



# Host–microbiome interactions in swine: intestinal microbiota, health, and growth performance

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**Abstract.** The porcine gut microbiome has emerged as a critical regulator of growth performance, intestinal health, and disease resilience, particularly in production systems with restricted antibiotic use. This mini-review synthesizes current knowledge on host–microbiome interactions in swine, focusing on the relationships between intestinal microbial communities, feed efficiency, mucosal immunity, and enteric disease. Evidence consistently demonstrates that specific bacterial taxa, including *Lactobacillus*, *Blautia*, *Dorea*, *Eubacterium*, and members of Ruminococcaceae, are positively associated with improved feed conversion efficiency, largely through enhanced short-chain fatty acid (SCFA) production and nutrient utilization. The microbiota also plays a central role in shaping mucosal immune responses and maintaining epithelial barrier integrity via microbial metabolites and host signaling pathways. In the context of antibiotic reduction, microbiome-targeted strategies such as probiotics, prebiotics, and fecal microbiota transplantation (FMT) have shown promising results in improving growth performance and mitigating disease. Conversely, dysbiosis—commonly induced by weaning stress, dietary changes, and pathogen exposure—remains a major driver of enteric disorders, including post-weaning diarrhea. Overall, the bidirectional interactions between host and microbiome represent a key axis for optimizing swine health and productivity, offering substantial potential for precision livestock management.

**Keywords:** porcine gut microbiome, feed efficiency, mucosal immunity, dysbiosis, probiotics, prebiotics, antibiotic alternatives, intestinal health, growth performance, short-chain fatty acids.

**Introduction.** The porcine gut microbiome has emerged as a central regulator of growth performance, intestinal health, and disease resilience in modern swine production systems, particularly under reduced or restricted antibiotic use. Its composition and functional capacity are shaped by diet, host genetics, and management practices, which together influence nutrient utilization, mucosal immunity, and susceptibility to enteric disorders (Bergamaschi et al., 2020; Nuñez et al., 2025; Wang et al., 2025). In this context, the microbiome represents a dynamic interface between the host and the environment, with direct implications for production efficiency and animal health.

Despite growing evidence supporting strong associations between gut microbial composition and economically important traits such as feed efficiency and growth performance, the underlying causal mechanisms remain incompletely understood. Most reported relationships are correlative rather than mechanistic, and are often influenced by substantial variability in diet composition, age, and production systems. Furthermore, differences in experimental design and microbial profiling methodologies complicate direct comparisons across studies, limiting the identification of universal microbial biomarkers for swine production traits (Bergamaschi et al., 2020; Aliakbari et al., 2021; Nuñez et al., 2025). Recent research also highlights bidirectional interactions between host genetics and the gut microbiome, suggesting that microbial composition may, in part, be genetically regulated. These findings support the concept that host–microbiome interactions jointly contribute to variation in feed efficiency, immune competence, and metabolic efficiency in

pigs, opening new perspectives for integrated selection and precision livestock management strategies (Aliakbari et al., 2021; Nuñez et al., 2025; Wang et al., 2025).

The aim of this mini-review is to critically evaluate current scientific evidence regarding host–microbiome interactions in swine, with particular emphasis on the role of the intestinal microbiota in regulating growth performance, feed efficiency, immune function, and susceptibility to enteric diseases. Additionally, the study assesses the effectiveness of microbiome-targeted interventions, including probiotics, prebiotics, and other antibiotic alternatives, in improving health and production outcomes in modern swine systems.

**Correlations Between Microbiome and Feed Conversion Efficiency.** Feed efficiency traits, including feed conversion ratio (FCR) and residual feed intake (RFI), have been consistently associated with the composition and functional potential of the gut microbiota in pigs. Several studies have identified specific bacterial taxa, such as *Lactobacillus*, *Blautia*, *Dorea*, *Eubacterium*, and members of the family Ruminococcaceae, as being positively correlated with improved feed efficiency. These associations are generally attributed to enhanced short-chain fatty acid (SCFA) production, improved energy harvesting from dietary substrates, and modulation of gut metabolic pathways (Bergamaschi et al., 2020; Nuñez et al., 2025).

Beyond individual taxa, overall microbial diversity has also been linked to feed efficiency, although results are not always consistent across studies. Higher  $\alpha$ -diversity is frequently associated with more stable gut ecosystems and improved metabolic outcomes; however, some studies report context-dependent effects depending on diet composition, production stage, and host genotype (Aliakbari et al., 2021; Wang et al., 2025). This variability highlights the complexity of microbiome–performance relationships and suggests that diversity alone is not a universal predictor of feed efficiency.

Importantly, emerging evidence indicates that a portion of microbiome variation is heritable and genetically correlated with feed efficiency traits. This suggests that host genetic background can influence microbial community structure, while microbial composition may, in turn, contribute to phenotypic variation in growth and feed utilization. Such bidirectional interactions support the concept that both host genome selection and microbiome modulation may be integrated to improve production efficiency in pigs (Aliakbari et al., 2021; Nuñez et al., 2025).

Despite these advances, most reported associations remain correlative rather than causal, and disentangling microbiome-driven effects from those induced by diet, environment, or host genetics remains a major challenge. Consequently, microbial markers of feed efficiency should be interpreted cautiously, particularly when extrapolating across different production systems.

A conceptual overview of the relationships between gut microbiota composition, microbial metabolites, and feed efficiency outcomes is presented in Figure 1. This figure illustrates the main bacterial genera associated with improved feed conversion efficiency (FCR, RFI) in pigs. Functional contributions to growth performance, including SCFA production and nutrient utilization, are indicated. Positive associations are highlighted, while interactions among microbial taxa and host traits are schematically represented.

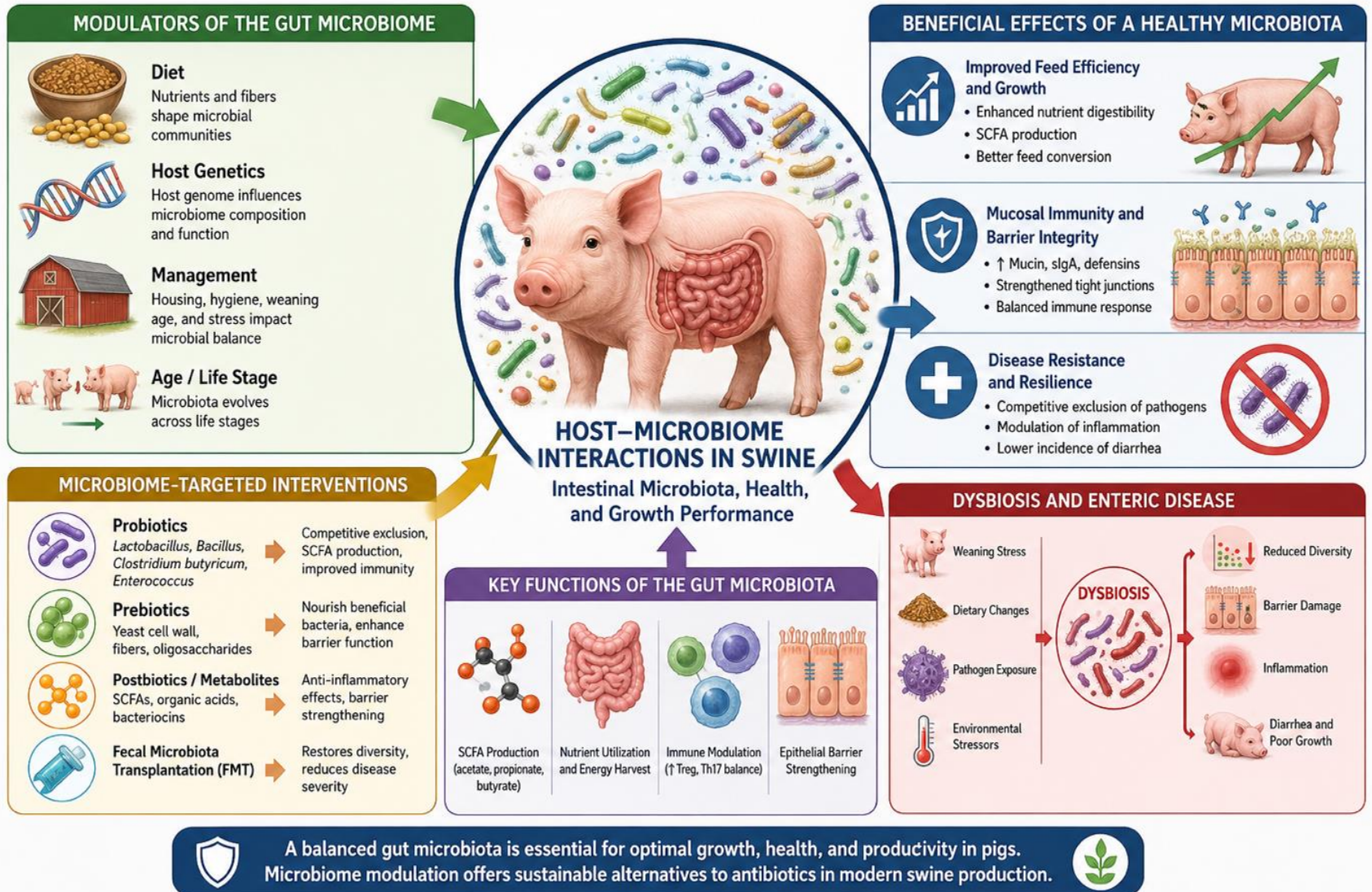


Figure 1. Host-microbiome interactions in pigs. Key gut microbial taxa and metabolites influence mucosal immunity, nutrient absorption, and gut barrier integrity, thereby affecting growth, feed efficiency, and disease resilience.

Key associations between gut microbiota composition and feed efficiency traits in pigs are summarized in Table 1. The table highlights bacterial taxa consistently associated with improved feed efficiency, the role of microbial diversity, and evidence for host genetic influences on microbiome composition.

Table 1

Links between gut microbiota and feed efficiency traits in pigs

Aspect	Key findings in pigs	References
Feed efficiency-associated taxa	<i>Lactobacillus</i> , <i>Blautia</i> , <i>Dorea</i> , <i>Eubacterium</i> and members of Ruminococcaceae are consistently associated with improved feed efficiency and nutrient utilization	Bergamaschi et al., 2020; Nuñez et al., 2025
Microbial diversity and feed efficiency	Higher microbial diversity is generally associated with more favorable feed efficiency profiles and greater ecosystem stability, although effects may vary among studies	Bergamaschi et al., 2020; Aliakbari et al., 2021; Wang et al., 2025
Genetic influence on microbiome composition	Several microbial taxa show moderate heritability and genetic correlations with feed efficiency traits, including RFI and FCR	Aliakbari et al., 2021; Nuñez et al., 2025
Proposed biological mechanisms	Improved SCFA production, enhanced nutrient digestion, increased energy harvesting, and modulation of host metabolism contribute to improved performance	Liao & Nyachoti, 2017; Bergamaschi et al., 2020; Wang et al., 2025
Aspect	Key findings in pigs	
Efficient-associated taxa	<i>Lactobacillus</i> , <i>Blautia</i> , <i>Dorea</i> , <i>Eubacterium</i> , Ruminococcaceae linked to higher FE	Bergamaschi et al., 2020; Nuñez et al., 2025
Diversity and FE	Higher $\alpha$ -diversity generally associated with more favorable FE profiles	Bergamaschi et al., 2020; Aliakbari et al., 2021; Wang et al., 2025
Genetic control	Many genera heritable; microbiome genetically correlated with RFI, FCR, intake	Aliakbari et al., 2021; Nuñez et al., 2025

Note: FE = feed efficiency; FCR = feed conversion ratio; RFI = residual feed intake; SCFA = short-chain fatty acids.

**Microbiota and Mucosal Immunity.** The porcine intestine represents the largest immune organ, and its microbiota plays a central role in regulating mucosal immunity and maintaining epithelial barrier integrity (Duarte & Kim, 2022; Huamán et al., 2024; Hu et al., 2024; Wang et al., 2025). Commensal microorganisms stimulate the production of mucins, secretory IgA, antimicrobial peptides, and tight junction proteins, while also promoting the differentiation of regulatory T cells and Th17 cells, thereby contributing to balanced immune responses and controlled inflammation.

Specific porcine-associated microbial taxa, including *Phascolarctobacterium succinatutens*, *Prevotella copri*, and *Oscillibacter valericigenes*, enhance epithelial integrity by upregulating proteins such as ZO-1, E-cadherin, and connexin-43, while also influencing crypt architecture and systemic immune cell populations in gnotobiotic models (Hu et al., 2024). In addition, microbiota-derived metabolites, such as 3-phenylpropionic acid produced by *Bacteroides fragilis*, strengthen epithelial barrier function through aryl hydrocarbon receptor (AhR) signaling pathways (Hu et al., 2023).

Mucosa-associated microbial communities are particularly important due to their close interaction with the host epithelium. Their composition is strongly influenced by diet, immune status, and growth stage, making them valuable biomarkers for assessing intestinal health and resilience in swine production systems (Duarte & Kim, 2022).

**Probiotics, Prebiotics and Alternatives to Antibiotics.** The restriction of in-feed antibiotics in modern swine production systems has accelerated the search for microbiome-targeted strategies aimed at maintaining growth performance, intestinal health, and

disease resilience. In this context, probiotics, prebiotics, and related alternatives to antibiotics have emerged as promising tools to modulate the gut microbiota and improve host physiological responses (Dowarah et al., 2017; Liao & Nyachoti, 2017; Duarte & Kim, 2022; Huamán et al., 2024).

Probiotics commonly used in pigs include *Lactobacillus*, *Bacillus*, *Clostridium butyricum*, and *Enterococcus* species, while prebiotics typically comprise yeast cell wall derivatives and non-digestible dietary fibers. These interventions have been consistently associated with improved gut health, enhanced immune responses, and better growth performance, particularly in weaned piglets under stress conditions (Liao & Nyachoti, 2017; Ali et al., 2023; Huamán et al., 2024; Saha et al., 2024).

At the mechanistic level, these microbiome-modulating strategies act through multiple complementary pathways. They promote competitive exclusion of pathogenic bacteria, stimulate the production of antimicrobial compounds such as bacteriocins, organic acids, and hydrogen peroxide, and enhance epithelial barrier integrity by strengthening tight junction proteins and mucus layer production. In addition, they modulate both innate and adaptive immune responses, contributing to improved mucosal immunity and reduced inflammatory burden (Dowarah et al., 2017; Duarte & Kim, 2022; Huamán et al., 2024; Liu et al., 2024).

In controlled experimental and field studies, supplementation with probiotics and prebiotics has been shown to positively influence microbial community structure, including increased abundance of beneficial taxa such as Lactobacillaceae, along with shifts in the Firmicutes/Bacteroidetes ratio. These changes are often associated with improved FCR, reduced incidence of post-weaning diarrhea, and enhanced nutrient utilization efficiency (Bergamaschi et al., 2020; Ali et al., 2023; Huamán et al., 2024).

In addition to single-strain or single-substrate approaches, multi-strain probiotic formulations and combined synbiotic strategies have demonstrated synergistic effects on gut health and performance, sometimes achieving outcomes comparable to antibiotic growth promoters under commercial conditions (Ali et al., 2023; Huamán et al., 2024; Saha et al., 2024).

Fecal microbiota transplantation (FMT) has also emerged as a novel strategy for restoring microbial balance in dysbiotic animals. By transferring a mature microbial community from healthy donors, FMT can enhance microbial diversity, strengthen epithelial barrier function, and reduce the severity of enteric diseases, including viral-induced diarrhea (Gresse et al., 2017; Peng et al., 2021; Hu et al., 2024).

Key microbiome-targeted interventions and their effects on pig health and performance are summarized in Table 2.

Table 2  
Microbiome-targeted interventions and their effects on gut health and feed efficiency in pigs

<i>Intervention / Microbiota change</i>	<i>Main effects on gut</i>	<i>Effect on growth / feed efficiency</i>	<i>References</i>
<i>Lactobacillus</i> spp.	Reduces <i>E. coli</i> , lowers luminal pH, increases SCFA	Improved growth and FCR	Dowarah et al., 2017; Bergamaschi et al., 2020; Ali et al., 2023
<i>Bacillus</i> -based probiotics	Reduces Enterobacteriaceae, strengthens intestinal barrier	Better performance, lower fecal score	Duarte & Kim, 2022; Huamán et al., 2024
<i>Clostridium butyricum</i>	Enhances tight junction proteins, modulates IL-1 $\beta$ /IL-18, IL-10	Improved growth	Huamán et al., 2024; Liu et al., 2024
Yeast cell wall prebiotics	Alters Firmicutes/Bacteroidetes ratio, modulates IL-8 and IL-10	Improved FCR vs AGP	Huamán et al., 2024
Fecal microbiota transplantation	Increases diversity, restores barrier, reduces viral diarrhea severity	Supports growth, reduces disease impact	Gresse et al., 2017; Peng et al., 2021; Hu et al., 2024

Note: FCR = feed conversion ratio; SCFA = short-chain fatty acids.

**Dysbiosis and Enteric Disease.** Intestinal dysbiosis in pigs represents a functional disruption of the host–microbiome equilibrium, rather than a simple compositional change in microbial communities. It is commonly triggered by weaning stress, abrupt dietary transitions, environmental challenges, and enteric pathogen exposure, all of which contribute to instability of the gut ecosystem during critical developmental stages (Gresse et al., 2017; Adhikari et al., 2019; Bergamaschi et al., 2020; Wang et al., 2025).

At the microbial level, dysbiosis is typically characterized by reduced bacterial diversity and a shift toward opportunistic taxa, particularly an increase in Proteobacteria and other inflammation-associated groups. These compositional changes are accompanied by a decline in beneficial commensals involved in SCFA production and epithelial support, resulting in impaired metabolic and protective functions of the microbiota (Bergamaschi et al., 2020; Da Rosa Dias et al., 2025).

Functionally, dysbiosis compromises intestinal barrier integrity through disruption of tight junction proteins and mucus layer degradation. This leads to increased intestinal permeability and enhanced translocation of microbial components, which activate innate immune pathways such as TLR4/MyD88/NF- $\kappa$ B signaling, thereby promoting local and systemic inflammatory responses (Gresse et al., 2017; Peng et al., 2021; Huamán et al., 2024).

Enteric pathogens exacerbate these effects. Enterotoxigenic *Escherichia coli* directly damages epithelial cells, induces fluid secretion, and amplifies inflammatory signaling, thereby worsening pre-existing microbial imbalance and contributing to post-weaning diarrhea (Kim et al., 2022; Huamán et al., 2024). Similarly, viral infections such as porcine deltacoronavirus disrupt microbial homeostasis and epithelial integrity, leading to severe but potentially reversible dysbiosis (Peng et al., 2021).

Clinically, these alterations manifest as post-weaning diarrhea, reduced feed efficiency, impaired nutrient absorption, and decreased growth performance, all of which have significant economic implications in commercial pig production systems (Bergamaschi et al., 2020; Da Rosa Dias et al., 2025; Wang et al., 2025). Importantly, dysbiosis is not only a consequence of disease but also a contributing factor, creating a self-reinforcing cycle between microbial imbalance, immune dysregulation, and pathogen susceptibility.

Restoration of microbial equilibrium represents a key therapeutic and preventive strategy. Approaches such as FMT and microbiome-targeted interventions have demonstrated the ability to restore diversity, reinforce epithelial barrier function, and reduce the severity of enteric disease, highlighting the plasticity of the porcine gut ecosystem (Gresse et al., 2017; Peng et al., 2021; Hu et al., 2024).

**Conclusions.** The integration of host genomics, microbiome research, and nutritional strategies has substantially advanced swine production systems by improving our understanding of growth, immunity, and disease resilience. Evidence increasingly shows that host genetic factors and gut microbiota are closely interconnected, forming a bidirectional system that influences key production traits such as feed efficiency, nutrient utilization, and growth performance.

Microbiome-targeted interventions, including probiotics, prebiotics, and FMT, offer promising approaches to stabilize gut ecosystems and mitigate the negative effects of dysbiosis, particularly under antibiotic-restricted conditions. However, their efficacy is strongly context-dependent and influenced by host genotype, diet, and environmental factors.

Dysbiosis remains a central challenge in swine production, especially during transitional stages such as weaning, where it contributes to impaired intestinal health, reduced performance, and increased disease susceptibility.

Future breeding and management strategies will likely rely on integrated frameworks combining genomic selection, microbiome modulation, and precision nutrition to improve both productivity and resilience in pig populations.

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