Immunity and Nutrigenomic Studies in Livestock

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Abstract. Nutrigenomics has emerged as a field of science that highlights the potential of dietary components to modulate gene expression and thereby shape immune responses, contributing to the overall effectiveness of the immune system. Studies have demonstrated that vitamins (A, D, E), trace minerals (zinc, selenium), omega-3 fatty acids, probiotics, and prebiotics enhance the activation of immunity-related genes, balance inflammatory responses, and support immune homeostasis (Musa et al., 2023; Ul Haq, 2022; Patil, 2021). Particularly in the neonatal period, immunoglobulins and bioactive peptides provided by colostrum promote the maturation of T and B lymphocytes, ensuring molecular-level programming of the immune system (Rosa et al., 2021; Loor, 2022). These findings suggest that nutrigenomics-based nutritional strategies may serve as a key tool in optimizing immune functions in animals, thereby improving both health and production performance. Nutrigenomic research clearly demonstrates that the immune system can be optimized at the molecular level in livestock production. Advances in high-throughput technologies have also enabled important investigations into disease resistance. The emergence of genotyping arrays has facilitated large-scale genome-wide association studies and global transcriptome analyses, giving rise to the field of “integrative genetics.” Other omics technologies, such as proteomics and metabolomics, are expected to continue making significant contributions to the daily methodology of biological research.

Keywords: Livestock, Disease, Resistance, Immunity, Nutrigenomics.

1 Introduction

In animal production, disease prevention and treatment are both essential steps in maintaining herd health. However, an animal’s natural resistance to disease also plays a crucial role in disease prevention. Disease resistance is a leading factor in sustainable productivity and food safety. Resistance and prevention protect herd health before the disease enters the herd and minimize losses. In contrast, treatment only reduces damage after the disease appears and cannot completely prevent losses. Therefore, the most effective approach is to strengthen resistance and focus on prevention, while treatment

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should be used only when necessary. Animals resistant to diseases help prevent production losses primarily by reducing mortality rates in herds (Göncü, 2013; Liang et al., 2020; Musa et al., 2023). Moreover, supporting genetically disease-resistant structures reduces the need for antibiotics, vaccines, and other veterinary drugs—lowering production costs and contributing to the prevention of global health issues such as antimicrobial resistance. Additionally, disease resistance improves animal welfare and enhances the resilience of production systems to environmental stressors. Especially in today's context, where climate change poses increasing pressure on livestock production, breeding resilient animal populations has become a strategic necessity for ensuring both economic sustainability for producers and safe, high-quality animal products for consumers.

Systematic research on disease resistance began in the mid-20th century, but scientific progress accelerated after the 1980s with advances in molecular biology and genetic technologies. Nutrigenomics is a scientific field that examines the effects of nutrition on gene expression and genetic potential. By uncovering the molecular responses of animals to nutrients and exploring gene–diet interactions, nutrigenomics helps optimize productivity, immunity, and product quality (Liang et al., 2020; Musa et al., 2023). In recent years, nutrigenomics has emerged as an important field that investigates genetic and molecular responses to nutrition, providing new insights for enhancing production efficiency and animal welfare.

Nutrigenomics utilizes molecular and omics-based approaches to understand animals' genetic responses to nutrition. Genomic analyses identify genetic profiles and detect genes sensitive to dietary factors (Liang et al., 2020). Transcriptomic and proteomic studies reveal which genes are upregulated or suppressed by specific nutrients, elucidating the molecular mechanisms of metabolism, immunity, and growth (Musa et al., 2023). Metabolomic analyses evaluate how feeds affect the metabolites produced in animals, thereby optimizing energy and nutrient utilization (Patil, 2021). The molecular and omic data obtained from these studies are used to develop individualized feeding strategies tailored to each animal's genetic potential and metabolic needs—simultaneously improving productivity, immune capacity, and product quality. Nutrigenomics integrates genetic information, nutrient composition, and molecular analyses to optimize efficiency, health, and product quality in livestock.

Nutrigenomic studies make significant contributions to improving productivity, product quality, and welfare by examining animals' genetic and molecular responses to nutrition. Transcriptomic and metabolomic analyses identify gene pathways related to energy and protein utilization, nitrogen metabolism, and growth performance, helping to determine individual feed efficiency (Liang et al., 2020). Research on the regulation of the rumen microbiota in ruminants has shown that probiotics, prebiotics, and plant-based additives can enhance energy utilization and reduce methane emissions (Malgwi et al., 2022). Nutrigenomic studies on milk and meat quality have revealed that omega-3-enriched diets alter milk fatty acid profiles and protein expression, thereby improving functional value (Osorio et al., 2017; Nowacka & Woszuk, 2020). Moreover, studies on vitamins and trace minerals have examined their effects on the immune system, with nutrigenomic approaches highlighting anti-inflammatory and immunomodulatory benefits that improve animal health (Hasin et al., 2017). Finally, nutrigenomic data are being integrated into genetic breeding programs to enable the selection of target genes, optimize feed efficiency, disease tolerance, and product quality (Martyniuk et al., 2020).

Nutrigenomic approaches also provide significant insights into rumen microbiota regulation, product quality, immunity, and disease resistance. These studies serve as valuable tools for understanding the genetic responses of animals to dietary interventions and highlight the strategic importance of nutrigenomics in achieving sustainable and efficient livestock production.

Optimizing productivity and welfare in animal production is achieved through the integrated application of genetics, nutrition, and management strategies. Genetic improvement programs enhance production capacity by selecting high-yielding and disease-resistant individuals, while nutrigenomic and molecular approaches analyze genetic responses to feeding to improve key parameters such as feed efficiency, immune function, and product quality. Simultaneously, sensors, biosensors, and monitoring technologies continuously track animal movement, feed intake, body temperature, and stress levels. These data enable the development of personalized feeding and care programs for each individual. When combined with rumen microbiota management, functional feed additives, and environmental management practices, these methods optimize both production efficiency and animal welfare.

In this context, modern livestock production increasingly adopts integrated strategies that combine molecular biology, nutrition science, and advanced technology applications to improve both productivity and welfare. Feed costs represent a major component of total production expenses. Nutrigenomic research aims to enhance feed efficiency by linking animals' genetic profiles to their ability to utilize dietary energy and protein. The addition of the term "-omics" to a molecular field indicates a comprehensive or global analysis of a group of molecules (Hasin et al., 2017). The earliest omic discipline—genomics—focuses on studying entire genomes, unlike traditional genetics, which examines single genes or variants. Genomic research provides a valuable framework for mapping and analyzing specific genetic variants associated with both Mendelian and complex diseases. The omics field has been largely driven by technological advances that enable cost-effective, high-throughput molecular analyses. For instance, expression array technology—based on hybridizing cDNA with oligonucleotide probe sequences—was developed in the late 1990s. As sequencing technologies evolved, they proved capable of quantitatively determining the levels of all protein-coding transcripts in a given tissue. The ability to study global gene expression patterns rapidly found applications across many areas of biology, including disease analysis. By the early 2000s, sequencing technologies enabled the mapping of loci controlling gene expression, known as expression quantitative trait loci (eQTLs). These loci significantly contributed to the interpretation of genome-wide association studies (GWAS) and the modeling of biological networks. Since then, various omic technologies capable of analyzing complete transcript, protein, and metabolite pools—as well as entire genomes—have been developed (Hasin et al., 2017).

Transcriptomic and metabolomic analyses identify gene pathways associated with nitrogen metabolism, energy conversion, and growth, thereby revealing molecular indicators of individual feed efficiency (Liang et al., 2020). This allows animals to be fed more efficiently and sustainably. In ruminants, the rumen microbiome plays a central role in nutrient degradation and energy production. Nutrigenomic approaches investigate how probiotics, prebiotics, and plant-based additives affect gene expression profiles within the rumen microbiota, providing key insights into methane emission reduction, improved energy gain, and the prevention of metabolic disorders (Malgwi et al., 2022).

Nutrigenomics is also applied to enhance milk and meat quality. Critical genetic and metabolic pathways related to milk fatty acid composition, protein profile, and biological value have been identified. Diets enriched with omega-3 fatty acids have been shown to alter gene expression in milk fat, thereby increasing functional value (Osorio et al., 2017). Lipidomic analyses identify biomarkers associated with meat fatty acid profiles and marbling, improving quality while contributing to the development of healthier products for human consumption (Nowacka & Woszuk, 2020).

Nutrigenomic data are increasingly integrated into genetic improvement programs to enable the targeted selection of genes, enhance nutrient utilization efficiency, and improve disease tolerance. Genetic markers and genotype × diet interactions, supported by omic data, make breeding programs more focused and efficient. As a result, genetic markers related to feed efficiency, milk composition, immunity, and meat quality are used as selection criteria, leading to the development of optimized animal lines in terms of both production and health (Martyniuk et al., 2020).

1.1 Disease Resistance

In livestock production, disease resistance refers to the innate (genetic) or acquired biological defense capacity of animals against infectious or non-infectious diseases (Göncü et al., 2013). In other words, it is the ability of an animal to withstand or recover quickly from exposure to a pathogen. Disease resistance is shaped not only by genetic factors but also by nutrition, environmental conditions, stress levels, and the preventive veterinary measures applied (Göncü et al., 2014).

Improving animal health through genetic selection is advantageous because genetic gains are cumulative and permanent, as beneficial genes added to a population can persist for generations. Understanding the genetic architecture of health and disease resistance not only provides insight into breeding potential for improved health but also contributes valuable information to biomedical research, including vaccine development, for both animals and humans.

There is considerable genetic variation among cattle breeds in susceptibility to diseases, indicating that genetic selection for disease resistance is a viable strategy (Bery et al., 2011; Sheldon, 2014). However, the lack of accurately recorded data on individual animals' disease susceptibility limits the inclusion of health and resistance traits in national breeding goals. Advances in genomic selection and other "omic" technologies can overcome some of the limitations of traditional breeding programs, especially for traits with low heritability that manifest after exposure to pathogens or environmental stressors in adulthood (Bery et al., 2011).

Doeschl-Wilson et al. (2021) highlight that control measures such as vaccination and selective breeding typically focus on increasing individual resistance to infection. However, they emphasize the need to consider subclinical carriers (infected animals without visible symptoms) that can influence herd health and productivity. Thus, enhancing herd-level disease resistance—not only individual resistance—is essential. Herd-level resistance includes both the direct effects on individual health and performance and the indirect effects on the environmental pathogen load within the herd. These authors also stress the importance of integrating technologies across scientific disciplines to achieve holistic resistance improvement.

From a genetic standpoint, immune system genes—particularly those within the Major Histocompatibility Complex (MHC) and Toll-Like Receptor (TLR) families—play a critical role in disease resistance (Bery et al., 2011; Sheldon, 2014; Doeschl-Wilson et al., 2021). These genes determine how individuals respond to pathogens, and breed differences in resistance have been observed. For example, Holstein and Simmental cattle are reported to be more sensitive to environmental stress factors.

Among environmental factors, nutrition, housing conditions, hygiene, and stress levels significantly influence cattle's resistance to disease. Poor nutrition and inadequate housing weaken the immune system and increase disease risk, while stress also impairs immune responses. Therefore, disease resistance in cattle results from the interaction between genetic and environmental factors, and optimizing these parameters is critical for disease control and productivity improvement in the livestock sector.

Local breeds' higher resistance to certain infectious diseases compared to exotic breeds underscores the importance of genetically based disease resistance. Furthermore, adequate nutrition, regular vaccination, and proper housing strengthen acquired immunity. The interaction between genetic profiles and nutritional strategies is essential for enhancing immune responses and preventing disease.

The neonatal period represents a critical stage for immune system development. During the first days after birth, the immune system is immature and relies on nutritional sources for protection. Colostrum, the primary postnatal nutrient source, contains high levels of immunoglobulins, growth factors, lactoferrin, cytokines, and various bioactive peptides. These bioactive compounds not only provide passive immunity but also modulate gene expression in immune cells, supporting the development of active immune responses (Göncü et al., 2013; Göncü et al., 2014; Rosa et al., 2021; Musa et al., 2023).

Nutrigenomic studies have shown that colostral growth factors and immune components affect T and B lymphocyte differentiation, cytokine production, and inflammatory regulation—all of which form the foundation of disease resistance mechanisms. B lymphocytes contribute by producing antibodies that neutralize and eliminate pathogens, while T lymphocytes differentiate into subtypes (Th1, Th2, Th17, Treg) to shape specific immune responses. Cytokines regulate communication between immune cells and determine the efficiency of both cellular and humoral responses. For instance, interferon-γ enhances macrophage activation to combat intracellular pathogens, while interleukin-4 and interleukin-10 strengthen humoral immunity.

Moreover, the regulation of the inflammatory response is vital for disease resistance, as excessive or insufficient inflammation can cause tissue damage or immune deficiencies (Asmelash et al., 2018). Lactoferrin and immunoglobulins activate NF-κB and

STAT pathways to enhance the expression of immune-related genes, strengthening neonatal immune responses (Patil, 2021). In addition, colostral peptides and prebiotic compounds can modulate the gut microbiota, supporting immune homeostasis and inducing epigenetic changes in gene expression (Ul Haq, 2022).

From a nutrigenomic perspective, colostrum and its bioactive compounds act as key molecular tools for early immune gene programming. Immunoglobulins and lactoferrin promote lymphocyte maturation, cytokines balance inflammatory responses, and bioactive peptides activate transcription factors such as NF-κB and STAT to enhance immune gene expression. Furthermore, prebiotic and microbiota-supporting components in colostrum promote immune stability and influence long-term immunity through epigenetic mechanisms. Thus, colostrum provides multilayered molecular support that reduces early infection risk while enhancing immune maturation and adaptive response capacity (Rosa et al., 2021; Musa et al., 2023; Patil, 2021).

In particular, proline-rich polypeptides (PRPs) in colostrum regulate immune cell differentiation and function by influencing gene expression. PRPs activate transcription factors such as NF-κB and STAT, increasing the expression of inflammation- and immunity-related genes. Additionally, growth factors like IGF-1 and EGF stimulate immune cell proliferation and maturation, thereby enhancing immune system efficiency.

The bioactive components of colostrum also affect immune function beyond the neonatal stage. Colostrum supplementation in adult animals has been shown to enhance immune cell activity and improve resistance to infections.

Transcriptomic and proteomic analyses have demonstrated that vitamins (A, D, E) and trace minerals (zinc, selenium) regulate the expression of immune-related genes. Furthermore, probiotic, prebiotic, and functional feed additives improve animal health by modulating the gut microbiota and immune responses (Musa et al., 2023; Patil, 2021; Ul Haq, 2022). These findings demonstrate that nutrigenomic approaches not only enhance productivity but also optimize animal welfare and immune capacity, making them a strategic tool for sustainable livestock production.

The interaction between nutrition and genetics plays a crucial role in shaping immune responses. Vitamins (A, D, E) and trace minerals (zinc, selenium) regulate immune-related gene expression, while nutrigenomics reveals the anti-inflammatory and immunomodulatory effects of feed additives that help prevent diseases (Hasin et al., 2017).

1.2 Microbiota and Immune System Interaction

In animal production, the immune system is a dynamic structure that constantly interacts with microorganisms. The microbiota, an ecosystem composed of microorganisms residing in the digestive tract, plays a crucial role in the development and function of the immune system. This interaction can be modulated through nutrition, and nutrigenomics helps us understand these processes at the molecular level.

After birth, the microbiota develops rapidly and plays a critical role in the maturation of the immune system. In particular, probiotic microorganisms such as Bifidobacterium and Lactobacillus support the development and maturation of immune cells. These microorganisms regulate immune responses by modulating gene expression through microRNAs (Loor, 2022).

The composition of the gut microbiota affects the homeostasis of the immune system. For example, probiotic supplementation can modulate the gut microbiota and improve immune functions. In a study conducted by Yao et al. (2020), supplementation with Bacillus megaterium was shown to enhance immune responses and reduce inflammation in neonatal dairy calves.

Nutrigenomics investigates the effects of dietary components on gene expression. Nutrition influences both the composition and function of the microbiota, thereby modulating immune system activity. For instance, beta-carotene can alter gut microbiota composition, reduce inflammation, and improve immune responses (Rosa et al., 2021). The gut microbiota functions as an ecosystem that interacts closely with the immune system. The use of probiotics and prebiotics helps modulate the gut microbiota, contributing to the strengthening of immune defenses. These microorganisms regulate immune cell activation and inflammatory responses, thereby improving overall health and resistance to disease.

1.3 Stress and Immune Responses

In animals, environmental and management-related stress factors such as temperature fluctuations, overcrowding, transportation, and disease risk can negatively affect the function of the immune system. In recent years, global warming has become a major source of multifactorial stress, impacting livestock at physiological, immunological, nutritional, productive, and behavioral levels, thereby reducing both productivity and animal health. Consequently, adaptation mechanisms, genetic selection, and climate-smart production strategies have become increasingly critical.

Under stress conditions, cortisol and other stress hormones rise, which can suppress the activity of immune cells and disrupt inflammatory responses (Dhabhar, 2014). Increased heat and humidity lead to heat stress, reducing feed intake, feed efficiency, and ultimately causing losses in milk and meat yield. Moreover, elevated cortisol levels associated with heat stress suppress the immune system, making animals more susceptible to infectious and parasitic diseases. High ambient temperatures also negatively affect ovulation and embryo development in females and reduce sperm quality in males, leading to significant declines in reproductive performance.

Additionally, the impacts of global warming on forage yield and quality and water scarcity increase the risks of nutritional and hydration stress. These adverse conditions not only threaten animal welfare but also economic sustainability for producers, emphasizing the urgent need for climate adaptation strategies in the livestock sector.

Such stressors elevate the secretion of cortisol and other stress-related hormones, impairing immune cell functions (Dhabhar, 2014). Chronic stress can reduce T and B lymphocyte activity, disrupt cytokine balance, and lead to irregular inflammatory responses. Nutrigenomic approaches aim to mitigate the negative effects of stress through targeted nutritional strategies. Antioxidant vitamins (A, C, E), omega-3 fatty acids, and trace minerals such as selenium and zinc protect immune function by reducing oxidative stress (Musa et al., 2023; Patil, 2021). Furthermore, probiotic and prebiotic supplementation can modulate the gut microbiota, helping to buffer the adverse immune effects of stress (Ul Haq, 2022).

For instance, antioxidants such as vitamins A, C, and E, omega-3 fatty acids, and selenium alleviate oxidative damage caused by stress, support immune responses, and regulate inflammation (Musa et al., 2023; Patil, 2021). Additionally, gut microbiota modulation through probiotics and prebiotics helps balance stress responses and enhances immune efficiency (Ul Haq, 2022). These findings demonstrate that nutrigenomic feeding strategies play a significant role in optimizing immune function under stress, thereby improving both animal welfare and production efficiency.

Although the concept of nutrigenomics in animal production is relatively new, its foundation dates back to the late 1990s and early 2000s. The earliest studies during this period aimed to explore the molecular-level effects of dietary components on gene expression. For instance, Wu et al. (2004) investigated the molecular effects of amino acids (particularly lysine and methionine) on the immune system and growth performance of calves, marking one of the first systematic studies linking nutrition, gene interaction, and immune response (see Table 1).

From the mid-2000s, more sophisticated approaches such as transcriptomics, proteomics, and metabolomics were adopted to investigate these interactions. After 2010, molecular-level studies began focusing on the effects of colostrum, probiotics, and prebiotics on gut microbiota and immune function.

Nutrigenomics now plays a key role in the molecular regulation of the immune system in animal production. By modulating gene expression related to immunity, nutrients can enhance disease resistance and improve overall health. Transcriptomic, proteomic, and metabolomic analyses have revealed how nutrients influence the activation of immune-related genes.

For example, using RNA-Seq technology, Soglia et al. (2022) examined the gene expression profiles in the liver, small intestine, and cecum tissues of broiler chickens fed with Tenebrio molitor (mealworm) larvae. The results indicated that these dietary components downregulated immune and inflammation-related genes. Similarly, Ali et al. (2022) studied the effects of nutrition on microbiota and immune interactions in geese raised on artificial pasture systems, showing that such feeding strategies improved gut barrier function and reduced inflammation.

As summarized in Table 1, early studies from the 2000s (Wu, 2004; Ballou, 2006; Loor, 2013) evaluated the effects of amino acid supplementation, probiotic applications, and colostrum on immune gene expression using transcriptomic and immunological parameters. More recent studies (Ali, 2022; Silva, 2024; Rostoll-Cangiano, 2025) have employed advanced omics approaches, gut microbiota analyses, and bioactive peptide assessments to invesigate the molecular modulation of immune responses.

Colostrum and amino acids have been identified as essential components supporting immune cell maturation during the neonatal period, while probiotics and prebiotics regulate inflammatory gene expression by modulating the gut microbiota, thereby strengthening immune responses. Recent findings reveal that these nutritional components not only provide passive immunity but also exert active molecular modulation through transcriptional pathways such as NF-κB and STAT.

Overall, Table 1 demonstrates that nutrigenomic approaches are effective in enhancing immune responses, particularly highlighting the neonatal period as a critical window for immune programming. These insights indicate that nutrition and management strategies can be designed at the molecular level to optimize animal health and production performance. Post-2020 studies, using more advanced molecular and omics tools, increasingly emphasize the role of gut microbiota and explore the epigenetic effects of bioactive compounds.

Table 1. Studies on nutrigenomics and immunity in animal production

Researcher	Species	Objective	Method	Findings
Wu et al., 2004	Calf	Effects of amino acid supplementation on immunity and growth	Amino acid supplementation, immune parameters	Lysine and methionine supplementation increased T-cell proliferation and supported growth
Ballou et al., 2006	Chicken	Effects of probiotics on gut microbiota and immunity	Nutritional modification, microbiota analysis	Probiotics activated immune-related genes and enhanced disease resistance
Loor et al., 2013	Cattle	Colostrum and immune gene expression	Transcriptomic analysis, molecular markers	Colostrum components modulated NF-κB and STAT pathways, supporting immune cell development
Kvidera et al., 2017	Cattle	Relationship between energy balance and immune response	Metabolomic and transcriptomic analyses	Energy deficit increased inflammatory gene expression and affected immune response
Ali et al., 2022	Goose	Effects of gut microbiota lipopolysaccharide production on immunity	Dietary modification, microbiota analysis, intestinal alkaline phosphatase activation	Pasture feeding reduced LPS production caused by commercial diets and supported immune response
Silva et al., 2024	Calf	Effects of colostrum components on neonatal immunity and growth	Literature review, molecular analyses	Colostrum immunoglobulins and bioactive peptides supported T and B cell maturation

Researcher	Species	Objective	Method	Findings
Rostoll-Cangiano et al., 2025	Calf	Role of colostrum in early immune development	Molecular analyses, gene expression studies	Colostrum regulated immune gene expression through NF-κB and STAT pathways
Petre et al., 2024	Goat	Effects of bioactive peptides in colostrum on neonatal health and immunity	Peptide analysis, immune response measurements	Bioactive peptides enhanced immune response by supporting gut microbiota
Poonia & Shiva, 2022	Review	Nutritional profile and health effects of colostrum	Review study	Colostrum activated immune genes and strengthened neonatal defense mechanisms
Arslan et al., 2021	Cattle	Effects of colostrum on immunity and disease resistance	Review	Colostrum modulated inflammation and immune responses, supporting animal health

Omics Approach	Objective	Methods	Applications
Transcriptomics	Analyze gene expression profiles to determine the effects of nutrients on genetic activity	Microarray, RNA-seq	Feed-induced gene expression changes, milk composition, feed efficiency, management of transition period metabolic stress
Proteomics	Identify proteins, quantify abundance, and elucidate functional pathways	Mass spectrometry, 2D gel electrophoresis, chromatography	Reproductive physiology analysis, disease biomarker identification, selection strategies
Metabolomics	Examine small molecule metabolites and characterize biochemical networks	NMR, mass spectrometry	Feed efficiency, energy metabolism, immune response, prevention of metabolic disorders
Lipidomics	Analyze lipid profiles and metabolic pathways	Lipid analysis techniques	Meat and milk quality, fatty acid composition, adipogenesis, study of vitamin A and D effects
Rumen microbiome studies	Understand microbial responses and optimize energy/methane conversion	Microbial gene expression analysis	Reduced methane emissions, improved energy utilization, prevention of metabolic disorders

Omics Approach	Objective	Methods	Applications
Nutrient-gene interactions	Enhance animal health, production, and immune response	Omics data + nutrient supplementation	Omega-3 enriched milk, high CLA content, improved meat fatty acid profile, regulation of immune-related gene expression
Integration into genetic selection	Target gene selection and improved nutrient utilization	Genotype × diet interactions, omics data	Optimized feed efficiency, milk and meat quality, disease tolerance, overall production efficiency

Table 1 demonstrates that studies on nutrigenomics and immunity in animal production encompass both basic and applied research perspectives. Moreover, nutrient-based strategies such as colostrum supplementation, amino acid fortification, and microbiota modulation have been shown to optimize immune function at the molecular level—confirming their critical role in achieving sustainable and efficient production systems. Immune responses to nutrition are also examined at the molecular level; vitamins (A, D, E) and trace minerals (zinc, selenium) regulate gene expression related to immunity, exhibiting anti-inflammatory and immunomodulatory effects (Hasin et al., 2017). Finally, nutrigenomic data can be integrated into genetic selection programs, enabling targeted selection of genes, enhanced feed efficiency, and improved disease tolerance. Genetic markers and genotype × diet interactions, supported by omics data, make breeding programs more precise and efficient, with selection criteria based on feed efficiency, milk composition, immunity, and meat quality (Martyniuk et al., 2020). Thus, production efficiency, animal health, and nutrient utilization are optimized simultaneously.

Nutrigenomics also aims to modulate animals' immune responses through diet at the molecular level. Nutrient components can influence the expression of genes related to immune function, thereby modulating immune responses. For example, micronutrients such as vitamins A and D regulate immune cell functions, while minerals like zinc and selenium enhance immune system efficacy. Additionally, anti-inflammatory nutrients such as omega-3 fatty acids help control inflammatory responses and prevent excessive immune reactions. Transcriptomic and proteomic analyses have revealed that certain nutrients activate anti-inflammatory and immunomodulatory genes, thereby strengthening immune responses (Musa, Ibrahim, & Alhaji, 2023; Patil, 2021). Furthermore, probiotics and prebiotics have been reported to modulate gut microbiota, enhancing immune efficiency and resistance to diseases (Ul Haq, 2022). These findings indicate that nutrigenomic strategies are not only essential for improving production efficiency but also play a vital role in optimizing animal health and welfare.

2 Conclusion

The integration of genetic and molecular data with nutritional strategies and management practices enables the development of sustainable, efficient, and ethical livestock

production systems. Nutrigenomic research clearly demonstrates that the immune system in animal production can be optimized at the molecular level. Advances in high-throughput technologies have also provided new opportunities for studying disease resistance mechanisms. The emergence of genotyping arrays has facilitated large-scale genome-wide association studies and methods for examining global transcript levels, leading to the rise of the field of integrative genetics.
Other "omics" technologies such as proteomics and metabolomics continue to make significant contributions to the daily methodologies of biological research. Future studies are expected to explore specific nutrient–gene interactions and the epigenetic effects of bioactive compounds in greater detail. These efforts will be essential for developing nutrigenomic protocols tailored to animal species and production conditions.

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