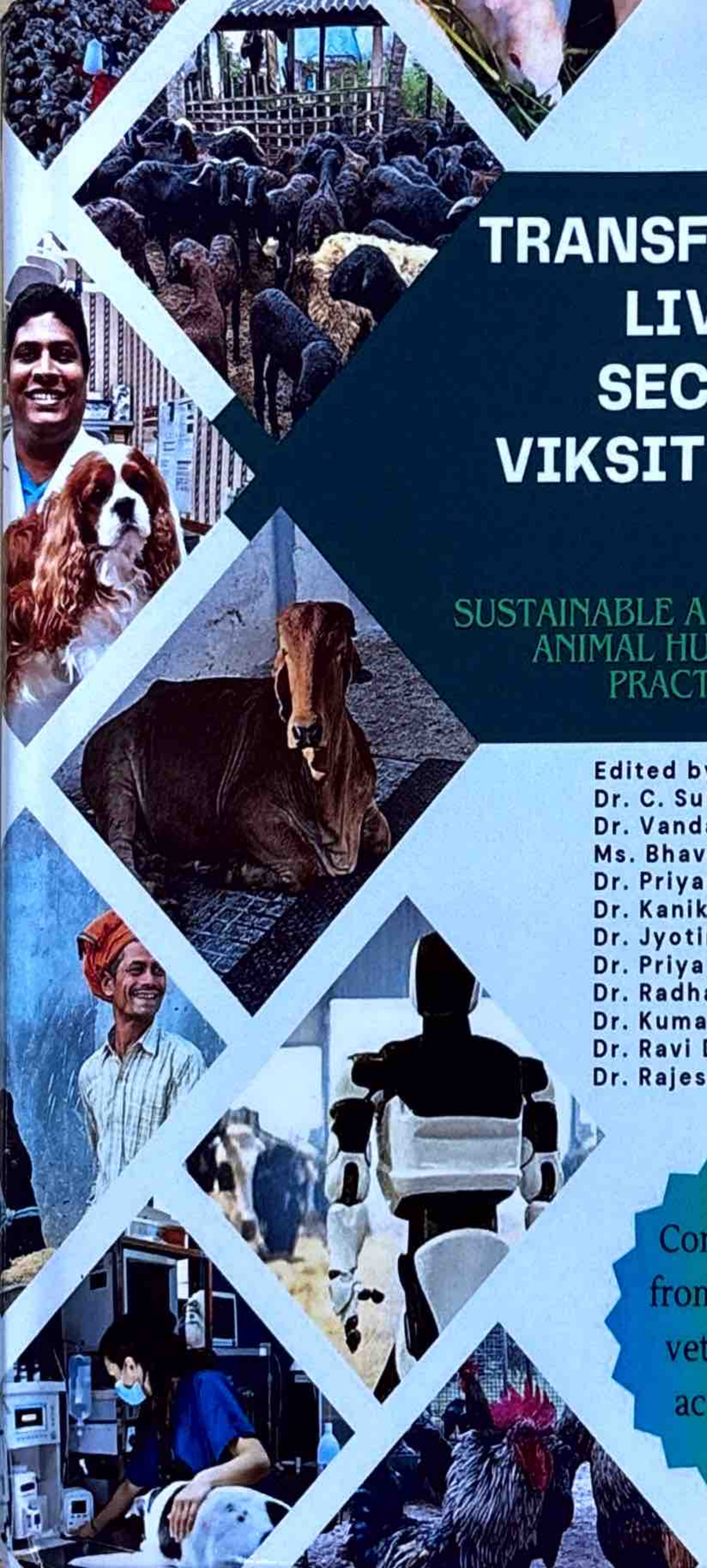

TRANSFORMING LIVESTOCK SECTOR FOR VIKSIT BHARAT @2047

SUSTAINABLE AND SCIENTIFIC ANIMAL HUSBANDRY PRACTICES

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Chapter 16

NUTRITIONAL REGULATION OF EPIGENETIC MODIFICATIONS IN LIVESTOCK

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Abstract

The regulation of gene expression through epigenetic mechanisms-such as DNA methylation, histone modifications, and non-coding RNAs-has emerged as a fundamental process influencing livestock growth, development, health, and productivity. Nutritional factors are now recognized as key modulators of these epigenetic processes, exerting long-term effects on animal phenotype and performance. This chapter provides a comprehensive overview of the current understanding of how dietary components, including vitamins, minerals, fatty acids, and amino acids, can alter epigenetic marks in livestock species. Special attention is given to the critical windows of developmental plasticity, during which nutritional interventions can induce stable epigenetic changes with lifelong consequences. By integrating insights from molecular biology, animal nutrition, and developmental programming, the chapter highlights the potential of nutritional epigenetics as a strategic tool for sustainable livestock production. It also addresses current challenges, methodological advancements, and future perspectives in applying nutriepigenomics to animal agriculture.

Keywords: Nutritional epigenetics, DNA methylation, Histone modification, Non-coding RNAs, Precision nutrition, Sustainable livestock production

Introduction

To meet the nutritional demands of the global population projected to reach 9.1 billion by 2050, the Food and Agriculture Organization (FAO, 2009) estimates that food production must increase by approximately 70%. This growth is largely driven by an ever-expanding human population, which is concurrently driving a surge in the demand for animal-based foods. Ensuring the sustainable development of the livestock industry is essential to address the dual challenge of climate change and the need for high-quality animal proteins with reduced environmental footprints.

In response to these pressures, current research is increasingly focused on enhancing livestock productivity and reducing production costs through improved nutritional and management practices. Modern livestock breeding programs are also undergoing a transformation through the adoption of advanced methods such as genetic selection, reproductive technologies, and genomic selection. These innovations contribute to increased selection intensity and accuracy, greater genetic diversity, and reduced generation intervals. The introduction of genomic breeding, in particular, has enabled more rapid genetic advancements in traits with low heritability-such as fertility, longevity, and health-while simultaneously enhancing the precision of breeding value predictions and accelerating genetic gain.

Moreover, the integration of cutting-edge sequencing technologies, genotype analyses, and genome profiling has driven substantial progress in genetic improvement programs. These tools have facilitated the identification of genetic determinants for numerous production traits However, despite significant progress in decoding both coding and non-coding genomic regions that influence productivity traits, molecular and regulatory genomic approaches have yet to fully account for the extent of variation required to sustain continued productivity improvements.

Genomic breeding often relies on single nucleotide polymorphism (SNP) data to estimate genomic breeding values. Nevertheless, genetic differences among individuals explain only a portion of total phenotypic variability (Ibeagha-Awemu& Khatib, 2017). Importantly, the DNA sequence alone cannot fully explain the observed diversity in function and morphology, nor can it account for environmentally responsive epigenetic factors that modulate gene expression.

The epigenome-comprising DNA methylation, histone modifications, chromatin remodeling, and non-coding RNAs (ncRNAs)-plays a critical role in regulating gene expression and maintaining genomic integrity and function (Do &IbeaghaAwemu, 2017). Epigenetic mechanisms have been increasingly recognized for their influence on key livestock traits (Wang &Ibeagha-Awemu, 2021), and they may provide additional variation necessary for further improvement in animal health and productivity.

Epigenetics refers to heritable biochemical modifications that affect gene activity and expression without altering the underlying DNA sequence (Greally, 2018). These changes can be induced by various environmental factors, including nutrition, and have important roles in regulating development, growth, metabolic pathways, and immune responses. The epigenome, a dynamic collection of chemical modifications on DNA and histones, represents the interface through which environmental cues interact with the genome throughout an organism's lifespan (Monk et al., 2019). Although epigenetics is relatively underexplored in livestock science, it represents a promising avenue for uncovering additional sources of phenotypic variation that can be harnessed for production gains. Investigating epigenetic mechanisms during key developmental stages may yield valuable insights into complex traits and productivity enhancement (Panzeri &Pospisilik, 2018).

In animal agriculture, nutrition constitutes one of the most significant costs and is a primary determinant of profitability. Post-conception, nutrition serves as a critical environmental input influencing genetic expression, developmental trajectories, and ultimate phenotype. The quality and composition of nutrients provided to livestock are crucial, as emerging evidence suggests that dietary components can directly impact the epigenome. Persistent nutritional exposures can result in epigenetic changes in somatic tissues that influence animal health and disease outcomes, some of which may be transmitted across generations (Ideraabdullah& Zeisel, 2018). Furthermore, both nutrient deficiencies and surpluses have been associated with epigenetic alterations in germ cells, which may propagate to future generations (Guo *et al.*, 2020). Although the heritability of these nutrition-induced epigenetic modifications is becoming evident, the molecular mechanisms remain poorly understood.

As a modifiable environmental factor, nutrition holds significant potential to influence epigenetic states in livestock, thereby affecting both immediate and longterm outcomes related to health, productivity, and welfare. The field of nutritional epigenetics seeks to elucidate how gene-diet interactions influence epigenetic regulation (Park et al., 2012). Foundational studies in this area have highlighted direct connections between specific nutrients-such as vitamins, macronutrients, and phytochemicals-and epigenetic modifications, particularly through their influence on methionine cycle intermediates and enzymatic activities. Diet may also impact the epigenetic landscape of progeny, influencing performance traits across generations. This effect is especially pertinent in rapidly reproducing species such as swine and poultry.

To understand how transgenerational epigenetic inheritance contributes to complex traits, it is essential to investigate the establishment of the epigenome during early development, along with nutrient-specific impacts on these processes. Nutritional regulation of epigenetic changes can be understood by examining the flow from dietary substrates to molecular targets and eventual phenotypic outcomes (Triantaphyllopoulos *et al.*, 2016). Epigenetic effects involve chemical modifications to DNA-such as the addition of methyl groups to cytosine bases-that do not change the DNA sequence itself but can modulate gene transcription, thus contributing to phenotypic variation. The overarching aim is to determine how epigenetic modifications can be harnessed to induce beneficial phenotypes in livestock.

With growing interest in sustainable and precision livestock farming, the role of nutrition in shaping the epigenome has garnered considerable attention. Understanding how individual nutrients influence epigenetic regulation can inform breeding strategies, enhance disease resistance, and improve productivity. This chapter explores the interaction between nutrition and epigenetics in livestock species, emphasizing key nutrients that influence epigenetic markers and discussing the implications for animal management and genetic improvement programs.

Epigenetic Mechanisms and Gene Regulation

Epigenetic modifications play a crucial role in regulating gene expression by influencing the chromatin structure and modulating the accessibility of DNA to transcriptional machinery. These modifications do not alter the DNA sequence but significantly impact gene activity. The principal forms of epigenetic regulation include DNA methylation, histone modifications, and the involvement of non-coding RNAs.

DNA Methylation

A growing body of evidence suggests that nutritional factors can influence DNA methylation patterns, either globally across the genome or at specific loci (Altmann et al., 2012). Nutritional regulation of DNA methylation occurs primarily through three interrelated pathways:

Supply of Methyl Donors and Substrates

Nutrients such as methionine, folate, choline, and betaine serve as substrates for methyl group donation. These are vital for the synthesis of S-adenosylmethionine (SAM), the primary methyl donor used in DNA methylation reactions. An adequate supply of these nutrients supports normal DNA methylation, whereas deficiencies can result in global hypomethylation or locus-specific methylation anomalies.

Provision of Cofactors for DNA Methyltransferase (DNMT) Activity

The activity of DNA methyltransferases, the enzymes responsible for transferring methyl groups to DNA, is influenced by the availability of SAM. Nutritional factors can modulate intracellular SAM levels, thereby indirectly regulating DNMT function. Moreover, some dietary components may directly impact DNMT expression or activity.

Modulation of One-Carbon Metabolism Enzymes

Enzymes involved in the one-carbon cycle, which generates methyl groups for SAM synthesis, also require vitamin-derived cofactors for proper function. For example, vitamin B6 is essential for serine hydroxymethyltransferase, vitamin B2 (as FAD) is required for methylene tetrahydrofolate reductase (MTHFR), and vitamin B12 is a cofactor for methionine synthase. These enzymes are critical in regulating the metabolic pathways that supply methyl groups for epigenetic modifications.

Together, these mechanisms highlight how dietary inputs can shape epigenetic landscapes by influencing the availability and utilization of methyl donors and the activity of associated enzymes. This underscores the dynamic interplay between nutrition and epigenetic regulation, particularly during key developmental windows or in response to environmental cues.

Epigenetic Mechanisms and Gene Regulation

Epigenetic modifications play a crucial role in regulating gene expression without altering the underlying DNA sequence. These modifications primarily function by modifying chromatin structure and controlling the accessibility of transcriptional machinery to specific genomic regions. The key epigenetic regulatory mechanisms include DNA methylation, histone modifications, and non-coding RNA activity.

DNA Methylation

DNA methylation is a fundamental epigenetic mark that typically involves the addition of a methyl group to the 5' position of cytosine residues, predominantly at CpG sites. This modification generally represses gene transcription by obstructing the binding of transcription factors or attracting proteins that induce chromatin condensation. Importantly, DNA methylation patterns are reversible and can be influenced by environmental factors, including dietary inputs.

A growing body of evidence suggests that nutritional components can significantly alter DNA methylation patterns both globally and at gene-specific sites. Nutrients may affect methylation in three major ways:

- Supplying methyl donors essential for methyl group transfer.
- Modulating the activity of DNA methyltransferases (DNMTs) through availability of necessary cofactors.
- Altering the function of enzymes involved in the one-carbon metabolism, which governs the biosynthesis of methyl groups.

These mechanisms often act in concert, meaning that dietary inputs can simultaneously influence several aspects of the DNA methylation machinery.

Dietary Methyl Donors

S-adenosylmethionine (SAM) acts as the primary methyl donor for methylation reactions involving DNA and proteins. SAM is synthesized through the methionine cycle, which relies on various dietary nutrients, including methionine, folate, choline, betaine, and vitamins B2, B6, and B12. Each of these nutrients contributes at specific stages of the cycle, facilitating efficient SAM production.

A deficiency in these methyl donors can lead to reduced SAM levels and hypomethylation of DNA, whereas adequate or high intake supports methylation activity. This relationship demonstrates how dietary composition can directly affect epigenetic gene regulation.

Regulation of DNMT Activity by Nutrition

DNMTs require SAM as a cofactor for catalyzing methylation reactions. Thus, fluctuations in SAM levels, governed by nutritional status, can influence DNMT function. Beyond this indirect regulation, some dietary bioactive compounds may directly affect the transcription and activity of DNMTs, further contributing to changes in DNA methylation patterns.

Enzyme Activity within the One-Carbon Metabolism

Vitamins such as B2, B6, and B12 play essential roles as cofactors in the enzymatic processes that generate methyl groups through one-carbon metabolism. Specifically:

- Vitamin B6 is essential for the activity of serine hydroxymethyltransferase (SHMT), which produces 5,10-methylene-tetrahydrofolate (THF).
- Vitamin B2 (as FAD) supports methylenetetrahydrofolate reductase (MTHFR), enabling the conversion of 5,10-methylene-THF to 5-methylTHF.
- Vitamin B12 is critical for methionine synthase activity, which facilitates the remethylation of homocysteine to methionine-an essential precursor for SAM formation.

By modulating the availability of these vitamins, diet can directly influence the methylation potential of the cell, with downstream effects on gene expression.

Histone Modifications

Histones are structural proteins around which DNA is wrapped to form chromatin. The N-terminal tails of histone proteins can undergo several posttranslational modifications, including acetylation, methylation, phosphorylation, and ubiquitination. These chemical modifications can either loosen or tighten chromatin structure, thereby regulating the accessibility of genes for transcription.For example, histone acetylation typically results in an open chromatin conformation conducive to gene activation, whereas certain types of methylation can either activate or repress gene expression, depending on the context and location of the modification.These histone modifications are dynamic and often responsive to external stimuli such as nutrition, stress, or toxins. Their role is particularly significant in coordinating gene expression during development and in response to environmental signals.

Chromatin Remodeling

Chromatin remodeling plays a pivotal role in regulating gene expression patterns essential for cellular differentiation and lineage commitment during development (Kishi & Gotoh, 2018). Beyond covalent modifications of DNA and histones, the repositioning and restructuring of nucleosomes are crucial for modulating chromatin accessibility. ATP-dependent chromatin remodeling complexes utilize the energy from ATP hydrolysis to reposition or evict nucleosomes, thereby controlling the access of transcription factors to DNA (Hota & Bruneau, 2016).

Among these remodeling complexes, the SWI/SNF family-also known as BRM/BRG1-associated factor (BAF) complexes-plays a significant regulatory role in both gene activation and repression during mammalian development and in various disease contexts (Alfert et al., 2019). Comprising more than 15 subunits, BAF complexes are dynamically assembled to fulfill distinct functions at various developmental stages, including embryogenesis, neural, cardiac, skeletal muscle, and immune system development (Hota & Bruneau, 2016).

Non-coding RNA (ncRNA) Regulation

Non-coding RNAs (ncRNAs), such as microRNAs (miRNAs) and long noncoding RNAs (lncRNAs), contribute to gene regulation by modulating mRNA stability and translation efficiency. miRNAs generally bind to complementary sequences on target mRNAs, leading to either their degradation or translational repression (Bartel, 2004).

In addition to canonical epigenetic mechanisms, ncRNAs have emerged as critical regulators of gene expression and chromatin structure. These RNAs include small interfering RNAs (siRNAs), piwi-interacting RNAs (piRNAs), miRNAs, and lncRNAs, all of which can influence transcriptional activity and post-transcriptional processes (Kaikkonen et al., 2011). For example, miRNAs under the regulation of DNA methyltransferase 1 (DNMT1) are implicated in lactation and mammary gland development in dairy cattle (Melnik & Schmitz, 2017).

Nutritional Regulation of Epigenetic Mechanisms

Dietary inputs significantly influence epigenetic modifications by supplying essential components such as methyl donors, enzymatic cofactors, and signaling molecules. These elements directly affect processes such as DNA methylation, histone modifications, and RNA-mediated gene regulation, thereby altering gene expression patterns relevant to animal health, development, and productivity.

Nutrients as Epigenetic Modulators

Nutritional epigenetics primarily focuses on how specific nutrients and their metabolic intermediates modulate key pathways, notably the folate and methionine cycles, and histone methylation processes. Nutrients such as folate, choline, and betaine function as methyl group donors and have been shown to enhance DNA methylation levels when supplemented in the diet (Crider et al., 2012). Additionally, B-complex vitamins-particularly B2, B6, and B12-serve as essential cofactors in these methylation pathways and facilitate the availability of S-adenosylmethionine (SAM), the principal methyl donor.While both choline and betaine participate in the remethylation of homocysteine to methionine, supplementation with these downstream metabolites has produced variable outcomes in terms of DNA methylation, possibly due to differences in their metabolic conversion and tissue-specific uptake (Waterland, 2006).

Vitamins and Co-Factors

Folate and Vitamin B12

Folate (vitamin B9) and vitamin B12 are integral to one-carbon metabolism, a pathway that supplies methyl groups necessary for DNA methylation. Folate, primarily in the form of tetrahydrofolate (THF), facilitates the remethylation of homocysteine to methionine, which subsequently contributes to the generation of Sadenosylmethionine (SAM), the universal methyl donor. Vitamin B12 functions as a coenzyme for methionine synthase, a key enzyme in this reaction.

Deficiencies in either vitamin can disrupt DNA methylation, potentially resulting in developmental anomalies, stunted growth, and heightened disease susceptibility (Waterland &Jirtle, 2003). In livestock, maintaining sufficient levels of these vitamins supports proper epigenetic control, fostering robust growth, immune function, and reproductive health.

Vitamin D

Beyond its classical roles in mineral homeostasis and skeletal health, vitamin D modulates gene expression through interaction with the vitamin D receptor (VDR). The active form, 1,25-dihydroxyvitamin D, binds to VDR, forming a complex that influences chromatin structure via histone modifications, DNA methylation, and regulation of non-coding RNAs.

In livestock, suboptimal vitamin D levels have been linked to diminished immunity, reproductive inefficiencies, and slower growth. This evidence underscores vitamin D's epigenetic significance in regulating genes critical to immune defense, inflammation, and bone physiology.

Vitamin A

The biologically active metabolite of vitamin A, retinoic acid, regulates gene expression through nuclear receptors. It modulates histone acetylation and DNA methylation, thereby influencing genes that govern cellular differentiation, immune function, and growth (Kong *et al.*, 2008). In animal husbandry, vitamin A supplementation is associated with enhanced immune competence and improved growth rates, effects that are likely mediated through epigenetic mechanisms.

Minerals and Trace Elements

Zinc

Zinc serves as a cofactor for numerous enzymes involved in DNA synthesis, repair, and gene expression. It has been shown to affect epigenetic processes, including DNA methylation, histone modifications, and the regulation of non-coding RNAs. Zinc deficiency disrupts these epigenetic pathways, impairing growth, immunity, and reproductive function in livestock.

Supplementation with zinc has demonstrated benefits such as increased immune resilience, better growth performance, and improved reproductive outcomes (King *et al.*, 2011), making it a key mineral in supporting livestock under stress or during periods of high physiological demand.

Selenium

As a constituent of selenoproteins, selenium is critical for maintaining cellular redox balance and protecting against oxidative stress. Selenium also influences DNA methylation and histone modifications, thereby affecting gene expression (Terry *et al.*, 2000). Inadequate selenium intake can lead to poor growth, compromised fertility, and weakened immunity (Combs, 2001).

Supplemental selenium has been found to modulate epigenetic marks, particularly those involved in immune response and metabolic regulation, highlighting its importance for livestock health and productivity (Yang *et al.*, 2015).

Fatty Acids

Omega-3 and Omega-6 Fatty Acids

Polyunsaturated fatty acids (PUFAs), especially omega-3 (n-3) and omega-6 (n-6) fatty acids, play a role in modulating gene expression via epigenetic mechanisms such as histone acetylation and DNA methylation. Omega-3 PUFAs, including EPA and DHA, exhibit anti-inflammatory effects and regulate genes involved in lipid metabolism, immune response, and inflammation (Calder, 2015).

The dietary balance of omega-3 and omega-6 is vital for maintaining epigenetic stability. An excess of omega-6 relative to omega-3 can promote chronic inflammation and disrupt normal gene regulation (Simopoulos, 2002). In livestock, omega-3 supplementation has been associated with enhanced immune function, improved feed efficiency, and better growth, potentially due to its influence on epigenetic gene regulation.

Amino Acids

Methionine

Methionine is an essential amino acid and a principal methyl donor in DNA methylation pathways. Its availability is crucial for SAM synthesis, and deficiencies can impair methylation processes, leading to disrupted gene expression (Pogribny *et al.*, 2006). Supplementation with methionine has been shown to enhance DNA methylation, promoting better growth, immune competence, and reproductive efficiency in livestock.

Leucine

Leucine, a branched-chain amino acid, activates the mechanistic target of rapamycin (mTOR) signaling pathway, which is central to cell growth and metabolism. In livestock, dietary leucine has been linked to increased muscle accretion and improved feed utilization (Barton *et al.,* 2015). These outcomes are potentially attributable to leucine's capacity to influence gene expression through epigenetic modifications.

Epigenetic Impacts on Livestock Reproduction, Growth, and Development

Epigenetic modifications are crucial in orchestrating gene expression during development, enabling dynamic responses to environmental stimuli (Del Corvo *et al.*, 2020; Thompson *et al.*, 2020). Mapping epigenomic landscapes across different tissues has expanded our understanding of how epigenetic regulation underlies key physiological processes in livestock.Various studies have demonstrated the involvement of epigenetic mechanisms such as DNA methylation and histone modifications-in placental development, embryogenesis, and postnatal growth in several livestock species (Das *et al.*, 2017; Franco, 2017; Hwang *et al.*, 2017). Genome-wide methylation analyses in cattle, sheep, swine, goats, and poultry have provided valuable insights into species-specific and tissue specific epigenetic patterns (Korkmaz & Kerr, 2017; Lee *et al.*, 2017; Zhang *et al.*, 2017; McKay *et al.*, 2018; Sevane *et al.*, 2019; Liu *et al.*, 2020; Wang *et al.*, 2020b). These findings reinforce the importance of epigenetic regulation in determining livestock health, development, and productivity outcomes.

Epigenetic Modifications in Response to Environmental and Maternal Stressors

DNA methylation alterations have been implicated in mediating the detrimental effects of maternal stress-such as heat stress, metabolic disturbances, and energy deficits-on the offspring's physiological performance (Akbarinejad *et al.*, 2017). In calves exposed to maternal heat stress or cooling strategies (e.g., fans and water soakers), differentially methylated cytosines (DMCs) in hepatic tissue have been identified within genes governing immune responses, cell proliferation, developmental processes, and enzymatic activities. Similarly, in mammary gland tissues, DMCs are enriched in genes associated with protein interactions, phosphorylation, enzyme activation, cellular signaling, and immune modulation (Skibiel *et al.*, 2018).

In the context of male reproduction, aberrant DNA methylation in sperm-as well as histone modifications, including acetylation and methylation-have been linked to compromised fertility and reproductive phenotypes (Kropp *et al.*, 2017; Perrier et al., 2018; Fang et al., 2019b; Kutchy et al., 2017, 2018). Regions of the genome exhibiting high methylation variability are strongly correlated with reproductive traits and are notably enriched for glycosyltransferase genes essential for spermatogenesis and fertilization. Additionally, these regions often co-localize with genes that regulate sperm motility (Liu S. *et al.*, 2019).

Epigenomic analyses of somatic tissues-such as the liver, brain, and mammary glands-have further highlighted the role of epigenetic modifications in modulating bovine development, health, and productivity (Wang et al., 2020). In pigs, investigations into the epigenetic landscape across various tissues, including the brain, intestine, teeth, and longissimus dorsi muscle, emphasize the regulatory significance of DNA methylation and histone marks during growth and development (Larsen *et al.*, 2018).

In avian species, particularly chickens, epigenetic variation has been explored across multiple strains, revealing its role in developmental and evolutionary processes (Sarah-Anne *et al.*, 2017). Detailed epigenetic mapping across chicken tissues such as the brain, retina, cornea, liver, and muscle demonstrates a strong association between DNA methylation and growth-related gene regulation (Liu *et al.*, 2016; Liu Z. *et al.*, 2019; Lee I. *et al.*, 2017). For example, during embryonic development, broilers exhibit lower DNA methylation levels compared to layers, with associated genes enriched for functions related to muscle formation, suggesting a role for methylation in muscle differentiation (Liu Z. *et al.*, 2019). Moreover, in chickens with fatty liver syndrome, the genes ACC and MTTP display elevated expression levels inversely related to reduced promoter methylation, indicating an epigenetic influence on lipid metabolism (Liu *et al.*, 2016).

In equine species, DNA methylation has been proposed as a biomarker of aging, with methylation patterns showing age-related variability in domestic horses (Andraszek *et al.*, 2016). Contrasting typical mammalian methylation profiles, honeybees exhibit unique methylation confined primarily to gene bodies, a pattern closely linked to transcriptional regulation (Wedd & Maleszka, 2016; Harris *et al.*, 2019). This gene-body methylation is particularly important for learning and memorytraits essential for behaviors such as foraging and hive maintenance-thus playing a critical role in honey production (Li *et al.*, 2017).

Nutritional Epigenetics and Livestock Development

Early-Life Programming

The fetal and neonatal stages represent critical periods during which nutritional inputs can exert profound effects on epigenetic programming. Maternal diet during gestation has been shown to influence the epigenetic regulation of gene expression in the developing fetus, with enduring effects on traits such as growth, immune competence, and metabolic health. This phenomenon, commonly referred to as nutritional programming, has garnered considerable attention in both human and animal studies.

Evidence suggests that maternal supplementation with micronutrients such as folate, vitamin B12, and omega-3 fatty acids can induce epigenetic alterations, including changes in DNA methylation and histone modifications, in the offspring. These epigenetic shifts are associated with modified gene expression profiles that impact growth performance, metabolic efficiency, and immune responses (Waterland &Jirtle, 2003). These findings emphasize the pivotal role of maternal nutrition in sculpting the epigenetic landscape of offspring and point to the potential of nutritional strategies to enhance livestock productivity.

Nutritional Interventions to Promote Livestock Health and Productivity

Because epigenetic modifications are dynamic and, in many cases, reversible, dietary interventions offer a valuable avenue for enhancing animal health and performance. Targeted supplementation with specific nutrients can modulate epigenetic markers that govern key physiological processes including growth, reproduction, immune function, and metabolism. By optimizing nutrient intake, producers can influence gene expression patterns in a direction that supports improved animal welfare, higher feed conversion efficiency, and reduced reliance on pharmaceutical interventions such as antibiotics.

Implications for Sustainable Livestock Production

Insights from nutritional epigenetics have profound implications for sustainable animal agriculture. Improved understanding and manipulation of nutrient epigenome interactions may enhance productivity while simultaneously reducing the environmental footprint of livestock systems. Specifically, better nutrient utilization, lowered disease incidence, and improved reproductive outcomes can be achieved through strategic nutritional management. Moreover, these approaches contribute to more sustainable practices by minimizing waste and optimizing resource inputs.

Conclusion

The epigenetic regulation of gene expression through dietary modulation presents a promising frontier in livestock science. Nutrients that influence DNA methylation, histone modifications, and the expression of non-coding RNAs can significantly affect animal growth, health, and productivity. A deeper understanding of the mechanisms underlying nutrition-epigenome interactions will enable the development of precision feeding strategies aimed at improving animal performance and welfare, as well as supporting the goals of sustainable livestock production.