

Animal Gut Microbiome: Recent Advances, Environmental Interactions, and Functional Implications

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Abstract

The animal gut microbiome represents a highly complex and dynamic consortium of microorganisms that plays a pivotal role in host nutrition, immunity, metabolism, and overall health. Over the past decade, advances in high-throughput sequencing, multi-omics technologies, and bioinformatics have significantly transformed our understanding of gut microbial communities across diverse animal taxa, including livestock, poultry, aquaculture species, companion animals, and wildlife. These studies have revealed that gut microbiota composition and function are shaped not only by host genetics and physiology but also by a wide range of environmental factors such as diet, climate, management practices, antibiotic exposure, and habitat conditions. Increasing evidence highlights the functional importance of the gut microbiome in nutrient utilization, immune modulation, disease resistance, growth performance, and stress adaptation, thereby influencing animal productivity and sustainability of animal production systems. Moreover, growing concerns regarding antimicrobial resistance and environmental degradation have intensified interest in microbiome-based interventions as eco-friendly alternatives to conventional practices. This review synthesizes recent advances in animal gut microbiome research, emphasizing microbial diversity, environmental interactions, and functional implications for animal health and performance. Current challenges, knowledge gaps, and emerging opportunities for microbiome manipulation within a One Health framework are also discussed, providing a comprehensive perspective on future directions in animal microbiome research.

Keywords

Animal gut microbiome; host–microbe interactions; environmental factors; multi-omics; animal health; One Health

1. Introduction

The gastrointestinal tract of animals harbors a vast and diverse community of microorganisms collectively referred to as the gut microbiome. This complex ecosystem comprises bacteria, archaea, fungi, protozoa, and viruses that coexist in close association with the host, forming a mutually influential biological system. The gut microbiome is now widely recognized as an integral component of animal biology rather than a passive inhabitant, contributing significantly to digestion, immune regulation, metabolic homeostasis, and protection against pathogens [1,2]. Across animal species, the gut microbiome plays a crucial role in shaping physiological functions and determining overall fitness, health, and productivity.

Historically, studies on gut microorganisms relied primarily on culture-based techniques, which provided limited insight due to the inability to culture a large fraction of gut microbes under laboratory conditions. The advent of culture-independent molecular approaches, particularly 16S rRNA gene sequencing and shotgun metagenomics, has revolutionized the field by enabling comprehensive profiling of microbial communities at unprecedented depth and resolution [3,4]. These approaches have revealed remarkable microbial diversity and functional specialization within animal gastrointestinal tracts, highlighting both conserved core microbiota and host-specific microbial signatures.

In animals, gut microbiome composition varies considerably depending on species, age, diet, gut anatomy, and environmental exposure. Ruminants such as cattle and sheep possess specialized microbial consortia capable of degrading complex plant polysaccharides, thereby enabling efficient conversion of fibrous feed into energy-rich metabolites such as volatile fatty acids [5]. In contrast, monogastric animals including poultry and swine host microbial communities that are more responsive to dietary composition and management practices [6]. Aquatic animals, such as fish and crustaceans, exhibit gut microbiomes that are strongly influenced by surrounding water microbiota, feed composition, and farming systems [7].

Environmental factors exert a profound influence on the structure and function of the animal gut microbiome. Diet is widely regarded as one of the most powerful modulators, capable of inducing rapid and reproducible shifts in microbial composition and metabolic output [8]. Additionally, exposure to antibiotics, pesticides, heavy metals, and other environmental contaminants can disrupt microbial balance, leading to dysbiosis and adverse health outcomes [9]. Climate-related stressors, including heat stress and altered feeding behavior, further complicate host–microbiome interactions, particularly in the context of global climate change [10].

Functionally, the gut microbiome contributes to a wide range of biological processes essential for animal health and productivity. Microbial fermentation enhances nutrient availability, synthesizes essential vitamins, and generates bioactive metabolites that influence host metabolism and immune function [11]. The gut microbiota also plays a critical role in the development and regulation of the host immune system, promoting immune tolerance while enhancing resistance to pathogens [12]. Emerging research has further linked gut microbes to neuroendocrine signaling pathways, implicating the microbiome in animal behavior, stress responses, and welfare [13].

Given its central role in animal biology, the gut microbiome has become a promising target for interventions aimed at improving animal health, productivity, and sustainability. Strategies such as dietary modulation, probiotic and prebiotic supplementation, and fecal microbiota transplantation are increasingly explored as alternatives to antibiotic growth promoters [14].

2. Composition of the Animal Gut Microbiome

The animal gut microbiome is a complex, multi-kingdom ecosystem composed of bacteria, archaea, fungi, protozoa, and viruses that collectively contribute to host physiology and metabolic potential. Although bacteria dominate numerically and functionally, non-bacterial members play critical and often underappreciated roles in shaping microbial community dynamics and host interactions [15].

2.1 Bacterial Communities

Bacteria constitute the most abundant and extensively studied component of the animal gut microbiome. Across most animal species, bacterial populations are primarily dominated by the phyla *Firmicutes* and *Bacteroidetes*, with additional contributions from *Proteobacteria*, *Actinobacteria*, *Verrucomicrobia*, and *Fusobacteria* [16]. The relative abundance of these phyla varies widely depending on host species, gut compartment, diet, and environmental conditions.

In ruminants, bacterial communities are highly specialized for lignocellulosic biomass degradation. Fibrolytic bacteria such as *Ruminococcus*, *Fibrobacter*, and *Butyrivibrio* play a key role in breaking down cellulose and hemicellulose, enabling the host to extract energy from plant-based diets [17]. In monogastric animals, including poultry and swine, bacterial communities are more dynamic and responsive to dietary changes, with *Lactobacillus*, *Clostridium*, *Bacteroides*, and *Prevotella* frequently reported as dominant genera [18]. In aquatic animals, gut bacterial composition is often shaped by surrounding water microbiota and feed, resulting in higher variability and a stronger influence of environmental bacteria [19].

2.2 Archaea

Although archaea represent a smaller fraction of the gut microbiome, they play a critical functional role, particularly in ruminants. Methanogenic archaea, such as members of the genus *Methanobrevibacter*, are responsible for hydrogen consumption and methane production during microbial fermentation [20]. By maintaining low hydrogen partial pressure, methanogens facilitate efficient microbial fermentation; however, methane emissions represent a significant environmental concern in livestock production.

In non-ruminant animals, archaeal populations are less abundant but still detectable, suggesting potential roles in hydrogen metabolism and microbial ecosystem stability [21]. Advances in metagenomics have improved the detection and characterization of gut-associated archaea, revealing greater diversity than previously recognized.

2.3 Fungi and Protozoa

Gut-associated fungi, collectively referred to as the mycobiome, contribute to fiber degradation, secondary metabolite production, and microbial interactions. In ruminants, anaerobic fungi belonging to the phylum *Neocallimastigomycota* are particularly important for the initial colonization and degradation of plant material [22]. These fungi produce powerful cellulolytic and hemicellulolytic enzymes that enhance feed digestion and nutrient availability.

Protozoa are another significant component of the ruminant gut microbiome, accounting for a substantial proportion of microbial biomass. Protozoa contribute to starch fermentation, bacterial predation, and nitrogen recycling, but they are also associated with increased methane production due to their symbiotic relationship with methanogens [23]. In monogastric and aquatic animals, protozoa and fungi are less abundant but may still influence microbial community structure and immune interactions.

2.4 Viruses and Bacteriophages

Viruses, particularly bacteriophages, represent a highly abundant yet understudied component of the gut microbiome. Phages influence bacterial population dynamics through predation, horizontal gene transfer, and modulation of microbial metabolism [24]. Emerging evidence suggests that phages contribute to microbiome stability and resilience, potentially acting as regulators of dysbiosis during environmental or dietary perturbations [25].

Animal gut viromes are highly diverse and host-specific, with significant implications for microbial evolution and ecosystem function. However, methodological challenges in viral detection and annotation continue to limit comprehensive understanding of gut viral communities.

2.5 Host-Specific and Developmental Patterns

Gut microbiome composition is strongly influenced by host species, genetics, and developmental stage. Early-life microbial colonization plays a crucial role in shaping immune system development and long-term health outcomes [26]. In many animals, microbial diversity increases with age and stabilizes upon dietary transition from milk to solid feed, although environmental exposure and management practices can induce long-term alterations [27]. Collectively, these findings highlight that the animal gut microbiome is a highly structured yet dynamic ecosystem, shaped by complex interactions among microbial taxa, host physiology, and environmental factors.

Table 1. Comparative overview of dominant gut microbial taxa and functional characteristics across major animal categories.

Animal Type	Dominant Bacterial Phyla	Key Functional Role	Notable Features
Ruminants	Firmicutes, Bacteroidetes	Fiber degradation, VFA production	Methanogens abundant
Poultry	Firmicutes, Proteobacteria	Nutrient absorption, pathogen resistance	Highly diet-responsive
Swine	Firmicutes, Bacteroidetes	SCFA production, gut integrity	Sensitive to antibiotics
Aquaculture species	Proteobacteria, Fusobacteria	Environmental adaptation	Influenced by water microbiota
Wildlife	Diverse taxa	Ecological adaptation	High biodiversity

3. Recent Advances in Animal Gut Microbiome Research

Recent technological innovations have fundamentally transformed animal gut microbiome research, enabling unprecedented insights into microbial diversity, functional potential, and host–microbe interactions. The integration of high-throughput sequencing, advanced bioinformatics, and multi-omics approaches has shifted the field from descriptive community profiling to functional and mechanistic understanding [28].

3.1 High-Throughput Sequencing Technologies

The widespread adoption of next-generation sequencing (NGS) platforms has revolutionized microbiome research. Amplicon-based sequencing of marker genes, such as the bacterial 16S rRNA gene, remains a cost-effective approach for characterizing microbial community structure and diversity across large sample sets [29]. However, limitations in taxonomic resolution and functional inference have prompted increased use of shotgun metagenomic sequencing.

Shotgun metagenomics enables comprehensive analysis of microbial genomes present within a sample, providing insights into metabolic pathways, antimicrobial resistance genes, and virulence factors [30]. In animal studies, metagenomics has been instrumental in identifying functional adaptations of gut microbes to specific diets, environments, and production systems.

3.2 Metatranscriptomics, Metaproteomics, and Metabolomics

Beyond metagenomics, functional omics approaches have further expanded understanding of active microbial processes. Metatranscriptomics captures gene expression profiles of gut microbes, revealing how microbial activity responds dynamically to dietary changes, stress, and disease [31]. Metaproteomics provides direct evidence of protein production and enzymatic activity, while metabolomics characterizes microbial-derived metabolites that mediate host–microbe interactions [32].

The integration of these approaches has revealed that microbial functional activity does not always correlate directly with taxonomic abundance, underscoring the importance of functional rather than purely compositional analyses.

3.3 Culturomics and Single-Cell Approaches

Despite advances in sequencing, cultivation of gut microbes remains essential for functional validation and mechanistic studies. Culturomics, which employs diverse culture conditions and high-throughput identification techniques, has led to the isolation of numerous previously uncultured gut microbes [33]. Single-cell genomics further complements these efforts by enabling genome reconstruction from individual microbial cells, providing insights into rare or low-abundance taxa [34].

3.4 Computational and Systems Biology Approaches

Advances in bioinformatics, machine learning, and systems biology have enhanced the analysis and interpretation of complex microbiome datasets. Predictive models linking microbial composition to host phenotypes are increasingly applied in animal production and health management [35]. These computational approaches facilitate the identification of microbial biomarkers and functional signatures associated with performance, disease resistance, and environmental adaptation.

4. Environmental Interactions and Modulators of the Animal Gut Microbiome

The structure and function of the animal gut microbiome are highly sensitive to environmental influences. Unlike host genetic factors, which remain relatively stable, environmental modulators can induce rapid and sometimes persistent changes in microbial composition and metabolic activity. Understanding these interactions is essential for interpreting microbiome variability and for designing effective microbiome-based interventions [36].

4.1 Diet and Nutrition

Diet is widely regarded as the most influential environmental factor shaping the animal gut microbiome. The quantity, quality, and chemical composition of feed directly determine substrate availability for microbial growth, thereby influencing microbial diversity and functional output [37]. In herbivorous animals, diets rich in structural carbohydrates promote the proliferation of fibrolytic microbes capable of degrading cellulose, hemicellulose, and lignin, whereas high-concentrate diets favor amylolytic and saccharolytic bacteria [38].

In ruminants, dietary shifts from forage-based to grain-rich diets can rapidly alter rumen microbial communities, often reducing microbial diversity and increasing the risk of metabolic disorders such as acidosis [39]. In monogastric animals, including poultry and swine, dietary protein levels, fat composition, and fiber content significantly influence gut microbial balance, short-chain fatty acid (SCFA) production, and gut integrity [40]. Aquatic animals exhibit particularly strong diet–microbiome interactions, as formulated feeds often replace natural diets in intensive aquaculture systems, leading to pronounced shifts in microbial composition and function [41].

Micronutrients and feed additives, such as minerals, vitamins, and plant-derived bioactive compounds, further modulate gut microbial communities. Phytochemicals, including polyphenols and essential oils, have been shown to selectively inhibit pathogenic bacteria while promoting beneficial taxa, offering potential alternatives to antibiotic growth promoters [42].

4.2 Antibiotics, Xenobiotics, and Environmental Pollutants

Antibiotic exposure remains one of the most disruptive environmental factors affecting the animal gut microbiome. While antibiotics are widely used for disease treatment and prevention, their non-selective activity often leads to reduced microbial diversity, altered metabolic functions, and the emergence of antimicrobial resistance genes within the gut microbiome [43]. Early-life antibiotic exposure is of particular concern, as it can permanently alter microbial colonization patterns and immune development [44].

Beyond antibiotics, animals are increasingly exposed to a wide range of xenobiotics, including pesticides, heavy metals, plasticizers, and industrial contaminants. These compounds can directly affect microbial viability or indirectly influence microbial communities by altering host physiology [45]. Heavy metals such as cadmium, lead, and arsenic have been shown to reduce beneficial microbial populations while enriching metal-resistant and potentially pathogenic taxa [46].

The gut microbiome also plays a dual role in xenobiotic metabolism, as microbes can both detoxify and bioactivate environmental contaminants. This bidirectional interaction highlights the importance of considering microbiome-mediated effects when assessing environmental toxicity in animals [47].

4.3 Climate Change and Environmental Stress

Climate change poses emerging challenges to animal gut microbiome stability through altered temperature regimes, water availability, and feed resources. Heat stress, in particular, has been shown to disrupt gut microbial balance, reduce microbial diversity, and impair intestinal barrier function in livestock and poultry [48]. These changes are often associated with reduced feed intake, altered metabolism, and increased susceptibility to disease.

In aquatic systems, rising water temperatures and changing salinity levels influence both host-associated and environmental microbiota, leading to shifts in gut microbial composition and increased prevalence of opportunistic pathogens [49]. Seasonal variations in temperature and feed availability further contribute to temporal fluctuations in gut microbiome structure, particularly in extensive and pasture-based production systems [50].

4.4 Farming Systems, Management Practices, and Habitat

Animal management practices strongly influence gut microbiome composition through differences in housing, hygiene, stocking density, and exposure to environmental microbes. Intensive farming systems often reduce microbial diversity due to controlled diets, limited environmental exposure, and frequent antimicrobial use [51]. In contrast, animals raised in extensive or pasture-based systems typically harbor more diverse gut microbiomes, which may enhance resilience against pathogens and environmental stressors [52].

In wildlife and free-ranging animals, habitat characteristics and ecological interactions play a dominant role in shaping gut microbiomes. Studies have demonstrated strong associations between habitat disturbance, dietary diversity, and gut microbial composition, emphasizing the role of environmental biodiversity in maintaining microbial ecosystem health [53].

5. Functional Implications of the Animal Gut Microbiome

Beyond taxonomic composition, the functional capacity of the gut microbiome is central to its influence on animal health and performance. Gut microbes collectively encode a vast array of metabolic pathways that complement host physiology and enable animals to exploit diverse ecological niches [54].

5.1 Digestion and Nutrient Metabolism

One of the primary functions of the gut microbiome is the fermentation of dietary components that are otherwise indigestible by host enzymes. Microbial fermentation of complex carbohydrates produces SCFAs such as acetate, propionate, and butyrate, which serve as major energy sources for intestinal epithelial cells and peripheral tissues [55]. In ruminants, microbial fermentation in the rumen supplies up to 70% of the host's energy requirements, highlighting the essential role of gut microbes in feed efficiency [56].

Gut microbes also contribute to nitrogen metabolism through protein degradation, amino acid synthesis, and urea recycling. Microbial synthesis of essential vitamins, including B vitamins and vitamin K, further supports host nutritional status [57].

5.2 Immune Modulation and Disease Resistance

The gut microbiome plays a critical role in shaping both innate and adaptive immune responses. Commensal microbes stimulate the development of gut-associated lymphoid tissue and promote immune tolerance toward beneficial microorganisms while enhancing defense against pathogens [58]. Microbial-derived metabolites, particularly SCFAs, modulate inflammatory responses and strengthen intestinal barrier integrity [59].

Disruptions to gut microbial balance, commonly referred to as dysbiosis, have been linked to increased susceptibility to infectious diseases, inflammatory disorders, and metabolic dysfunctions across animal species [60]. Consequently, maintaining a balanced gut microbiome is essential for disease prevention and overall health.

5. Functional Implications of the Animal Gut Microbiome

5.3 Growth Performance, Productivity, and Reproduction

The gut microbiome exerts a strong influence on animal growth, feed efficiency, and overall productivity by regulating nutrient utilization, metabolic signaling, and immune competence. Numerous studies in livestock and poultry have demonstrated clear associations between gut microbial composition and feed conversion efficiency, weight gain, and carcass quality [61]. Animals with a higher abundance of SCFA-producing bacteria often exhibit improved energy harvest and growth performance.

In ruminants, microbial efficiency within the rumen directly affects milk yield, milk composition, and methane emissions [62]. Selective enrichment of propionate-producing bacteria has been linked to improved feed efficiency and reduced energy loss as methane [63]. In poultry, balanced gut microbiota enhance nutrient absorption, gut morphology, and resistance to enteric pathogens, thereby improving growth rates and production efficiency [64].

The gut microbiome also plays an emerging role in animal reproduction. Microbial metabolites influence hormonal regulation, energy balance, and inflammatory status, all of which are critical determinants of reproductive success [65]. Dysbiosis has been associated with reduced fertility, impaired embryonic development, and increased incidence of reproductive disorders in several animal species [66].

5.4 Gut–Brain Axis and Animal Behavior

Recent research has expanded the functional relevance of the gut microbiome beyond digestion and immunity to include neuroendocrine signaling via the gut–brain axis. Microbial metabolites such as SCFAs, neurotransmitter precursors, and bile acids influence neural pathways, stress responses, and behavior [67]. In animals, gut microbiota have been implicated in modulating stress tolerance, social behavior, and cognitive functions.

In livestock, stress-induced alterations in gut microbiota are associated with reduced productivity and compromised welfare [68]. In aquatic animals, microbiome-mediated neurochemical signaling has been linked to feeding behavior and stress adaptation [69].

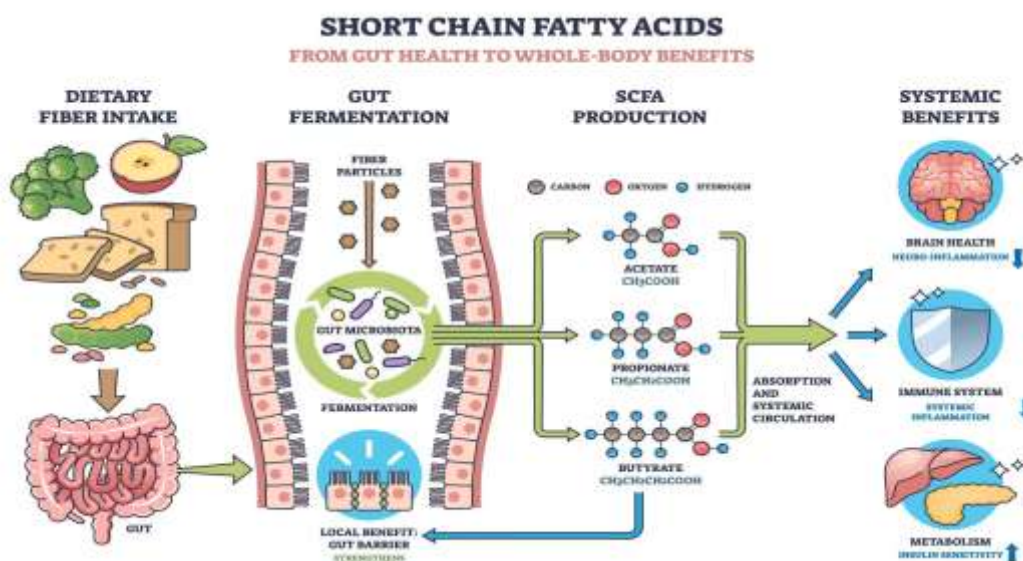


Figure 1. Functional Implications of the Gut Microbiome

6. Microbiome Manipulation Strategies

Growing recognition of the gut microbiome's functional importance has stimulated the development of strategies to manipulate microbial communities for improved animal health and sustainability.

6.1 Probiotics, Prebiotics, and Synbiotics

Probiotics—live beneficial microorganisms administered through feed or water—are among the most widely applied microbiome-based interventions. They enhance gut microbial balance, inhibit pathogens, and improve immune function [70]. Prebiotics, non-digestible feed components that selectively stimulate beneficial microbes, and synbiotics, which combine probiotics and prebiotics, further enhance microbial stability and functional output [71].

These approaches are increasingly promoted as alternatives to antibiotic growth promoters, particularly in the context of antimicrobial resistance mitigation.

6.2 Fecal Microbiota Transplantation and Precision Nutrition

Fecal microbiota transplantation (FMT) has shown promise in restoring microbial balance in diseased or dysbiotic animals, although its application in animal production systems remains limited due to regulatory and logistical challenges [72]. Advances in precision nutrition aim to tailor diets based on individual or population-level microbiome profiles, optimizing microbial functionality and host performance.

7. Challenges and Knowledge Gaps

Despite rapid progress, several challenges limit the translation of gut microbiome research into practical applications. These include high inter-individual variability, limited functional validation of microbial taxa, methodological inconsistencies, and insufficient long-term studies. Additionally, ethical, regulatory, and biosafety considerations must be addressed before widespread adoption of microbiome-based interventions.

8. Future Perspectives

Future research is expected to focus on integrative multi-omics approaches, longitudinal studies, and mechanistic investigations linking microbial functions to host phenotypes. The One Health framework emphasizes the interconnectedness of animal, human, and environmental health, positioning the animal gut microbiome as a critical nexus for sustainable development. Harnessing microbial ecosystems offers transformative potential for improving animal welfare, reducing environmental impacts, and enhancing food security.

9. Conclusions

The animal gut microbiome is a dynamic and multifunctional ecosystem that profoundly influences host nutrition, immunity, metabolism, behavior, and productivity. Advances in sequencing technologies and systems biology have expanded understanding from descriptive microbial catalogs to functional and ecological insights. Environmental factors such as diet, antibiotics, climate, and management practices act as major drivers of microbial composition and activity. By integrating microbiome science into animal health and production systems, sustainable and environmentally responsible solutions can be developed. Continued interdisciplinary research will be essential to unlock the full potential of the animal gut microbiome within a global One Health framework.

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