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"- OMICS" Based approaches in sheep nutrition

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Abstract

The term '-omics' denotes many biological disciplines in biology characterised by titles ending in the -omics prefix, including genomics, proteomics, metabolomics, transcriptomics,. The purpose of omics is to facilitate the comprehensive identification and measurement of groups of biomolecules that govern the structure, function, and dynamics of organisms. The application of emerging omics technologies is seeing a growing prevalence within the realm of animal agriculture. Omics technology significantly enhances comprehension of the genetic structure of animals that influences important economic characteristics. Utilising these omics technologies enables the investigation of animal metabolism in response to a particular stimulus. This methodology enables the examination of how environmental factors (such as temperature and humidity), diet, sex, and welfare affect the physiological processes of animals at the molecular level. Currently, nutrigenomics is a rapidly advancing field of research that investigates how dietary components affect genome functioning in terms of gene expression patterns and epigenetic alterations, including DNA methylation and histone modifications. The novel RNA-Seq technology for transcriptome studies of animals is acknowledged as a potent method to elucidate molecular processes related to nutrient-gene interactions. The present review centres on the potential applications of '-omics' based methodologies in the field of livestock husbandry, specifically highlighting the domain of sheep nutrition.

Key words: Sheep, Nutrition, -omics, nutrigenomics, Transgenomics, Metabolomics

INTRODUCTION

In order to guarantee the availability of nourishing food, the overall health and well-being of humans and animals, and the preservation of the environment, it is imperative to implement livestock production in the most efficient and sustainable manner feasible for a successful food security programme supporting a growing population. Fundamental research will yield innovative and technical advancements that enhance all facets of food production. A significant obstacle confronting the livestock sector is the need to satisfy the increasing demand for products derived from cattle. Diminished fertility, immunological response, feed efficiency, and production efficiency in animals adversely affect the cattle sector. Enhancing animal health, performance, and overall wellbeing is the proposed answer. The application of emerging omics technologies is more prevalent in the realm of animal production. In biology, the term "-omics" encompasses various disciplines with

names ending in the -omics prefix, including genomics, proteomics, metabolomics, transcriptomics, and others. The purpose of omics is to facilitate the comprehensive identification and measurement of groups of biomolecules that govern the structure, function, and dynamics of organisms (Subedi et al., 2022). The analysis enables the examination of how environmental factors (such as temperature and humidity), nutrition, sex, and wellbeing affect the physiological processes of farm animals at the molecular level (Ribeiro et al., 2020). The term "-omics" originates from the suffix '-ome', which is derived from a Greek word that signifies 'whole', 'all', or 'complete'. The suffix '-omics' commonly denotes a discipline within the biological sciences that focusses on analysing extensive and high-throughput data/information to get insights into life, defined by 'omes' (Yadav, 2007). The past twenty years have seen the development of several omics tools for the collection and analysis of high-throughput data on proteins (proteomics), mRNA

transcripts (transcriptomics), gene sequences (genomics), microbial diversity (metagenomics), epigenetic control of gene expression (epigenomics), metabolic profile (metabolomics), lipid profile (lipidomics), and other aspects of a specific cell, tissue, organ, or whole organism at a certain moment in time. Genomics, metagenomics, metabolomics, proteomics, transcriptomics, epigenomics, translomics and other omics technologies can facilitate the quick and effective identification of phenotypic alterations, dietary responses, and inherent phenotypic tendencies in animals (Mu et al., 2022; Wang et al., 2022). Therefore, the use of omics tools in animal selection and breeding programmes is expected to provide an accurate estimate of breeding value for early selection, reduce the production interval and increase the rate of genetic gain (Figure 1). Omics technologies are effective tools, especially when used in combination with advanced molecular and breeding methods. In particular, genomic research has the potential to improve the precision and efficiency of traditional breeding and advanced breeding approaches by increasing consistency and predictability (Ahmad et al., 2023).

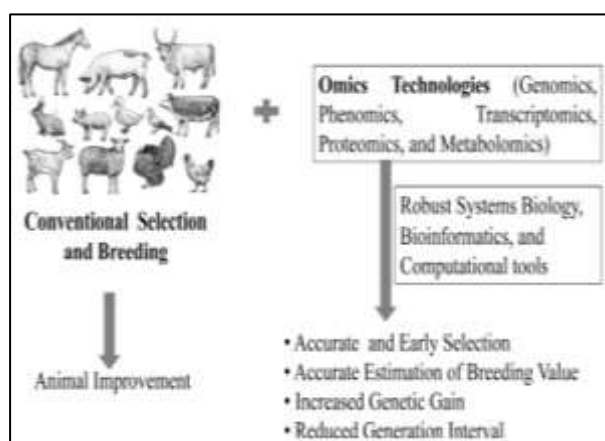


Figure 1. Impact of omics technology in animal improvement (Chakraborty et al., 2023)

The application of -omics technologies (genomics, transcriptomics, proteomics, and metabolomics) has revolutionized our understanding of sheep nutrition by unraveling molecular mechanisms underlying dietary interactions and

metabolic pathways. This comprehensive review explores the current applications and future potential of -omics based approaches in advancing sheep nutrition research. By elucidating molecular insights into gene expression, protein synthesis, metabolic profiles, and the interplay with dietary components, -omics technologies offer valuable tools to optimize nutritional strategies for enhanced productivity and health in sheep.

Genomics in Sheep Production

Genomics has significantly advanced our understanding of sheep nutrition by identifying genetic markers associated with important production traits and metabolic pathways. Kijas et al. (2012) conducted a genome-wide association study (GWAS) to explore SNP variation across different sheep breeds, revealing genetic markers linked to traits such as wool production and quality. Their findings underscored the genetic diversity within sheep populations and highlighted genomic regions influencing economically relevant traits, providing a foundation for selective breeding programs aimed at improving productivity and adaptability.

In sheep, the use of GWAS has been facilitated by the development of microarrays or DNA chips, which identify genetic markers associated with traits of interest. Companies like Illumina and Affymetrix have developed various genotyping platforms, with the OvineSNP50 chip being the most commonly used. This chip contains over 54,000 SNPs and has been employed to analyze samples from multiple sheep breeds, including both domestic and wild species (Zhang et al. 2012).

Early GWAS in sheep identified key genetic factors for traits such as horn development. For example, the RXFP2 gene was associated with horn presence and type (Johnston et al., 2011). Additionally, studies on diseases like rickets in Corriedale sheep pinpointed the R145X mutation in the DMP1 gene as a cause (Zhao et al., 2011). Research on meat quality traits linked the Callipyge gene with improved muscle deposition (Nanekarani and Goodarzi, 2014), while other studies identified genes associated with muscle

formation, fatty acid profiles, and stress responses (Guðmundsdóttir, 2015; Pant et al., 2016; Aali et al., 2017).

Recent research has also explored the genetic underpinnings of body size and wool characteristics, revealing several new genes and markers. Notable findings include associations with genes involved in pigmentation, morphology, and milk production (Kominakis et al., 2017; Rochus et al., 2018).

Rovadoscki et al. (2018) investigated the genetic basis of fatty acid composition in Brazilian sheep breeds using GWAS and identified promising genomic regions associated with lipid metabolism. Their study highlighted genetic variants influencing the synthesis and deposition of fatty acids in sheep tissues, offering insights into dietary strategies to modulate meat quality and lipid profiles in sheep production systems.

To further understand the genetic underpinnings of nutritional efficiency in sheep, recent studies have applied advanced genomic techniques such as whole-genome sequencing (WGS) and transcriptomic profiling. In their work, Xiang et al. (2024) performed a genome-wide association analysis (GWAS) including four distinct periods of baby weight (BW) development: birth, weaning, six months, and 12 months. Their investigation revealed the presence of five novel candidate genes, namely MAP3K1, ANKRD55, ABCB1, MEF2C, and TRNAW-CCA-87. Upon additional analysis, these genes were shown to be involved in pathways associated with growth hormone and energy metabolism. The findings suggest that these genes have the ability to impact the growth and development of sheep, so offering meaningful understanding of the genetic processes that underlie characteristics related to body weight and guiding sheep breeding methods. Their study emphasized the role of genomic diversity in shaping dietary responses and metabolic adaptations in sheep, highlighting opportunities for precision breeding to enhance nutritional efficiency and sustainability in sheep production.

Nutrigenomics Approach

Utilising genomic information in ruminant production systems can help alleviate

concerns about food safety and sustainability of production. Nutritional genomics (nutrigenomics) is the field of research concerned with any interplay between nutrients and the genomes of organisms, i.e. variable patterns of gene expression and the impact of genetic variations on the nutritional environment (Mathers, 2017; Müller and Kersten, 2003; Sales et al., 2014). Ruminant nutrigenomics, a relatively new field that has developed a revolutionary analytical approach to traditional ruminant nutrition research, has several studies on different aspects of animal production systems (Kızılaslan et al., 2022). Comprehending the precise binary interactions between genes and nutrients will eventually facilitate the tailoring of diets to promote the development of specific traits in individuals or groups. In pursuit of this objective, nutrigenomics, a recently established scientific discipline, applies information from several clearly defined disciplines as outlined in Figure 2 (Kızılaslan et al., 2022).

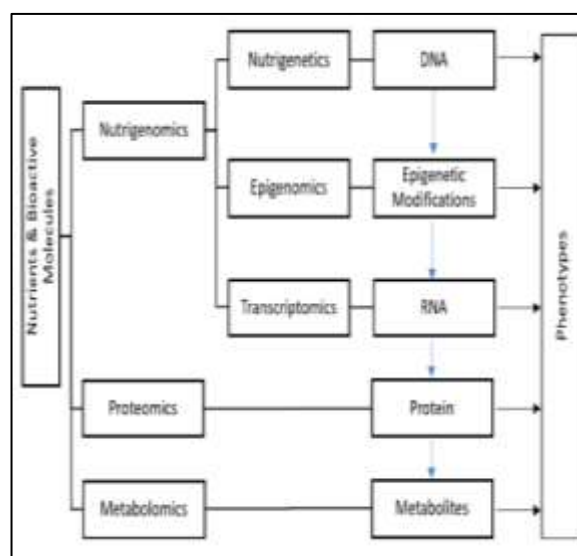


Figure 2. Investigation of phenotypic interactions between nutrigenomics and several other life sciences (Kızılaslan et al., 2022).

Currently, nutrigenomics is a rapidly advancing field of research that investigates how dietary components affect genome functioning in terms of gene expression patterns and epigenetic modifications, including DNA methylation and histone

modifications (Bordoni and Gabbianelli, 2019 Figure 3).



Figure 3. Summary of nutritional factors investigated in nutrigenomic research (Nowacka-Woszek, 2020).

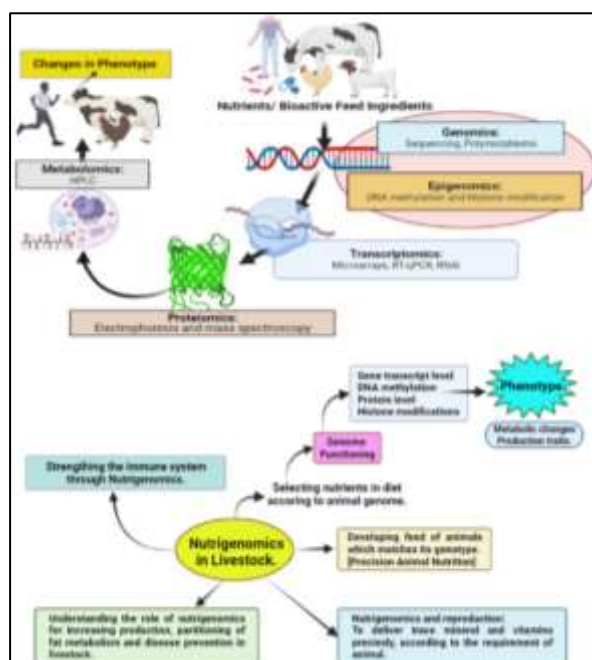


Figure 4. Utilisation and integration of omics technology in nutrigenomics and animal nutrition research (ul Hag et al., 2022).

Transcriptomics Insights

In sheep, transcriptomics provides a dynamic perspective on gene expression patterns in reaction to nutritional treatments and environmental conditions. This field of study is very recent in the realm of ruminant animals, particularly in sheep and goats.

Genetic expression is influenced by dietary chemicals either directly or indirectly by their interactions with transcription factors, such as ligand-dependent nuclear receptors. This paper discusses novel findings derived from the application of functional analysis to transcriptome, proteomic, and metabolomic data sets in goats and sheep (Osorio et al. 2017). In their study, Osorio et al. (2017) highlighted the potential of omics and bioinformatics tools to enhance our comprehension of the various degrees of regulation caused in small ruminants by dietary nutrients when used for milk, meat, wool, or reproduction. The initial findings suggest that adopting a nutrigenomic approach may eventually result in more accurate management of goats and sheep, hence facilitating a more efficient use of feed resources.

The study conducted by Wu et al. (2020) employed multi omics approaches to integrate feed nutrient value, sheep microbiome, transcriptome, metabolome, and fatty acid profile in order to examine the mechanisms that influence meat quality in twin ewes that were fed either high fibre low protein (HFLP) roughage (Ceratoides) or low fibre high protein (LFHP) roughage (alfalfa) dishes. The findings indicated that the performance of lamb production and the composition of muscle were notably influenced by the feed. Gas chromatography-mass spectrometry study revealed an increase in the essential fatty acid (linoleic acid and arachidonic acid) content of muscle in lambs fed HFLP. Moreover, the bacteria Bacteroidetes and Firmicutes in the rumen of ewes fed with LFHP were 2.6 times more abundant than in the group fed with HFLP. Comparative transcriptome analysis of muscle showed significant differential expression of genes associated with glucose metabolic pathways and fatty acid production in the two groups. An investigation revealed possible intercommunication across the four omics data layers, elucidating the process by which feed components impact the meat quality of lambs.

Utilising microarrays and RNA arrays, it is now possible to quantify the expression of nearly all transcribed genes in a given sample, hence establishing the

transcriptome. A transcriptome is a comprehensive collection of all transcripts that are currently encoded in a cell (Lowe et al., 2017). Advancements in transcriptome research have enhanced our comprehension of RNA-based gene regulation networks as a cutting-edge high-throughput sequencing method. In 2007, Osorio et al. conducted the first nutrigenomic analysis of goat mammalian transcriptome responses in feed-deprived goats, marking the first instance of such an analysis in small ruminants. The findings of this study indicate that genes associated with the reduction of milk fat, lactose, and protein, as well as genes relevant to the inhibition of cell proliferation and differentiation in mammalian cells, and an elevation in programmed cell death, play a role in the early development of mammals. RNA sequencing has been employed since 2011 and has lately superseded microarray techniques in the field of applied genomics. Previous research has employed this method to investigate the transcriptome and micro RNAome of small ruminants, including goats and sheep (Martyniuk et al., 2020).

High-throughput RNA-seq has emerged as the preferred technique for animal nutritionists to create meal or feed additives and to provide a foundation for enhancing animal growth, health, and productivity. This approach has been employed to examine worldwide patterns of gene expression in tissues associated with economically significant characteristics such as livestock productivity (Alexandre et al. 2015) or to quantitatively identify genes or transcripts that may serve as potential indicators for production characteristics (Han et al., 2015). Thus, the new RNA-Seq technology for transcriptomic studies of living organisms is acknowledged as a potent method to enhance our understanding of molecular processes related to nutrient-gene interactions. However, its implementation encounters certain technical obstacles in both experimental and computational aspects (ul Haq et al. 2022).

Three recent studies explored different aspects of rumen development in lambs and dairy calves in response to varying diets and dietary fiber sources.

Sun et al. (2021) investigated how solid diets influence rumen growth and maturation in Hu lambs. They found that feeding lambs goat milk powder alone or with alfalfa hay or concentrate starter led to increased concentrations of volatile fatty acids (VFA) and microbial crude protein (MCP), along with greater rumen weight and papilla area in the hay and concentrate groups compared to milk alone. Transcriptomic analysis revealed that different diets affected gene expression related to VFA metabolism and immune responses. Specifically, alfalfa hay improved immune function, while concentrate starter enhanced nutrient transport and metabolism.

Nishihara et al. (2023) focused on the weaning transition in dairy calves, examining how short-chain fatty acid (SCFA) levels and associated microbial communities affect the rumen epithelium. Their study showed that SCFA metabolism pathways were up-regulated and apoptosis pathways down-regulated after weaning. They also observed a positive correlation between SCFA levels and genes involved in SCFA absorption and metabolism, with certain microbes like Rikenellaceae and Campylobacter influencing these processes. The findings suggest that SCFA levels and microbial communities play significant roles in rumen epithelial function during weaning.

Liu et al. (2023) compared the effects of different fiber sources-alfalfa hay (forage) versus soybean hull (non-forage)-on rumen development in Hu lambs. They identified that soybean hulls increased immune function and nitrogen utilization, while alfalfa hay supported better rumen morphological development. This study highlighted the differential impact of fiber sources on rumen structure and function.

Together, these studies underscore the importance of diet and fiber source in shaping rumen development, with implications for optimizing feeding strategies in lambs and calves to enhance growth and health.

Antioxidants And Sheep Welfare / Omics Based Approaches

Antioxidants are essential for preserving redox equilibrium, reducing oxidative stress, and improving immunological function in

sheep. Various dietary antioxidants, including vitamins C and E, selenium, and polyphenols, effectively neutralise free radicals and reactive oxygen species (ROS), therefore safeguarding cellular components against oxidative assault. Various field investigations have shown that dietary antioxidant supplementation is effective in enhancing antioxidant status and health outcomes in sheep subjected to different stress situations.

Recent advancements in -omics technologies have facilitated the characterization of antioxidant metabolism and oxidative stress responses in sheep. Genomic studies have identified genetic variants influencing antioxidant enzyme activities and redox regulation in sheep breeds adapted to different environmental conditions. Transcriptomic analyses have elucidated gene expression profiles of antioxidant enzymes and stress-responsive pathways in sheep tissues under oxidative stress conditions. Proteomic and metabolomic approaches have provided insights into protein expression patterns, metabolic biomarkers, and antioxidant metabolites associated with dietary antioxidant interventions in sheep.

Numerous field studies assessing the impact of dietary antioxidants on the health and performance of sheep have yielded significant knowledge regarding their mechanisms of action and practical uses (Ochoa et al., 1992; Lopez-Bote et al., 2001; Lauzurica et al., 2005; Leal et al., 2018; Leal et al., 2019). In a recent study, Leal et al. (2020) examined the effects of adding vitamin E and rosemary extracts to lamb diets on the quality of meat and the ability of sheep to withstand oxidation. They found that the inclusion of these supplements resulted in increased antioxidant capacity and decreased lipid oxidation in the meat samples. Their study emphasised the significance of dietary antioxidants in enhancing the quality and maintaining the shelf life of products in sheep production systems.

Research has indicated that comparable therapies can effectively decrease oxidative stress on proteins and lipids in broiler chickens. Additionally, piglets exhibit reduced omega 6 / omega 3 and

PUFA/MUFA ratios compared to the control group. This reduction in oxidative stress may also have a positive impact on the health of ruminants (Skaperda et al., 2019). The aforementioned observations highlight the need of providing natural antioxidants with advantageous characteristics to enhance the redox state of farm animals and further animal welfare. Quantification of oxidative damage in livestock is crucial for comprehending the fundamental processes associated with illnesses and metabolic pathologies. Hence, to prevent the high mortality rates of sheep and other farm animals caused by oxidative diseases and safeguard their tissues from the detrimental oxidation process, it would be beneficial to examine and investigate their redox molecular status by quantifying particular redox markers (Figure 5) (Skaperda et al., 2019).

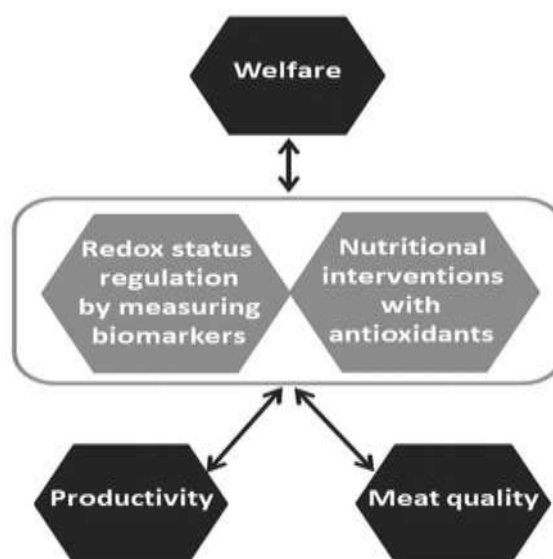


Figure 5. Interactions between welfare of livestock and antioxidant supplementation to diets (Skaperda et al., 2019).

CONCLUSIONS

In conclusion, -omics based approaches have transformed sheep nutrition research by providing molecular insights into gene expression, protein synthesis, metabolic pathways, and the interplay with dietary antioxidants. Genomics, transcriptomics, proteomics, and metabolomics offer powerful tools for identifying genetic markers, gene expression profiles, protein

biomarkers, and metabolite signatures relevant to sheep nutrition and antioxidant metabolism. These technologies enable targeted nutritional interventions tailored to individual sheep genotypes, environmental conditions, and production goals, enhancing productivity, health, and sustainability in sheep production systems.

Future research efforts should focus on integrating multi-omics data to develop precision nutrition strategies, leveraging technological advancements and interdisciplinary collaborations to address emerging challenges and opportunities in sheep nutrition. By harnessing the synergistic potential of -omics technologies and antioxidants, researchers can advance sustainable and resilient sheep production systems that meet global demands for high-quality protein and nutritional security.

Based on current info gathered from various studies, future research directions in -omics based approaches in sheep nutrition may include;

- **Epigenetic Modulations:** Exploration of epigenetic mechanisms influencing antioxidant gene expression and oxidative stress responses in sheep.
- **Gut Microbiome Interactions:** Investigation of gut microbiome-host interactions affecting antioxidant metabolism, immune function, and metabolic health in sheep.
- **Climate Resilience:** Assessment of antioxidant strategies to mitigate heat stress and enhance resilience in sheep exposed to climate variability and extreme weather events.
- **Precision Antioxidant Nutrition:** Development of personalized antioxidant interventions based on -omics data to optimize metabolic health, immune function, and production outcomes in sheep.
- **Data Integration and Interoperability:** Standardization of -omics data pipelines, bioinformatics tools, and data sharing platforms to enhance reproducibility and scalability of antioxidant research in sheep nutrition.
- **Advancements in Computational Biology:** Continued advancements in computational biology, machine learning, and predictive modeling will facilitate the analysis of complex -omics datasets and the

development of actionable insights for precision livestock management.

REFERENCES

- Aali M, Moradi-Shahrbabak H, Moradi-Shahrbabak M, Sadeghi M, Yousefi AR. 2017. Association of the calpastatin genotypes, haplotypes, and SNPs with meat quality and fatty acid composition in two Iranian fat- and thin-tailed sheep breeds. *Small Ruminant Res*, 149:40-51.
- Alexandre PA, Kogelman LJ, Santana MH, Passarelli D, Pulz LH, Fantinato-Neto P, et al. 2015. Liver transcriptomic networks reveal main biological processes associated with feed efficiency in beef cattle. *BMC genomics*, 16(1), 1-13.
- Bordoni L, Gabbianelli R. 2019. Primers on nutrigenetics and nutri(epi)genomics: origins and development of precision nutrition. *Biochimie*, 160:156-171.
- Chakraborty D, Sharma N, Kour S, Sodhi SS, Gupta MK, Lee SJ, Son YO. 2022. Applications of omics technology for livestock selection and improvement. *Frontiers in Genetics*, 13, 774113.
- Guðmundsdóttir ÓÓ. 2015. Genome-wide association study of muscle traits in Icelandic sheep. *Agricultural University of Island*.
- Han Y, Gao S, Muegge K, Zhang W, Zhou B. 2015. Advanced applications of RNA sequencing and challenges. *Bioinformatics and Biology Insights*, 9, BBI-S28991.
- Johnston SE, McEwan JC, Pickering NK, Kijas JW, Beraldi D, Pilkington JG, et al. 2011. Genome-wide association mapping identifies the genetic basis of discrete and quantitative variation in sexual weaponry in a wild sheep population. *Mol*, 20(12):2555-2566.
- Kijas JW, Lenstra JA, Hayes B, Boitard S, Porto Neto LR, et al. 2012. Genome-Wide Analysis of the World's Sheep Breeds Reveals High Levels of Historic Mixture and Strong Recent Selection. *PLOS Biology* 10(2): e1001258.
- Kızılaslan M, Arzik Y, Cinar MU, Konca Y. 2022. Genome-wise engineering of ruminant nutrition-nutrigenomics: applications, challenges, and future perspectives-A review. *Annals of Animal Science*, 22(2), 511-521.

- Kominakis A, Hager-Theodorides AL, Zoidis E, Saridaki A, Antonakos G, Tsiamis G. 2017. Combined GWAS and 'guilt by association'-based prioritization analysis identifies functional candidate genes for body size in sheep. *Genet Sel Evol*, 49(41):1-16.
- Lauzurica S, de la Fuente J, Diaz MT, Alvarez I, Perez C and Canequé V. 2005. Effect of dietary supplementation of vitamin E on characteristics of lamb meat packed under modified atmosphere. *Meat Sci* 70:639–646.
- Leal LN, Beltrán JA, Alonso V, Bello JM, den Hartog LA, Hendriks WH et al. 2018. Dietary vitamin E dosage and source affects meat quality parameters in light weight lambs. *J Sci Food Agric* 98:1606–1614.
- Leal LN, Beltran JA, Belles M, Bello JM, den Hartog LA, Hendriks WH, Martín-Tereso J. 2020. Supplementation of lamb diets with vitamin E and rosemary extracts on meat quality parameters. *J Sci Food Agric.*, 100(7): 2922–2931.
- Leal LN, Jensen SK, Bello JM, den Hartog LA, Hendriks WH and Martín-Tereso J. 2019. Bioavailability of α -tocopherol stereoisomers in lambs depends on dietary doses of all-rac or RRR- α -tocopheryl acetate. *Animal* 13:1874–1882.
- Liu T, Li F, Xu J, La Y, Zhou J, Zheng C. 2021. Transcriptomic analysis reveals that non-forage or forage fiber source promotes rumen development through different metabolic processes in lambs. *Animal Biotechnology*, 34(4), 1058–1071.
- López-Bote CJ, Daza A, Soares M and Berges E. 2001. Dose–response effect of dietary vitamin E concentration on meat quality characteristics in light-weight lambs. *Anim Sci* 73:451–457.
- Lowe R, Shirley N, Bleackley M, Dolan S, Shafee T. 2017. Transcriptomics technologies. *PLoS computational biology*. 13, e1005457.
- Martyniuk CJ. 2020. Perspectives on transcriptomics in animal physiology studies. *Comparative Biochemistry and Physiology Part B: Biochemistry and Molecular Biology*, 250, Article 110490.
- Mathers JC. 2017. Nutrigenomics in the modern era. *Proc. Nutr. Soc.*, 76: 265–275.
- Mu Y, Qi W, Zhang T, Zhang J, Mao S. (2022). Multi-omics analysis revealed coordinated responses of rumen microbiome and epithelium to high-grain-induced subacute rumen acidosis in lactating dairy cows. *Msystems* 7 (1), e0149021.
- Müller M, Kersten S. 2003. Nutrigenomics: goals and strategies. *Nat. Rev. Genet.*, 4: 315–322.
- Nanekarani S, Goodarzi M. 2014. Polymorphism of candidate genes for meat production in Lori sheep. *IERI Procedia*, 8:18-23.
- Nishihara K, van Niekerk J, Innes D, He Z, Canovas A, Guan LL, Steele M. 2023. Transcriptome profiling revealed that key rumen epithelium functions change in relation to short-chain fatty acids and rumen epithelium-attached microbiota during the weaning transition. *Genomics*, 115:5, 110664.
- Nowacka-Woszuć J. 2020. Nutrigenomics in livestock-recent advances. *Journal of Applied Genetics*, 61(1), 93-103.
- Ochoa L, McDowell LR, Williams SN, Wilkinson N, Boucher J and Lentz EL. 1992. α -Tocopherol concentrations in serum and tissues of sheep fed different sources of vitamin E. *J Anim Sci* 70:2568–2573.
- Osorio JS, Vailati-Riboni M, Palladino A, Luo J, Lóor JJ. 2017. Application of nutrigenomics in small ruminants: Lactation, growth, and beyond. *Small Ruminant Research*, 154, 29–44.
- Pant SD, You Q, Schenkel LC, Voort GV, Schenkel FS, Wilton J, et al. 2016. A genome-wide association study to identify chromosomal regions influencing ovine cortisol response. *Livest Sci*, 187:40-47.
- Ribeiro DM, Salama AA, Vitor AC, Argüello A, Moncau, CT, Santos EM, Almeida AM. 2020. The application of omics in ruminant production: A review in the tropical and sub-tropical animal production context. *Journal of proteomics*, 227, 103905.
- Rochus CM, Tortereau F, Plisson-Petit F, Restoux G, Moreno-Romieux C, Tosser-Klopp G, et al. 2018. Revealing the selection history of adaptive loci using genome-wide scans for selection: An example from domestic sheep. *BMC Genomics*, 19:1-17.
- Rovadoscki G.A, Pertile SFN., Alvarenga AB, Cesar ASM, Pértile F, Petrini J, et al. 2018.

- Estimates of genomic heritability and genome-wide association study for fatty acids profile in Santa Inês sheep. *BMC Genomics* 19:375. doi: 10.1186/s12864-018-4777-8
- Sales NMR, Pelegrini PB, Goersch MC. 2014. Nutrigenomics: Definitions and advances of this new science. *J. Nutr. Metab.*, 202759.
- Skaperda Z, Aristidis SV, Demetrios K. 2019. Farm animal welfare, productivity and meat quality: Interrelation with redox status regulation and antioxidant supplementation as a nutritional intervention (Review). *World Academy Of Sciences Journal*. 1: 177-183.
- Subedi P, Moertl S, Azimzadeh O. 2022. Omics in Radiation Biology: Surprised but Not Disappointed. *Radiation*. 2:124–129.
- Sun D, Yin Y, Guo C, Liu L, Mao S, Zhu W, Liu J. 2021. Transcriptomic analysis reveals the molecular mechanisms of rumen wall morphological and functional development induced by different solid diet introduction in a lamb model. *J Animal Sci Biotechnol* 12, 33.
- ul Haq Z, Saleem A, Khan AA, Dar MA, Ganaie AM, Beigh YA, Hamadani H, Ahmad SM. 2022. Nutrigenomics in livestock sector and its human-animal interface-a review. *Vet. Anim. Sci.* 17, 100262.
- Wang Y, Li J, Lu D, Meng Q, Song N, Zhou H, et al. (2022). Integrated proteome and phosphoproteome analysis of interscapular brown adipose and subcutaneous white adipose tissues upon high fat diet feeding in mouse. *J. proteomics* 255, 104500.
- Wu J, Yang D, Gong H, Qi Y, Sun H, Liu Y, Qiu X. 2020. Multiple omics analysis reveals that high fiber diets promote gluconeogenesis and inhibit glycolysis in muscle. *BMC genomics*, 21, 1-13.
- Xiang X, Peng C, Cao D, Chen Z, Jin H, Nie S, Xie Y, Chen X, Wang Z. 2024. Whole genome sequencing reveals that five genes are related to BW trait in sheep. *Animal*, 101282.
- Yadav SP. 2007. The Wholeness in Suffix-Omics,-Omes, and the Word Om. *J. Biomol. Tech.*, 18 (5), 277.
- Zhang H, Wang Z, Wang S, Li H. 2012. Progress of genome wide association study in domestic animals. *J Anim Sci Biotechnol*, 3:1-10.
- Zhao X, Dittmer KE, Blair HT, Thompson KG, Rothschild MF, Garrick DJ. 2011. A novel nonsense mutation in the DMP1 gene identified by a genome-wide association study is responsible for inherited rickets in Corriedale sheep. *PLoS ONE*, 6(7):1-6.