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Nutrigenomics: A tool to unlock genetic potential of Nigerian indigenous goat breeds

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ABSTRACT

Nigerian indigenous goats represent a valuable genetic resource for meat and milk production. However, their productivity often falls below their genetic potential because of sub-optimal nutrition. Nutrigenomics offers a revolutionary approach to bridge this gap by exploring the interactions between nutrients and goat genes. This study explores how nutrigenomic tools can be used to identify gene variants associated with feed efficiency, meat quality, and milk production. Various technologies are designed to ensure the realization of genetic potential. Nutrigenomics is aimed at exploiting the noncoding section of an individual's genome, which is disregarded in traditional animal nutrient requirement assessment. Nutrigenomic technology has the potential to unlock the genetic potential of animals and essentially help to confront nutritional challenges and sub-optimal use of available feed resources, particularly in Nigerian indigenous goats, of which there is a dearth of information on their nutritional needs and requirements. This review discusses the potential of nutrigenomics to unlock the genetic potential of Nigerian indigenous goats. In addition, the review discusses the challenges and future directions of nutrigenomic research in Nigerian goats. By implementing nutrigenomic strategies, Nigerian goat production can be revolutionized, leading to increased productivity, improved product quality, and enhanced farmer livelihoods. It is hoped that this review will provide vital information to aid research into the nutrigenomics potential of unlocking the genetic potentials and reproductive performance of Nigerian indigenous goats through nutrition.

Keywords: Breeds, Diversity, Genetics, goats, Nutrigenomics.

Introduction

Livestock plays at least two major roles in human society: they are a major component of the food supply, mainly because of their value as food-producing units, and they provide vital services. The identification of genes governing these biological processes has been made possible by recent advances in genomics and molecular biology (Herrero *et al*., 2013). The use of high-throughput omic technologies to gain a worldwide understanding of nutritional pathways is referred to as "nutrigenomics." Understanding nutrient-mediator gene interactions may help identify important genetic variations in animals through the use of nutrigenomics, also known as nutrigenetics (Vyas, 2022).

The resilience and adaptability of native/indigenous Nigerian goats to arid and harsh environments make them unique (Adeloye, 1998; Oseni and Ajayi, 2014; Daramola *et al*., 2021). They exhibit considerable genetic diversity, which is a valuable asset for breeding programs (Ojo *et al*., 2015; Okpeku *et al*., 2016; Akintunde *et al*., 2024a). Determining the genes that respond positively to nutritional interventions requires an understanding of the genetic makeup of these goats. Growth rate, milk yield, reproductive efficiency, and disease resistance are important characteristics of interest.

The creation and application of ecologically sustainable farming techniques are central to sustainable livestock

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production. Precision nutrition is essential to sustainable agriculture, just as it is to livestock production. Over the past years, the process of identifying ideal nutrient requirements for Nigerian indigenous goats and then feeding them has been a relatively static process (Sejian *et al*., 2023). Nowadays, the primary goals are to guarantee higher productivity and genetic advancement. The need for a more dynamic feed area arose from the development of technologies such as nutrigenomics, which are based on changes in gene expression observed in response to nutrients from the subject's diet. Overall, nutrigenomic technologies are very helpful in the diagnosis of diseases and the development of transfer capacities, especially when the broad range of economic traits has enough relevance to warrant investment. Specific dietary recommendations for feedlot ruminants could be developed using the information gathered from the transcriptional and proteomic profiling of a variety of tissues, potentially leading to improved carcass quality.

According to Okpeku *et al*. (2019), genomics holds great promise for unlocking the genetic potential of indigenous goats in Nigeria. Considering the distinctive characteristics of these breeds, as well as their low productivity and production, this is particularly crucial. The application of nutrigenomics in this context could help in the genetic improvement of these goats, as seen in the case of the West African Dwarf (WAD) goats, where genetic resistance to gastrointestinal nematode infections has been identified (Chiejina *et al*., 2015). The need for detailed phenotypic and genetic characterization of these goats, as well as the design of breeding strategies, has also been emphasized (Oseni and Ajayi, 2014). The evaluation of genetic diversity and conservation in native goat ecotypes found in South Africa also emphasizes the significance of prioritizing conservation and sustainable use top priority (Magoro *et al*., 2022). The review, as a whole, emphasizes how nutrigenomics can be used to increase the productivity and sustainability of indigenous goats in Nigeria.

Moreover, this information may be utilized to create diet plans that are specifically tailored and incorporate components chosen to act as modulators in particular metabolic or functional processes, such as meat quality, disease resistance, and fertility. Nutrigenomics holds the potential to provide more accurate control over nutrient supply—a crucial factor in optimizing production processes, mitigating nutritionally related genetic defects, and maintaining environmental sustainability (Farhud *et al*., 2010). In particular, the potential use of nutrigenomics in health promotion and management is great, especially for farm animals, many of which have adaptively evolved to select diets based on nutrient content (Fenech *et al*., 2011). Nutrigenomics holds great promise not only for health-related connections but also for performance control.

Nevertheless, there are restrictions on the advancement of nutrigenomics technologies, particularly when it comes to using them to unlock the genetic potential of native goat breeds in Nigeria. The future of nutrigenomics is bright and uncertain because of the complexity of food and its constituent parts, as well as the complex interactions between the genes involved in health, function, and nutrient responses. It is probable that the field of nutrigenomics is likely to have an incremental effect on livestock devices. The ultimate phase of this process will encompass the creation and application of tools for genotypic and phenotypic analysis, as well as the amalgamation of biological and economic domains in the formulation of nutritional models.

Significance of nutrigenomics in livestock production

The identification of the critical molecular actors involved in the physiological adaptations to alterations in nutrient supply and environmental conditions is a major objective of applying nutrigenomics at the animal level (Loor, 2022). Nutrigenomics enhances the understanding of the relationship between nutrition and gene expression by elucidating how the genetic code and DNA influence the requirements for specific nutrients and amounts (German, 2005; Miggiano and De Sanctis, 2006). According to Naji *et al*. (2014) and Banerjee *et al*. (2015), knowledge of the physiological, biochemical, and metabolic pathways as well as gene expression in livestock is necessary in order to investigate the significance of diet and diet formulation. Certain genes' expression and structural makeup can be influenced by nutrients found in foods and supplements. The application of nutrigenomics spans several disciplines, including the diagnosis of health status and disease trajectory. To investigate how nutrition affects genomic stability, epigenome alterations, RNA and micro-RNA expression, protein expression, and metabolite changes, these fields can be investigated separately or in combination (Fenech *et al*., 2011; Banerjee *et al*., 2015).

Nutrigenomics and its applications

Given its importance in nutrition and medical science, nutrigenomics, also known as nutritional genomics, has become a prominent field (Farhud *et al*., 2010). It is a helpful treatment for both preventing and curing the many kinds of cancer as well as treating chronic illnesses. It is related to the molecular interactions between genes and the body's nutrition (nutrigenetics), and transcriptomics, metabolomics, and proteomics are all affected by these interactions (Ferguson *et al*., 2016). The expression of metabolic response and gene expression alters people's health and illness vulnerability. These correlations can specifically affect how bioactive food ingredients are absorbed, digested, metabolized, and excreted (Farhud *et al*., 2010). Nutrigenomics is the study of how dietary factors affect genetic variants and how nutrients and bioactive food elements individually affect gene expression (Simopoulos, 2010; Riscuta, 2016).

Epigenetics, transcriptomics, and nutrigenetics are all included in nutrigenomics, along with other "omic" analyses such as metabolomics and proteomics that clearly show the wide variation in tumor risk across individuals with similar dietary choices (Kaput, 2008; Hurlimann *et al*., 2014). Numerous research on various food components, such as phytochemicals, vital nutrients, and compounds derived from zoo chemicals, bacteria, and fungo chemicals, have produced varying findings regarding their ability to reduce the incidence of cancer and tumors (De Vasconcelos, 2010). Numerous rulings have demonstrated that not all animals react to a diet in the same way; there are breed-specific and within-breed differences (Akintunde and Toye, 2014). According to Akintunde *et al*. (2020, 2021, 2024b) and Akintunde and Toye (2021, 2023), genotypes significantly influence the use of nutrients for growth performance, as well as the generation of eggs and sperm. However, Akintunde (2018) came to the conclusion that nutrition and genotypes significantly interact. Food ingredients have an impact on metabolism, cells, and organs, in addition to affecting overall health. Two observations form the basis of nutrigenomics: the impact of nutrients on gene expression and nutrient metabolism may vary depending on an individual's genotype, thereby influencing health in different ways (Fenech *et al*., 2011). Therefore, in order to customize diet and nutrition and prevent disease, nutrigenomics incorporates an individual's genotypes, genes, and nutritional environment (Iacoviello *et al*., 2008; Kussmann and Van Bladeren, 2011; Akintunde *et al*., 2019).

Genome-wide association studies (GWAS) have received a lot of attention in an effort to identify genes that contribute to chronic illnesses like cancer (Chung *et al*., 2010). Contrary to the vast majority of GWASs, some GWASs are regarded as dietary variables. Furthermore, at this point, GWAS has extensively reaffirmed the established facts and continues to reveal that identifying the most important genetic variables will not be a simple task, most likely as a result of discontinued cellular controlled techniques (Fenech, 2008; Ferguson, 2009).

Principles of nutrigenomics

The principles of nutritional genomics encompass transcriptomics, proteomics, metabolomics, and epigenetics (Lagoumintzis and Patrinos, 2023). Nutrition is considered a significant influencing factor for a number of diseases under certain conditions. Dietary components then modify gene expression or gene structure, which modifies the animal genome (Mierziak *et al*., 2021). Individual differences in genotype can shed light on the balance between health and illness. Commencement, progression, and extent may be influenced by genes that are regulated by dietary variables (Fenech, 2008; Ardekani and Jabbari 2009; Hardy and Tollefsbol, 2011; Nicastro *et al*., 2012; Elsamanoudy *et al*., 2016). As shown in Figure 1, with a growing understanding of genetics, illness preventive monitoring, lifestyle recommendations, and treatment might then be customized to each person's needs.

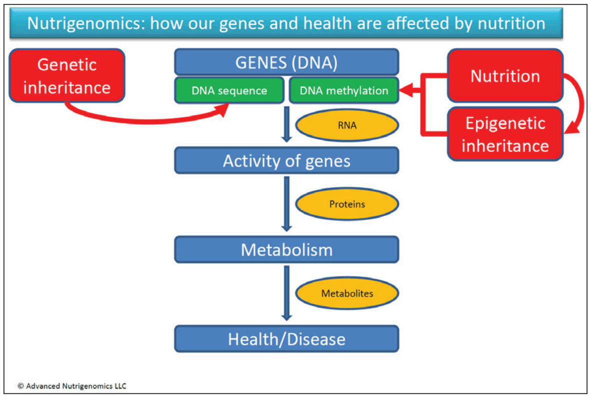

Fig. 1. Nutrigenomics: How genes and health are affected by nutrition.

All things considered, a nutrigenomic approach offers a picture of the genes that are turned on or off (the genetic potential) at any given time; an insight into how gene/protein networks might work together to produce the observed response; and a way to ascertain how nutrients affect the expression of genes and proteins. To minimize the emergence of chronic diet-related disorders, it is hoped that expanding research in this field would foster a better understanding of how nutrition affects metabolic pathways and homeostatic control (Pathak *et al*., 2000; Ramachandran *et al*., 2006; Ramya *et al*., 2011).

Techniques and tools for nutrigenomic research

To learn how foods affect gene expression, several nutrigenomic studies have used technical techniques, including microarrays, genomics, and bioinformatics. Together with nutrigenomics, these new technologies have the potential to improve nutrition and health (Masotti *et al*., 2010).

Microarray technologies, the main transcriptomics tools, have enabled new insights into the physiological impacts of different dietary proteins, omega-3 polyunsaturated fatty acids (PUFA), and dietary conditioning in colon cancer. The relationship between diet and genes, as determined by variations in genetic expression, has been successfully assessed using quantitative real-time polymerase chain reaction (PCR) and DNA microarray technology (Deepak *et al*., 2007). The use of proteomics tools, particularly two-dimensional electrophoresis, has allowed for the discovery of new information regarding the protein composition of egg and poultry meat proteins, the effect of dietary methionine on breast meat accretion, the toxicity of dioxin, and the safe use of transgenic crops in animal nutrition (Zduńczyk and Pareek, 2009). Metabolomic analysis was used to identify metabolite profiles in the liver of rats used as an animal model and to identify alterations in the biochemical profiles of plasma and urine from pigs fed different diets in order to examine the toxicity of triazole fungicides (Ekman *et al*., 2006). Microarray technology was assessed as a possible nutrigenomics tool for livestock species given its economic benefits and ability to improve food quality and safety in the dairy and meat industries (Neeha and Kinth, 2013). This commonly used microarray or DNA chip technology in nutrigenomics research will not only enable the simultaneous screening of multiple genes and provide a comprehensive picture of the variation of gene expression patterns, but it will also clarify complex regulatory interactions, including those between genes, diet, and nutrients (Zduńczyk and Pareek, 2009).

Single-nucleotide polymorphisms

Munshi and Duvvuri (2008) explained how nutrients affect the results of gene expression, that is, synthesis of mRNA (transcriptomics), protein synthesis (proteomics), and metabolite production (metabolomics), using the example of genetic polymorphisms [single nucleotide polymorphisms (SNPs)], which may be partially responsible for variations in an individual's response to bioactive food components. Siddique *et al*. (2009) also investigated the impact of different nutrients on the normal expression of genes in the body and how these genes are applied to different aspects. Scientists have discovered the genes that produce nutritionally significant proteins, including digestive enzymes and transport molecules that deliver nutrients and cofactors to their intended location, using molecular biology and genomics methods (Fenech *et al*., 2011). Nutrient needs are influenced by several common SNPs. An illustration is provided by research on SNPs that altered the likelihood of organ malfunction in humans fed choline-deficient diets (da Costa *et al*., 2006). Choline deficiency symptoms were 15 times more common in premenopausal women [carriers of a very common SNP (methylenetetrahydrofolate dehydrogenate MTHFD1-G1958A)] than in noncarriers when they were following a low-choline diet (Zeisel, 2007). Compared with women consuming diets in the highest quartile for choline intake, moms with this SNP had a four-fold higher chance of giving birth to a child with a neural tube abnormality. Zeisel (2011) also proposed that choline in the mother's diet affects the development of the fetus's brain in mouse models.

Scientific studies on alternative therapies, with a focus on nutritional approaches to health and well-being, have been prompted by growing interest in preventive medicine and the pursuit of organic animal production (Vignesh *et al*., 2024). The creation of SNP arrays, which aid in identifying distinct haplotypes, is one example of a recently developed technology. Majeed and Prakash (2006) discussed how nutraceuticals affect health and illness. Such methods would gain scientific legitimacy from nutrigenomics, which examines the relationship between nutrition and illness development based on a person's genetic profile.

A study by Neeha and Kinth (2013) examined SNPs and the diseases they are linked to, including cancer, obesity, diabetes, cardiovascular vascular diseases, neural tube defects, leukemia, down syndrome, and spina bifida. The results also highlighted the relationship between folate nutrigenomics, which is the study of folate-dependent enzyme polymorphism and folate nutrition. In healthy Indians, Ghodke *et al*. (2011) investigated SNPs along the intracellular folate metabolic route. Acute lymphoblastic leukemia's relationship to folate, vitamin B12, and homocysteine levels raises the possibility that gene-environment interaction plays a significant role in disease development (Adiga *et al*., 2008).

Biomarkers

Nutrigenomics is a groundbreaking perspective that views food as a medicine that reverses sickness and slows down the effects of aging, rather than just as a source of nourishment (Bhatt and Sharma, 2011). Finding indicators of diet-related disorders in the early stages, when nutritional intervention might restore health, is a component of the nutrigenomics approach (Kore *et al*., 2008; Lau *et al*., 2008; Ramesha *et al*., 2010; Murray *et al*., 2010).

Through the use of nutrients or their combinations, markers can alter gene expression to enhance an animal's overall performance and productivity (Haq *et al*., 2022). Today's nutrigenomic research requires the identification of these markers associated with commercially significant features, such as the production of milk, meat, wool, and leather, whose expression can be enhanced by dietary regimens. This will support the production of animals in a sustainable manner. It may be feasible to achieve the intended livestock performance in terms of health and productivity by modifying some genes through diet, particularly in the rise in the production of premium leather for which Sokoto Red goats are known (Kore *et al*., 2008).

Coudron *et al*. (2006) used *Perillus bioculatus* (F.) (Heteroptera: Pentatomidae) to demonstrate the possible identification of genetic markers when raised on an optimal versus substandard diet and examined the presence of differentially expressed genes as a result of the treatment. The discovery of biomarkers in this study may result in the creation of a quick and easy way to assess the fitness and quality of insect populations both in the field and in the lab, which might lead to more effective rearing techniques and the manufacture of high-quality insects (Siddiqui *et al*., 2023). In the long run, these advancements will probably result in better agricultural sustainability and more efficient use of biological control techniques. Ten PCR-Simple Sequence Repeats microsatellite markers were employed by Ramesha *et al*. (2010) to gain a better understanding of the genotyping of particular nutrigenomic gene loci in nutritionally efficient silkworm breeds and hybrids. They found that farmers in the sericulture sector could benefit from this advanced molecular analysis of silkworms. The use of nutritionally efficient silkworm strains as marker-assisted selection or gene-transmission methods in silkworm breeding programs emphasizes the potential for future research into the functioning mechanism of silkworms in nutrigenomics studies.

In order to unlock the genetic potential of indigenous goat breeds in Nigeria, nutrigenomics serves as the foundation for the development of the concept of "personalized diets," the identification of molecular biomarkers or new bioactive feed ingredients, and the validation of the efficacy of these bioactive ingredients as functional feed components or nutraceuticals.

Nutrigenomic studies of livestock

Because feed makes up over 70% of production costs and the livestock industry is one of the main sources of income for farmers in rural Nigeria, the profitability of the sector is heavily reliant on how well the animals use their feed (Adeloye, 1998; Rauw *et al*., 2020). Nutrigenomics differs significantly from traditional nutritional approaches in livestock farming by focusing on how nutrients interact with genes to influence animal health, growth, and productivity. The traditional nutritional approaches usually center on standardized nutrient requirements, which are usually based on the temperate regions' breeds of goats, whereas the nutrigenomics approach is individualized. Effective bio-fermentation in the rumen is achieved via the symbiotic and synergistic actions of the intricate and highly varied rumen microbial community. There are effective anaerobic processes in the rumen that break down lignocellulosic diets (Gharechahi *et al*., 2023). However, only a small portion of the potential energy in lignocellulosic diets can be extracted by rumen bacteria (Liang *et al*., 2020). Feed energy waste causes significant financial losses for the cattle business. Rumen microbiologists and nutritionists have been attempting to comprehend the complex microbial ecosystem and minimize losses (Matthews *et al*., 2019). The molecular age and sophisticated molecular tools are used to address genetically based dietary mysteries. Nutrigenomics opens the door to the prevention or clinical management of nutritional illnesses and metabolic disorders. The identification of putative genes and pathways responsible for economically significant traits will be made possible by differential gene expression studies. Nutrigenomics investigates how nutrition affects gene expression or regulatory systems that may be connected to a variety of biological processes affecting animal health and productivity in the context of changing diets (Asmelash *et al*., 2018).

In addition to adjusting to environmental stressors, there has been a remarkable surge in tackling the significant obstacles posed by the sharply anticipated rise in the world's demand for food and premium animal proteins (Apalowo *et al*., 2024). In order to create efficient nutritional strategies, nutrigenomics research seeks to identify the required molecular signatures and to explain the molecular relationships between genes and diet. Because certain gene transcripts determine biochemical parameters, gene expression analysis is performed in response to dietary regimens (Mierziak *et al*., 2021). The dairy cattle experiments were centered on milk content and yield. On the other hand, research on beef cattle focuses on determining the fatty acid composition of their muscle tissue in order to adjust their diet. Supplements such as amino acids, vitamins, and prebiotics are used because animal health is important for both pigs and poultry. These supplements influence gene transcription and are crucial for enhancing immune system performance (Alagawany *et al*., 2021).

Nuclear receptors within cells are activated by a variety of lipid-soluble signaling substances, including retinoids, thyroid hormones, steroid hormones, and vitamin debye metabolites. To promote gene production, ligand-activated transcription factors attach to the appropriate DNA segments (Osz *et al*., 2020; Rochette-Egly, 2020). It is believed that vitamin debye regulates adipogenesis and plays a part in bone metabolism and calcium balance (Nimitphong *et al*., 2020). Vitamin D has been shown to influence tissue sensitivity to insulin, insulin production, and eventually systemic inflammation in obesity. Direct and paracrine actions of vitamin D caused local synthesis of 1, 25(OH) 2D, CYP27B1 expression, and Vitamin D receptor (VDR) activation in pancreatic beta-cells (Maestro *et al*., 2003). Genes involved in the generation and signaling of vitamin debye have polymorphisms that lower obesity and diabetes. Vitamin D reduces adipogenesis in both *in vitro* and *in vivo* studies. Adipogenic gene expression is downregulated and 3T3-L1 preadipocyte development is suppressed in a dose-dependent manner by 1, 25-dihydroxy vitamin D, the active metabolite of vitamin D (Blumberg *et al*., 2006). It has been determined that 1, 25-dihydroxyvitamin D activates the 1, 25-dihydroxyvitamin D receptor, which in turn controls adipogenesis (VDR). VDR inhibits adipogenesis by downregulating the expression of C/EBP when 1, 25-dihydroxyvitamin D is present (Lu *et al*., 2018; Miao *et al*., 2020).

The consistency of ruminant meat should be enhanced because it influences flavor and juiciness. All things considered, this problem has received a lot of attention recently because the fatty acid concentration of lipids in meat is essential for human health (Geletu *et al*., 2021). Researchers now have a better knowledge of the biological processes influencing fatty acid composition and meat mixing based on nutrigenomic studies. The cattle sector may benefit from this knowledge if it is inspired to create chemicals or substances that can alter gene expression and improve the quality of meat

(Aiken and Ozanne, 2014). Because of this experience, nutritionists will now be able to employ feedstuffs and other foods. The womb is where adipogenesis and marbling are programmed. Adipogenesis takes place in the womb and affects meat quality and fat accumulation over time (Desoye and Herrera, 2021). Until the direct influence of nutrients on genes during the finishing phase can be sufficiently investigated, the effect of dam nutrition on offspring adipogenesis should be investigated through the influence of nutrients on gene expression in the fetus. The concept of fetal programming is connected to this influence. It has been proposed that mothers may influence the phenotypes of their offspring by contributing half of the fetal genes together with epigenetic markers through ooplasmic input to the fetus, intrauterine environment, and somatic epigenetic reprogramming (Vahmani *et al*., 2015).

The possible positive or negative effects of meat's fatty acid composition on human health raise concerns regarding its manipulation. The risk of diabetes, hyperlipidemia, and cancer is decreased by conjugated linoleic acid (CLA) C9 and t11-C18:2, but high-density lipoprotein cholesterol is raised by certain saturated fatty acids (Berton *et al*., 2016). Numerous biological processes essential to human health include PUFAs, which can be accomplished via nutrigenomic methods (Wood *et al*., 2004). Figure 2 shows the interactions between diet and gene expression.

Adult animals can also exhibit how nutrition affects their gene expression profiles and, consequently, their meat quality characteristics. Teixeira *et al*. (2017) investigated how the lipid metabolism gene expression profile and intramuscular fat contents of the muscle tissue of Angus and Nellore cattle breeds were affected by varying starch delivery regimes (whole shelled corn *vs*. ground and silaged corn). They discovered that the fatty acid binding protein 4 (FABP4), acetyl-CoA carboxylase alpha (ACACA), and stearoyl-CoA desaturase (SCD1) genes were more highly expressed in Nellore bulls fed ground corn. Sterol regulatory element-binding transcription factor 1 (SREBF1) gene transcription was decreased in both breeds, while the expression of the peroxisome proliferator-activated receptor alpha (PPARA) gene was elevated in response to the whole shelled maize. However, as the whole shelled corn diet decreased the rumen's pH and raised its linoleic acid content, the authors believed that the lack of effect on marbling was due to the lower level of SREBF1 (c9, c12–C18:2). According to Oliveira *et al*. (2014), when cattle were supplemented with soybeans, their muscle tissue showed changes in the expression of genes related to lipid metabolism, including PPARA, SCD, ACACA, FABP4, lipoprotein lipase (LPL), and glutathione peroxidase. However, in order to enhance starch fermentation and boost animal performance, the alpha-amylase enzyme is frequently added to the diet of beef cattle. A study of this practice was also published by Elolimy *et al*. (2018), who supplemented finishing steers with amylase to ascertain its impact on carcass characteristics and performance in connection with global gene expression profiles of the liver and muscles. Although there were no changes in carcass characteristics or serum metabolites, animals in the experimental group had lower average daily gain and gain/feed ratios. The adipogenesis-related genes forkhead box O1, actin-binding rho activating protein,

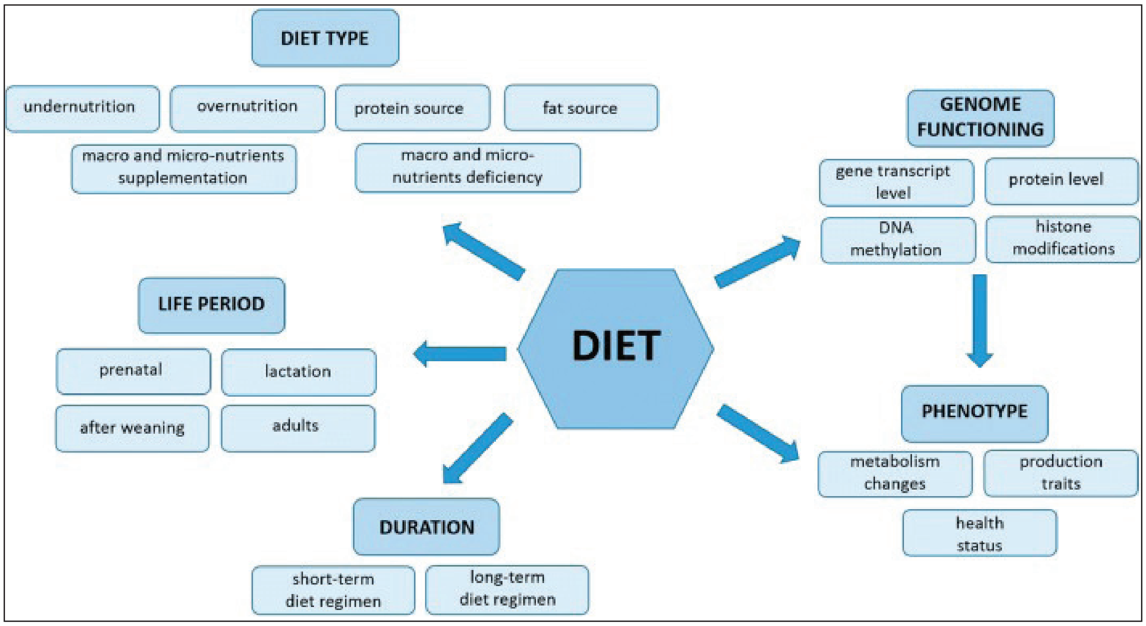

Fig. 2. Gene–diet interactions (Nowacka-Woszuk, 2020).

and peroxisome proliferator-activated receptor gamma coactivator 1 alpha were all upregulated in muscle tissue. The liver's decreased expression of 3-hydroxybutyrate dehydrogenase 1 and fatty acid binding protein 1 indicated that the amylase-supplemented animals may have less hepatic lipid catabolism (Elolimy *et al*., 2018).

Variations in the fatty acid composition and content of an experimental diet can vary the fatty acid profile of beef through modifications to the expression of genes related to lipid metabolism, potentially leading to healthier meat. Choi *et al*. (2016) investigated the effects of oil supplementation on cattle by feeding them palm oil (high in oleic acid) and soybean oil (rich in PUFAs) hoping that the palm oil would increase the expression of adipogenic genes in intramuscular and subcutaneous adipose depots. The mRNA level of CCAAT enhancer binding protein-beta decreased in both adipose depots in rats administered palm oil, whereas the expression of AMP-activated protein kinase alpha decreased in subcutaneous adipose tissue. In contrast to palm oil, which was thought to play a critical role in promoting adipogenesis, soybean oil more successfully reduced the level of the SCD transcript in the subcutaneous adipose (Choi *et al*., 2016). SCD and SREBF1 gene expression in muscle was likewise decreased in cattle fed a diet rich in n-3 PUFA-enriched fish oil; however, both genes' expression was positively connected with n-6 PUFA muscle content (Waters *et al*., 2009). It was demonstrated that giving lambs of the Aragonesa breed vitamin E supplements in the form of alpha tocopherol changed the transcript levels of SREBF1 and PPARG in their muscle and adipose tissue, respectively (González-Calvo *et al*., 2014). In response to food supplementation with essential oils extruded from eucalyptus leaves, dill seeds, and cinnamon bark, extensive studies of the liver and muscle transcriptome in lambs have also been conducted (Sabino *et al*., 2018). Essential oils had a sex-dependent impact on the transcription of genes in both tissues, according to the RNA-seq data. The majority of the genes with differential expression were connected to immune response and inflammation pathways.

A dairy dam's diet can significantly affect the amount of milk she produces as well as the protein and fat content of that milk. Certain fatty acids included in the food, particularly trans-10 and cis-12 CLA, have been demonstrated to be responsible for diet-induced milk fat depression (MFD), which results in decreased milk fat production in the mammary gland (Bauman *et al*., 2011). Important lipogenic genes, such as SREBF1, FAS, LPL, ACACA, and thyroid hormone-inducible hepatic protein, exhibit changed expression in MFD syndrome (Peterson *et al*., 2003; Harvatine *et al*., 2018). Similar findings were noted in MFD-fed dairy sheep, in which there was a change in the expression of lipogenic genes in the mammary tissue (Carreño *et al*., 2016; Toral *et al*., 2017). Studies on adding various oils to the diet of cattle and goats, including fish oil and sunflower oil with starch additions, have recently been conducted. The composition of fatty acids in milk and the expression of lipogenic genes in the mammary system were determined. Both species' milk fat content and yield showed notable variations; however, the types of diets under study had no effect on the expression levels of the genes under analysis; instead, only species-specific variations in mRNA profiles were discovered (Bernard *et al*., 2017; Fougère *et al*., 2018; Fougère and Bernard, 2019). The study by Faulconnier *et al*. (2018) involved giving dairy goats linseed oil either alone or in combination with fish oil. Both diets changed the fatty acid composition of the milk, but they had no effect on the expression of specific potential lipogenic genes in the mammary gland. Conversely, the global transcriptional profile revealed variations in the responses of genes involved in protein metabolism and transport to dietary supplementation.

Genetic potential of Nigerian indigenous goats

Goats native to Nigeria are a valuable genetic resource for the country's livestock development; the WAD, Red Sokoto (RS), and Sahel goat breeds in particular have developed special adaptations and potentially advantageous traits as a result of their long history of natural selection in the harsh environment of the region (Akintunde *et al*., 2024a).

Research has indicated that there is a great deal of genetic variation both within and among native goat breeds in Nigeria (Adeyinka *et al*., 2011; Ogah, 2016; Rotimi *et al*., 2020). This diversity suggests a rich pool of genes with favorable features, including disease resistance, heat tolerance, prolificacy, and mothering skills. In tropical regions, disease tolerance is particularly important. WAD goats exhibit trypan resistance, enabling them to flourish in regions where tsetse flies are common (Adeloye, 1998; Daramola *et al*., 2010; Ogah, 2016). All three races exhibit resistance to severe weather conditions and effective foraging skills on low-quality foliage, demonstrating their tolerance to heat (Adeloye, 1998; Ogah, 2016; Daramola *et al*., 2021). Effectiveness of WAD compared with other breeds, goats have the capacity to generate more children. Research on mothering skills reveals that the indigenous Nigerian people possess a strong maternal instinct (Adeloye, 1998; Daramola *et al*., 2021).

Genetic potential for improvement

Breeding programs can benefit from the genetic diversity of local goats in Nigeria. The use of genetic markers for trypan tolerance and other disease resistance traits to create more resilient livestock; adaptation to climate change, as heat-tolerant breeds can serve as the foundation for breeding programs aimed at producing animals that thrive in warm climates; and selective breeding within breeds or crossbreeding with superior breeds to increase production of meat, milk, and hide are some ways to capitalize on this potential (Cartwright *et al*., 2023).

Challenges and conservation efforts

Uncontrolled breeding resulting from traditions that frequently lack selective breeding tactics and uncontrolled breeding with foreign breeds might cause genetic dilution, which are obstacles to achieving the full potential of indigenous goats in Nigeria (Oseni and Ajayi, 2014; Akintunde *et al*., 2024a). Implementing breeding programs with specific selection goals that can boost output while preserving genetic variety and teaching farmers the importance of native breeds and sustainable breeding methods are crucial components of conservation initiatives (Darmawan *et al*., 2023).

Indigenous goats from Nigeria have a great deal of genetic potential for producing meat, milk, and skin, and they are especially well-suited to the country's climate (Adebambo *et al*., 2011). The continued importance of these species to food security and farmer livelihoods can be ensured by acknowledging their distinct genetic composition and establishing smart breeding plans into place. To optimize their potential and promote their conservation, more study is required.

Roles of nutrition in gene expression

Gene expression, the process by which the instructions in DNA are used to generate proteins, is influenced by nutrition in a surprising and important way (Carthew, 2021). Nutrients in animal feed have the ability to affect the on/off regulation of genes. Nutrigenomics is the study of the intricate relationship between diet and gene expression (Farhud *et al*., 2010). Some nutrients have the ability to regulate gene expression, affecting which genes are active and to what degree.

Nutrition can affect gene expression in a number of ways, including by altering signaling pathways, directly affecting transcription factors, and causing epigenetic modifications. Transcription factors are molecules that can bind to nutrients and control which genes are replicated into RNA (Oksuz *et al*., 2023). Vitamins A and D, for instance, have the ability to directly bind to DNA and affect gene activity. Vitamin A can also bind to transcription factors, which promote the expression of genes involved in cell growth and differentiation (Carazo *et al*., 2021). Through modifications to cellular signaling pathways, nutrition can also have an indirect impact on gene expression (Lal *et al*., 2022). The body of the animal excretes nutrients into smaller molecules known as metabolites. Gene expression-regulating signaling pathways may be affected by these metabolites (Bogush *et al*., 2023). These pathways carry messages from outside the cell to the nucleus, where genes are located. For instance, the hormone insulin, which is produced in reaction to blood sugar levels, has the ability to trigger signaling pathways that alter the expression of genes related to metabolism (Rahman *et al*., 2021). Nutrition can cause epigenetic alterations, which are modifications to DNA molecules that impact gene expression without changing the underlying DNA sequence (Tiffon, 2018). For instance, methylation, a form of epigenetic change that can silence genes, can be affected by specific diets.

Gene expression is also influenced by the gut microbiome, which is the community of bacteria that reside in an animal's gut. Diet can affect the gut microbiota, which can then generate metabolites that affect gene expression in the gut and other parts of the body (Conlon and Bird, 2014). Depending on a person's genetic composition, diet can have different effects on gene expression. Scientists can develop novel approaches to illness prevention and treatment by understanding how nutrition influences gene expression. For instance, studies indicate that encouraging healthy gene expression patterns, and a diet high in fruits, vegetables, and whole grains may help prevent chronic illnesses such as diabetes, heart disease, and cancer (Clemente-Suárez *et al*., 2023).

Understanding the implications

The health and well-being of animals are greatly affected by the intricate interplay between gene expression and nutrition. Understanding how diet can affect gene activity could lead to the creation of individualized nutrition plans that consider an individual's genetic composition, the identification of diets that prevent disease and promote health, and the development of novel therapeutic approaches based on the dietary manipulation of gene expression.

Potential applications and implications of nutrigenomics for Nigerian indigenous goats

The resilience and adaptability of Nigerian native goats, including the Sahel, RS, and WAD, make them an invaluable resource (Chiejina and Behnke, 2011). The indigenous goat of Nigeria is an important genetic resource for the production of meat, milk, and leather (Adebambo *et al*., 2011). The study of nutrigenomics, which examines how genes and diet interact, holds enormous promise for improving productivity, health, and product quality (Fenech *et al*., 2011). The following lists the possible uses and consequences of nutrigenomics in indigenous Nigerian goats:

Tailored diets

The relationship between a goat's genes and nutrition can be determined using nutrigenomics. Researchers can create diets that are ideal for each breed or even for individual animals by examining these connections (Haq *et al*., 2022). Growth, milk output, reproductive function, and illness resistance may all increase as a result.

Precision livestock farming

Nutrigenomics paves the way for precision livestock farming, a technique that tailors management practices to each individual animal. This can lead to better animal welfare since nutrigenomics can help maintain optimal health and well-being by tailoring to the needs of each individual animal, and less feed waste because genetically modified diets can prevent overfeeding and improve resource utilization (Papakonstantinou *et al*., 2024).

Exploitation of undiscovered potential

The indigenous goat of Nigeria possesses a distinct genetic adaptability to its surroundings. Understanding the genes that affect how goats use local feed resources could increase their productivity on locally available feedstock, and nutrigenomics can assist in identifying the genes linked to these adaptations (Siddiki *et al*., 2020). For example, researchers can identify genes linked to heat tolerance, which could result in breeding programs or nutritional strategies designed to improve performance in hot climates.

Challenges and future directions

The application of nutrigenomics to indigenous Nigerian goats is promising, but it faces difficulties because further study is required to identify the precise gene-nutrient correlations in this breed. Furthermore, nutrigenomic testing might necessitate a large infrastructure and skill investment. To completely comprehend the combined effects of the intricate relationships between nutrition and genes on goat performance, more research is necessary. Combining genomic, proteomic, and metabolic data is necessary for data integration in order to offer thorough insights and account for the impact of environmental factors on gene–nutrient interactions (Jendoubi, 2021).

Researchers, government organizations, and private players must work together to address these issues. The sequencing of indigenous Nigerian goat breeds' genomes, examining the roles of genes found through nutrigenomic analysis, combining nutrigenomics with conventional breeding and management techniques, creating individualized feeding plans based on each animal's genetic profile, examining the ways in which nutrigenomics can support environmentally sustainable livestock production, and creating affordable and user-friendly nutrigenomic tools are among the top research priorities.

However, there is no denying its potential advantages. Nutrigenomics has enormous potential to unlock the genetic potential of Nigerian native goats, resulting in a more ethical, sustainable, and productive livestock business as research progresses and expenses become more affordable.

Conclusion

Nutrigenomics offers a groundbreaking approach to unlocking the genetic potential of indigenous Nigerian goats. By harnessing this technology, researchers can develop targeted feeding strategies that optimize feed utilization, enhance meat quality, and improve milk production. Overcoming existing challenges and prioritizing future research directions will pave the way for a revolution in Nigerian goat production, leading to increased productivity, improved product quality, and, ultimately, enhanced livelihoods for Nigerian goat farmers.

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Conflict of interest

The authors declare no conflict of interest.

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Author's contributions

AOA, LCN-O, and AAA drafted the manuscript. ARK and OOO revised and edited the manuscript. RZA and IM participated in preparing and critical checking this manuscript. CDN, LA, and LL edited the references. All authors have read and approved the final manuscript.

Data availability

All references are open-access, so data can be obtained from the online web.

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