UNIVERSITY OF SINDH JOURNAL OF ANIMAL SCIENCES
DOI: https://doi.org/10.57038/usjas.v9i02.7742
Uni. Sindh. J. Anim. Sci., vol. 9(2); 35-45, 2025
Email: editors.usjas@usindh.edu.pk
ISSN (P): 2521-8328
ISSN (E): 2523-6067
Published by University of Sindh, Jamshoro.

ROLE OF THE GUT MICROBIOME IN NUTRIENT ABSORPTION, IMMUNE DEFENSE AND ANIMAL HEALTH

OLUWAFEMI ABEL AGBETUYI[*1], EMMANUEL KEHINDE ASANIYAN[2], ADEMIJU ADEOLU AGANGA[1], ADETUNMBI TELLA[1], TOMILOLA AYO ARILEKOLASI[1], KEHINDE LUKE AKINSOLA[1]

[1]Department of Animal Production and Health, Federal University, Oye Ekiti, Nigeria
[2]Department of Animal Production and Health, Olusegun Agagu University of Science and Technology, Okiti Pupa, Nigeria

ARTICLE INFORMATION

Article History:
Received: 13th August 2025
Accepted: 17th December 2025
Published online: 30th December 2025

Author Contributions:
All authors contributed equally

Key words:
Gut Microbiome, Immune Defense, Animal health, microorganisms, metabolism

Similarity Index:
14%

SDGs Targeted:
SDG 3 – Good Health and Well-Being
SDG 2 – Zero Hunger

ABSTRACT

The gut microbiome, a complex network of microorganisms that flourish in the gastrointestinal tract, is crucial for immune defense, nutrient absorption, and preservation of physiological balance in animals. This influences the development and function of the immune system, which aids in the synthesis of essential vitamins and complex carbohydrates conversion with a focus on how microbial ecosystems aid in the digestion, absorption, and metabolism of nutrients. This study highlights the complex interactions among gut microbiomes, their metabolic products (metabolomics), and the animals. More information was given about how this microbiome affects immune responses, particularly inflammation regulation and pathogenic resistance. A balanced gut microbiome is necessary because any disruption to this ecosystem can result in a number of health problems. New evidence suggests that the gut microbiome must be balanced to maintain homeostasis and prevent various diseases. Understanding of intricate microorganism colonies can be utilized to improve animal well-being and productivity using microbiome-based techniques.

1. INTRODUCTION

The primary processes of digestion and nutrient assimilation take place within the gastrointestinal tract of animals. The health and immune responses of such animals can be boosted by a balanced diet that contains essential nutrients (Magalhaes *et al.,* 2024). In animals, the gut microbiome is essential for maintaining good health by influencing digestion, immunity and disease prevention (Kumar *et al.,* 2025). More so, the gut must function efficiently to support various functions that will benefit the animals in terms of healthiness, productivity, and sustainability. However, changes in the early colonization of gut microbes in these animals often have enduring effects on the microbiome's formation and can affect the host physiology (Arshad *et al.,* 2021).

Phycology: the essential constituents of diet that promote the growth of beneficial bacteria, such as polyphenols, alkaloids, capsaicin and polysaccharides lead to an improved gastrointestinal health and overall well-being in animals (Chenbo *et al.,* 2022). The intestinal barrier's function, diet, and composition are factors that affect gut health, while the immune response of the animal is influenced by efficient digestion and assimilation factors.

The gut microbiome produces metabolites as by-products that affect both the bacteria and host, controlling its composition and function (Liu *et al.,* 2022). Short-chain fatty acids (SCFA), secondary bile acids (SBA), and neurotransmitters, among other metabolic, immune activation, and neurological functions, are all part of the constituent molecules in animal physiology (Rindels and Loman, 2024).

---

*Corresponding Author: femzyright@gmail.com

Various regions of the gut have distinct microbiomes, including jejunum, ileum, and cecum, regions like the mucosal microbiome to luminal microbiome, contain some bacteria during the growing periods from early life to maturity, in terms of density and diversity (Sun *et al*., 2024). Animal welfare is dependent on a vast and diverse microbial ecosystem. While the age, diet, and environment as factors, have varying effects on the gut microbiome (Chen *et al*., 2019). In a diverse ecological community, the microbiome is made up of commensal, symbiotic, and pathogenic microorganisms, such as bacteria, fungal, virus, or protozoa. Bacteria and other microbial groups, such as bacteriophages and fungi that play a significant role in maintaining gut homeostasis, make up the gut microbiome, which is characterized by its complex structure.

In the gastrointestinal tract, there are numerous viruses known as phages, which play a crucial role in shaping bacterial communities through predation and horizontal gene transfer (Shkoporov and Hill, 2019). Bacterial diversity, antimicrobial resistance, and metabolic functions can be influenced by phage-bacteria dynamics, which play an important role in microbial ecology (Lin *et al*., 2021). Incorporating phages to regulate gut microbial balance has been proposed as a method for engineering the microbiome of animals (Lin *et al*., 2021). The modulation of inflammation, immune signaling, and metabolic pathways through microbial interactions with dietary components like fibers, polyphenols, and omega-3 fatty acids also affects health outcomes (Sultan *et al*., 2021). Numerous studies have been conducted to clarify the specific functions and mechanisms of these microbes concerning various diseases (Lavelle and Sokol, 2020; Liu *et al*., 2022). The gastrointestinal tract of humans and animals is home to numerous microbes, which account for more than 10 times the number of human and animal cells and 150 times as many genes as the host genome (Paul, 2024).

Production animals contain significant amounts of phylogenetic diversity in the gut microbiome, as evidenced by the estimation of approximately 375 types in pigs (Shoaib *et al*., 2025), the range of 300 to 1000 bacterial species in cow rumen, roughly 915 operational taxonomic units in chickens, and from 2000 to over 3000 operational taxonomic units in sheep (Ma *et al*., 2019). Advances in microbiome profiling technologies such as metagenomics, metabolome analysis and personalized nutrition techniques have been reported to provide knowledge of the variability within gut microbes' responses (Roy and Singh, 2025). The recent technological advancements in omics, including metagenomics data analysis, have led to an increased understanding of microbial composition, health-related diseases, new therapeutic possibilities, and personalized medicine (Roy and Singh, 2025). The methods involve sequencing millions of DNA fragments at the same time, which enables strain-level insights into genome structure, genetic variations, gene activity, and change in gene behavior (Satam *et al*., 2023). Moreover, metabolomic studies aid in determining the characteristics of host-microorganism interactions (Roy and Singh, 2025). This molecular approach has led to growing evidence of the effects of dietary interventions on modulating the microbiome, which could improve health and potentially treat chronic diseases (Hick *et al*., 2024; Riegelman *et al*., 2024).
Various gut compartments are affected by environmental and physiological factors that shape the microbial communities within the gut compartments. Osmolarity, feed retention time, oxygen levels, availability of nutrients, and pH are all important physiological factors that must be considered when selecting particular microbial populations (Bickhart *et al*., 2020). Microbial composition is heavily influenced by the pH gradient that runs through the gut. For instance, the rumen maintains pH levels between 5.5 and 7.0, which promote fibre-digesting bacteria such as *Fibrobacter* and *Ruminococcus* (Tardiolo *et al*., 2025). On the contrary, the acidic environment of the monogastric stomach (pH 1.5-3.5) favors acid-resistant microorganisms like *Lactobacillus* and *Streptococcus* (Tugnoli *et al*., 2020). The osmotic pressure in the gut is altered by diet composition and water absorption. High-starch diets can lead to an increase in osmolarity in the intestines, which may cause microbial populations to shift towards amylolytic bacteria like Prevotella (McCallum and Tropini, 2024). Our current review aims to focus on the gut microbiome of animals by investigating existing knowledge about it. Furthermore, there were knowledge gaps regarding the absorption of nutrients,

immunity, and general health that can improve the productivity in animals.

2. MATERIALS AND METHODS

This review was prepared through a structured literature search focusing on the gut microbiome and its relationship with nutrient absorption, immune defense, and animal health. Peer-reviewed articles were consulted from major scientific databases (e.g., PubMed, Google Scholar, and ScienceDirect) using combinations of keywords such as "gut microbiome", "animals", "nutrient absorption", "probiotics", "prebiotics", "SCFAs", "immune responses", and "dysbiosis". Priority was given to recent studies, reviews, and meta-analyses, while older landmark studies were also included where necessary for conceptual background. Relevant papers were screened based on title/abstract, and full texts were reviewed to extract information on (i) microbiome functions in digestion and nutrient metabolism, (ii) microbiome–immune interactions, and (iii) dietary and probiotic/prebiotic interventions affecting microbiome composition and host health.

3. RESULTS

The reviewed evidence shows that the gut microbiome contributes substantially to animal health through three main pathways. First, microbial fermentation supports nutrient utilization by producing short-chain fatty acids (SCFAs), supporting vitamin synthesis, and improving mineral bioavailability, thereby enhancing digestion and metabolic efficiency. Second, the microbiome strengthens immune defense by maintaining gut barrier integrity, regulating inflammation, and improving resistance against pathogens; disruption of this balance (dysbiosis) is linked with increased susceptibility to disease and reduced productivity. Third, dietary strategies—including probiotics, prebiotics, enzyme supplementation, and resistant starch—consistently demonstrate potential to shift microbial communities toward beneficial taxa, improve gut morphology, and enhance performance and health indicators in several animal species. Overall, the literature supports microbiome-based nutritional interventions as promising tools for improving animal productivity and welfare.

Role of gut microbiome

Among the major defensive barriers in the body, the intestinal mucosal barrier is made up of physical and chemical components as well as microbial and immunological components (Matsuoka *et al.*, 2025). This safeguard against the invasion of bacteria stops foreign antigens and toxic substances from gaining entrance into the body, thereby reduces water and nutrients loss (Verma *et al.*, 2025). The barrier regulates molecular exchange and facilitates the cohabitation and colonization of gut bacteria. The gut microbiome's composition can be disrupted, leading to the development of significant diseases. Host animals' normal physiological functions are dependent on the gut microbiome. It has been established that the gut microbiome is associated with and functions as a commensal to metabolic organ, which can affect systemic inflammation, immunity regulation or nutrition (Stephens *et al.*, 2018; Matsuoka *et al.*, 2025). It includes an association of microbes that are often beneficial in promoting the normal functioning of the gastrointestinal tract (Agbetuyi *et al.*, 2024a). Its main functions include directing the normalization or progression of gut structure and morphology, strengthening immune responses, providing protection against luminal pathogens, and participating in digestion and nutritional absorption (Figure 1). There are several important positive and negative effects of microbiome on host physiology and performance (Verma *et al.*, 2025).

The gut microbiome can cause both direct and indirect harm to chickens, including reduced fat digestibility, increased cell turnover rate, and production of toxic metabolites due to protein fermentation (Kumar *et al.*, 2025) decomposing into smaller particles or compounds, the rumen's microbiome is the first to interact with forage biomass. As the microbiome becomes more intricate, it is possible to manipulate it in a way that maintains biotic relationships and reduces emissions of greenhouse gases while increasing feed efficiency (Matsuoka *et al.*, 2025).

Dietary enhancement of gut microbiome

The misuse of antibiotics in animals and poultry has become a serious issue with public health concern (Agbetuyi *et al.*, 2024b). Some studies have shown the presence of antibiotic residues in eggs; however, using probiotics as feed additives can help breeders improve their quality and to benefit the health of breeders and other egg producers (Reuben *et al.*, 2021). β-mannanase and probiotics were found to have an impact on the growth performance, serum levels, gut morphology, and egg quality traits of hens in a recent study by Wang *et al.* (2025). Egg-laying potential of 11% was increased by the hens with diet rich in probiotics and β-mannanase, as well as 7% for their health. Through the use of β-mannanase and probiotics, yolk characteristics and serum biochemical parameters such as total cholesterol, uric acid, and triglycerides were enhanced. Morphological changes in the villus height and crypts were also observed, which led to an increase in nutrient absorption levels (Wang *et al.,* 2025). Fungus is bolstered by feed additives like resistant starch that boost intestinal short-chain fatty acids (SCFAs) levels and minimize gut inflammation. Improved gut health and SCFA production were observed in experimental pigs that were fed raw potato starch to supplement their diet (Yi *et al.,* 2023; Lee *et al.,* 2024). In comparison to control group, the treated groups showed reduced histopathological lesions (Yi *et al*., 2023). When 16S rRNA gene sequencing was used to analyze the microbiome, it reveals the high numbers of Firmicutes, Bacteroidetes, and Proteobacteria phyla (Lin *et al.,* 2025). Rikenellaceae_RC9 and Oscillospiraceae-UCG-005 were closely linked to lipid metabolism and fatty acid composition, respectively (Lin *et al*., 2025).

The rumen microbiome's relative abundance had an impact on goat fattening, meat quality and nutritional indices (Zhou *et al.,* 2023). The gut microbiome produces short-chain fatty acids (SCFAs) by digesting dietary carbohydrates through microbial control of metabolism, which is essential for maintaining the gut's microenvironment (Figure 2). Roughly 20% of the carbohydrates that are digested cannot be broken down by amylase. Bacteroides, Bifida, *Enterobacterium*, Roseburia and *Fecalibacterum* are gut microbiome that produce SCFAs including acetate, butyrate and propionate by fermenting indigestible carbohydrates such as non-starch polysaccharides and cellulose (Roy and Singh, 2025). The animal's large intestine is responsible for the absorption of these SCFAs.

Probiotics and assimilation of nutrients

Probiotics are live microorganisms that offer the host several health advantages when consumed in sufficient quantities (Reuben *et al*., 2021). Probiotics are mainly associated with gut health enhancement, but their impact on nutrient absorption is highly variable and depends on the type and strain of probiotic ingredient (Markowiak and Slizewska, 2017). Probiotics can stimulate the production of SCFAs, improve the gut lining, reduce inflammation, and increase the synthesis of certain digestive enzymes, thereby enhancing the bioavailability of specific nutrients and phytonutrients. Additionally, probiotics play a vital role in preserving the integrity of the intestinal barrier, which is essential for effective nutrient absorption. The proteolytic property of certain *Lactobacillus species* aids in the formation of little bioactive soluble peptides that are more readily absorbed than their indigenous protein counterparts, thereby enhancing the nutritional value of some proteins (Manus *et al*., 2021). The absorption of certain *Lactobacillius species* through fermentation can be boosted by reducing the anti-metabolite substances such as tannins, phytate and trypsin inhibitors (Manus et al., 2021; Walden *et al*., 2022). Additionally, fermentation can reduce the pH and its antibiotics concentration, decrease trypsin inhibitor property, and inhibit the presence of phytates and tannins in pulsed food preparations (Jager *et al.,* 2020). Furthermore, certain probiotics are critical in the synthesis of specific B-Complex vitamins, including thiamin, B_{12}, and B_9 (folate) within the gut.

Prebiotics and assimilation of nutrient

Prebiotics, which are fermented in the colon by gut bacteria, can enhance the proliferation and functionality of beneficial bacteria such as *Bifidobacterium* and *Lactobacillus*. According to existing evidence, these non-digestible oligosaccharides can also improve the absorption of nutrients and phytonutrients (Reuben *et al.,* 2021). Although existing studies suggest that specific prebiotics may positively influence the bioavailability of certain minerals, including calcium and magnesium, thereby contributing to physiological advantages that enhance bone mineralization and structure (Zakrzewska *et al.,* 2022). The SCFAs generated in the colon, particularly butyrate, may significantly impact nutrient bioavailability. This occurs through the production of an osmotic effect, the expansion of the gut absorption surface area, and the reduction of intestinal lumen pH, which in turn increases mineral solubility (Zakrzewska *et al.,* 2022). Additionally, SCFAs may stimulate the production and secretion of pancreatic lipase, which is essential for the breakdown of dietary fats. Moreover, prebiotics have been demonstrated to improve gut barrier function, which regulates nutrient passage through the intestinal lining while simultaneously obstructing the absorption of harmful compounds such as toxins and pathogens (Reuben *et al.,* 2021). In contrast, Prebiotics stimulate mucus production in the gut, which acts as a protective barrier and prevents damage to the intestinal lining. In general, they can impact gut health and enhance nutrient bioavailability.

Gut microbiome and assimilation of nutrient

The microbiome is recognized for its ability to convert polyphenols, fibers, nucleic acids, and fats into short-chain fatty acids (SCFAs), modified B-Complex vitamins, conjugated fatty acids, polyphenols, and various metabolites (Barone *et al.,* 2022; Gebrayel *et al.,* 2022). By breaking down complex food molecules that passes through the digestive system, the gut microbiome is essential for nutrient absorption (Uebanso *et al.,* 2020). Microbes in the gut possess the necessary enzymes to breakdown these molecules and release nutrients and metabolites, such as glucose and SCFAs. The gut microbiome is also responsible for the metabolism of amino acids, lipids, and other nutrients, which can affect nutrient absorption and utilization (Roy and Singh, 2025). Additionally, some cellular processes contain many small molecule precursors called METALS. The production of bile acids by gut bacteria is essential for the emulsification of fats and their absorption; they can also assist in the breakdown of vitamin K and vitamin B_{12} (Uebanso *et al.,* 2020). Gut bacteria are not only involved in managing the metabolism of nutrients but also play a role in nutrient assimilation by controlling gut barrier function and immune system regulation (Table 1). Either way, another cellular organism may absorb some nutrients. To maintain the integrity of the gut barrier and manage inflammatory responses, the microbiome can produce mucus and other protective compounds to regulate immune function (Uebanso *et al.,* 2020; Barone *et al.,* 2022; Agbetuyi *et al.,* 2024a). Moreover, the gut microbiome is essential for the absorption of nutrients, as it facilitates the breakdown of complex food molecules, the production of vitamins and other nutrients through digestion, as well as regulating gut membrane function and immune system property. The gut microbiome's imbalances, such as dysbiosis, can result in nutrient loss and adverse health effects (Roy and Singh, 2025).

Gut microbiome, immunity, and health

By modulating the immune system and enhancing health and productivity in animals, the gut microbiome provides protection to the host against environmental hazards (Ghosh and Ray, 2025; Roy and Singh, 2025). When this commensal microbiome is disturbed, it can cause gut disorders such as rumen acidosis, bloat, and nutrient toxicity, as well as diarrhea. In the intensive production systems, health issues are major welfare and economic concerns that have traditionally been addressed by the "one-pathogen one-disease" approach (Barone *et al.,* 2022). There is increasing evidence that symbiotic microbiomes are major players in modulating and reducing the incidence of gut disorders, mastitis, and respiratory disease (Barone *et al.,* 2022; Yu *et al.,* 2025). The interaction between the microbes and their host offers new perspectives on how the gut microbiome can impact on metabolic efficiency, resistance to disease and host stress.

Gut microbiome immune responses

The immune system's role in maintaining health is crucial as it can respond to microbes, tumors and other obstacles (Yu *et al.,* 2025). Specific cell populations, such as macrophages, neutrophils and mast cells, eosinophilds, natural killer, and other innate lymphoid cells are part of the 'non-specific' arm. They respond immediately to microbes and tissue damage typically induced by pattern recognition receptors, including pathogen-associated molecular patterns (PAMPs) and damage-associated molecular patterns (DAMPs), as illustrated in the study of Li *et al.* (2021). Along with acute inflammation and the intestinal mucosa, anatomical barriers are also present (Cronkite and Strutt, 2018). Different populations of T and B cells, which are essential for responses to non-self-antigens such as immune memory upon re-exposure, make up the adaptive or specific arm instead (Lam *et al.,* 2024). Over time, the role of the gut microbiome remains influential in shaping the immune cell types (Ghosh and Ray, 2025). The major ways of achieving this are pathogen-associated molecular patterns produced by microbiological factors, which function through Toll-like receptors (TLRs) and nucleotide-binding oligomerization domain-containing proteins (NODs), as well as microbiome derivative metabolites such as SCFAs butyrate and propionate, that can perform both locally and systemically (Mann *et al*., 2024). However, Bi-directional interaction between the gut microbiome and immunity is influenced by multiple mechanisms (Zheng *et al*., 2020). For instance, B cells generate significant amounts of immunoglobulin (IgA) against commensal bacteria and the intestinal mucosa produces mucin (Bamias *et al.*, 2023). A protective barrier created by the intestinal lumen neutrophils serves to modulate the microbiome, recruiting bacteria to the mucosal epithelium to limit segmental filamentous bacteria through the induction of antimicrobial proteins (Roy and Singh, 2025). This is achievable through intestinal mucous membrane and then moving to their location to control bacterial overgrowth primarily through reactive oxygen species production (Zhang and Frenette, 2019).

Microbiome impact on intestinal flora

While intestinal disorders are common among companion animals, diarrhea is a significant issue for animal owners and the leading reason for frequent veterinary treatment. The root cause of diarrhea is diverse and involves multiple factors such as microbial metabolite dysregulation, medication, and pre-existing conditions (Guo *et al*., 2024). The impact of bile acid dysregulation, antibiotic use, and gastrointestinal diseases on companion animal's diarrhea has been highlighted. Treatment strategies that can address multi-causal diarrhea include utilizing microbiological targeted interventions (Li *et al*., 2025). The gut microbiome and metabolome (a collection of all metazoans) undergo significant changes due to diarrhea occurrence (Li *et al*., 2025). To study the connections between changes in metabolome, as some microbial substances can either worsen or improve health conditions, and such substances may be produced uniformly or separately within gut microbiomes (Roy and Singh, 2025). Primary, animal-produced bile acids are then biota converted into secondary metabolites (SBA), where microbial metabolism is involved. Antibiotics are frequently prescribed by veterinarians to treat diarrhea caused by pathogens (Agbetuyi *et al*., 2024b). Despite this, recent research indicates that antibiotics are not only ineffective for the treatment of diarrhea but also tend to worsen the problem in animals. A condition that leads to antibiotic resistance and drug residue in animal products with altered composition of gut microbiome (Chaitman *et al*., 2020; Stavroulaki *et al*., 2021; Agbetuyi *et al*., 2024b).

4. CONCLUSION

In animals, gut microbiome is essential for nutrient absorption and immune function, as well as general health. Detailed interactions between the gut microbiome and its host's physiological makeup determine important aspects of metabolic processes, such as access to nutrients, or immune responses. Complex carbohydrates are broken down, vitamins are produced, and minerals are more readily available to the body due to the presence of these microbes. A relationship that fosters the optimal absorption of nutrients is essential for growth and development. Healthy gut microbiome is essential for a robust immune system, which can help train the body's immune response, improve barrier stability, and protect against pathogenic infections. In animals, immunological disorders and increased susceptibility to diseases can be caused by a microbiome imbalance called dysbiosis, which results in significant economic losses. The better health outcomes are linked to a healthy microbiome, which has been shown to have reduced systemic inflammation. Overall, the gut microbiome is of utmost importance to animal welfare, and current studies have revealed its functions more clearly over time, leading to better health strategies and interventions. Present study suggests that Future research should focus on identifying specific bacterial strains that improve nutrient absorption and immunity in animals, supporting the development of targeted probiotic therapies. As knowledge of the gut microbiome advances, personalized nutrition plans can be designed based on an animal's needs and key microorganisms. Further intervention studies are needed to evaluate how diet changes, probiotics, and prebiotics affect microbiome composition and function across animal species. Exploring the microbiome's role in preventing metabolic and autoimmune diseases may reveal new strategies for better animal health management. Combining advanced sequencing with bioinformatics will be essential to understand microbiome dynamics and their impact on health.

5. CONFLICT OF INTEREST

All authors have declared that there is no conflict of interest regarding the publication of this article.

REFERENCES

Agbetuyi, O. A., Ekeocha, A. H., Aganga, A. A., & Oloruntola, O. D. (2024a). *Moringa oleifera* and *Allium sativum* in broiler nutrition: carcass traits, biochemical characterization, and economic analysis. Discover Food, 4(1), 86. https://doi.org/10.1007/s44187-024-00155-y

Agbetuyi, O. A., Ekeocha, A. H., & Aganga, A. A. (2024b). Assessing the impact of moringa and garlic supplementation on egg production and quality in laying hens. Dysona-Applied Science, 5(2), 41-51. http://dx.doi.org/10.30493/DAS.2024.451601

Arshad, M. A., Hassan, F., Rehman, M. S., Huws, S. A., Cheng, Y., & Din, A. U. (2021). Gut microbiome colonization and development in neonatal ruminants: strategies, prospects, and opportunities. Animal Nutrition, 7, 883–895.

Bamias, G., Kitsou, K., & Rivera-Nieves, J. (2023). The underappreciated role of secretory IgA in IBD free. Inflammatory Bowel Diseases, 29(8), 1327-1341. https://doi.org/10.1093/ibd/izad024

Bickhart, D. M., McClure, J. C., Schnabel, R. D., Rosen, B. D., Medrano, J. F., & Smith, T. P. L. (2020). Symposium review: advances in sequencing technology herald a new frontier in cattle genomics and genome-enabled selection. Journal of Dairy Science, 103, 5278–5290.

Barone, M. D., Amico, F., Brigidi, P., &Turroni, S. (2022). Gut microbiome-micronutrient interaction: the key to controlling the bioavailability of minerals and vitamins? Biofactors, 48(2), 307-314. https://doi.org/10.1002/biof.1835.

Chaitman, J., Ziese, A. L., Pilla, R., Minamoto, Y., Blake, A. B., Guard, B. C., Isaiah, A., Lidbury, J. A., Steiner, J. M., & Unterer, S. (2020). Fecal microbial and metabolic profiles in dogs with acute diarrhea receiving either fecal microbiota transplantation or oral metronidazole. Frontiers in Veterinary Science, 7, 192. https://doi.org/10.3389/fvets.2020.00192

Chen, S., Xiang, H., Zhang, H., Zhu, X., Wang, D., Wang, J., Yin, T., Liu, L., Kong, M., & Li, H. (2019). Rearing system causes changes of behavior, microbiome, and gene expression of chickens. Poultry Science, 98, 3365–3376.

Chenbo, Y., Chuanq, C., Jianxi, Z., Ha, Z., Wei, C., &Qixiao, Z. (2022). Dietary strategies to promote the abundance of intestinal *Akkermansiamuciniphila*, a focus on the effect of plant extracts. Journal of Functional Foods, 93, 105093. https://doi.org/10.1016/j.jff.2022.10509

Cronkite, D. A., & Strutt, T. M. (2018). The regulation of inflammation by innate and adaptive lymphocytes. Journal of Immunological Research, 2018, 1467538.

Gebrayel, P., Nicco, C., Al Khodor, S., Bilinski, J., Caselli, E., Comelli, E. M., Egert, M.,

Giaroni, C., Karpinski, T. M., Loniewski, I., Mulak, A., Reygner, J., Samczuk, P., Serino, M., Sikora, M., Terranegra, A., Ufnal, M., Villeger, R., Pichon, C., Konturek, P., & Edeas, M. (2022). Microbiota medicine: towards clinical revolution. Journal of Translational Medicine, 20(1), 111. https://doi.org/10.1186/s12967-022-03296-9.

Ghosh, S., & Ray, R. R. (2025). Use of alternative sources (AMP, Nanomaterials, Phytocompounds) for handling biofilm-associated infections in livestock. In: Lahiri, D., Nag, M., Bhattacharya, D., Ray, R.R. (eds) biofilm associated livestock diseases and their management. Livestock Diseases and Management. Springer, Singapore. https://doi.org/10.1007/978-981-96-1885-9_13

Guo, S., Ma, T., Kwok, L., Quan, K., Li, B., & Wang, H. (2024). Effects of postbiotics on chronic diarrhea in young adults: a randomized, double-blind, placebo-controlled crossover trial assessing clinical symptoms, gut microbiota, and metabolite profiles. Gut Microbes, 16, 1 https://doi.org/10.1080/19490976.2024.2395092

Hick, E., Suarez, M., Rey, A., Mantecón, L., Fernandez, N., Solis, G., Gueimonde, M., &

Arboleya, S. (2024). Personalized nutrition with banked human milk for early gut microbiota development: in pursuit of the perfect match. Nutrients, 16, 1976.

Jager, R., Zaragoza, J., Purpura, M., Iametti, S., Marengo, M., Tinsley, G. M., Anzalone, A. J.,

Oliver, J. M., Fiore, W., Biffi, A., Urbina, S., & Taylor, L. (2020). Probiotic administration increases amino acid absorption from plant protein: a placebo-controlled, randomized, double-blind, multicenter, crossover study. Probiotics and Antimicrobial Proteins, 12(4), 1330-1339. https://doi.org/10.1007/s12602-020-09656-5.

Kumar, S., Mukherjee, R., Gaur, P., Leal, E., Lyu, X., Ahmad, S., Puri, P., Chang, C., Raj, V. S. & Pandey, R. P. (2025). Unveiling roles of beneficial gut bacteria and optimal diets for health. Frontiers in Microbiology, 16, 1527755. https://doi.org/10.3389/fmicb.2025.1527755

Lam, N., Lee, Y., & Farber, D. L. (2024). A guide to adaptive immune memory. Nature Reviews Immunology, 24, 810-829.

Lavelle, A., & Sokol, H. (2020). Gut microbiota-derived metabolites as key actors in inflammatory bowel disease. Nature Reviews Gastroenterology and Hepatology, 17, 223-237. https://doi.org/10.1038/s41575-019-0258-z

Lee, J., Gonzalez-Vega, J. C., Htoo, J. K., &Nyachoti, C. M. (2024). Effects of dietary crude protein content and resistant starch supplementation on growth performance, intestinal histomorphology and microbial metabolites in weaned pigs. Archives of Animal Nutrition, 78(2), 191-206. https://doi.org/10.1080/1745039X.2024.2376093

Li, D., Li, C., Liu, N., Liu, H., Yu, Z., Liu, Q., Shu, G., Lin, J., Zhang, W., Peng, G., Zhao, L.,

Tang, H., Li, H., Xu, F., & Fu, H. (2025). Integrated metabolomics and intestinal microbiota analysis to reveal anti-post-weaning diarrhea mechanisms of Modified Yupingfeng Granule in Rex rabbits. Frontiers in Microbiology, 16. https://doi.org/10.3389/fmicb.2025.1470731

Li, Q., Larouche-Lebel, E., Loughran, K. A., Huh, T. P., Suchodolski, J. S., & Oyama, M. A. (2021). Gut dysbiosis and its associations with gut microbiota-derived metabolites in dogs with myxomatous mitral valve disease. MSystems, 6(2), e00111-e00121. https://doi.org/10.1128/msystems. 00111-21

Lin, Y. C., Wu, C.C., Li, Y.E., Chen, C. L, Lin, C.R., & Ni, Y.H. (2025). Full-length 16S rRNA Sequencing Reveals Gut Microbiome Signatures Predictive of MASLD in children with obesity. BMC Microbiology, 25, 146. https://doi.org/10.1186/s12866-025-03849-0

Lin, Y., Zhou, B., & Zhu, W. (2021). Pathogenic *Escherichia coli*-specific bacteriophages and polyvalent bacteriophages in piglet guts with increasing coliphage numbers after weaning. Applied and Environmental Microbiology, 87, e00966-21.

Liu, M. J., Yang, J. Y., Yan, Z. H., Hu, S., Li, J. Q., & Xu, Z. X. (2022). Recent findings in *Akkermansiamuciniphila*-regulated metabolism and its role in intestinal diseases. Clinical Nutrition, 41, 2333-2344. https://doi.org/10.1016/j.clnu.2022.08.029

Ma, Y., Ma, S., Chang, L., Wang, H., Ga, Q., Ma, L., Bai, Z., Shen, Y., & Ge, R. L. (2019). Gut microbiota adaptation to high altitude in indigenous animals. Biochemical and Biophysical Research Communications, 516, 120-126.

Mann, E. R., Lam, Y. K., & Uhlig, H. H. (2024). Short-chain fatty acids: Linking diet, the microbiome and immunity. Nature Reviews Immunology, 24, 577-595.

Magalhaes, M. I., Azevedo, M. J., Castro, F., Oliveira, M. J., Costa, A. M., & Sampaio Maia, B. (2024). The link between obesity and the gut microbiota and immune system in early-life. Critical Reviews in Microbiology, 51(2), 264-284. https://doi.org/10.1080/1040841X.2024.2342427

Manus, J., Millette, M., Uscanga, B. R. A., Salmieri, S., Maherani, B., & Lacroix, M. (2021). *In vitro* protein digestibility and physico-chemical properties of lactic acid bacteria fermented beverages enriched with plant proteins. Journal of Food Sciences, 86(9), 4172-4182. https://doi.org/10.1111/1750-3841.15859

Markowiak, P., &Slizewska, K. (2017). Effects of probiotics, prebiotics, and Synbiotics on human health. Nutrients, 9, 1021. https://doi.org/10.3390/nu9091021

Matsuoka, M., Soria, S. A., Pires, J. R., Sant'Ana, A. C. P., & Freire, M. (2025). Natural and induced immune responses in oral cavity and saliva. BMC Immunology, 26(34) https://doi.org/10.1186/s12865-025-00713-8

McCallum, G., &Tropini, C. (2024). The gut microbiota and its biogeography. Nature Reviews Microbiology, 22, 105–118.

Paul, J. (2024). Gastrointestinal tract infections. in: disease causing microbes. Springer, Cham. 149-215.

Reuben, R. C., Sarkar, S. L., Roy, P. C., Anwar, A., Hossain, M. A., & Jahid, I. K. (2021).

Prebiotics, probiotics and postbiotics for sustainable poultry production. World's Poultry Science Journal, 77(4), 825-882. https://doi.org/10.1080/00439339.2021.1960234

Riegelman, E., Xue, K. S., Wang, J. S., & Tang, L. (2024). Gut-brain axis in focus: polyphenols,

microbiota, and their influence on α-synuclein in parkinson's disease. Nutrients, 16, 2041.

Rindels, J. E., & Loman, B. R. (2024). Gut microbiome – the key to our pets' health and

happiness? Animal Frontiers, 14 (3), 46-53. https://doi.org/10.1093/af/vfae015

Roy, S., & Singh, S. (2025). Metabolomics approaches for microbiome analysis. In: Kesheri, M.,

Kanchan, S., Hader, DP., Sinha, R.P. (eds) Multi-Omics in Biomedical Sciences and Environmental Sustainability. Springer, Singapore. https://doi.org/10.1007/978-981-96-7067-3_9

Satam, H., Joshi, K., Mangrolia, U., Waghoo, S., Zaidi, G., Rawool, S., Thakare, R. P., Banday, S., Mishra, A. K., & Das, G. (2023). Next-generation sequencing technology: current trends and advancements. Biology, 12, 997.

Shkoporov, A. N., & Hill, C. (2019). Bacteriophages of the human gut: the “known unknown” of the microbiome. Cell Host Microbe, 25, 195–209.

Shoaib, M., Gul, S., Majeed, S., He, Z., Hao, B., Tang, M., Zhang, X., Wu, Z., Wang, S., Pu, W. (2025). Pathogenomic characterization of multidrug-resistant *Escherichia coli* strains carrying wide efflux-associated and virulence genes from the dairy farm environment in Xinjiang, China, Antibiotics, 14(5), 511. https://doi.org/10.3390/antibiotics14050511

Stavroulaki, E. M., Suchodolski, J. S., Pilla, R., Fosgate, G. T., Sung, C. H., Lidbury, J. A., Steiner, J. M., &Xenoulis, P. G. (2021). Short- and long-term effects of amoxicillin/clavulanic acid or doxycycline on the gastrointestinal microbiome of growing cats. PLoS One. 16(12), e0253031. https://doi.org/10.1371/journal.pone.0253031

Stephens, R. W., Arhire, L., &Covasa, M. (2018). Gut microbiota: From microorganisms to metabolic organ influencing obesity. Obesity, 26, 801-809.

Sun, W., Zhang, Y., Guo, R., Sha, S., Chen, C., Ullah, H., Zhang, Y., Ma, J., You, W., Meng, J., Lv, Q., Cheng, L., Fan, S., Li, R., Mu, X., Li, S., & Yan, Q. (2024). A population-scale analysis of 36 gut microbiome studies reveals universal species signatures for common diseases. npj Biofilms Microbiomes, 10, 96. https://doi.org/10.1038/s41522-024-00567-9

Sultan, S., El-Mowafy, M., Elgaml, A., Ahmed, T., Hassan, H., &Mottawea, W. (2021). Metabolic influences of gut microbiota dysbiosis on inflammatory bowel disease. Frontiers in Physiology, 12, 715506. https://doi.org/10.3389/fphys.2021.715506

Tardiolo, G., La Fauci, D., Riggio, V., Daghio, M., Di Salvo, E., Zumbo, A., & Sutera, A. M. (2025). Gut microbiota of ruminants and monogastric livestock: an overview. Animals, 15(5), 758. https://doi.org/10.3390/ani15050758

Tugnoli, B., Giovagnoni, G., Piva, A., & Grilli, E. (2020). From acidifiers to intestinal health enhancers: how organic acids can improve growth efficiency of Pigs. Animals, 10, 134.

Uebanso, T., Shimohata, T., Mawatari, K., & Takahashi, A. (2020). Functional roles of B-vitamins in the gut and gut microbiome. Molecular Nutrition & Food Research, 64, e2000426. https://doi.org/10.1002/mnfr.202000426

Verma, M., Randhawa, S., Bathla, M., Tejiab, N., & Acharya, A. (2025). Strategic use of nanomaterials as double-edged therapeutics to control carcinogenesis via regulation of dysbiosis and bacterial infection: current status and future prospects. Journal of Materials Chemistry B, 16.

Walden, K. E., Hagele, A. M., Orr, L. S., Gross, K. N., Krieger, J. M., Jager, R., & Kerksick, C. M. (2022). Probiotic BC30 improves amino acid absorption from plant protein concentrate in older women. Probiotics and Antimicrobia Proteins. https://doi.org/10.1007/s12602-022-10028-4

Wang, X. Y., Ding, Z. L., Xu, Y. X., Yang, D. Z, Yang, S., & Fei, H. (2025). Effect of supplementing exogenous glucanase or/and mannanase to diets containing Torula yeast on growth performance, biochemical indices, liver and intestinal morphology, and intestinal microbiota and metabolism of largemouth bass (*Micropterussalmoides*). Probiotics and Antimicrobial Proteins, 1-15. https://doi.org/10.1007/s12602-025-10560-z

Yi, S., Lee, H. G., Kim, E., Jung, Y., Bok, E., Cho, A., Jung Do, Y., Hur, T., & Oh, S. (2023). Raw potato starch diet supplement in weaned pigs could reduce *Salmonella Typhimurium* infection by altering microbiome composition and improving immune status. Frontiers in Veterinary Science, 10. https://doi.org/10.3389/fvets.2023.1183400

Yu, J., Liu, C., Wang, D., Wan, P., Cheng, L., & Yan, X. (2025). Integrated microbiome and metabolome analysis reveals altered gut microbial communities and metabolite profiles in dairy cows with subclinical mastitis. BMC Microbiology, 25, 115. https://doi.org/10.1186/s12866-025-03810-1

Zakrzewska, Z., Zawartka, A., Schab, M., Martyniak, A., Skoczen, S., Tomasik, P. J., Wędrychowicz, A. (2022). Prebiotics, probiotics, and postbiotics in the prevention and treatment of anemia. Microorganisms, 10(7), 1330. https://doi.org/10.3390/microorganisms10071330

Zhang, D., & Frenette, P. S. (2019). Cross talk between neutrophils and the microbiota. Blood, 133, 2168-2177.

Zheng, D., Liwinski, T., &Elinav, E. (2020). Interaction between microbiota and immunity in health and disease. Cell Research, 30, 492–506.

Zhou, G., Liang, X., He, X., Li, J., Tian, G., Liu, Y., Wang, X., Chen, Y., & Yang, Y. (2023). Compound enzyme preparation supplementation improves the production performance of goats by regulating rumen microbiota. Applied Microbiology and Biotechnology, 107, 7287-7299. https://doi.org/10.1007/s00253-023-12804-w

Table 1: Gut microbiome's roles and their examples

Roles	Examples
Immune system regulation	Interaction with regulatory T cells to reduce inflammation and SCFAs promote anti-inflammatory pathways
Metabolic effects	Production of acetate, propionate, and butyrate for energy and metabolic regulation
Pathogenic protection	Development of bacteriocins and lowering of *Clostridioidesdifficile*
Nutrient synthesis	Synthesis of both vitamin K and B such as B_{12}

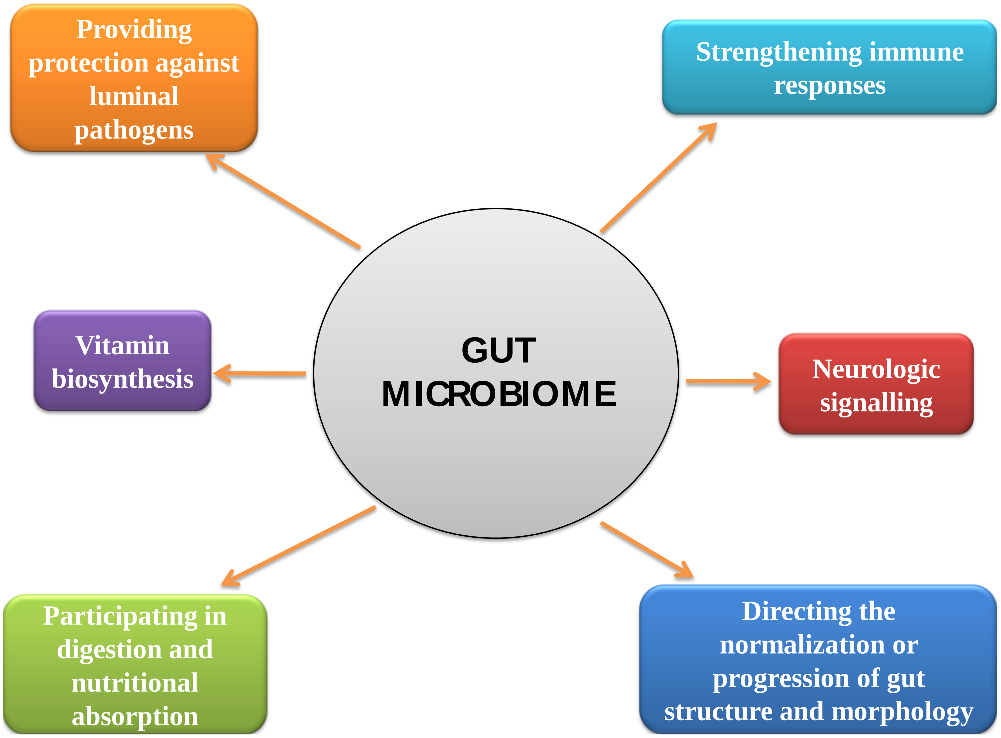

Figure 1: The main functions of gut microbiome

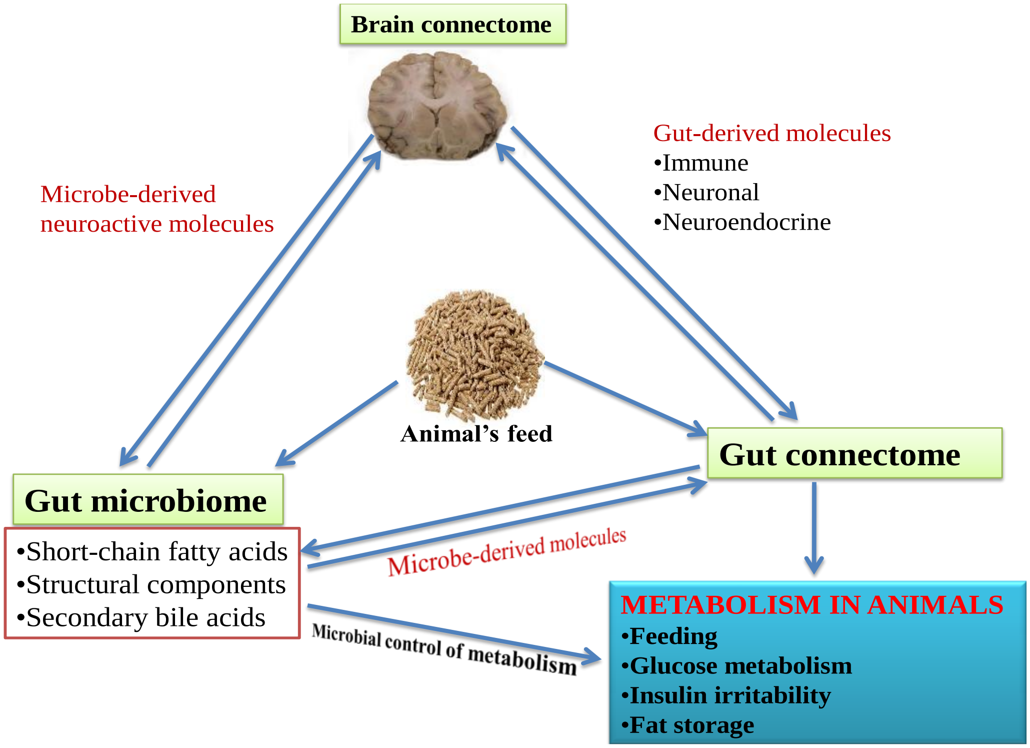

Figure 2: Dietary enhancement of gut microbiome