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Editorial

UNRAVELLING THE GUT MICROBIOME: FOUNDATIONS AND FRONTIERS IN ANIMAL HEALTH AND PRODUCTIVITY

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The microbiome comprises a complex community of bacteria, archaea, viruses, and eukaryotic microbes that inhabit both the internal and external surfaces of animal bodies. These microbial populations exert profound influences on animal health and disease, facilitating metabolic processes, pathogen defence, immune system modulation, and a variety of other physiological functions. Consequently, their collective impact is integral to virtually all aspects of host biology.

The gut microbiota, in particular, is a dynamic assemblage of bacteria, archaea, and eukaryotes residing within the gastrointestinal tract. Over millennia, these microorganisms have coevolved with their hosts, establishing intricate, and mutually beneficial relationships. Given the vast number of microbial cells present, the host and its resident microbes are often conceptualized as a superorganism. The gut microbiota confers numerous physiological benefits, including the maintenance of gut integrity, modulation of the intestinal epithelium, energy generation, protection against pathogens, and regulation of host immunity. However, disturbances in microbial composition, collectively referred to as dysbiosis, may compromise these critical functions. Advancements in high-throughput genomic profiling and ecosystem characterisation have highlighted the microbiota's crucial roles in a wide range of gut-related pathological conditions. The prevailing comprehension of gastrointestinal microbiota formation and composition underscores its impact on gut integrity and host health.

In livestock, the gastrointestinal microbiota is central to gut development, feed digestion and utilization, and immune responses. Patterns of microbial colonisation in early life have lasting impacts, determining the composition and functional capabilities of the microbiota and ultimately affecting host phenotypes. The gut microbiota itself is a highly diverse community, encompassing bacteria, archaea, fungi, protozoa, and viruses. The broader concept of the gut microbiome includes not only these living microorganisms but also plasmids, dead cells, extracellular DNA, and various macromolecular structures such as proteins and polysaccharides. This diversity reflects the evolutionary adaptation of the host-microbe consortium to dietary habits and environmental pressures.

While the gut microbiota is predominantly composed of bacteria, the other microbial constituents including bacteriophages and fungi play essential roles in maintaining ecosystem stability. Bacteriophages or phages, are abundant in the gastrointestinal tract and are instrumental in shaping bacterial communities through predation and horizontal gene transfer. These phage-bacteria interactions influence microbial diversity, antimicrobial resistance, and metabolic functions. In livestock, phages are increasingly viewed as potential tools for microbiota engineering. Fungi, although less prevalent, are particularly important in ruminants, where anaerobic genera such as Piromyces and Neocallimastix facilitate the breakdown of recalcitrant plant fibres by producing potent hydrolytic enzymes. These fungi interact synergistically with fibrolytic bacteria and methanogenic archaea, enhancing lignocellulose degradation in the rumen. In monogastric animals, commensal fungi such as Candida and Saccharomyces are common, though dysbiosis lead to health disorders. Further, it is vital to recognize the interdependence among bacteria, phages, and fungi in shaping microbial ecosystems in livestock. Future research integrating multi-kingdom microbial interactions will advance our understanding of microbiota function and its implications for animal health and productivity.

The composition of gut microbial communities is influenced by several environmental and physiological factors that differ across the gastrointestinal tract. The key determinants include pH, osmolarity, nutrient availability, oxygen concentration, and feed retention time, each influencing microbial selection and

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colonization. For example, the rumen's neutral pH favours fibre-degrading bacteria such as *Fibrobacter* and *Ruminococcus*. In contrast, the acidic environment of the monogastric stomach supports acid-resistant species like *Lactobacillus* and *Streptococcus*. Dietary composition and water intake influence gut osmolarity, with high-starch diets promoting amylolytic bacteria such as *Prevotella*. The retention time of digesta is extended in ruminants and reduced in monogastrics, influencing microbial fermentation and nutrient absorption. Despite the gut being predominantly anaerobic, microaerophilic niches are present too, allowing facultative anaerobes like *Escherichia coli* to flourish, especially in reaction to host metabolic changes. These factors jointly promote niche specialisation and interspecies variations in microbiota composition, underscoring the complex interaction between host physiology and microbial ecology.

In recent years, the core gut microbiome has evolved from a novel concept to a central focus of biomedical research, with an exponential increase in the scientific literature on the gut microbiome in the past two decades. Although the microbiome is highly personalised, the term "core" denotes a shared set of microbial taxa, genes, or functional capabilities that are present in the vast majority of healthy individuals. The core gut microbiome in livestock consists of a stable consortium of bacteria, archaea, fungi, and protozoa shared among individuals of the same species, irrespective of diet or environment. This core community is essential for health, nutrient assimilation, and immune function, and is central to production parameters such as growth and milk yield via the breakdown of fibre and synthesis of volatile fatty acids. Core taxa also produce essential metabolites, including amino acids and vitamins, and encode key fibre-degrading enzymes critical for host nutrition. Through cross-feeding networks, core microorganisms support the broader microbial community, underpinning ecosystem stability. Manipulating these core microbial groups holds potential to enhance microbiome function and ruminant metabolism, with far-reaching implications for food security and environmental sustainability.

Identifying and characterizing the core gut microbiota established in early life represents a promising avenue for improving animal health and productivity, though significant conceptual and methodological challenges remain. Advances in multi-omics technologies, high-resolution sequencing, and artificial intelligence have opened new opportunities to elucidate microbial communities that drive growth efficiency, immune maturation, and disease resilience. However, distinguishing true "core" taxa from transient or environment-specific populations demands rigorous longitudinal and cross-cohort studies utilizing standardized sampling and analytical methods. Moreover, mechanistic insights linking microbial composition and function to host physiology and long-term performance require integrative approaches bridging microbiology, animal genetics, and nutritional sciences. The principal challenge moving forward lies in translating these insights into sustainable, microbiome-informed strategies that enhance animal production while mitigating environmental impact.

In conclusion, as our understanding evolves, it is clear that in livestock, the gut microbiome represents a highly complex and dynamic consortium of microorganisms that profoundly influence health, metabolism, immunity, and disease resistance. The gut microbiota, in particular, forms intricate and co-evolved relationships with its host, playing a pivotal role in maintaining gut integrity and overall physiological balance, and production performances. Disruptions in microbial composition, or dysbiosis, can compromise these essential functions. The gut microbiota, comprising bacteria, archaea, fungi, protozoa, and viruses, contributes to digestion, immune development, and nutrient assimilation, with its composition shaped by species, diet, and environmental factors. Ensuring the stability of the core gut microbiome is fundamental for optimal health, growth, and productivity in livestock. Advancing our understanding and management of these microbial communities offers promising avenues for enhancing animal performance and sustainability, while simultaneously addressing the intricate challenges associated with host–microbe interactions.

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