Journal of Animal Science and Veterinary Medicine
Volume 11(3), pages 208-218, June 2026
Article Number: FA0DBE118
ISSN: 2536-7099
https://doi.org/10.31248/JASVM2026.670
https://integrityresjournals.org/journal/JASVM

Review Article

Integrating host genomics and the gut microbiome in livestock breeding: Toward a holobiont-based selection paradigm. A review

Udoh, J. E[1]., Inyang, I. U[2]., Isaac, L. J[1] and Etukudo, O. M[1]*

[1]Department of Animal Science, University of Uyo, Akwa Ibom State, Nigeria.
[2]Department of Animal Science, Akwa Ibom State University, Obio Akpa Campus.

*Corresponding author. Email: owoidiheetukudo@uniuyo.edu.ng; Tel: +2348132080471.

Received Date: 29 May 2026 | Accepted Date: 25 June 2026 | Published Date: 30 June 2026

ABSTRACT: There is an increasing need to boost livestock efficiency and sustainability as well as the ability to cope while meeting global protein demands. Genomic selection has made significant genetic gains but has been able to explain only a portion of the phenotype in complex characters such as feed efficiency, growth rates, methane emissions, and resistance to diseases. Recent studies have shown that the microbiome plays a crucial role in modulating the host metabolism and other processes including immune regulation. The microbiome is involved in nutrient breakdown, the production of short-chain fatty acids, vitamin formation, and immune regulation, making the host use it like an "organ." This resulted in the introduction of the holobiont idea, which regards the host organism and its associated microbiota as a single biological entity (hologenome). The selection strategy was thereby transformed from one focused solely on the host to a more holistic approach centered around the entire system. Incorporating information from the microbiome into host genomics via multi-omics, metagenomics, and artificial intelligence improves the precision of predicting complex traits and discovers new biomarkers for productivity and efficiency in the environment. However, obstacles persist, including high levels of microbiome diversity, non-standardization, insufficient causal knowledge, and technical difficulties. Nevertheless, combining the study of host genomics and gut microbiomes presents an innovative avenue for improving livestock.

Keywords: Metagenomics, genomic prediction, host-microbe interactions, quantitative genetics, precision agriculture, functional traits, sustainable production.

INTRODUCTION

The livestock industry has become faced with the task of producing more animal proteins to meet the demands of the growing population, with sustainability, efficiency, and resilience being at the heart of their operations. In conventional breeding practices, the most common method has been on host genomic selection, which involves the use of molecular markers spread throughout the whole genome to estimate the breeding value for economically important traits. While the technique has shown great genetic improvements, it has not been able to provide an explanation for the phenotypic variance for complex traits like feed efficiency, disease resistance, and metabolic efficiency (Cammack *et al*., 2018).

The emergence of high-throughput sequencing technology and advancements in microbial ecology has brought forth the knowledge that the guts of livestock animals contain complex microbiomes that contribute immensely in areas such as digestion, metabolic processing, immune regulation, and well-being (Wei *et al*., 2025). These microbiomes aid in the decomposition of nutrients from feed that would otherwise remain undigested and produce certain metabolites like short-chain fatty acids, which affect the well-being of the host animal (Tardiolo *et al*., 2025). There is increasing evidence showing that variations in the microbiome are directly linked with economically valuable traits like body size and productivity (Tian *et al*., 2024).

It is crucial to highlight that apart from being affected by the environment like diet and management, the gut microbiome partially depends on host genetics. There are numerous studies conducted in various livestock species, including pigs, cows, and birds, that show a substantial impact of host genotypes on the structure and functioning of the gut microbiome (Liufu *et al*., 2024). The heritability estimates of specific taxa of microorganisms and their derived characteristics, though being rather low or medium, indicate that these characteristics can be improved through selection (Cammack *et al*., 2018). The interaction between genetics and the microbiome of the host is involved in various processes like heterosis and adaptation (Huang *et al*., 2024).

It is based on such knowledge that the concept of the holobiont has evolved. The hologenome, comprising the genome of the host and all of its associated microbiomes, has the effect of affecting phenotypic outcomes. Such a framework goes against the conventional host-centric approach that has been employed in livestock production, since it proposes that both the genetic makeup of the host and the microbiome should be considered during selection processes (Martinez-Boggio *et al*., 2024).

The integration of host genomics with gut microbiome genomics provides an exciting opportunity to enhance the precision of genetic evaluation and selection. Indeed, research conducted by Tian *et al*. (2024) has demonstrated the potential of integrating microbiome genomic data within the process of genome-based complex trait prediction for traits such as feed efficiency and growth. In addition, metagenomic and metabolomic analysis of the microbes present in the gut could provide a means of identifying novel biomarkers of animal efficiency, productivity, and environmental performance such as methane production.

However, despite all these achievements, there are still quite a few issues related to using such a strategy of breeding. First of all, the composition of the gut microbiome depends on many different factors, among which the most significant include diet, age, environmental conditions, and management (Tardiolo *et al*., 2025). Secondly, it should be noted that it is rather complicated to compare results obtained by various researchers because of the lack of standards for procedures, bioinformatic pipelines, and models.

As a result, the integration of host genomics and studies on gut microbiota is a revolutionary trend in selecting livestock towards the development of a holobiont selection system. Indeed, taking into account host and its microbial community as one entity will help to have a deeper insight into the factors determining the performance of animals. In this way, there are good chances that this approach will become very helpful in increasing livestock productivity and sustainability.

METHODOLOGY

A systematic review methodology using a narrative approach was employed in reviewing the current literature on the relationship between the genomics of hosts and gut microbiota research in animal breeding, with special focus on the formulation of a holobiont-based selection strategy. Articles were sourced from prominent databases such as PubMed, Scopus, Web of Science, and Google Scholar. Articles ranging from 2010 to 2025 were considered in the review, with priority given to recent advancements in genomic selection and microbiome studies.

A set of key terms such as “host genomics,” “gut microbiome,” “breeding of livestock,” “genomic selection,” “holobiont,” “hologenome,” and “metagenomics” were employed using Boolean logic (AND and OR). Studies were considered for inclusion if they were peer reviewed, had a focus on livestock animals (cattle, pigs, sheep, goats, and poultry), and involved host genomics, gut microbiome, or both in association with their performance or breeding or health issues. Those studies that failed to provide a clear methodology, were only conference proceedings without data, not written in English, or unrelated to livestock were excluded.

The articles that were identified underwent screening through titles and abstracts, with subsequent full-text assessment of eligibility. Screening resulted in the elimination of duplicate articles. Data from the eligible articles were then collected using an extraction form that considered author details, date of publication, type of animal involved, methodology used (genetics wide association study, metagenomics, sequencing of 16S rRNA gene), and other key results and implications for livestock breeding.

Qualitative analysis through thematic analysis was applied to the generated data considering the diversity of methods and design used in the selected articles. The data findings were structured according to different themes including host genotype selection, microbiome functions, host-microbiome interaction, integration of omics, and breeding approaches based on holobiont.

Based on the findings that were identified through the synthesis process, a conceptual model was formulated to demonstrate the interplay between host genome and gut microbiome and the impacts of both factors in terms of growth, immune response, feed utilization, and production capabilities. The quality of selected studies was taken into account through methodological considerations, sample sizes, use of next-generation sequencing techniques, and statistical strength.

BIOLOGY OF HOST–MICROBIOME INTERACTIONS

Host-microbe relationships refer to the interaction dynamics between a multicellular organism and microorganisms like bacteria, archaea, fungi, protozoa,

Table 1. Biology of host–microbiome interactions and functional roles in livestock systems.

Biological component	Function in host–microbiome system	Mechanism of Action	Livestock outcome/significance	References
Gut microbial community	Extends host metabolic capacity	Fermentation of dietary fibers into short-chain fatty acids (SCFAs) such as acetate, propionate, and butyrate	Improves energy yield, feed efficiency, and gut health	Berg *et al*. (2020); Krautkramer *et al*. (2021)
Microbial metabolites	Act as signaling molecules	SCFAs and other metabolites regulate host gene expression and epigenetic modifications	Influences growth, fat deposition, and immune responses	Wei *et al*. (2025); Han *et al*. (2026)
Host immune system	Controls microbial colonization	Pattern recognition receptors (e.g., Toll-like receptors) mediate microbial recognition and immune tolerance	Maintains gut microbial balance and disease resistance	Chen *et al*. (2024); Zhang *et al*. (2024)
Host genetics	Shapes microbiome composition	Genetic regulation of gut environment (mucus layer, antimicrobial peptides, gut pH)	Determines microbial diversity and stability across individuals	Rothschild *et al*. (2018); Zhang *et al*. (2024)
Microbial vitamin synthesis	Provides essential micronutrients	Biosynthesis of B-complex vitamins and vitamin K by gut microbes	Supports metabolism, growth, and enzymatic functions	Oke *et al*. (2025); Han *et al*. (2026)
Microbial fermentation system	Converts indigestible feed components	Anaerobic breakdown of cellulose and hemicellulose in rumen/gut	Enhances utilization of fibrous feeds in Ruminants	Berg *et al*. (2020); Ortiz-Chura *et al*. (2025)
Holobiont interaction system	Integrated host–microbe functioning	Host and microbiome function as a combined biological unit (hologenome concept)	Basis for microbiome-informed breeding and selection strategies	Bordenstein & Theis (2015); Cammack *et al*. (2018)

and viruses inhabiting the body. Host-microbe interactions in livestock animals are most evident in the gut microbiota, which is characterized by high microbial density and metabolism (Rothschild *et al*., 2018; Han *et al*., 2026). The major biological components underlying host–microbiome interactions in livestock systems are summarized in Table 1.

Functionally, the gut microbiome increases the metabolic capability of the host through its ability to produce enzymes not encoded in the host genome. The gut microbiome breaks down complex polysaccharides, ferments dietary fibers, synthesizes important vitamins (such as B-complex vitamins), and produces short-chain fatty acids (SCFAs) like acetate, propionate, and butyrate. SCFAs provide energy and act as signaling molecules that affect host metabolism and immune development and protect the intestines (Berg *et al*., 2020; Oke *et al*., 2025). In ruminant animals, gut microbiomes are crucial in breaking down fibrous feeds into digestible forms, thus affecting feed utilization and growth (Ortiz-Chura *et al*., 2025).

On the other hand, the host contributes significantly to microbial composition through genetic, physiological, and immunological approaches. The influence of the host genome on the environment of the host gut in terms of the nature of mucus layer, tight junctions' properties, antimicrobial peptide production, and expression of immune receptors will determine colonization and stabilization of microbes (Zhang *et al*., 2024). Immune-related genes such as those encoding pattern recognition receptors including toll-like receptors contribute immensely to microbial colonization and tolerance, hence affecting the composition of the microbiome (Chen *et al*., 2024).

There is a considerable level of bidirectionality in this relationship, especially when considering the contribution of microbial metabolites towards regulation of host genes. SCFAs serve as epigenetic modifiers by influencing DNA and histone acetylation status, leading to alterations in transcriptional activity in both metabolic and immune-related pathway s (Krautkramer *et al*., 2021). These interactions influence host traits such as growth rate, feed efficiency, and metabolic efficiency**.**

For livestock animals, studies have demonstrated that the microbiome composition impacts economically valuable traits such as methane production in cattle, feed efficiency ratio in pigs, and growth performance in chickens (Huang *et al*., 2024; Martinez-Boggio *et al*., 2024). Notably, both host genetics and the microbiome play a role in shaping the phenotypic variations, as the presence of heritability has been confirmed for particular taxa and functions related to the microbiome (Cammack *et al*., 2018), thus allowing the inference that the microbiome composition is genetically regulated.

Table 2. Heritability of microbiome traits and their implications in livestock.

Microbiome trait	Estimated heritability range (h^2)	Host genetic influence	Environmental influence	Livestock relevance	References
Individual bacterial taxa abundance	0.05 – 0.30	Low to moderate genetic control	High (diet, housing, antibiotics)	Influences gut microbial composition and stability	Cammack *et al*. (2018); Rothschild *et al*. (2018)
Microbial functional pathways (e.g., carbohydrate metabolism)	0.15 – 0.40	Moderate genetic influence	Moderate	Affects feed efficiency and nutrient utilization	Zhang *et al*. (2024); Han *et al*. (2026)
Short-chain fatty acid (SCFA) production	0.20 – 0.45	Moderate genetic regulation via host–microbe interaction	Moderate (diet-dependent)	Energy metabolism, growth performance, gut health	Cammack *et al*. (2018); Krautkramer *et al*. (2021)
Methane-producing microbial activity (ruminants)	0.10 – 0.35	Genetic influence through rumen environment	High (feed type, management)	Environmental impact and feed efficiency	Cammack *et al*. (2018); Ortiz-Chura *et al*. (2025)
Immune-associated microbial composition	0.15 – 0.35	Moderate through immune gene variation	Moderate to High	Disease resistance and immune development	Chen *et al*. (2024); Zhang *et al*. (2024)
Overall microbiome diversity index	0.10 – 0.25	Low to moderate	High	Indicator of gut stability and resilience	Rothschild *et al*. (2018); Han *et al*., 2026
Vertical microbial transmission (parent–offspring)	Variable (0.10 – 0.30)	Moderate genetic and maternal effects	Moderate	Early-life microbiome establishment	Cammack *et al*. (2018); Martinez-Boggio *et al*. (2024)

The above evidence reinforces the holobiont idea according to which the host and its microbiome are considered one biological entity. Specifically, the phenotype is determined by the combined action of the genes of the host and its microbes, together called the hologenome (Bordenstein and Theis, 2015). This paradigm transforms the livestock biology perspective towards considering host-microbe interactions rather than only host genetics when explaining the emergence of particular traits.

In summary, host–microbiome interactions can be regarded as a fundamental biological system integrating genetics, immunity, metabolism, and adaptation, which offers scientific evidence-based rationale for improving livestock via genomics and microbiomes (Wei *et al*., 2025; Han *et al*., 2026).

HERITABILITY OF MICROBIOME TRAITS

Heritability of microbiota features implies the share of variations in microorganism population composition or abundance caused by genetic characteristics rather than by environmental components. In agricultural applications, heritability of the gut microbiota is essential to reveal whether it is possible to include microbial features in the breeding program as they can change accordingly. The heritability estimates of key microbiome traits in livestock species are summarized in Table 2, highlighting the relative contributions of host genetics and environmental factors.

Research carried out on cattle, pigs, and poultry has proved that despite considerable impact of external factors like feeding, environment, and husbandry conditions, a significant part of the gut microbiota depends on genetics. Heritability of individual microorganisms appears to be medium to low, while it reaches higher values for some functional microbial pathways and metabolites (Cammack *et al*., 2018; Zhang *et al*., 2024).

The impact of host genetics on microbiome composition is mediated by physiological factors, including immune system control, gut development, mucin production, and the synthesis of antimicrobial peptides. Such features provide a selection pressure that promotes or discourages certain microbes within the ecosystem. For instance, variants of immune-associated genes will change the ability to recognize and tolerate different microbes, thus influencing their structure (Chen *et al*., 2024).

Table 3. Influence of gut microbiome on economically important traits in livestock.

Economically important trait	Microbiome mechanism involved	Microbial groups/functions	Effect on livestock performance	References
Feed efficiency	Fermentation of dietary fiber into short-chain fatty acids (SCFAs)	Fibrolytic bacteria (e.g., *Ruminococcus*, *Fibrobacter*)	Improved nutrient extraction, reduced feed cost, better conversion ratio	Han *et al*. (2026); Ortiz-Chura *et al*. (2025)
Growth performance	Regulation of energy metabolism and host gene expression	SCFA-producing microbes; bile acid-transforming bacteria	Enhanced weight gain, muscle development, and feed utilization	Krautkramer *et al*. (2021); Han *et al*. (2026)
Immune response and disease resistance	Immune modulation through gut barrier integrity and immune signaling	Commensal bacteria interacting with Toll-like receptors	Reduced infection risk, improved vaccine response	Chen *et al*. (2024); Zhang *et al*. (2024)
Methane missions (ruminants)	Hydrogen utilization and methanogenesis in rumen	Methanogenic archaea (e.g., *Methanobrevibacter*)	Reduced greenhouse gas emissions and improved feed efficiency	Cammack *et al*. (2018); Ortiz-Chura *et al*. (2025)
Milk and meat quality	Lipid and amino acid metabolism influencing product composition	Lipid-metabolizing and proteolytic Bacteria	Improved fatty acid profile, nutritional value, and sensory quality	Han *et al*. (2026)
Nutrient absorption efficiency	Enzymatic breakdown of complex arbohydrates and proteins	Diverse gut microbial consortia	Increased bioavailability of nutrients	Krautkramer *et al*. (2021)
Stress and adaptation traits	Modulation of gut–brain and Endocrine signaling pathways	SCFA-producing microbes affecting neuroendocrine signaling	Improved stress tolerance and adaptation to environmental changes	Chen *et al*. (2024)

The heritability of the gut microbiome features is highly variable, typically between 0.05 and 0.30 for each taxon but usually larger for functional traits like short-chain fatty acid biosynthesis or metabolism. This implies that although specific microbes are sensitive to environmental fluctuations, microbial functions might be relatively genetically driven (Rothschild *et al*., 2018; Han *et al*., 2026).

Of particular importance, certain taxa show host-specific heritability, implying that there is vertical transmission from parents to offspring in addition to environmental transmission. This confirms the assumption that the composition of microbiomes depends on both genetic transmission and environmental influence, which further proves the semi-heritability nature of this feature (Cammack *et al*., 2018).

With regards to animal breeding, the partially inheritable nature of microbiome traits means that host genotypes can be selected to change the composition of microbial communities. The practice known as microbiome-assisted selection consists in selecting host genotypes, whose features promote beneficial microorganisms that increase feed efficiency, growth rates, and resistance to pathogens.

At the same time, a low-to-moderate heritability of many microbial traits implies that there should be environmental management in place, such as proper diet design, probiotics, and housing management, along with genetic breeding techniques. Thus, breeding programs should incorporate both the principles of host genetics and microbiology.

MICROBIOME AND ECONOMICALLY IMPORTANT TRAITS IN LIVESTOCK

The microbiome within the gastrointestinal tract is an essential factor when it comes to creating economically relevant characteristics such as digestion, metabolism, energy extraction, and immune response in livestock. All of these characteristics are important for measuring the productivity and sustainability of livestock farming. There is substantial evidence indicating that variations in the composition of the microbiome influence traits related to feed efficiency, growth rate, milk/lean meat productivity, methane output, and disease resilience. The role of the gut microbiome in economically important livestock traits is summarized in Table 3.

One of the most well-studied traits in livestock is feed efficiency, as animals having a beneficial microbiome are characterized by an effective breakdown of carbohydrates into energy and increased synthesis of short-chain fatty acids (SCFAs). Microbes involved in the fermentation of fiber are beneficial in the process of obtaining nutrients from poor-quality feed, which makes this trait profitable and improves the growth rate (Han *et al*., 2026; Ortiz-Chura *et al*., 2025).

Table 4. Integration of microbiome data into livestock breeding models.

Breeding model component	Data type used	Analytical approach	Role of microbiome	Expected outcome in selection	References
Conventional genomic selection	SNP markers, phenotypic records	GBLUP, BLUP, Bayesian models	Not included	Selection based only on host genetics	Cammack *et al*. (2018); Zhang *et al*. (2024)
Microbiome-assisted genomic selection	SNP data + microbial abundance	Extended GBLUP / multi-trait models	Microbial taxa used as covariates	Improved prediction accuracy for complex traits	Martinez-Boggio *et al*. (2024)
Microbiability models	Host genome + microbiome + phenotype data	Variance partitioning models	Estimates microbiome contribution to traits	Quantifies microbial influence on heritability	Cammack *et al*. (2018)
Multi-omics integration models	Genomics + metagenomics + metabolomics	Machine learning (RF, SVM, deep learning)	Functional microbial pathways included	High-accuracy prediction of feed efficiency, growth, methane	Han *et al*. (2026)
Holobiont-based selection model	Host genome + microbiome + environment	Systems biology frameworks	Treats host + microbiome as single selection unit	Selection of combined host–microbe performance	Bordenstein & Theis (2015); Zhang *et al*. (2024)
Microbiome-informed selection indices	Genomic EBVs + microbial traits	Selection index models	Beneficial microbial profiles weighted in selection	Enhanced productivity and disease resistance	Cammack *et al*. (2018); Ortiz-Chura *et al*. (2025)

Growth performance, on the other hand, is facilitated through the regulation of energy metabolism in the host and altering the expression of genes associated with muscle development and fat deposition. Some microbial metabolites like the SCFAs and secondary bile acids affect the metabolism of lipids and the sensitivity to insulin. These have direct effects on body mass gain and carcass quality (Krautkramer *et al*., 2021).

With regard to disease resistance, beneficial microbial communities improve gut barrier functions and trigger immune signaling pathways in the host. This promotes an optimal microbial balance that results in a decrease in mortality and morbidity rates because of resistance to infection and high vaccine effectiveness (Chen *et al*., 2024).

Methane emission is another important economic trait affected by the microbiome, especially for ruminant species. The ruminal methanogens contribute to greenhouse emissions. The manipulation of the microbiome results in a significant reduction in methane release from ruminants without compromising production (Cammack *et al*., 2018; Ortiz-Chura *et al*., 2025).

Product quality is also affected by microbiomes. They regulate product quality by determining the composition of the milk and the profile of fatty acids and nutrients in meat products (Han *et al*., 2026).

INTEGRATION INTO BREEDING MODELS

The application of gut microbiome knowledge in livestock breeding programs has marked a paradigm shift in selection strategies from traditional host genome selection to a more integrated approach that considers both the host genome and microbial communities in breeding decisions. Such efforts are driven by scientific knowledge indicating that economic performance traits such as feed efficiency, growth, methane production, and disease resistance are not solely determined by host genetic factors but also by the microbiome structure and activities (Cammack *et al*., 2018; Han *et al*., 2026). The integration of gut microbiome data into livestock breeding models is summarized in Table 4, highlighting different analytical frameworks from conventional genomic selection to holobiont-based approaches.

Conventional breeding involves selecting animals based on estimated breeding values (EBVs), which rely on genotypes and phenotypes of individuals. In contrast, microbiome-guided breeding broadens the scope of conventional breeding practices by including microbial traits as predictors in statistical and genomic predictions. This has been facilitated by the incorporation of metagenomic data, microbial abundance, and functional pathways within the multi-omics prediction platforms alongside host SNPs (Zhang *et al*., 2024).

The most commonly suggested strategy has been the incorporation of microbiome characteristics in genomic selection methods (GBLUP and Bayesian models). Here, the microbiome characteristic, including abundance of particular taxa, microbial diversity measures, or concentration of metabolites, can be considered as covariate together with the genomic markers. It would enhance the predictive capacity of complex traits with substantial interaction between the host and environment (Martinez-Boggio *et al*., 2024).

An alternative approach includes the creation of microbiability models to decompose the variance of phenotype into host genetics, microbiome, and environment. It would help in determining the role of microbiome in explaining the variance of traits and evaluating if there exists indirect or direct selection for microbial traits (Cammack *et al*., 2018).

Moreover, machine learning algorithms and artificial intelligence are being utilized to combine high-dimensional genomic and microbiome data sets. Random forest, support vector machine, and deep learning algorithms are employed to model complicated, non-linear associations between the microbiome communities and their impacts on various host phenotypic traits. Such modeling helps in predicting the desired phenotype characteristics with greater accuracy, such as feed efficiency and methane production in cattle (Han *et al*., 2026).

Incorporation of microbiome information into breeding models also facilitates microbiome-assisted selection practices in which breeding choices focus on selecting genotypes of the host species capable of supporting beneficial microbiomes. Selecting genotypes that encourage higher fiber-degrading microbiomes or low methanogen communities, for instance, will enhance host productivity while minimizing its environmental footprint (Ortiz-Chura *et al*., 2025).

FUNCTIONAL ROLES OF THE MICROBIOME IN LIVESTOCK SYSTEMS

The gut microbiome carries out several interrelated activities vital for proper host functioning, productivity, and adaptability. For livestock animals, besides digestion, the microbiome regulates metabolism, modulates immunity, reduces the effects of environmental changes, and impacts development processes. Together, all of these processes make the microbiome a part of a "metabolic organ" of the host animal, which significantly affects animal productivity and well-being.

Nutrient digestion and energy provision

The digestion process by the microbiome involves the enzymatic cleavage of undigestible compounds present in the diet. For example, in ruminants, fermentation by the gut microbiome allows breaking down of cellulose and hemicellulose into SCFAs such as acetate, propionate, and butyrate, which comprise 70% of host's energy requirements. Metabolites like SCFAs are used for glucose and lipids synthesis, which have an impact on the growth and productivity of the host organism (Krautkramer *et al*., 2021; Han *et al*., 2026).

Metabolic effects on host

Metabolism of the host is affected by the microbiota in terms of bioactive substances that influence lipid metabolism, glucose homeostasis, and hormone regulation. SCFAs and bile acid analogs function as signaling molecules that affect insulin sensitivity, fat accumulation, and appetite control. These processes result in changes in body weight gain, carcass characteristics, and feed conversion ratio (Krautkramer *et al*., 2021).

Immune system formation and disease resistance

Formation of the immune system of the host is highly dependent on the microbiota. The interaction between commensal bacteria and host's cells results in improved GALT development and regulation, enhanced mucosal barrier function, and regulated inflammation response. All these factors contribute to decreased vulnerability to pathogen-induced infections and better immunization responses in animals (Chen *et al*., 2024; Han *et al*., 2026).

Environmental effect and methane reduction

Methane-producing Archaea play an important role in the processes of methanogenesis in ruminant microbiomes. Alterations in rumen microbial population allow achieving lower methane levels without negative effects on productivity in ruminants. Thus, manipulation of ruminant microbiomes is considered one of the key approaches for climate-resilient livestock production systems (Cammack *et al*., 2018; Ortiz-Chura *et al*., 2025).

Nutrient biosynthesis and synthesis of vitamins

There is synthesis of nutrients by bacteria that inhabit the gut, and these include vitamin K and B vitamins. Synthesis of nutrients helps to improve metabolism in the body because there is less dependence on diets, especially in cases where there is poor feeding (Han *et al*., 2026).

Adaptation to stress and gut-brain communication

The latest information indicates that gut bacteria communi-

Table 5. Holobiont-based selection framework in livestock breeding.

Component of framework	Data inputs	Biological level	Role in trait expression	Application in breeding	References
Host genome (SNPs)	Genotyping data	Host level	Determines baseline genetic potential for traits such as growth, immunity, and reproduction	Genomic selection using GEBVs	Cammack *et al*. (2018); Zhang *et al*. (2024)
Microbiome composition	Metagenomic sequencing, 16S rRNA profiling	Microbial level	Influences digestion, metabolism, immune modulation, and energy harvest	Identification of beneficial microbial profiles	Han *et al*. (2026)
Microbial metabolites	SCFAs, bile acids, vitamins	Functional microbial output	Regulates host metabolism, hormone signaling, and immune response	Functional trait prediction and biomarkers	Krautkramer *et al*. (2021)
Host–microbiome interaction	Integrated multi-omics data	System (holobiont) level	Determines synergy between host genes and microbial functions	Improved prediction accuracy of complex traits	Bordenstein & Theis (2015)
Environmental inputs	Diet, management, climate	External ecosystem level	Shapes microbiome composition and stability	Management strategies to optimize microbiome	Cammack *et al*. (2018)
Integrated breeding value	Genomics + microbiome + environment	Holobiont level	Combined effect on productivity, efficiency, and resilience	Holobiont-based selection index	Ortiz-Chura *et al*. (2025)

cate with their hosts using the gut-brain axis to affect stress responses in terms of adaptation through hormone modulation (Chen *et al*., 2024).

HOLOBIONT-BASED SELECTION FRAMEWORK IN LIVESTOCK BREEDING

A novel selection strategy that uses the concept of holobionts as a basis can be viewed as the paradigm shift in the genetics of livestock, where both the animal and its microbes are considered to form one biological unit known as a holobiont. Holobiont-based selection framework in livestock breeding is summarized in Table 5. Within this framework, both the genetic constitution of the host organism and the structure of its microbiomes are responsible for the economically significant characteristics of the animal, including growth rates, food efficiency, immunity, reproductive function, and adaptation to the environment (Bordenstein & Theis, 2015; Han *et al*., 2026).

The concept underlying the new selection strategy is based on the integration of information regarding host genomes, microbiomes, and the environment into a selection model where microbiomes are no longer viewed as an external environment factor but as a heritable part of the phenotype, which is also influenced by the host's genome and management (Cammack *et al*., 2018). There is evidence supporting the vertical transmission of microbial communities and their indirect modification under the influence of host genetic material.

The key point in this paradigm is the decomposition of phenotypic variation into host genome, microbes, and interactions between the two components. Thus, estimates of breeding values and the effects of the microbiome on animal health can be performed; this increases the precision of predicting complex traits shaped via biological interactions at various levels (Zhang *et al*., 2024). In such a manner, an additional factor influencing the selection process is the functional importance of the microbiota for the host's survival.

Multi-layer selection made possible by the holistic approach allows one to select animals based on the host genotype, improve microbial community composition, or enhance interaction between the host and microbiome. Specifically, animals genetically predisposed to have a large number of microorganisms that efficiently degrade fibers can have higher feed efficiency, and those capable of inhibiting the growth of methane-producing Archaea reduce greenhouse emissions without losing productivity (Ortiz-Chura *et al*., 2025).

In addition, progress achieved in metagenomics, metabolomics, and machine learning has made it more feasible to apply the holistic approach. High-resolution analysis of the host microbiome using these techniques facilitates the construction of predictive models based on genomic estimates of breeding value as well as microbiome-based characteristics (Han *et al*., 2026).

On the whole, the selection model using the concept of the holobiont offers a holistic approach to livestock production whereby the host genome and microbiome are considered interrelated factors influencing livestock performance. Such an approach can ensure greater precision and sustainability in animal breeding.

CHALLENGES AND LIMITATIONS OF INTEGRATING HOST GENOMICS AND THE MICROBIOME IN LIVESTOCK BREEDING

Despite the potential in combining host genomics information and microbiomes within animal breeding schemes, there are scientific and technical issues that prevent the use of such approaches from being fully realized at this time.

The first issue lies with the complexity of the microbiome itself. While the genotype of an individual is relatively constant throughout their life, the microbiome varies significantly based on nutrition, the environment, illness, and management strategies. Thus, it is difficult to establish a microbial trait that is reliable enough for use in a selective model (Cammack *et al*., 2018; Han *et al*., 2026).

A second problem relates to the establishment of a causal relationship between microbial communities and phenotypes of interest. Although the existence of a connection has been proved multiple times, the question of cause-and-effect persists. It can be difficult to determine if these bacteria are causing certain variations or merely a reflection of them, reducing the potential for prediction without functional testing (Ortiz-Chura *et al*., 2025).

Then, there are issues related to the technicalities involved. The adoption of high-throughput sequencing technologies and multi-omics research creates massive and complex data, which calls for advanced bioinformatics approaches. However, in many developing countries, such tools are not readily available for practical applications. Moreover, there is no standardization in terms of sample collection, DNA isolation, sequencing depth, and analyses, resulting in poor comparability (Zhang *et al*., 2024).

In addition, the inheritance pattern of microbiome traits may pose another potential problem in plant breeding. Although certain microbiome traits have been found to be moderately heritable, most traits depend significantly on the environment and thus would not directly respond to selection pressure (Cammack *et al*., 2018).

Other ethical and managerial considerations also need to be taken into account. The manipulation of microbial communities via diet-based and probiotic treatments can have unforeseen ecological or physiological impacts. Moreover, the process of microbiome analysis still carries substantial costs, which restricts its widespread use in practical breeding.

Finally, the problem of longitudinal validation studies needs to be addressed. Most current studies are conducted on a short-term basis or using experimental animal populations, and there is a lack of information regarding the performance of microbiome-guided selection across generations in the real world.

FUTURE PERSPECTIVES IN INTEGRATING HOST GENOMICS AND THE GUT MICROBIOME IN LIVESTOCK BREEDING

In the future, the breeding approach for livestock will not only be based on traditional genetic improvement but also incorporate the holistic nature of the holobiont, which involves consideration of the relationship between the genome of the host, its microbiota, and the environment as well. This will be informed by increasing proof of the role of the microbiota in influencing economically important characteristics such as feed efficiency, growth rate, methane emission, and disease resilience (Cammack *et al*., 2018; Han *et al*., 2026).

One of the key areas for the future will involve the creation of platforms for integrating multi-omics information. Multi-omics will include genomics, metagenomics, transcriptomics, proteomics, and metabolomics. These platforms will enable researchers to go beyond the description phase and start creating models that are predictive and mechanistic, and that explain interactions at the molecular level (Zhang *et al*., 2024).

Developments in machine learning and artificial intelligence technologies will also be very important in terms of developing breeding strategies in the future. AI tools will analyze vast amounts of data that may contain nonlinear associations between various microorganisms, genes, and phenotypes. As a result, prediction models for complex traits, such as efficiency in converting feed to energy and disease resistance, will become more accurate (Han *et al*., 2026).

The next important issue in the future is the application of microbiome engineering methods based on the use of probiotics, prebiotics, symbiotic, and microbial transfer. With the help of these techniques, it is possible to engineer the microbiome and improve the necessary characteristics in livestock populations. The application of genome selection along with microbiome engineering is expected to produce an optimal result (Ortiz-Chura *et al*., 2025).

Another area where the notion of breeding indices will evolve further is the inclusion of microbiome into it. It is predicted that in the future, microbial biomarkers could be introduced routinely as additional parameters to estimated breeding value indices within national breeding programs. As a result, not only the genetic qualities but also the ability of animals to form beneficial microflora will come into play.

Moreover, the need for long-term experimental testing and validation of heritability and stability of microbiome properties is important as well. It should be determined whether the microbe-related characteristics would be responsive to genetic selection in practice.

At the same time, ethical and sustainability aspects cannot be overlooked since the manipulation of animals' microbiome can lead to severe consequences related to animal welfare, ecology, and food security. Therefore, the development of protocols for microbiome research in livestock is crucial in such circumstances.

Thus, it can be concluded that in the future, the use of the systems biology perspective in breeding will allow for creating more effective and sustainable livestock production systems that would cope with modern challenges of climate change and global warming.

CONCLUSION

The integration of host genomics and gut microbiome science represents a paradigm shift in livestock breeding, moving beyond conventional host-centric selection toward a holistic, holobiont-based framework. Mounting evidence demonstrates that the gut microbiome is not merely an environmental factor but a critical biological component that interacts dynamically with host genetics to influence productivity, feed efficiency, health, disease resilience, methane emissions, and overall animal performance. By capturing both host and microbial contributions to phenotype, holobiont-based selection offers an unprecedented opportunity to explain previously unaccounted sources of variation and substantially improve the accuracy of breeding decisions.

Although challenges remain, including microbiome instability, environmental influences, methodological standardization, and the need to establish causal relationships, these limitations are increasingly being addressed through advances in sequencing technologies, bioinformatics, and systems biology. The convergence of genomics, metagenomics, multi-omics integration, artificial intelligence, and microbiome engineering is expected to accelerate the practical implementation of this approach.

Ultimately, the future of livestock improvement lies in recognizing the animal and its microbiome as a single, interconnected biological unit. Embracing this holobiont perspective has the potential to revolutionize breeding programs by delivering more productive, resilient, environmentally sustainable, and economically efficient livestock systems. As research continues to mature, holobiont-based selection is poised to become a cornerstone of next-generation animal breeding strategies.

CONFLICT OF INTEREST

There is no conflict of interest involved in writing the paper.

ACKNOWLEDGMENT

All authors are duly acknowledged for their significant contributions to the conception, design, analysis, and preparation of this manuscript.

REFERENCES

Berg, G., Rybakova, D., Fischer, D., et al. (2020). Microbiome definition re-visited: Old concepts and new challenges. *Microbiome*, *8*, 103. https://doi.org/10.1186/s40168-020-00875-0.

Bordenstein, S. R., & Theis, K. R. (2015). Host biology in light of the microbiome: ten principles of holobionts and hologenomes. *PLoS Biology*, *13*(8), e1002226. https://doi.org/10.1371/journal.pbio.1002226.

Cammack, K. M., Austin, K. J., Lamberson, W. R., Conant, G. C., & Cunningham, H. C. (2018). Ruminnat nutrition symposium: Tiny but mighty: The role of the rumen microbes in livestock production. *Journal of animal science*, *96*(2), 752-770. https://doi.org/10.1093/jas/skx053.

Chen, L., Zhang, L., Hua, H., Li, L., Mao, Y. & Wang, R. (2024). Interactions between toll-like receptors signaling pathway and gut microbiota in host homeostasis. *Immunity, Inflammation and Disease*, *12*(7), e1356. https://doi.org/10.1002/iid3.1356.

Han, Y., Wang, Z., Xie, J., Yang, G., Su, M., Wang, S., Yang, M., Yu, H., Li, M., Wang, L., Zhang, Y., & Hou, B. (2026). Host–gut microbiota interactions in health and disease: mechanisms and intervention strategies. *Frontiers in Microbiology*, 17, https://doi.org/10.3389/fmicb.2026.1785607.

Huang, Q., Wen, C., Gu, S., Jie, Y., Li, G., Yan, Y., Tian, C., Wu, G., & Yang, N. (2024). Synergy of gut microbiota and host genome in driving heterosis expression of chickens. *Journal of Genetics and Genomics*, *51*(10), 1121-1134.

Krautkramer, K. A., Fan, J., & Bäckhed, F. (2021). Gut microbial metabolites as multi-kingdom intermediates. *Nature Reviews Microbiology*, *19*(2), 77-94. https://doi.org/10.1038/s41579-020-0438-4.

Liufu, S., Wang, K., Chen, B., Chen, W., Liu, X., Wen, S., Li, X., Xu, D., & Ma, H. (2024). Effect of host breeds on gut microbiome and fecal metabolome in commercial pigs. *BMC Veterinary Research*, *20*(1), 458. https://doi.org/10.1186/s12917-024-04308-0

Martinez-Boggio, G., Monteiro, H. H., Lima, F. S., Figueiredo, C. C., Bisinotto, R. S., Santos, J. E. P., Mion, B., Schenkel, F. S., Ribeiro, E. S., Weigel, K. A. & Penagaricano, F. (2024). Host and rumen microbiome contributions to feed efficiency traits in Holstein cows. *Journal of Dairy Science*, *107*(5), 3090-3103. https://doi.org/10.3168/jds.2023-23869

Oke, O. E., Fasasi, L. O., Opowoye, I. O. & Akosile, O. A. (2025). The role of gut microbiota-derived metabolites in modulating poultry immunometabolism. *Frontiers in Physiology*, *16*, https://doi.org/10.3389/fphys.2025.1700406.

Ortiz-Chura, A., Corral-Jara, K. F., Tournayre, J., Cantalapiedra-Hijar, G., Popova, M., & Morgavi, D. P. (2025). Rumen microbiota associated with feed efficiency in beef cattle are highly influenced by diet composition. *Animal Nutrition*, *21*, 378-389. https://doi.org/10.1016/j.aninu.2024.11.027

Rothschild, D., Weissbrod, O., Barkan, E., et al. (2018). Environment dominates over host Genetics in shaping gut microbiota. *Nature*, *555*, 210–215. https://doi.org/10.1038/nature25973

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.

Tian, X., Zhou, J., Qin, Y., Zhang, K., Sun, W., Lai, S-J., Jia, X. & Chen, S-Y. (2024). Parameter Estimation of Host Genomic and Gut Microbiota Contribution to Growth and Feed Efficiency Traits in Meat Rabbits. *Microorganisms, 12*(10), 2091. https://

doi.org/10.3390/microorganisms12102091.

Wei, J., Wei, L., Ullah, A., Geng, M., Zhang, X., Wang, C., Khan, M. Z., Wang, C. & Zhang, Z. (2025). Metagenomic Applications to Herbivore Gut Microbiomes: A Comprehensive Review of Microbial Diversity and Host Interactions. *Animals*, *15*(20), 2938; https://doi.org/10.3390/ani15202938.

Zhang, W., Lan, F., Zhou, Q., Gu, S., Li, X., Wen, C., Yang, N. & Sun, C. (2024). Host genetics and gut microbiota synergistically regulate feed utilization in egg-type chickens. *Journal of animal Science and Biotechnology*, *15*, 123. https://doi.org/10.1186/s40104-024-01076-7.