streptococcus agalactiae.* The coagulase-negative *Staphylococci* and *Corynebacterium* species are examples of minor pathogens (Dalanezi et al., 2020). Persistent diarrhea is a hallmark of Johne's illness, which causes emaciation, malnutrition, and large financial losses for the global livestock business (Rathnaiah et al., 2017). The non-motile, slow-growing mycobacteria known as Mycobacterium avium subsp. Johne's sickness is due to paratuberculosis (MAP) (Britton, Cassidy, O'Donovan, Gordon, & Markey, 2016).

6. Dynamics of Microbe-Animal Symbiosis in Antibiotic Resistance

6.1. Evolution of Antibiotic Resistance in Symbiotic Microorganisms:

Livestock gastrointestinal environments frequently include low and sublethal amounts of antibiotics, which promote the formation of ARGs and help avoid sickness. Merely 5–15% of studies on antibiotic-resistant genes published between 2000 and 2020 explored the role that cattle may play in potential hazards, even though livestock utilizes over half of all antibiotics used worldwide. As of 2020, the proportion of relevant research on livestock out of all published articles on antibiotic resistance is still less than 17%, despite an increase in this area. Thus, to lessen the risk of antibiotic resistance, funding for this kind of study is required. The prolonged use of antibiotic to encourage animal development and prevent diseases may be the reason for the higher content of residual antibiotics in livestock farmyard waste when compared to human waste (Sim et al., 2011). As a result, microorganisms on animal farms are under more pressure to evolve resistance genes through natural selection. Layer and sow dung had higher levels of ARG pollution than chicken and piglet/fattening pig manure, respectively, however the ARG level in chicken manure appeared to be higher in virtually all kinds of poultry and livestock farms than in pig and cow farms (Qian et al., 2018).

Tetracycline and sulfa resistance genes were measured in terms of number and variety in chicken manure from small- and medium-sized chicken farms in Hangzhou, Eastern China by Cheng et al. (Cheng, Chen, Su, & Yan, 2013). The results showed that the relative abundance of various ARGs in the feces of medium-sized chicken farms was higher than that of small chicken farms. Moreover, tetQ exhibited the highest relative abundance in these farms, followed by tetM and sul2. According to a study, hatcheries were common place for blaOXA-1, blaMOX-like, blaCIT-like, blaSHV, and blaFOX (Osman et al., 2018). Antibiotics containing tetracycline are frequently used to treat illnesses and also encourage growth in pig farms (Q. Q. Zhang, Ying, Pan, Liu, & Zhao, 2015). As a result, pig feces frequently include tetracycline resistance genes, with the genes that safeguard ribosomal proteins being the most common.

6.2. Impact of Antibiotic Use on Livestock Microbiomes:

Shortly after the extensive use of antibiotics as growth promoters in cattle in the 1950s, there have been multiple cases of drug-resistant pathogen-related outbreaks in humans and farm animals worldwide (Datta, 1962). Antibiotic-resistant microorganism infections now cause large healthcare and financial losses, as well as longer hospital admissions, higher death rates, and an increased risk of complications (Carmeli, Troillet, Karchmer, & Samore, 1999; Cosgrove, Kaye, Eliopoulous, & Carmeli, 2002; Lautenbach, Patel, Bilker, Edelstein, & Fishman, 2001). Antibiotics that do not have adequate safety profiles must be used to treat infections brought on by resistant bacteria. For example, colistin, an antibiotic of last resort, can successfully treat infections caused by highly resistant *Pseudomonas aeruginosa* and *Acinetobacter baumannii*; however, patients who take it suffer from severe renal failure and deterioration (Levin et al., 1999). The discovery in 2016 of plasmid-mediated resistance to colistin in Escherichia coli isolates isolated from pigs raises even more concerns over the possibility that the drug's therapeutic benefits may be short-lived (Y. Y. Liu et al., 2016). If all of our prescription antibiotics are eventually rendered ineffective by resistant bacteria, humanity will return to the pre-antibiotic era, when even little cuts can become infected and have fatal consequences (Ventola, 2015).

6.3.Strategies to Mitigate Antibiotic Resistance:

The numbers of *Campylobacter* jejuni in broiler chicks were consistently reduced in experiments employing bacteriophage treatments in vivo (Carvalho et al., 2010; Loc Carrillo et al., 2005). According to Chinivasagam and colleagues, phage cocktails were used to manage *Campylobacter* in broiler chickens at the farm. The bacteriophage mixtures were chosen using *E. coli* and *C. jejuni* as their targets. Before the birds were killed, the phages were given orally to 47-day-old birds for a whole day. The market-ready broilers' levels of *Campylobacter* were shown to be effectively reduced by the phage cocktails, according to the study the authors recommended extending the therapy for more than 24 hours to ensure continued phage replication for the biocontrol of *Campylobacter* in vivo, nevertheless, because some of the birds in farm B had low phage titres (Chinivasagam et al., 2020). Animal feeds have traditionally included probiotics, prebiotics, and synbiotics to promote the expansion of aquaculture and animal husbandry (Tan, Chan, Lee, & Goh, 2016).

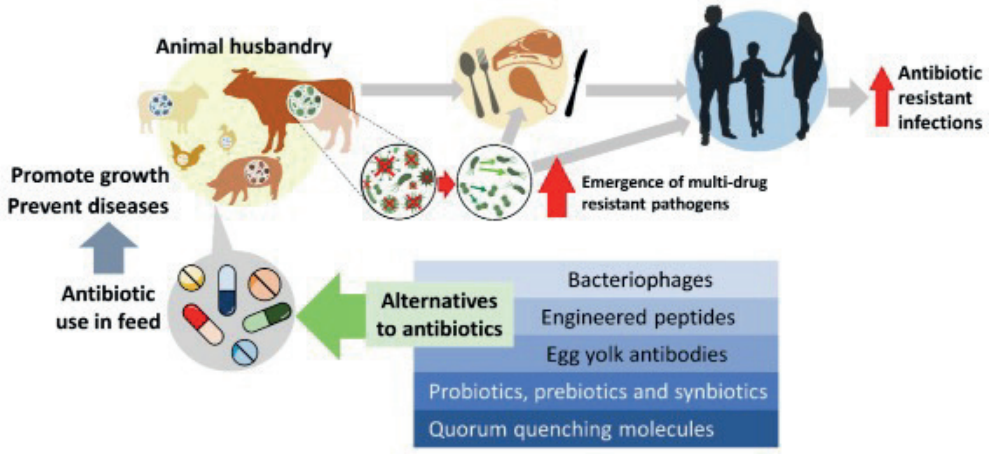


Figure 2. Process of antibiotic resistance development in microbial communities of livestock

7. Biotechnological Applications of Microbe-Animal Symbiosis

7.1. Probiotics and Animal Health:

The use of probiotics in animals has increased since the mid-1970s (Fuller, 2012). Probiotic supplements have been administered to farm animals as therapeutic supplements to lower morbidity and mortality, enhance feeding behavior, and boost yields of meat, milk, and eggs yield (Kabir, Rahman, Rahman, Rahman, & Ahmed, 2004; Naglaa, 2013; Rai, Yadav, & Lakhani, 2013). Probiotics have been shown to have the ability to limit the growth of undesirable microbes through at least two different mechanisms direct cell-to-cell contacts and/or the creation of inhibitory chemicals (Jonkers, 2016). According to Chaucheyras-Durand and Durand (2010), probiotics produce compounds known as organic acids, hydrogen peroxide, bacteriocins, and biosurfactants, which are antimicrobials and can inhibit the growth of pathogenic bacteria. Lactic and acetic acids are the most often produced compounds by probiotic bacteria; they lower pH and prevent the growth of infections. Additionally, probiotics strengthen immunity against intestinal infections by competitively colonizing intestinal adhesion sites and nutrients (Boirivant & Strober, 2007; Parvez, Malik, Ah Kang, & Kim, 2006).

Probiotics are thought to upregulate the expression of toll-like receptors (TLRs), which is one complex way in which they stimulate the innate immune system. Tumor necrosis factor-α (TNF-α), interleukin-4 (IL-4), and interferon-γ (IFN-γ) are among the cytokines that are released as a result ((R. Ashraf & Shah, 2014). According to Casas and Dobrogosz (2000); Ezema (2013) it has been shown that taking probiotics increases illness resistance and reduces metabolic stress and mortality. A basic diet supplemented with a probiotic blend containing *Lactobacillus casei, Lactobacillus acidophilus, Bifidobacterium thermophiles,* and *Enterococcus faecium* increased the content of immunoglobulins (Ig) M and G in turkeys. This enhanced the illness resistance and growth efficiency of the turkeys (ÇEtïn, Güçlü, & Cetin, 2005).

7.2. Microbial Bioremediation and Environmental Applications:

The use of microorganisms for example bacteria to enhance the environment is known as bioremediation, which goes beyond probiotics. Additionally, garbage and other hazardous pollutants are neutralized, detoxified, removed, cleaned up, broken down, and/or decomposed into less toxic or non-toxic chemicals using microorganisms in the bioremediation process. In an aquaculture setting, microorganisms have easy access to the digestive tracts of the animals and come into close touch with them through their gills and food supply.

Probiotics can be applied in two different ways directly to food (combined into the diet formulation) or indirectly to the environment (mixed with water and/or sediment). The first method involves adding probiotics, which are beneficial microbes, and decomposers to the feed. These additives work to improve feed quality by changing the feed's constituents into forms that are easier for the intestines to absorb, which increases feed digestibility. The ecology around the second application will be better since it will break down harmful substances like ammonia, sulfur, fish excrement, and surplus feed that could attract pathogens and other undesirable micro- and macroflora.

Meanwhile, adding compost to the soil is one approach to enhance its environmental quality and it also introduces bacteria to the soil. Using a starter or microbes to speed up the organic material's beneficial decomposition for plants is a more efficient way to create compost. Applying compost to agricultural land has two advantages it increases the amount of organic matter in the soil and improves the microbial biota of the soil. Effectively employing microbes to enhance agriculture, animal husbandry, and fisheries requires the development of tailored microbial cocktails for each specific type of plant, animal, or fish (Kompiang, 2009).

7.3. Agricultural Innovations: Enhancing Animal Productivity:

Animal breeding primarily focuses on the genetic development of economically important qualities such as meat output, meat quality, and illness resistance. The CRISPR/Cas system is a fantastic resource for animal biotechnology research and cattle production. It has transformed the field of genetic manipulation and dramatically expanded its applicability. Along with base editing and gene editing, post-transcriptional engineering using CRISPR/Cas system-based technologies and transcriptional control have advanced quickly, prime editing and transcriptional regulation (Gaj, 2021; Kantor, McClements, & MacLaren, 2020).

One of the most important applications of genome editing is to increase the resistance in farm animals against diseases. In addition to causing the animal husbandry industry to incur significant financial losses, infectious illnesses in farm animals also present a risk to human health producing anti-foot-and-mouth disease virus (FMDV) shRNA through the breeding of antiviral animals, such as pigs and cattle devoid of prion protein has been successfully accomplished through the use of transgenic and gene targeting techniques (Hu et al., 2015; Richt et al., 2007). Recently, the efficiency of raising animals resistant to disease has greatly increased thanks to genome editing technology, when the leukotoxin from *Mannheimia haemolytica* interacts with the uncleaved signal peptide of CD18 protein, ruminant leukocytes are cytolyzed causing acute severe lung tissue damage and acute inflammation, which causes a significant financial loss for the global cow sector (Shanthalingam

& Srikumaran, 2009). Zinc finger nuclease (ZFNs), a protein used in first-generation gene editing technology, has been used to create a single amino acid mutation in the bovine CD18 protein (Shanthalingam et al., 2016). Cattle with the CD18 gene altered had leukocytes that expressed CD18 protein without the signal peptide; as a result, the leukocytes were immune to the cytolysis caused by leukotoxin.

8. Techniques for Studying Animal-Microbe Symbiosis

8.1. Omics Technologies: Metagenomics, Metatranscriptomics and Metaproteomics:

The microbial communities (microbiota) that exist in the gastrointestinal tract (GIT) of cattle are being studied using state-of-the-art omics technologies instead of traditional cultivation methods and pure culture characterization. Culture-independent molecular techniques are widely used because of the discrepancy between in situ and cultivable diversity. The 16S ribosomal RNA gene-based techniques for microbial community profiling have grown as tools for describing microbial communities and the relationships amongst the microbes inhabiting the gastrointestinal tract. Shotgun pyrosequencing of the cDNA and total DNA yields metagenomic or metatranscriptomic data, respectively. The reads need to be quality filtered, contig assembled, binned, and allocated to potential gene functions and taxonomy. Metaproteomic studies investigate a sample's protein inventory at a particular moment in time. This makes it possible to identify the metabolic pathways expressed by the active microbial fraction. To obtain a pure protein sample and prevent the co-extraction of eukaryotic proteins, the first crucial step is to identify an optimal sample preparation strategy. The technological equipment that is available determines the workflow that follows.

8.2. In vivo and In vitro Models:

Scientists studying symbiosis are resorting to model systems. Fortunately, a number of potent models that were crucial for understanding developmental biology have also been used to research host-microbe interactions, such as hydra, the fruit fly, worm, and mouse (Bosch, 2013; Burns & Guillemin, 2017; Charroux & Royet, 2012; Clavel, Lagkouvardos, Blaut, & Stecher, 2016; Davis, Bryda, Gillespie, & Ericsson, 2016; Douglas, 2018; Klimovich & Bosch, 2018; Martino, Ma, & Leulier, 2017; Schulenburg & Félix, 2017; Shapira, 2017; Stagaman, Burns, Guillemin, & Bohannan, 2017; F. Zhang et al., 2017; Zhu et al., 2016).

Nematostella vectensis, the starlet sea anemone, is a good model for understanding the mechanisms driving dynamic colonization processes throughout host development because of the distinct microbiota it has for each of its three developmental life phases (Har et al., 2015; Mortzfeld et al., 2016).The ontogenetic core signature of N. vectensis´ was preserved despite significant changes in the microbiological composition caused by environmental fluctuations. Moreover, analysis of the bacterial communities of N. vectensis polyps from five different populations revealed a strong correlation between host biogeography and bacterial diversity, despite years of laboratory culturing (Mortzfeld et al., 2016).

Without being constrained by ethical considerations, in vitro fermentative models are thought to be excellent tools for screening a wide range of substances, including pathogens, medications, toxic or radioactive compounds, and ingredients in food, to determine how they affect and are affected by microbial populations and gastrointestinal environments. More complex continuous in vitro models include one or more connected, pH-controlled chemostats that simulate different parts of the human colon and are infected with fecal bacteria (Venema & Van den Abbeele, 2013). Batch incubations using anaerobic conditions and dense fecal microbiota are another type of in vitro model.

Fermenters are usually inoculated with liquid fecal suspension obtained from a single individual or from a combination of feces from several subjects. In the last example, fecal samples are used to inoculate a fed-batch fermenter, producing a standardized inoculum that is frozen for storage. A method for immobilizing fecal microbiota in mixed xanthan-gellan gum gel beads was created by to maintain microbial variety and reach high cell densities throughout lengthy, continuous colonic fermentations. The model was recently improved to create PolyFermS, enabling the development of complex intestinal ecosystems in several reactors in a stable and repeatable manner (Cinquin, Le Blay, Fliss, & Lacroix, 2004). This makes it possible to compare the impacts of different treatments to a control reactor and examine their effects in parallel (Zihler Berner et al., 2013).

Because of its transparent body that makes it possible to visualize microbial infection and colonization, and its genetic tractability, Caenorhabditis elegans has become a valuable model for studying host-microbe interactions. Furthermore, there are morphological and functional similarities between the intestinal cells of C. elegans and other animals, such as vertebrates (Brenner, 1974). The bacteria that inhabit the intestinal lumen spontaneously make up the C. elegans gut microbiome. Feeding fluorescently tagged C. elegans bacteria and watching for fluorescence in the lumen is a typical way to see the presence of bacteria in the intestine. However, research has demonstrated that fluorescence is unable to differentiate living, intact bacteria from dead ones, with GFP-expressing E. coli OP50-1 demonstrating TEM revealed no intact bacteria, although there was fluorescence in the gut lumen (Hsiao, Chen, Yang, & Ho, 2013). When fluorescently tagged transgenic bacteria are used in trials to explore the microbiome colonization of the C. elegans gut, this disparity might cause confusion and possibly lead to inaccurate findings about the ability of bacteria to develop a niche and proliferate in the gut lumen.

Confocal laser scanning microscopy (CLSM) is one of the methods that is utilized often (Pawley, 2006). Fungi, plants, and other plant-like creatures have deep relationships and complex structural relationships with their substrates. In the heyday of their existence, CLSM emerged as a common tool for analyses of their interactions with microorganisms.

With CLSM, three different categories of objects can be identified (1) genetically modified organisms (GMOs) producing fluorescent proteins; (2) autofluorescent substrates, cells, and tissues; and (3) cells, tissues, and molecules stained with one or more fluorochromes. Since autofluorescent signals on biological and synthetic substrates are usually viewed as a negative aspect of CLSM images, efforts are often undertaken to prevent them (Lo Piccolo et al., 2010).

8.3. Bioinformatics and Computational Approaches:

With CLSM, three different categories of objects can be identified (1) genetically modified organisms (GMOs) producing fluorescent proteins; (2) autofluorescent substrates, cells, and tissues; and (3) cells, tissues, and molecules stained with one or more fluorochromes. Autofluorescence of synthetic and biological substrates is usually viewed as a negative. A plethora of bioinformatic tools have been developed and are extensively employed in the processing of metagenomic and amplicon sequence data. Researchers can now perform integrated metagenomic analyses and visualize results without command-line operations or strong computational knowledge thanks to web servers like MG-RAST (Meyer et al., 2008), IMG/M (Markowitz et al., 2014), EBI Metagenomics (Hunter et al., 2014), and SILVAngs (Quast et al., 2013), as well as pipelines like MEGAN (Schloss et al., 2009), QIIME (H. M. Chen & Lifschitz, 1989), and Mothur (Schloss et al., 2009).

By dividing reads into distinct species using particular sequence features found in a metagenomic dataset, composition-based methods enhance the efficiency of de novo metagenomic assembly. For instance, bin sequences based on the composition and coverages of tetra-nucleotide frequencies, such as MaxBin (Y. W. Wu, Tang, Tringe, Simmons, & Singer, 2014), metaBAT (Kang, Froula, Egan, & Wang, 2015), and CONCOCT (Alneberg et al., 2014).

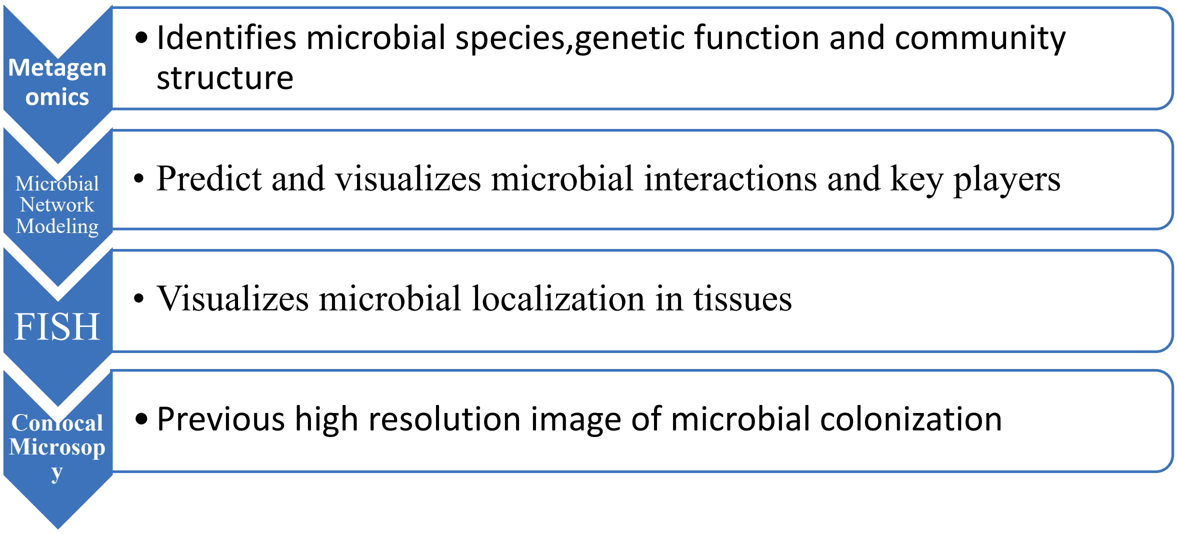


Figure 3. Schematic showing various techniques and their applications in studying symbiosis in livestock.

9. Genomic Insights into Prokaryote–Animal Symbioses

Due to the ecological ubiquity of bacteria, it is common to discover a number of prokaryotic species interacting closely with members of different eukaryotic taxa, frequently resulting in the long-lasting partnership known as symbiosis (Moya, Peretó, Gil, & Latorre, 2008). The link between the host and symbiont in the majority of prokaryotic and eukaryotic symbioses is so intimate that the microorganisms cannot be cultivated, making them challenging to research (Moya et al., 2008). Advances in transcriptomics, genome sequencing, and metagenomics have opened new avenues for studying symbiosis, enabling cross-species comparisons of bacterial evolution and host integration stages (J. P. McCutcheon & Moran, 2007; Shigenobu, Watanabe, Hattori, Sakaki, & Ishikawa, 2000).

9.1. Comparative Genomics of Host and Symbionts:

Symbionts genome;

The genomes of intracellular etiologic and protocooperative bacteria are smaller and include more AT (J. J. J. N. R. G. Wernegreen, 2002). Reductive-genome evolution occurs due to population dynamics and new environment requirements. Many genes are eliminated, while others become redundant, promoting genetic drift and allowing accumulation due to natural selection (Itoh, Martin, & Nei, 2002; N. A. J. P. o. t. N. A. o. S. Moran, 1996; Moya et al., 2008). These factors work together to advance the range of genes that can vanished and decrease the likelihood of the hereditary interchange through crossing over. These genes include those that are involved in genetic material healing and recombination, which can be advantageous but are not essential (Moya et al., 2008). Despite their small size, the smallest bacterial genomes prioritize genes essential for basic cellular processes like transcription, translation, and replication. Surprisingly, the only other consistently preserved genes are those involved in protein folding and stability, specifically Hsp70 molecular chaperone complex. These microscopic creatures' survival and ability to function depend heavily on these enzymes (J. P. J. C. o. i. m. McCutcheon, 2010).

Endosymbiont genomes have smaller, higher AT contents, likely due to DNA repair loss and mutational bias towards AT, affecting protein structure and function, impacting numerous genes (J. J. J. C. o. i. g. Wernegreen & development, 2005). The size reduction and AT content increase in endosymbionts vary based on the age of the association, with younger associations having smaller genomes and higher AT content (Baumann, 2005; Dale, Maudlin, & Microbiology, 1999; Moya, Latorre, Sabater-Muñoz, & Silva, 2002).

After transitioning to an obligate symbiosis, there was a massive loss of genes (10-20% retention) (Dale & Moran, 2006) likely due to large deletions and chromosomal rearrangements facilitated by mobile elements like insertion sequences (N. A. Moran & Mira, 2001). These mobile elements were abundant in recently acquired endosymbionts but were later removed as they became detrimental, leading to genome degradation and streamlining in older associations (N. A. Moran, Plague, & development, 2004; Plague, Dunbar, Tran, & Moran, 2008). When a genome shrinks, it's mainly because genes are being lost over time, spread out across the genome. This happens in a specific pattern a gene becomes inactive due to small changes, then gets shorter and shorter until it's completely gone (Gómez-Valero, Silva, Simon, & Latorre, 2007; Silva, Latorre, & Moya, 2001). The main reason for genome shrinkage is gene downsizing due to deletion or mutation, not just their shortening (Pérez-Brocal et al., 2006).

It is implied by host specialization that the host is now reliant on the bacterium for survival and procreation. The host's adaptive alterations comprise the creation of focused cells where microbes live, functional mechanisms for regulating microbial inhabitants, and adjustments to its immune system to combat the invader cells (Moya et al., 2008).

9.2. Genomic Adaptations in Symbiotic Relationships:

The hologenome theory of evolution suggests that genetic variation in symbiotic microbiota or host can be caused by microbial amplification, novel strain acquisition, and horizontal gene transfer, while host genome variation during sexual reproduction and development promotes symbiotic interaction.

Larger endosymbiont genomes preserve genes involved in multiple metabolic pathways, while smaller genomes have most disappeared. Endosymbionts have limited transport capacities, despite conserved pathways for nutrient production (Ren & Paulsen, 2005). Cellulolytic microorganisms are crucial for livestock animal nutrition, with their early emergence in newborn ruminants indicating quick development and fiber utilization (Jami, Israel, Kotser, & Mizrahi, 2013; Moraïs & Mizrahi, 2019). Ruminal cellulolysis is primarily attributed to protists, fungi, and bacteria, but their specific roles remain a topic of debate (Delfosse-Debusscher, Thines-Sempoux, Vanbelle, & Latteur, 1979; Lee, Ha, Cheng, & microbiology, 2000). Because LAB and yeasts (S. cerevisiae) can influence the subtleties of microbial community in the rumen and the process by which dietary factors degrade and utilized as probiotics and ruminal activators (Doyle et al., 2019; Mohammed, Mahmood, & Abas, 2018). In order to identify microbial membrane patterns such as peptidoglycan via receptors, hosts have built molecular systems (Moya et al., 2008). Microbial sensors are evolutionary pathogen recognition receptors crucial for defense against invasive microbes. Probiotic strains may modify TLR expression to exert their defense against infections (Akira, Uematsu, & Takeuchi, 2006).

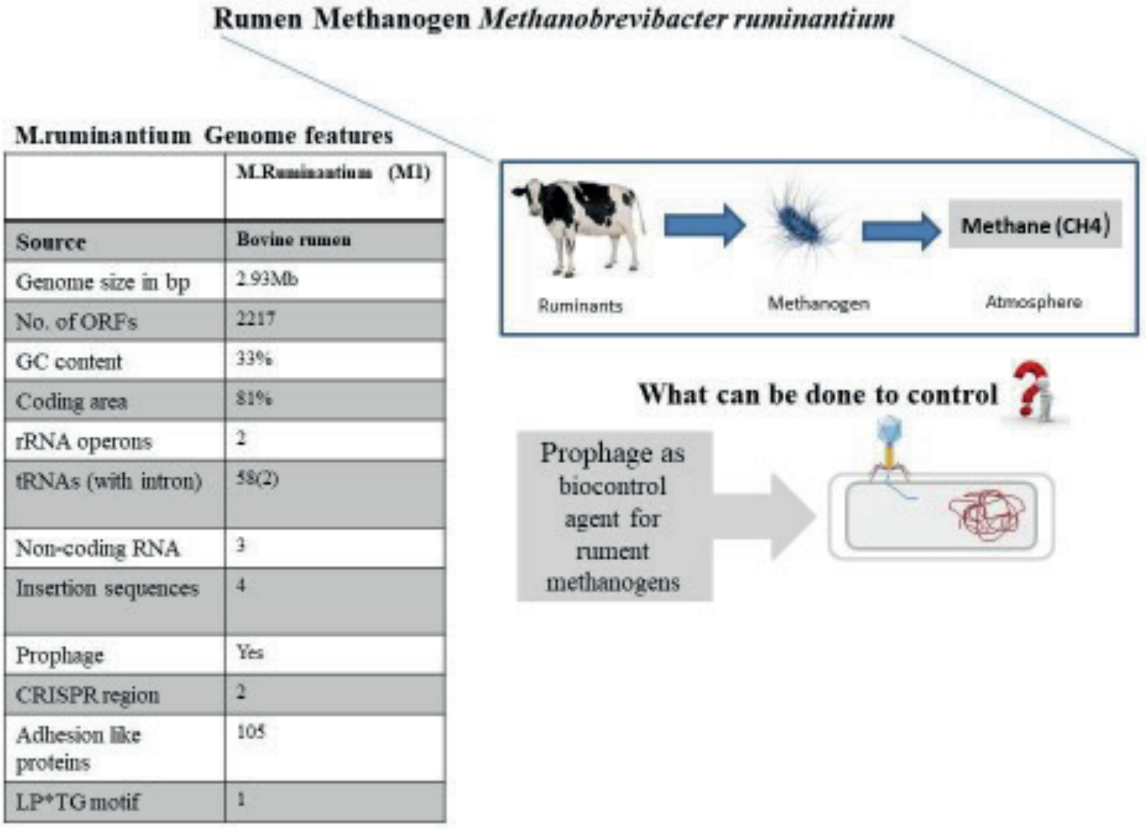
10. Applications in Synthetic Biology and Genetic Engineering:

It has been shown in recent years that these vast microbiomes and diversified microbiota have a tremendous impact on the life of both plants and animals.

10.1 Designing genetically modified probiotics

Nutritional supplements featuring active microbial entities that settle and reshape the enteric microbiota are known as probiotics (Dowarah, Verma, & Agarwal, 2017). Scientists first concentrated on using probiotics for treating and preventing abdominal infections brought on by specific bacterial strains that could replace unhealthy bacteria in the gut and stop the development of hazardous germs (Salas-Jara, Ilabaca, Vega, & García, 2016). Advanced probiotics (APs) and microbial-based therapeutic agents (MBTAs) with enhanced characteristics such as those engineered through precision microbiology have gained significant attention in the industry (T. P. Singh & Natraj, 2021; Steidler & gastroenterology, 2003).

Probiotics can affect the host in several ways, such as altering the enteric microbiota, regulating the defense system, and producing beneficial compounds. This enhances the host's defenses and promotes a balanced relationship between the host and microorganisms (Mugwanda et al., 2023). These peptides are essential for the immune system's stimulation, pathogen-killing, gut microbiota maintenance, and defense against harmful microbes (Mandal, Silva, & Franco, 2014). Additionally, probiotics aid in the digestion of fiber in cattle and lipids in humans. Certain probiotic strains have the capacity to activate certain facets of native protection (Alvarez-Olmos & Oberhelman, 2001; Torres-Sanchez et al., 2022). Genetic engineering has been used to enhance the health benefits of NGPs, targeting various illnesses and health problems in humans and animals (Abouelela & Helmy, 2024; T. P. Singh & Natraj, 2021). For example *Saccharomyces boulardii* and *cerevisiae*, two types of yeast, have been found to have probiotic properties in farm animals, altering the balance of gut bacteria, lowering the likelihood of microbial imbalance and generating essential nutrients and biological catalysts (Garcia-Mazcorro et al., 2020; Latorre et al., 2015; Ugwuoke, Okwesili, Dim, Okonkwo, & Ndofor-Foleng, 2021). Two beneficial bacteria, *Lactobacillus salivarius* and *Pediococcus parvulus*, found in the gastrointestinal tract of poultry, have shown to be resistant to harsh conditions like acidic environments, high salt concentrations, and bile salts. Moreover, they have been found to settle the spread of harmful germs like Salmonella, *E. coli*, and *Campylobacter* in laboratory tests (Menconi et al., 2014).



M.ruminantium Genome features

	M.Ruminantium (M1)
Source	**Bovine rumen**
Genome size in bp	2.93Mb
No. of ORFs	2217
GC content	33%
Coding area	81%
rRNA operons	2
tRNAs (with intron)	58(2)
Non-coding RNA	3
Insertion sequences	4
Prophage	Yes
CRISPR region	2
Adhesion like proteins	105
LP*TG motif	1

Figure 4. Genome comparison between a livestock host and its symbiont (Rumen Methogen Methanobrevibacter ruminantium); Ruman harbors methanogenic archea. Methane (a greenhouse gas) in ruminants is produced through the activity of methanogenic archaea, such as Methanobrevibacter ruminantium, which shows main role in ruminal methanogenesis process. Phage have been proposed as biocontrol agents for rumen methanogens and have main ecological impact on bacterial communities in the rumen (Hegarty & Klieve, 1999). The genomic sequence provides new insight

of this methanogen and helps for developing therapeutic interventions for methane mitigation

11. Innovative Perspectives on Pathogenic Relationships

11.1. Molecular Mechanisms of Pathogenesis

The term pathogenicity describes the potential of a pathogen to infect and inflict harm on host, making it a pathogen (Van Baarlen, Van Belkum, Summerbell, Crous, & Thomma, 2007). The host-pathogen interaction is like a lock and key, requiring a precise genetic match to enable colonization or infection. The genetic compatibility of both parties determines the outcome, with genetic variation, mutant selection, and interaction progression influencing the dynamics of this complex relationship (Lynch & Conery, 2003). Microbes and hosts can form relationships like parasitism, commensalism, or mutualistic symbiosis, with delicate balance. Disruptions can cause mutualists or commensals to become pathogenic, or introduce pathogenic bacteria to new hosts (Tanaka, Christensen, Takemoto, Park, & Scott, 2006). Animals sense helpful commensal microbes through receptors, which are crucial for preserving the host's health (Villena, Kitazawa, Van Wees, Pieterse, & Takahashi, 2018).

When a harmful pathogen enters the body, it triggers a rapid response from the immune system's "first line of defense" cells like stromal and epithelial cells, which act like sensors to detect and alert the body to potential threats (Matzinger, 2007). These ancient defense mechanisms, found in all animals and plants, help distinguish between harmless and harmful substances, and initiate a response to protect the body (Fontana & Vance, 2011; Glass, 2012). Bodies have an early warning system that detects harmful pathogens, like bacteria and viruses, through special receptors called Pattern Recognition Receptors (PRRs) (Kersse, Bertrand, Lamkanfi, & Vandenabeele, 2011). These receptors recognize specific patterns on pathogens that are different from our own cells and trigger an immune response to fight the infection. This early detection system is present in many cell types, including immune cells and cells lining our bodily surfaces (Kumar, Kawai, & Akira, 2011). Particularly most familiar PRRs are called toll-alike Receptors, and small changes in their sequence can affect how they respond to different pathogens (Werling, Jann, Offord, Glass, & Coffey, 2009). There are many other types of PRRs, including those that detect genetic material like RNA and DNA.

Damaged cells release "danger signals" that trigger an inflammatory response, alerting the immune system to potential threats (Glass, 2012). These signals, also known as "alarmins", are detected by specific receptors, including some that also detect pathogens (Manson, Thiemermann, & Brohi, 2012). Once pathogens enter the body, they trigger a cascade of signals that alert the immune system (Glass, 2012). This leads to a coordinated response, involving various signaling cascades and gene regulators, which ultimately activates production of particles that fight inflammation and infection, such as cytokines. If the immune response is strong and rapid, it can effectively clear the infection and prevent disease (Bianchi, 2007). The defense system has two essential arms natural and specific. The natural response happens quickly and triggers the adaptive response, which takes longer to develop. The adaptive response involves cells called T & B lymphocytes, which synergize to fight infection (Hill, 2012). There are different types of T cells, such as Th1 and Th2, which have different roles in fighting infection and regulating the immune response (Ouyang, Rutz, Crellin, Valdez, & Hymowitz, 2011). Macrophages, a type of immune cell, can also have different roles, such as pro-inflammatory and anti-inflammatory macrophages, which are involved in fighting infection as well as regulating the immune response (Mills, Kincaid, Alt, Heilman, & Hill, 2000). Understanding how these cells work together and how they are influenced by genetics can help us develop new ways to improve immune function and resistance to disease in animals (Calenge, Kaiser, Vignal, & Beaumont, 2010; Glass, 2012).

For example, Salmonella is an opportunistic cytosolic microbe that infects phagocytic or non-phagocytic cells and reproduces there. It uses protein export machines (injectosome system) and enters enterocytes and accessory cells in the intestine. Salmonella enters macrophages through phagocytosis, injects effector proteins, and travels to lymph nodes, liver, spleen, and lymphoid follicles (Ibarra & Steele-Mortimer, 2009). Host immune cells recognize Salmonella through conserved pathogenic molecular patterns (CPMPs) and host cell-derived danger signals (HCDDS), stimulating an immune defense response. This recognition is modulated by innate immune sensors (IISs) and pattern-recognition receptors (PRRs), which activate downstream signaling pathways, including NF-κB and triggering the production of immune-activating cytokines, to combat the invasive microorganism (Crawford et al., 2010; Kobayashi et al., 2002).

11.2. Host-Pathogen Interaction Studies

Our knowledge for control of animal protection systems against pathogens and their interactions with beneficial microorganisms has significantly improved because of the post-genomic era's technological advancements. Animal-microbe associations can so now be researched more quickly and thoroughly than ever before. Two of the main practical advantages of probiotic ingestion are immune activation and an even gut microbiota (Hammes & Hertel, 2002; Parracho, McCartney, & Gibson, 2007; Salminen & Isolauri, 2006).

Enterocin-producing Enterococci have been shown to promote health in food animals (poultry and rabbits) by fighting off harmful bacteria like Salmonella, Staphylococci, and others (A Lauková, Guba, Nemcová, & Mareková, 2004; Andrea Lauková et al., 2006; Simonová et al., 2009). These beneficial bacteria produce enterocins, which work in various ways to provide antimicrobial activity (Guillermo et al., 2015). For example, Enterococcus faecium (EF 55) has been found to increase the number of lymphocytes and boost the immune system in poultry infected with Salmonella (Levkut et al., 2012).

The pathogenic E. Coli, which can cause severe disease in humans, is often carried and shed by cattle (Guillermo et al., 2015). However, research has shown that a specific probiotic blend containing Lactobacillus gallinarum and Streptococcus bovis, derived from cattle rumen, can significantly decrease enterohemorrhagic E. Coli excretion in infected calves. This reduction is associated with an increase in gut-derived fatty acids (Ohya, AKIBA, & ITO, 2001), indicating a positive impact on the animal's digestive health (Guillermo et al., 2015).

11.3. Novel Approaches to Controlling Pathogenic Microbes

The world is currently faced with the formidable task of increasing crop and livestock productivity without resorting to the careless use of antibiotics (Reid, 2011). A whole new field of study has emerged as a result of the promise of microbiota-based treatments for treating Salmonella infections (De Jong, Parry, van der Poll, & Wiersinga, 2012). Beneficial microorganisms, used as biocontrol agents, offer a promising solution to manage plant diseases by outcompeting pathogens or directly combating them through the production of antimicrobial compounds, thereby protecting plants from harm (Mansfield, 2000). By adding specific beneficial fungus like *Tricoderma harzianum* and *Gloicocadium virens* to organic mulch, "bioenhanced mulches" were produced that successfully inhibited the growth of a dangerous disease (*P. cinnamomi*) in avocado roots. When crop disease burden is modest, using beneficial microorganisms as biocontrol agents is a safe and efficient way to manage crops (Costa, Menge, & Casale, 2000). The research of microbiome interactions among various farm animal groups is part of Customized Combination of Microbial-Based Therapies (CCMBT), which aims to identify the most effective combinations for disease control and promoting animal health (Peixoto, Harkins, & Nelson, 2021).

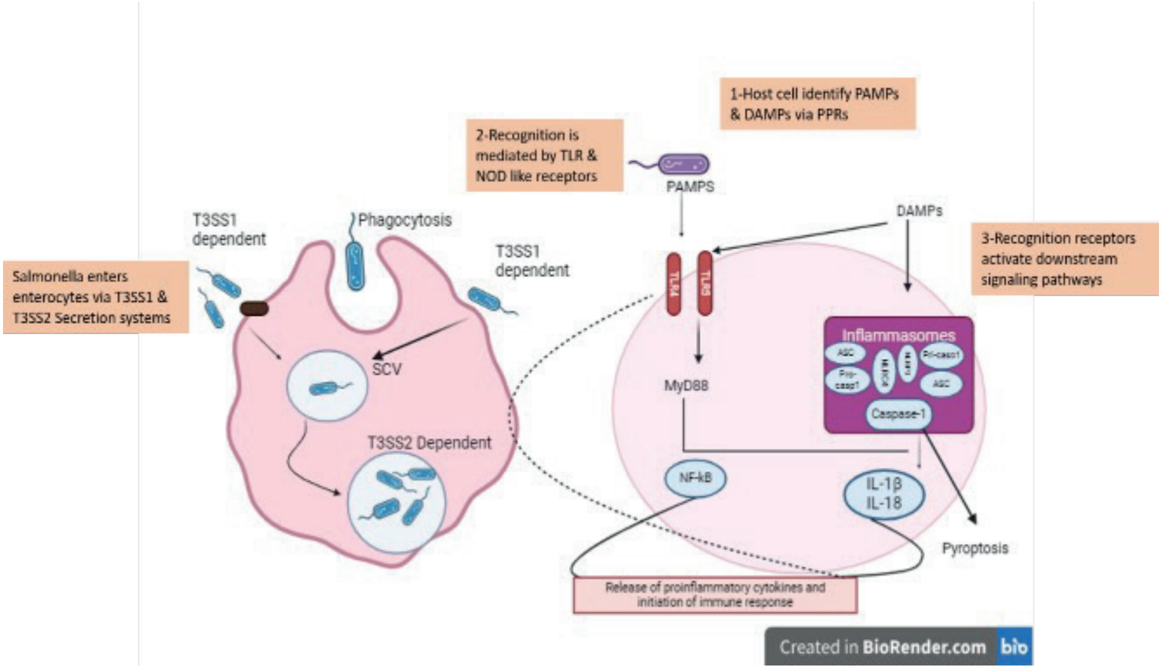


Figure 5. Host-Pathogen Interaction; Host immune cells recognize Salmonella through pathogen-associated molecular patterns (PAMPs) and danger-associated molecular patterns (DAMPs), triggering an immune response. This recognition is mediated by microbial sensors, which activate downstream signaling pathways, including Inflammatory response, to combat the infection. On the other side, salmonella enters the cell via 3 mechanisms a) T3SS1 dependent b) T3SS2 dependent c) phagocytosis.

12. Future Directions and Emerging Trends

12.1. Prospects for New Symbiosis-Based Technologies

Antibiotic resistance genes are being transferred by pathogens, leading to multidrug resistance. Scientists suggest using beneficial microorganisms to modify plant and animal immune systems as a viable substitute for antimicrobials (Jones, Vance, & Dangl, 2016). Current probiotics are modified using gene editing technologies ZFNs, TALEN, CRISPR, CRISPR-Cas and CRISPR-Cas 9, ensuring their effectiveness in fighting pathogen infections and controlling beneficial interactions (Ma et al., 2022). Probiotics that have been engineered utilized to treat numerous illnesses and health problems in humans & animals (Abouelela & Helmy, 2024). Host-pathogen systems biology has various applications and is expected to play a crucial role in personalized medicine, with ultimate goal of creating individualized digital models to simulate and predict disease progression and treatment outcomes (Forst, 2010).

Molecular biology boosts animal production (Peixoto et al., 2021). We have now entered an era where the scientific community has access to vast amounts of genomic data, ranging from traditional sequencing to pacific biosciences & portable sequencing as well as second generation sequencing and genome analyzers (Peixoto et al., 2021). Thanks to sequencing, analysis, and comparison, metagenomic technologies have increased our understanding of rumen microbiomes and revealed a wide universe of previously undiscovered microbial species (Peixoto et al., 2021). To better understand ruminant greenhouse gas emissions, recent research have used meta-omics methodologies (Peixoto et al., 2021). The goal of the Hungate 1000 project (Wallace et al., 2019) is to create a reference set of rumen microorganisms and sequence the genomes of rumen microbes (Seshadri et al., 2018). The Global Rumen Census measures the variety of microbes in rumen samples from different farming environments and geographical areas. The Rumen Microbial Genomics (RMG) Network includes these initiatives. There are now 501 genomic sequences in the database.

A different study discovered a core microbiome connected to host genetics and phenotype, and concluded that the rumen microbiome is heritable (Andersen, Kunath, Hagen, Arntzen, & Pope, 2021; Denman, Morgavi, & McSweeney, 2018). The research of microbiome interactions among various farm animal groups is part of Customized Combination of Microbial-Based Therapies (CCMBT), which aims to identify the most effective combinations for disease control and promoting animal health (Peixoto et al., 2021).

12.2. Challenges and Opportunities in Biotechnology

Despite the progress made in developing probiotics for use in commercial poultry, more commercially beneficial microorganisms that are feed-durable, economically viable and storage stable are desperately needed to boost adoption and compliance. The production of NGPs is fraught with difficulties. Some of these are the Selection and characterization of suitable probiotic strains (Stanton et al., 2003); Probiotic survival during storage and gastrointestinal transit (Soccol et al., 2014); Commercial probiotic production (Foligné, Daniel, & Pot, 2013); Probiotic stability and shelf life (Ranjan et al., 2022); There is an pressing need for advanced microbial cultivation techniques, cost-effective genetic and metagenetic analysis, robust bioengineering tools for precision editing and modification of microbial genetic material (Abouelela & Helmy, 2024); The conclusion of biocompatibility testing; and safety and efficacious trials in humans (O'Toole, Marchesi, & Hill, 2017); The application of genetically engineered microbes in next-generation products (NGPs) presents further regulatory compliance challenges & public perception hurdles (Abouelela & Helmy, 2024).

To overcome these difficulties in biotechnology, we should encourage the improvement of novel, particular transport methods, including inclusion or micro inclusion, to safeguard probiotic strains throughout storage and gastrointestinal transit (Abouelela & Helmy, 2024). Refining artifact stability, steadiness, and quality switch can be achieved through optimizing manufacturing processes (Abouelela & Helmy, 2024).

12.3. Future Research Directions and Emerging Fields

Researchers are working to pinpoint the precise bacterial strains that will help everyone the most through methods such as metagenomic sequencing. Advanced delivery technologies, such as time-release formulations and nanoparticles, are being developed to guarantee tailored administration to enteric zones or enterocytes, maintaining exposure to beneficial bacteria. With biotechnological advancements emerging fields work for microbiome associated benefits. Recent literature explores various strategies for creating probiotics, including heterologous protein expression, incorporating foreign enzymes, and metabolic engineering. These strategies allow for the use of complex byproducts of DNA technology, modified lipopolysaccharides, and detoxification through novel metabolic pathways (Steidler & gastroenterology, 2003). Neutralizing antibodies from recombinant bacteria can now be produced thanks to the development of single chain (ScFv) antibody technology (Steidler & gastroenterology, 2003).

A novel strategy for avoiding microbial illnesses is replacement treatment (Steidler & gastroenterology, 2003). A synthetic genome was successfully inserted into a Mycoplasma cell envelope, demonstrating groundbreaking artificial genome technology, resulting in a simple, fully functional artificial cell (Cordova, Hoeltgebaum, Machado, & SANTOS, 2016). Genome transplantation in Mycoplasma species allows comparative genomics studies, identifying crucial proteins and functional capabilities, despite being limited to unusual bacteria like Mollicutes (Karas et al., 2019). Research is now being conducted to create a novel, affordable, feed-stable probiotic that is clinically beneficial for both human and animal use, has a broad range of applications, and is easy to administer. Products containing Bacillus spores should reduce *Salmonella* as effectively as possible as well as be comparable to the antibiotic bacitracin in terms of preventing necrotic enteritis in both experimental and commercial field testing (Guillermo et al., 2015); engage closely with the microbiota or host cells to maximize any potential probiotic effects (Guillermo et al., 2015); lessen pathogens that are transmitted through food (Aureli, Fiore, Scalfaro, Casale, & Franciosa, 2010); Avoid certain gastrointestinal conditions (Guillermo et al., 2015); Colon carcinogenesis can be prevented by either live vegetative cells or endospores from certain isolates (Park, Jeon, Park, Paik, & Bulletin, 2007); release antibiotic agents against bacteria that are Gram-positive, including *Clostridium difficile, E. faecium,* and *Staphylococcus aureus* (O'mahony et al., 2001); and the present objective is to create an innovative probiotic that is clinically successful for both human and animal use, has a simple administration system, and is widely utilized. In both experimental and commercial field trials, that isolate of Bacillus subtilis spores is as effective for reducing *Salmonella* as FloraMaxTM, and is comparable to the antibiotic bacitracin for preventing necrotic enteritis (Shivaramaiah et al., 2011; Wolfenden et al., 2010).

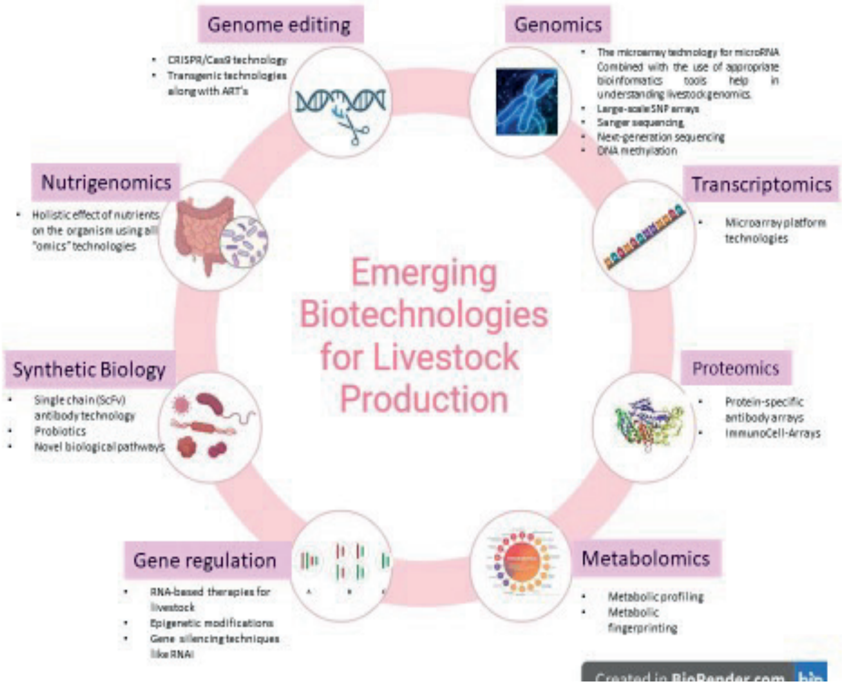


Figure 6. Emerging Biotechnologies for Livestock production; Livestock production rely more heavily on existing and emerging biotechnologies those including genomics, transcriptomics, proteomics, metabolomics, CRISPR, Nutrigenomics etc. (Gohar, Shah, Sarwar, Akram, & Mukhtar, 2021).

12. Summary

In conclusion, the symbiotic relationships between microorganisms and animals are complex and multifaceted, playing a crucial role in animal health, productivity, and sustainability. This chapter has explored the diversity of microorganisms in various livestock hosts, the different types of symbiotic relationships, and the mechanisms of symbiosis formation. We have also discussed the role of symbiosis in health and disease, antibiotic resistance, biotechnological applications, and future research directions. The study of animal-microbe symbiosis has significant implications for biotechnology and animal health, offering opportunities for improving livestock productivity, disease resistance, and environmental sustainability. However, there are also challenges and limitations to be addressed, such as the need for further research on symbiotic mechanisms and the development of effective biotechnological applications.

In addition, the study of genomics has greatly advanced our understanding of symbiosis as a common and vital aspect of life, particularly through the sequencing of genomes from organisms that cannot be cultured in a lab. Symbiosis is vibrant and transformative procedure where the primitive partner granting the host innovative physiological talents, undergoes significant genetic and physiological changes assimilate into new culture, distinct from its free-living counterparts. The subject of NGP research is fast developing and has considerable potential for creating medicinal treatments. There is now more interest in discovering novel beneficial microorganisms for use in biomedical applications due to rapid advancement of sophisticated Genome analyzers, DNA decoding machines, and potent genome-editing utensils for bacteria. Novel molecular methodologies provide precise evaluation of the floral composition, leading to enhanced approaches to clarify the distinct mechanisms of action exhibited by probiotics in augmenting the performance of livestock animal species. Although a lot of research has been done, much more needs to be done to fully comprehend and utilize the advantageous properties of non-pathogenic bacteria. The properties of the pathogen and the host are what determine the host-pathogen interactions. Pathogens' aptitude to proliferate in their host species and spread to additional entities is a prerequisite for their reproductive success, which has led to the evolution of very diverse methods. In the future, to create our food animal farming will depend increasingly on recent and next biotechnology developments. Technological developments in molecular biology have given us new means of enhancing animal production, such as growth and yields, and have also made it possible to investigate the microbial lodgers of animals Product development and manufacturing optimization, especially concerning growth enhancement, disease tolerance and reproductive improvement. Through cloning techniques, we might eventually be able to create cattle that are free of prion, scrapie, and BSE by utilizing the DNA of naturally resistant animals.

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About The Authors

Dr. Saba Saba

Affiliation: Department of Microbiology and Molecular Genetics, The Women University Multan, Multan, Pakistan

Email: saba.6395@wum.edu.pk ORCID: 0000-0002-9182-4667

Dr. Mohsin Tassawar Cheema

Affiliation: Department of Microbiology, Faculty of Science and Technology, University of Central Punjab, Lahore, Pakistan

Email: Mohsin.tassawar@ucp.edu.pk ORCID: 0000-0002-4399-8110

Dr. Momena Habib

Affiliation: Department of Microbiology and Molecular Genetics, University of Okara, Okara, Pakistan

Email: momena.habib@uo.edu.pk ORCID: 0000-0001-8501-0707

Dr. Naila Noureen

Affiliation: Department of Microbiology, Faculty of Science and Technology, University of Central Punjab, Lahore, Pakistan

Email: naila.noureen@ucp.edu.pk ORCID: 0000-0002-8045-5923

Adeela Naeem

Affiliation: Institute of Microbiology and Molecular Genetics, University of the Punjab, Lahore, Pakistan

Email: adeelanaeem20@gmail.com ORCID: 0009-0003-7937-4354

Memoona Siddiqua

Affiliation: Institute of Microbiology and Molecular Genetics, University of the Punjab, Lahore, Pakistan

Email: memoonasiddiqua62@gmail.com ORCID: 0009-0008-7552-5220

Fakhr-Un-Nisa

Affiliation: Institute of Microbiology and Molecular Genetics, University of the Punjab, Lahore, Pakistan

Email: fakhrunisa309@gmail.com ORCID: 0009-0009-5504-4565

Dr. Abid Hussain

Affiliation: Department of Microbiology and Molecular Genetics, University of Okara, Okara, Pakistan

Email: abihqureshi@gmail.com ORCID: 0000-0001-8661-9522

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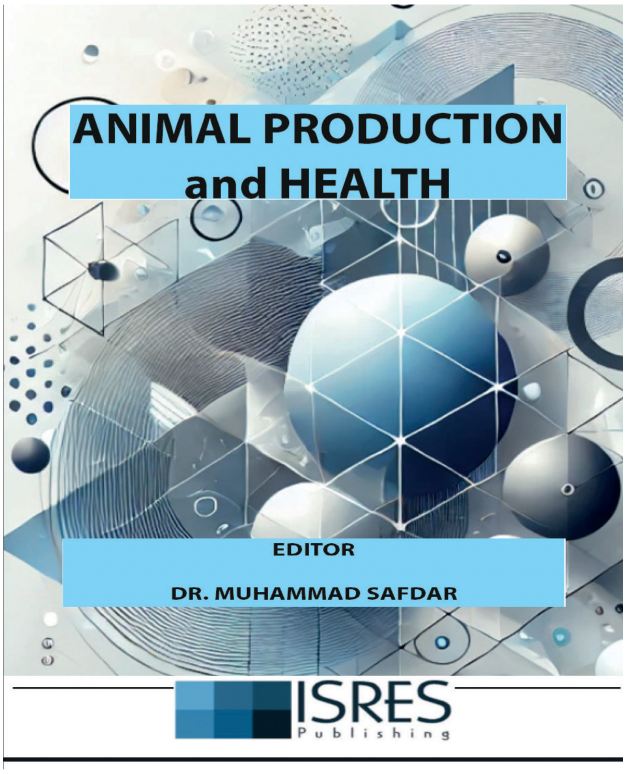

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