Indian J. Anim. Nutr. 2024. 41 (2): 181-188
doi: 10.5958/2231-6744.2024.00023.4

Indian Journal of
Animal Nutrition

Nutrigenomics in Livestock Nutrition: A Pathway to Enhanced Animal Health and Productivity

D. Chandaka[1*], R.K. Swain[2], P. K. Regulagadda[1], U. Chandaka[3], H. Mekapothula[4] and S. Salur [5]
[1,2] Centurion University of Technology and Management, Paralakhemundi, Odisha, India
[3] NHPC Ltd, Baira Siul Power Station, Surangani, Himachal Pradesh, India
[4,5] Institute of Veterinary and Animal Sciences, SOADU, Bhubaneswar, Odisha, India
Correspondence: deeptichandaka@gmail.com

ABSTRACT

Nutrigenomics represent emerging discipline that scrutinizes the intricate relationship between diet and genetic expression. These fields investigate how bioactive compounds in food influence gene expression and ultimately impact animal and human metabolism. In livestock, the study of nutrigenomics is constrained by high costs, long generational distances, and ethical considerations. Recent research in livestock nutrigenomics has primarily focused on elucidating the effects of dietary modifications on breeding efficiency, production traits, and animal health. By integrating disciplines such as nutrition, molecular biology, genomics, bioinformatics, molecular medicine, and epidemiology, nutrigenomics aims to elucidate the epigenetic mechanisms underlying disease occurrence. This review provides a comprehensive overview of nutrigenomics, highlighting its significance in understanding the interaction between diet and gene expression in livestock. By deciphering the intricate molecular pathways involved, nutrigenomics holds promise for personalized nutrition strategies tailored to individual genotypes, ultimately improving health outcomes for animals.

KEYWORDS: Genes, Health, Livestock, Nutrition, Poultry, Production

Article received: 18 March 2024; Article accepted: 30 April 2024

INTRODUCTION

The livestock industry plays a crucial role in the livelihoods of farmers in India, with a significant portion of input costs allocated to animal feed. However, the efficiency of feed utilization by animals greatly impacts the economics of the industry (Rauw et al., 2020). The rumen, housing a complex microbial ecosystem, plays a vital role in the bio-fermentation of feed within the digestive system. Despite the efficiency of anaerobic systems in the rumen for degrading lignocellulosic feeds, a considerable fraction of potential energy remains unutilized, resulting in economic losses for the industry. Efforts by rumen microbiologists and nutritionists aim to minimize these losses and decipher the intricacies of the microbial ecosystem. The molecular era and sophisticated molecular techniques are utilized to address unanswered questions in nutrition at the genetic level (ul Haq et al., 2022). Nutrigenomics, as a comprehensive and burgeoning discipline, delves into the intricate and multifaceted landscape of the genome-wide impact of nutrition, where genes are dynamically regulated, activated, or silenced in response to metabolic cues emanating from both internal factors such as hormonal signaling and external stimuli, notably nutrients, which exert profound and pervasive influence on genetic expression and cellular function. Across evolutionary epochs, nutrients served as rudimentary signals, orchestrating complex pathways of synthesis or storage, a trait conserved as organisms ascended the evolutionary ladder into more intricate life forms, sustaining the ability to responsively tune gene expression to govern pivotal biological processes including energy metabolism, cellular differentiation, and growth (Asmelash et al., 2018). The overarching goal of nutrigenomics is to furnish a comprehensive foundation for dietary management aimed at the preservation and optimization of health, with the overarching aim of seamlessly integrating nutrients within the intricate mosaic of individual genetic backgrounds, ensuring tailored nutritional strategies (Ghormade et al., 2011). This cutting-edge technique facilitates rapid and comprehensive assessments of nutrient-induced physiological changes while furnishing efficacious methodologies to discern and optimize nutrient interactions, thereby fostering enhanced production outcomes and promoting robust health in animal populations (Banerjee et al., 2015). Moreover, nutrigenomics illuminates the central and multifaceted role that nutrients play in governing the cellular protein landscape, elucidating their regulatory functions in gene transcription, nuclear RNA processing, and mRNA stability and degradation, thus underscoring its profound potential in ameliorating chronic diseases and catalyzing advancements in feed conversion efficiency, production, and product quality within the agricultural sector (Harland, 2005). Studies on differential gene expression enable the identification of candidate genes and pathways influencing economically important traits. With advancements in molecular techniques, such as transcriptomics, proteomics, and metabolomics, there is a growing potential for understanding diet-gene interactions and discovering novel nutritional biomarkers (ul Haq et al., 2022). Contrary to expensive transgenesis, nutrigenomics offers cost-effective strategies to enhance animal production, growth rates, milk production, feed utilization, disease resistance, and fertility. Nutrigenomics, through large-scale gene expression methods, investigates the effects of nutrition on gene expression, providing valuable insights into observed phenotypic differences and metabolic pathways involved.

TECHNIQUES IN NUTRIGENOMICS

Nutrients present in food and supplements have the potential to modulate the expression and structure of specific genes. The application of Nutrigenomics spans multiple disciplines, encompassing dietary effects on genome stability, epigenome alterations, RNA and micro-RNA expression, protein expression, and metabolite changes, which collectively contribute to diagnosing health status and disease trajectory (German, 2005; Miggiano and De Sanctis, 2006). Traditionally, Nutrigenomics studies have relied on small-scale techniques like PCR and quantitative real-time PCR for measuring gene expression. However, advancements in genomic analysis now offer more robust approaches to biological inquiries. Large-scale gene expression studies are feasible today, owing to innovations such as microarrays and massive transcriptome sequencing (RNAseq), enabling high-throughput data accumulation through automated and parallelized protein and DNA/RNA chemistry. Omics technologies, including transcriptomics, proteomics, and metabolomics, have become widely adopted for gathering comprehensive biological data (Susmitha and Sagar, 2023). Transcriptomics, facilitated by microarray technologies, yields valuable insights into the physiological impacts of dietary proteins, while Proteomics tools such as two-dimensional electrophoresis offer a means to explore the influence of individual amino acids on protein composition (Asmelash et al., 2018). Leveraging newly emerging bioinformatics techniques alongside biological data generated from genomics and transcriptomics studies, researchers can employ modern systems approaches to study interactions within living systems. Understanding the physiological, biochemical, and metabolic pathways, along with gene expression in livestock including poultry, is imperative for comprehending the significance of diet and diet formulation.

APPLICATIONS OF NUTRIGENOMICS

Nutrigenomics applications contribute to improving health outcomes by elucidating the impact of dietary nutrients on gene expression and metabolic pathways, optimizing reproductive performance in animals through understanding how diet influences fertility, gestation, and offspring development, enhancing milk quality by identifying dietary factors affecting milk composition, yield, and nutritional value, boosting meat quality by investigating the effects of diet on muscle development, composition, and post-mortem characteristics, promoting longevity and extending lifespan by identifying dietary interventions positively influencing cellular aging and overall health, and strengthening immunity in animals by uncovering the relationship between diet, gene expression, and immune system function, leading to the development of nutritionally tailored strategies for enhancing immune response.

Improving health and disease resistance

Feeding animals with diets deficient in selenium can induce significant alterations in protein synthesis at the transcriptional level, which has profound implications for their overall health and productivity. Selenium deficiency poses a considerable threat to animal well-being, as it can exacerbate stress responses by up regulating specific gene expression and signaling pathways. This heightened stress, in turn, triggers a cascade of physiological changes, including alterations in genes responsible for protecting against oxidative damage and facilitating detoxification mechanisms within the body. The repercussions of selenium deficiency extend beyond mere biochemical processes; they have tangible effects on the phenotype of the animals. These alterations in gene expression and associated biochemical pathways can manifest in observable changes in traits critical to agricultural productivity, such as milk, meat, and wool production. For instance, compromised detoxification mechanisms may result in increased susceptibility to diseases or reduced metabolic efficiency, directly impacting an animal's ability to produce milk or grow muscle mass effectively (Kore et al., 2008).

Plant extracts like Curcuma longa, anethole, and garlic metabolites have been investigated for their ability to protect against avian coccidiosis in poultry. Studies have shown that these extracts can alter gene expression related to inflammatory responses, indicating their potential as immune protective agents against coccidiosis. Waste products like olive mill wastewater, rich in polyphenols, have been used in chicken feeding, impacting gene expression related to intestinal functioning and viral processes (Nowacka-Woszuk, 2020). Broiler strains from both Cobb and Aviagen possess quantitative trait loci associated with disease resistance against pathogens like salmonella or campylobacter. Research has identified feed additives and components that enhance resistance to various diseases, including bacteria and viruses. These components influence the immune system, with nutrients like energy, PUFA, vitamins (A, C, E), lectin, carotenoids, and fiber playing vital roles in lymphocyte responses and immune modulation (Susmitha and Sagar, 2023).

Improving production

Nutrigenomics in ruminants targets enhanced milk fat production by regulating mammary gland synthesis. This process is influenced by bioactive fatty acids (FAs), with certain FAs from rumen biodegradation inhibiting milk fat synthesis. Notably, Tran-10, cis-12 conjugated linoleic acid has been identified as a key regulator, with its effects characterized by dose-response relationships (Bauman et al., 2011). Hiller et al. (2011) found down regulation of lipid metabolism genes in muscle and adipose tissue with a grass-silage/n-3 fatty acid diet compared to a maize silage/n-6 fatty-acid-based control diet in German Holstein bulls. Early to mid-gestation under nutrition increases adipocyte diameter, FATP1 gene transcription in adipose tissue, and reduces yield grade in beef carcasses (Long et al., 2012). Under nutrition during early and middle gestation phases reduces secondary muscle formation, while late gestational nutrient deficiencies decrease intramuscular adipocyte numbers, impacting progeny marbling (Yan et al., 2013). Negative energy status during mid gestation affects progeny fat deposition without altering muscle mass (Mohrhauser et al., 2015). Rumen-protected methionine supplementation in pregnant dairy cattle alters hepatic expression of methionine metabolism genes in offspring, affecting methylation potential and DNA methylation (Jacometo et al., 2017). Teixeira et al. (2017) investigated starch administration (whole shelled corn vs. ground and silaged corn) effects on lipid metabolism gene expression and intramuscular fat content in Angus and Nellore cattle. Ground corn increased FABP4, ACACA, and SCD1 expression in Nellore bulls, while whole shelled corn increased PPARA expression and reduced SREBF1 transcription in both breeds. Maternal over nutrition in cattle increases PPARG expression in fetal skeletal muscle at mid gestation but has no effect in late pregnancy (Gionbelli et al., 2018). Elolimy et al. (2018) studied amylase supplementation in finishing steers, observing reduced average daily gain and gain/feed ratio with up regulated adipogenesis genes in muscle tissue and reduced hepatic lipid catabolism gene expression. Down regulation of mammary lipogenic genes during milk fat depression (MFD) involves pathways like sterol response element-binding protein-1 (SREBP1) and Spot14 (Susmitha and Sagar, 2023). Understanding these mechanisms can inform strategies to improve milk fat yield and fatty acid profile.

Vitamin E acts as a potent lipid-soluble antioxidant, protecting biological membranes against lipid peroxidation. Supplementation above dietary requirements in pigs improves meat color stability, reduces drip loss during storage, and enhances sensory qualities like freshness, tenderness, and juiciness. Optimal effects are achieved with supplementation at levels around 200 mg/kg of feed or 600 IU/kg of Vitamin E, leading to improved muscle pH, color, and juiciness in pork (Dirinck et al., 1996). The top three essential feed additives for enhancing the composition and quality of pork are Ractopamine, Linoleic acid, and Vitamin E. Ractopamine, a â-1 agonist, boosts average daily gain and feed conversion efficiency during the finishing phase of pigs. It reduces carcass fatness while increasing leanness and lean deposition without raising feed consumption. Although it may slightly affect meat quality characteristics, its impact is minimal (Anderson, 2000). Linoleic acid, a component of conjugated linoleic acid (CLA), offers various health benefits, such as reducing atherosclerosis and certain types of cancer in laboratory animals. It improves pork meat quality by reducing subcutaneous fat, increasing intramuscular fat, and enhancing meat palatability. CLA supplementation also increases fat hardness and counteracts the softening effect of canola oil on subcutaneous fat in swine (Martin et al. 2008). Meat quality in pork is influenced by factors like breeds, nutritional status, and feeding systems of swine. Intramuscular fat (IMF) positively affects meat quality and is influenced by genetic alleles. Selecting specific pig breeds with favorable genes is crucial for achieving desired meat quality traits. Porcine IMF is less influenced by genetic background and nutritional status, making it challenging to pinpoint major genes affecting these traits (Jing and Defa, 2009).

González-Calvo et al. (2014) demonstrated altered transcript levels of SREBF1 and PPARG in muscle and adipose tissue of Aragonesa lambs supplemented with vitamin E.

Oregano supplementation has been shown to affect hepatic gene expression associated with insulin signaling pathways and fatty acid metabolism, potentially reducing fat deposition in broiler chickens. Trivalent chromium supplementation altered micro RNA expression related to muscle growth and development. Methionine and cysteine deficiencies in the diet have been shown to impact gene expression involved in one-carbon metabolism and skin quality, respectively (Nowacka-Woszuk, 2020).

Improving reproduction and fertility

The reproductive performance of cattle and other livestock species can be influenced by dietary-induced alterations in specific gene functions. Understanding the connection between nutrients and gene expression regulation is exemplified in studies like Rao et al. (2001), where dietary selenium's impact on gene expression in mice was explored. This research unveiled how selenium affects protein synthesis patterns in mice by modulating the expression of specific genes at the transcriptional level. By directly observing the effects of nutritional strategies or diets on the expression of fertility-related genes in male or female animals, we can potentially unravel the significance of the interplay between individual nutrients and gene expression regulation. Selenium deficiencies, for instance, have been shown to modify protein synthesis patterns in mice by orchestrating the expression of particular genes at the transcriptional level. Recent advancements in pig productivity, achieved through genetic selection, improved management practices, enhanced health measures, and refined nutritional strategies, have transformed reproductive performance from previously unpredictable to highly consistent. Over the past 15 years, feed efficiencies during the growing and finishing phases of production have surged by approximately 25% (Fremaut, 2003). The addition of organic trace minerals to the diets of working boars has been shown to improve semen concentration and increase the number of doses of extended semen per ejaculate (Mahan et al., 2002). Another promising supplement for enhancing reproductive performance in sow nutrition is chromium. Supplementation of lactating sows with chromium has been found to boost reproductive performance, likely through its influence on glucose-insulin relationships and consequent metabolic effects on reproduction. These innovative feed ingredients hold the potential to significantly enhance reproductive productivity under commercial conditions (Lindemann et al., 2004).

Improving immune response

Sabino et al. (2018) revealed sex-dependent effects of essential oils from cinnamon bark, dill seed, and eucalyptus leaves on gene transcription in liver and muscle of lambs, primarily impacting inflammatory and immune response pathways. Enhancing immune response in pigs not only promotes better overall animal health but also enhances their performance. Recent studies have explored the use of novel protein sources in pig diets, yielding promising results in terms of reproductive performance improvement. Incorporating yeast cell proteins such as NuPro® from Alltech Inc. into sow diets has been found to not only boost piglet growth rate and weaning weight but also reduce variability in growth and incidences of diarrhea (Kocher, 2004). Long-term selenium supplementation has been found to increase the transcriptional level of genes associated with both innate and acquired immunity, suggesting an improvement in immunity in pigs. Glutamine supplementation has been found to prevent intestinal dysfunction and atrophy in weaned piglets by up regulating genes important for cell growth and immune response while down regulating immune activation genes. Threonine-deficient diets have been shown to alter the expression of genes involved in immune and defense responses, protein synthesis, and energy metabolism in the ileal tissue of young piglets (Nowacka-Woszuk, 2020).

Prebiotic supplementation of poultry with inulin has been found to affect gene expression related to metabolic pathways, growth, immune status, and lipid metabolism. Adding phytonutrients like carvacrol, cinnamaldehyde, and Capsicum oleoresin to chicken feed has been studied for its potential to protect against infections. These supplements have shown to alter gene expression related to lipid metabolism, small molecule biochemistry, and immune response, suggesting a natural alternative to antibiotics in poultry feeding (Nowacka-Woszuk, 2020).

Improving longetivity

Supplementation of sow diets with select commercial trace minerals such as Bioplex® and Sel-Plex® has been found to increase the number of sows remaining in the herd after completing parity 4 (Close and Cole, 2001). Soy-based diets in pigs have been shown to impact oxidative stress response genes in the liver (Nowacka-Woszuk, 2020).

CONCLUSION

The application of nutrigenomics in livestock nutrition holds immense promise for improving animal health, production efficiency, and overall welfare. By elucidating the intricate relationship between dietary nutrients and gene expression, nutrigenomics offers tailored nutritional strategies that optimize various aspects of livestock management, including reproduction, immunity, and product quality. Cutting-edge techniques such as transcriptomics, proteomics, and metabolomics provide invaluable insights into the molecular mechanisms underlying dietary effects on gene expression and metabolic pathways. Furthermore, the utilization of plant extracts, waste products, and supplementation with specific nutrients has demonstrated significant potential in enhancing disease resistance, improving feed efficiency, and promoting desirable production traits in livestock. From selenium supplementation to prebiotic intervention, nutrigenomics offers a diverse array of tools to address key challenges faced by the livestock industry, ultimately leading to sustainable and profitable animal production systems. As we continue to unravel the complexities of nutrition-genome interactions, it is essential to integrate these findings into practical feeding strategies that benefit both producers and consumers. By leveraging the power of nutrigenomics, we can pave the way for a more resilient, efficient, and ethically sound livestock industry that meets the growing demands for high-quality animal products while safeguarding animal welfare and environmental sustainability.

ACKNOWLEDGMENT

The authors acknowledge Centurion University of Technology and Management for its continuous support and encouragement.

REFERENCES

Anderson, P.T. 2000. Mechanisms by which metabolic modifiers alter growth rate and carcass composition of meat animals. In Recipr. Meat Conference .53: pp. 31-35.

Asmelash, B., Mahlet, D. and Brhane, H. 2018. Livestock nutrigenomics applications and prospects. Journal of Veterinary Science and Technology. 9: 1-4.

Banerjee, G., Pal, R. and Ray, A.K. 2015. Applications of nutrigenomics in animal sectors: A review. Asian Journal of Animal and Veterinary Advances. 10(9): 489-499.

Bauman, D.E., Harvatine, K.J. and Lock, A.L. 2011. Nutrigenomics, rumen-derived bioactive fatty acids, and the regulation of milk fat synthesis. Annual Review of Nutrition. 3: 299-319.

Close, W.H. and Cole, D.J.A. 2001. Protein and amino acids. In: Nutrition of Sows and Boars. Nottingham University Press, UK. p. 71-96.

Dirinck, P., Winne, A.D. and Frigg, M.C.M. 1996. Studies on vitamin E and meat quality. Effect of feeding high vitamin E levels on time-related pork quality. Journal of Agriculture and Food Chemistry. 44: 65-68.

Elolimy, A.A., Moisá, S.J., Brennan, K.M., Smith, A.C., Graugnard, D., Shike, D.W. and Loor, J.J. 2018. Skeletal muscle and liver gene expression profiles in finishing steers supplemented with Amaize. Animal Science Journal. 89(8): 1107-1119.

Fremaut D. 2003. Trace mineral proteinates in modern pig production: reducing mineral excretion without sacrificing performance. In: Nutritional Biotechnology in the Feed and Food Industries, Proceedings of Alltech's 19th Annual Symposium (T.P. Lyons and K.A. Jacques, Eds.). Nottingham University Press, UK. 171-178.

German, J.B. 2005. Genetic dietetics: nutrigenomics and the future of dietetics practice. Journal of the Academy of Nutrition and Dietetics. 105(4): 530-531

Ghormade, V., Khare, A. and Baghel, R.P.S. 2011. Nutrigenomics and its applications in animal science. In Veterinary Research Forum, Faculty of Veterinary Medicine, Urmia University. 2(3): 147-155.

Gionbelli, T.R.S., Veloso, C.M., Rotta, P.P., Valadares Filho, S.C., C. Carvalho, B., Marcondes, M.I., S. Cunha, C., Novaes, M.A.S., Prezotto, L.D., Duarte, M.S. and Gionbelli, M.P. 2018. Foetal development of skeletal muscle in bovines as a function of maternal nutrition, foetal sex and gestational age. Journal of animal Physiology and Animal Nutrition. 102(2): 545-556.

Harland, J.I. 2005. Nutrition and genetics: mapping individual health. ILSI, Europe.

Hiller, B., Herdmann, A. and Nuernberg, K. 2011. Dietary n-3 fatty acids significantly suppress lipogenesis in bovine muscle and adipose tissue: a functional genomics approach. Lipids. 46: 557-567.

Jacometo, C.B., Zhou, Z., Luchini, D., Corrêa, M.N. and Loor, J.J. 2017. Maternal supplementation with rumen-protected methionine increases prepartal plasma methionine concentration and alters hepatic mRNA abundance of 1-carbon, methionine, and transsulfuration pathways in neonatal Holstein calves. Journal of Dairy Science. 100(4): 3209-3219.

Jing, D. Y. and Defa, Li. 2009. Nutrigenomics Approach-A strategy for identification of nutrition responsive genes influencing meat edible quality traits in swine. Asian-Australasian journal of animal sciences. 22(4): 605-610.

Kocher, A. 2004. The potential for immune saccharides to maximize growth performance. Interfacing immunity, gut health and performance.107-115.

Kore, K.B., Pathak, A.K. and Gadekar, Y.P. 2008. Nutrigenomics: emerging face of molecular nutrition to improve animal health and production. Veterinary World. 1(9): 285.

Lindemann, M.D., Carter, S.D., Chiba, L.I., Dove, C.R., LeMieux, F.M. and Southern, L.L. 2004. A regional evaluation of chromium tripicolinate supplementation of diets fed to reproducing sows. Journal of Animal Science. 82(10): 2972-2977.

Long, N.M., Tousley, C.B., Underwood, K.R., Paisley, S.I., Means, W.J., Hess, B.W., Du, M. and Ford, S.P. 2012. Effects of early- to mid-gestational under nutrition with or without protein supplementation on offspring growth, carcass characteristics, and adipocyte size in beef cattle. Journal of Animal Science. 90: 197–206.

Mahan, D., Zawadzki, J. and Guerrero, R. 2002. Mineral metabolism and boar fertility: observations from Latin American to Europe. In: Biotechnology in the Feed and Food Industries, Proceedings of Alltech's 18th Annual Symposium (T.P. Lyons and K.A. Jacques, Eds.). Nottingham University Press, UK. p. 411-418.

Martin, D., Muriel, E., Gonzalez, E., Viguera, J. and Ruiz, J. 2008. Effect of dietary conjugated linoleic acid and monounsaturated fatty acids on productive, carcass and meat quality traits of pigs. Livestock Science. 117(2-3): 155-164.

Miggiano, G.A. and De Sanctis, R. 2006. Nutritional genomics: toward a personalized diet. La Clinica Terapeutica. 157(4): 355-361.

Mohrhauser, D.A., Taylor, A.R., Underwood, K.R., Pritchard, R.H., Wertz-Lutz, A.E. and Blair, A.D. 2015. The influence of maternal energy status during midgestation on beef offspring carcass characteristics and meat quality. Journal of Animal Science. 93(2): 786-793.

Nowacka-Woszuk, J. 2020. Nutrigenomics in livestock—recent advances. Journal of Applied Genetics. 61(1): 93-103.

Rao, L., Prolla, T.A. and Puschner, B. 2001. Gene expression profiling of low selenium status in the mouse intestine: transcriptional activation of genes linked to DNA damage, cell cycle control and oxidative stress. The Journal of Nutrition. 131(12): 3175-3181.

Rauw, W.M., Rydhmer, L., Kyriazakis, I., Øverland, M., Gilbert, H. and Dekkers, J.C. 2020. Prospects for sustainability of pig production in relation to climate change and novel feed resources. Journal of the Science of Food and Agriculture. 100(9): 3575–3586.

Sabino, M., Carmelo, V.A.O., Mazzoni, G., Cappelli, K., Capomaccio, S., Ajmone-Marsan, P., Verini-Supplizi, A., Trabalza-Marinucci, M. and Kadarmideen, H.N. 2018. Gene co-expression networks in liver and muscle transcriptome reveal sex-specific gene expression in lambs fed with a mix of essential oils. BMC genomics. 19: 1-15.

Susmitha, T. and Sagar, L.V. 2023. Nutrigenomics: An emerging tool in Nutrition. The Pharma Innovation Journal. SP-12(9): 2141-2146

Teixeira, P.D., Oliveira, D.M., Chizzotti, M.L., Chalfun-Junior, A., Coelho, T.C., Gionbelli, M., Paiva, L.V., Carvalho, J.R.R. and Ladeira, M.M. 2017. Subspecies and diet affect the expression of genes involved in lipid metabolism and chemical composition of muscle in beef cattle. Meat Science. 133: 110-118.

ul Haq, Z., Saleem, A., Khan, A.A., Dar, M.A., Ganaie, A.M., Beigh, Y.A., Hamadani, H.

and Ahmad, S.M. 2022. Nutrigenomics in livestock sector and its human-animal interface-a review. Veterinary and Animal Science. 17: 100262.

Yan, X., Zhu, M.J., Dodson, M.V. and Du, M. 2013. Developmental programming of fetal skeletal muscle and adipose tissue development. Journal of Genomics. 1: 29.