DOI: 10.21088/ijab.2454.7964.12126.9

Indian Journal of Agriculture Business
Volume 12 Number 1, January – June 2026

REVIEW ARTICLE

Feeding the Microbiome: A Growing Frontier in Pig Production

Abhilasha Singh[1], Kumar Govil[2], Mamta[3], Nishtha Kushwah[4]

HOW TO CITE THIS ARTICLE:

Abhilasha Singh, Kumar Govil, Mamta, et al. Feeding the Microbiome: A Growing Frontier in Pig Production. J Agri Busi 2026; 12(1): 83–94.

ABSTRACT

Pig production is a major contributor to global animal protein supply but faces challenges of high feed costs, disease risks, and restrictions on antibiotic growth promoters. Recent advances highlight the gut microbiome as a key regulator of nutrient utilization, immune function, and overall health in pigs. This review summarizes the development and composition of the gut microbiota across life stages and its roles in digestion, energy harvest, barrier protection, and immune modulation. Nutritional interventions such as prebiotics, probiotics, synbiotics, phytogenic compounds, organic acids, functional amino acids, enzymes, and unconventional feed resources are discussed for their ability to beneficially modulate the microbiome and enhance pig performance. In addition, emerging strategies including precision feeding, microbiome-informed biomarkers, multi-omics integration, and next-generation approaches such as phage therapy, fecal microbiota transplantation, and engineered probiotics are explored. While these developments are promising, challenges remain in terms of mechanistic understanding, cost-effectiveness, regional adaptability, and standardization of microbiome-based interventions. The integration of host genetics, microbial ecology, and digital technologies holds future potential for precision and sustainable pig nutrition. Overall, feeding the microbiome represents a paradigm shift in swine production, offering avenues to improve productivity, animal welfare, and environmental sustainability in the post-antibiotic era.

KEYWORDS

• Swine Nutrition • Gut Microbiota • Probiotics • Growth Performance • Immune Modulation • Feed Additives

AUTHOR'S AFFILIATION:

[1] Assistant Professor, Animal Nutrition, College of Veterinary Science & Animal Husbandry, NDVSU, Rewa, Jabalpur, M.P, India.

[2] Assistant Professor, Animal Nutrition, College of Veterinary Science & Animal Husbandry, NDVSU, Rewa, Jabalpur, M.P, India.

[3] Assistant Professor, Livestock Production Management, Pandit Deen Dayal Upadhyaya Pashu Chikitsa Vigyan Vishwavidyalaya Evam Go Anusandhan Sansthan, Mathura, India.

[4] Assistant Professor, Veterinary Physiology and Biochemistry, Animal Nutrition, College of Veterinary Science & Animal Husbandry, NDVSU, Rewa, Jabalpur, M.P, India.

CORRESPONDING AUTHOR:

Abhilasha Singh, Assistant Professor, Animal Nutrition, College of Veterinary Science & Animal Husbandry, NDVSU, Rewa, Jabalpur, M.P, India.

E-mail: abhilasha1495@gmail.com

➢ **Received:** 23-09-2025 ➢ **Accepted:** 18-12-2025

INTRODUCTION

Pig production is a critical contributor to global animal protein supply, accounting for more than 35% of all meat consumed worldwide (FAO, 2023). Feed and nutrition remain the largest input cost in pig farming, representing nearly 60–70% of total production expenses (NRC, 2012). Traditionally, nutritionists formulated rations to meet the pig's nutrient requirements for growth, reproduction, and maintenance. However, this approach has expanded in recent decades to include the pig's gut microbiome, which is now recognized as a key determinant of health, productivity, and welfare. The gut microbiota, often described as a "forgotten organ," consists of trillions of microorganisms, including bacteria, archaea, fungi, and viruses, inhabiting the gastrointestinal tract. This microbial ecosystem contributes to digestion, energy harvest, vitamin synthesis, immune modulation, and pathogen resistance (Yang *et al.,* 2021). Importantly, disruptions to microbial balance, such as those occurring during weaning, can result in diarrhea, poor growth, and increased disease susceptibility (Dowarah *et al.,* 2018). With the global push to reduce antimicrobial growth promoters due to concerns over antimicrobial resistance, nutrition strategies are shifting towards feeding the microbiome using diet, feed additives, and novel technologies to deliberately nurture beneficial microbial communities. This review highlights the development, composition, and functional roles of pig gut microbiota, examines dietary strategies to modulate it, and explores emerging opportunities and challenges in microbiome-targeted pig nutrition.

DEVELOPMENT AND COMPOSITION OF PIG GUT MICROBIOTA

1. Early Colonization

Microbiota colonization in pigs begins immediately after birth, influenced by maternal microbiota, the farrowing environment, and colostrum intake. Piglets born via natural delivery acquire a richer and more diverse microbiome than those delivered via caesarean section, reflecting maternal vaginal and fecal microbial exposure (Liu *et al.,* 2020). Colostrum and milk are also rich in oligosaccharides and immunoglobulins that promote the establishment of Lactobacillus and Bifidobacterium spp., supporting early immune development (Trevisi *et al.,* 2020).

2. Weaning Transition: Weaning represents one of the most stressful events in pig production, often causing gut microbial dysbiosis. Piglets are abruptly shifted from a milk-based diet to solid feed, accompanied by separation stress and environmental changes. This transition reduces beneficial lactic acid bacteria and allows opportunistic pathogens such as Escherichia coli and Clostridium perfringens to proliferate, predisposing piglets to post-weaning diarrhea (Gresse *et al.,* 2017; Ma *et al.,* 2024). Weaning is thus a "critical window" for interventions to stabilize the microbiome and prevent health setbacks.

3. Growth and Finishing Phases

As pigs mature, the gut microbiome stabilizes and increases in diversity. In grower and finisher pigs, Firmicutes and Bacteroidetes dominate, followed by Proteobacteria and Actinobacteria (Holman *et al.,* 2017). Genera such as Prevotella, Ruminococcus, and Faecalibacterium are enriched, contributing to fiber degradation and short-chain fatty acid (SCFA) production (Wang *et al.,* 2021). Microbial profiles during this stage correlate with feed efficiency, carcass quality, and fat deposition, making them valuable biomarkers for performance (Li *et al.,* 2022).

4. Typical Microbiota Across Growth Stages

Content presented in table, 1. showing the typical gut microbiota across growth stage (Gresse *et al.,* 2017; Holman *et al.,* 2017; Wang *et al.,* 2021).

Table 1: Typical Microbiota Across Growth Stages

Growth Stage	Dominant Taxa	Functional Role	Key Issues
Neonatal (0–1 wk)	Lactobacillus, Bifidobacterium	Milk digestion, immune priming	High susceptibility to pathogens
Weaning (3–6 wk)	↓ Lactobacillus, ↑ E. coli, Clostridium	Stress adaptation, diarrhea risk	Gut dysbiosis, diarrhea outbreaks
Grower–Finisher	Prevotella, Ruminococcus, Faecalibacterium	Fiber degradation, SCFA production	Links to feed efficiency, fat deposition
Adult	Stable diverse microbiome	Homeostasis, resilience	Relatively stable but diet-sensitive

FUNCTIONAL ROLES OF GUT MICROBIOTA IN PIGS

The gut microbiome is not a passive community but an active metabolic and immunological organ. It contributes to digestion, nutrient utilization, immune system development, epithelial integrity, and host metabolism. These functions collectively determine growth performance, health, and resilience in pigs.

1. Digestion and Energy Harvest

One of the most fundamental roles of gut microbiota is the breakdown of dietary components that escape digestion in the upper gastrointestinal tract.

- **Fermentation of non-digestible carbohydrates (NDCs):** Pigs lack endogenous enzymes to degrade complex polysaccharides such as cellulose, hemicellulose, arabinoxylans, and resistant starch. Microbiota in the large intestine ferment these substrates into short-chain fatty acids (SCFAs), primarily acetate, propionate, and butyrate (Louis & Flint, 2017).
- **SCFA functions:**
  - *Acetate:* absorbed into circulation and serves as an energy substrate for peripheral tissues.
  - *Propionate:* transported to the liver, where it contributes to gluconeogenesis.
  - *Butyrate:* preferential fuel for colonocytes, maintaining epithelial energy balance and integrity (Tan *et al.*, 2014).
- **Energy contribution:** SCFAs provide up to 10–15% of total maintenance energy in pigs (Heo *et al.*, 2013). Butyrate supplementation or diets promoting butyrate-producing bacteria (e.g., Faecalibacterium prausnitzii) improve gut health and feed efficiency (Jha & Berrocoso, 2016).
- **Protein fermentation:** Microbiota degrade undigested proteins and amino acids into bioactive metabolites such as branched-chain fatty acids, amines, and indoles. While some metabolites (e.g., indole-3-propionic acid) are beneficial, excessive protein fermentation may generate toxic compounds like ammonia and hydrogen sulfide, impairing growth (Pieper *et al.*, 2012).

2. Modulation of the Immune System

The gut microbiota serves as a trainer of the immune system, helping piglets develop balanced immune responses.

- **Immune education:** Early exposure to microbial-associated molecular patterns (MAMPs) such as lipopolysaccharides and peptidoglycans stimulates pattern recognition receptors (PRRs) (e.g., TLRs, NOD-like receptors) on immune cells (Belkaid & Hand, 2014). This shapes both innate and adaptive immunity.
- **Regulation of inflammation:** SCFAs, particularly butyrate, promote differentiation of regulatory T cells (Tregs) and increase production of anti-inflammatory cytokines (IL-10) while suppressing pro-inflammatory cytokines (TNF-α, IL-6) (Furusawa *et al.*, 2013; Liu *et al.*, 2018).
- **Vaccine responsiveness:** A balanced gut microbiota enhances vaccine efficacy by providing adjuvant-like signals (Ma *et al.*, 2024). In contrast, dysbiosis reduces immune competence, leaving piglets vulnerable to enteric and systemic infections.

3. Barrier Protection and Gut Integrity

The intestinal mucosa is a critical barrier separating host tissues from luminal antigens and pathogens. The microbiota actively strengthens this barrier.

- **Mucin production:** Commensal bacteria stimulate goblet cells to secrete mucins, which form a protective mucus layer (Johansson *et al.*, 2011).
- **Tight junction integrity:** Butyrate enhances the expression of tight junction proteins such as occludin and claudins, reducing intestinal permeability or "leaky gut" (Peng *et al.*, 2009).
- **Antimicrobial peptides (AMPs):** Beneficial bacteria stimulate epithelial cells to produce AMPs (e.g., defensins, cathelicidins), which inhibit pathogenic overgrowth (Ganz, 2003).
- **Competitive exclusion of pathogens:**
  - Probiotic Lactobacillus spp. lower gut pH by producing lactic acid, making the environment unfavorable for pathogens like E. coli.
  - Bifidobacterium spp. produce acetate, which directly blocks pathogen adherence (Fukuda *et al.*, 2011).

Thus, microbiota act as both physical and biochemical defenders of gut integrity in pigs.

4. Host Metabolism and Growth Performance

Beyond digestion, the microbiota influences whole-body metabolism and growth.

- **Feed efficiency and weight gain:** Pigs with higher microbiome diversity and greater abundance of **fiber-degrading bacteria** (e.g., Prevotella, Ruminococcus) tend to have better feed conversion ratios (FCRs) (McCormack *et al.*, 2017).
- **Lipid metabolism:** Gut microbiota regulate fat deposition by influencing bile acid metabolism. Microbial bile salt hydrolases (BSHs) modify bile acids, which in turn regulate lipid absorption and host metabolism through **farnesoid X receptor (FXR)** and **TGR5** signaling (Joyce & Gahan, 2016).
- **Amino acid utilization:** Specific taxa metabolize dietary amino acids into bioactive derivatives. For instance, tryptophan is converted to **indoles**, which activate the aryl hydrocarbon receptor (AhR), promoting mucosal immunity and reducing inflammation (Agus *et al.*, 2018).
- **Gut–brain axis:** Microbial metabolites such as serotonin precursors and SCFAs influence pig behavior, stress responses, and feed intake regulation (Wang *et al.*, 2025). This is an emerging area with implications for welfare in intensive pig production.

8. Summary of Functional Roles

Function	Microbial Contribution	Key Benefits in Pigs
Digestion & Energy	Fermentation of fibers → SCFAs	Improved feed efficiency, energy supply
Immune Modulation	SCFA–Treg axis, PRR stimulation	Balanced immunity, reduced inflammation
Barrier Protection	Mucin induction, tight junction strengthening	Reduced diarrhea, pathogen resistance
Metabolism	Bile acid modification, indole production	Enhanced growth, lean mass, stress resilience

FEEDING STRATEGIES TO MODULATE GUT MICROBIOTA

Targeted feeding strategies can shift the gut microbial community in favor of beneficial taxa, enhance fermentation efficiency, suppress pathogens, and improve pig health and productivity. These strategies are particularly critical in the post-antibiotic era, as producers seek sustainable alternatives to antimicrobial growth promoters (AMGPs). Below, we discuss major nutritional approaches.

1. Prebiotics and Dietary Fibers

Definition: Prebiotics are non-digestible food ingredients that selectively stimulate the growth or activity of beneficial microbes in the gut (Gibson *et al.*, 2017). In pigs, prebiotics are typically fermentable fibers, oligosaccharides, and resistant starches.

Mechanism:

- Fermentation of prebiotics → SCFA production → lower gut pH → suppression of pathogens (Salmonella, E. coli).
- Promote proliferation of Bifidobacterium and Lactobacillus spp.
- Enhance mucosal immunity via SCFA–Treg pathways.

Examples:

- Inulin and fructooligosaccharides (FOS) → increase Lactobacillus abundance and reduce diarrhea in weaned piglets (Lallès *et al.*, 2020).
- Galactooligosaccharides (GOS) → improve villus height and gut integrity (Xu *et al.*, 2021).
- Resistant starch → enrich Ruminococcus bromii and butyrate-producing bacteria (Yang *et al.*, 2021).

2. Probiotics and Synbiotics

Definition: Probiotics are live microorganisms which, when administered in adequate amounts, confer health benefits on the host. Synbiotics combine prebiotics with probiotics for synergistic effects.

Mechanism:

- Direct colonization of beneficial bacteria.
- Competitive exclusion of pathogens.
- Secretion of antimicrobial substances (bacteriocins, organic acids).

- Immune modulation (enhanced IgA, reduced pro-inflammatory cytokines).

- **Examples in pigs:**
  - Lactobacillus plantarum → reduces post-weaning diarrhea, improves ADG (average daily gain) (Dowarah *et al.*, 2018).
  - Bacillus subtilis → spore-forming probiotic, improves feed efficiency under heat stress (Sun *et al.*, 2022).
  - Multi-strain probiotics outperform single strains in stabilizing microbiota during weaning (Ma *et al.*, 2024).
  - Synbiotic supplementation (e.g., inulin + Lactobacillus) shows additive benefits on gut morphology and performance (Markowiak & Slizewska, 2018).

3. Phytogenics (Plant-Derived Additives)

Phytogenics (essential oils, plant extracts, polyphenols) are emerging as natural alternatives to antibiotics.

Mechanism:

- Antimicrobial action via membrane disruption.
- Antioxidant and anti-inflammatory properties.
- Modulation of microbial diversity, favoring Lactobacillus and Ruminococcus.

Examples:

- Oregano oil (carvacrol, thymol) → suppresses E. coli and Clostridium spp. (Zhai et al., 2020).
- Curcumin → upregulates tight junction proteins, reduces gut inflammation (Zhang et al., 2018).
- Green tea catechins → promote SCFA production, inhibit lipid peroxidation (Lee et al., 2019).

4. Organic Acids

Organic acids are well-established alternatives to antibiotic growth promoters.

Mechanism:

- Lower luminal pH → inhibit growth of acid-sensitive pathogens.
- SCFAs like butyrate → fuel colonocytes, strengthen barrier.
- Medium-chain fatty acids (MCFAs) → direct antimicrobial activity.

Examples:

- Formic and lactic acid → reduce Salmonella colonization (Partanen & Mroz, 1999).
- Sodium butyrate → enhances villus height and growth rate in weaned piglets (Hu *et al.*, 2022).
- Caprylic acid (MCFA) → inhibits Clostridium difficile growth (Hinton *et al.*, 2021).

5. Amino Acids as Functional Nutrients

Beyond their role in protein synthesis, amino acids regulate gut microbiota and mucosal health.

Glutamine: Preferred fuel for enterocytes, reduces oxidative stress, prevents villus atrophy during weaning (Wu *et al.*, 2011).

Threonine: Essential for mucin production, enhancing the protective mucus layer (Wang *et al.*, 2010).

Tryptophan: Microbial metabolism produces indoles → activate AhR pathway → enhance mucosal immunity (Agus *et al.*, 2018).

Arginine: Promotes nitric oxide production and gut barrier defense (Yin *et al.*, 2014).

6. Enzyme Supplementation

Enzymes improve digestibility of complex feed ingredients, reducing undigested substrates that promote pathogen growth.

- **Xylanase and β-glucanase:** Hydrolyze non-starch polysaccharides, generating oligosaccharides that act as prebiotics (Kiarie *et al.*, 2013).
- **Proteases:** Reduce undigested proteins, lowering ammonia and harmful metabolites in hindgut (Adeola & Cowieson, 2011).
- **Phytase:** Improves phosphorus utilization and indirectly modifies microbial fermentation by altering mineral balance (Lei *et al.*, 2013).

7. Alternative Feed Resources

- **Fermented Feed:** Rich in lactic acid bacteria and organic acids; improves gut microbiota diversity and reduces pathogens (Canibe & Jensen, 2012).

- **Insect Meal (e.g., black soldier fly larvae):** Contains chitin, which stimulates lactic acid bacteria and immune responses (Biasato *et al.*, 2019).
- **Algae-derived polysaccharides:** Promote SCFA production and beneficial taxa (Mateos-Aparicio *et al.*, 2020).
- **Rice- and cereal-based fermented products:** Locally adapted options in Asia, with LAB dominance and improved piglet gut health (Singh *et al.*, 2023).

8. Summary Table

Strategy	Example Additives	Microbiota Effects	Benefits in Pigs
Prebiotics/Fibers	Inulin, FOS, GOS, resistant starch	↑ Bifidobacterium, SCFA producers	Reduced diarrhea, better gut integrity
Probiotics/Synbiotics	Lactobacillus, Bacillus, multi-strain blends	Competitive exclusion, ↑ IgA, ↓ pathogens	Improved ADG, FCR, immune modulation
Phytogenics	Oregano oil, curcumin, catechins	↓ Pathogens, ↑ lactobacilli, antioxidant	Reduced inflammation, growth promotion
Organic Acids	Butyrate, formic acid, MCFAs	↓ Pathogens, ↑ barrier strength	Enhanced villus height, feed efficiency
Amino Acids	Glutamine, threonine, tryptophan, arginine	Support mucin, immunity, indole production	Stronger gut lining, reduced weaning stress
Enzymes	Xylanase, protease, phytase	Release prebiotic oligosaccharides, ↓ toxins	Better digestibility, less gut dysbiosis
Alternative Feeds	Fermented feed, insect meal, algae	↑ LAB, ↑ SCFA, immune stimulation	Sustainable protein, pathogen control

GUT MICROBIOTA AND PIG HEALTH

The pig gut microbiota is now recognized as a pivotal determinant of swine health, performance, and welfare. It contributes not only to nutrient digestion but also to immune system maturation, pathogen control, and even behavior through the gut–brain axis. A balanced microbial community improves digestive efficiency, suppresses enteric pathogens, and reduces systemic inflammation (Pluske *et al.*, 2018). Conversely, dysbiosis is associated with diarrhea, reduced feed efficiency, impaired nutrient absorption, and poor growth outcomes.

1. Microbiota and Diarrhea Control

Post-weaning diarrhea remains one of the most significant health and economic challenges in pig production. It is often triggered by the decline in *Lactobacillus* and *Bifidobacterium* and the concurrent expansion of pathogenic *Escherichia coli* and *Clostridium perfringens* populations (Guevarra *et al.*, 2019). Beneficial commensals produce organic acids (lactic acid and SCFAs) that lower gut pH and inhibit pathogen growth. They also compete for epithelial adhesion sites and nutrients, preventing colonization by enterotoxigenic *E. coli* (Dowarah *et al.*, 2018).

Microbial metabolites such as butyrate and propionate play protective roles by stimulating mucus secretion and enhancing tight junction protein expression, which limit intestinal permeability. Nutritional strategies including probiotics, prebiotics, and organic acids help re-establish microbial balance and significantly reduce diarrhea incidence, thus improving piglet survival.

2. Immunomodulation by Gut Microbiota

The gastrointestinal tract is the largest immune organ in pigs, and commensal microbes are critical for the development of gut-associated lymphoid tissue (GALT) and the maturation of immune cells. Short-chain fatty acids, particularly butyrate, act as epigenetic modulators, promoting anti-inflammatory gene expression and enhancing regulatory T-cell activity. These immunomodulatory mechanisms not only reduce systemic inflammation but also improve responsiveness to vaccines in pigs (Schokker *et al.*, 2014).

3. Microbiota–Pathogen Interactions

The gut microbiota provides ecological resistance against pathogens through niche exclusion, antimicrobial metabolite production, and stimulation of host defenses. Antibiotic overuse, stress, or poor diet disrupts this balance, creating opportunities for *Salmonella, Clostridium difficile,* and pathogenic *E. coli* to proliferate (Gresse *et al.,* 2017). Such infections not only impair pig health but also reduce growth and increase production costs. Sustainable feeding strategies that reinforce commensals and reduce reliance on antibiotics are therefore critical for future swine production (Dowarah *et al.,* 2018).

4. The Gut–Brain Axis in Pigs

An emerging research frontier is the gut–brain axis, the bidirectional communication between the gut microbiota and the central nervous system. Microbial metabolites such as SCFAs, tryptophan derivatives (indoles, serotonin precursors), and neurotransmitter-like compounds (GABA) influence neurodevelopment, behavior, and stress resilience (Berding & Donovan, 2016; Pohl *et al.,* 2017). Dysbiosis during weaning has been linked with elevated cortisol levels and stress-related behaviors, suggesting that microbiota management could improve both pig health and welfare.

EMERGING TECHNOLOGIES IN MICROBIOME RESEARCH AND APPLICATIONS IN PIG NUTRITION

The rapid advancement of sequencing technologies, metabolomics, and computational biology has transformed pig microbiome research. These tools have shifted our understanding from simply identifying "who" is present in the gut to uncovering "what they do" and "how they interact" with the host, paving the way for precision microbiome-informed pig nutrition.

1. High-Throughput Sequencing and Metagenomics

High-throughput sequencing, including 16S rRNA gene sequencing and whole-genome shotgun metagenomics, now enables comprehensive taxonomic and functional profiling of microbial communities (Xiao *et al.,* 2016). These tools have been used to link microbial profiles with feed efficiency, growth rates, and fat deposition in pigs (McCormack *et al.,* 2017; Bergamaschi *et al.,* 2020).

2. Metabolomics and Nutritional Biomarkers

Metabolomics complements sequencing by identifying bioactive microbial metabolites such as SCFAs, bile acids, and amino acid derivatives. These metabolites act as functional biomarkers, connecting dietary interventions with host responses. For instance, fecal SCFA profiles indicate fiber fermentation efficiency, while bile acid shifts reflect fat digestion and microbial imbalance (Xu *et al.,* 2020). Metabolomics-based biomarkers are increasingly being used to predict pig performance and monitor dietary effects (Ramayo-Caldas *et al.,* 2019).

3. Multi-Omics Integration

Integration of metagenomics, transcriptomics, proteomics, and metabolomics offers a systems-level view of host–microbiome interactions. For example, studies demonstrate that dietary protein levels alter microbial fermentation products, which in turn regulate host immune and metabolic gene expression (Niu *et al.,* 2019; Chen *et al.,* 2023). This integrative approach underpins personalized nutrition strategies in pigs.

4. Precision Feeding and Digital Technologies

Precision livestock farming (PLF) technologies such as automated feeders, near-infrared spectroscopy (NIRS), and real-time sensors allow dynamic, individualized diet adjustments. Coupled with microbiome insights, these tools enhance nutrient use efficiency and minimize nitrogen and phosphorus excretion, reducing environmental impact (Pomar *et al.,* 2019). AI and machine learning are now applied to analyze microbiome datasets, enabling prediction of microbial biomarkers linked to feed efficiency or health risks.

5 Microbiome Editing and Next-Generation Interventions

The future of pig microbiome management includes direct manipulation of gut microbial communities. Fecal microbiota transplantation (FMT) from healthy donors shows promise in restoring microbial balance (Hu *et al.,* 2018). Phage therapy is being explored as a targeted antimicrobial approach to eliminate pathogens while sparing commensals (Clavijo & Flórez, 2018). Engineered probiotics and CRISPR-based microbiome editing represent futuristic methods to selectively silence undesirable microbial genes, including antibiotic resistance determinants (Barrangou & Doudna, 2016). Although still experimental, these interventions hold transformative potential for sustainable swine production.

CHALLENGES, KNOWLEDGE GAPS, AND FUTURE PERSPECTIVES

Despite rapid advances in understanding the pig gut microbiome, several challenges and unanswered questions remain before microbiome-targeted nutrition can be fully integrated into commercial swine production.

1. Challenges in Application

1 Individual Variability

Microbiome composition varies widely among pigs depending on genetics, age, environment, maternal microbiota, and diet. This individual variability makes it difficult to standardize microbiome-based nutritional interventions across farms. For instance, a probiotic strain effective in one herd may show limited efficacy in another due to different baseline microbiota.

2. Cost and Practicality

Novel feed additives such as probiotics, synbiotics, and enzymes often increase feed costs. Their adoption depends on demonstrated cost–benefit ratios under field conditions, particularly in developing countries where feed resource constraints already limit profitability.

3. Regulatory Frameworks

While feed additives targeting the microbiome are gaining popularity, regulations on their safety, efficacy, and labeling vary across regions. Lack of harmonization in global regulatory standards slows down commercialization of innovative products such as engineered probiotics or bacteriophages.

4. Knowledge Gaps in Mechanisms

Although many studies demonstrate positive effects of microbiota-targeted feeding strategies, the mechanistic pathways are often poorly defined. For example, while probiotics improve piglet health, it is not always clear whether benefits are due to competitive exclusion, metabolite production, or immune modulation. More mechanistic insights are needed for rational feed design.

2. Knowledge Gaps in Research

- **Early-life programming:** The role of maternal microbiota and early dietary exposures in shaping long-term pig performance remains underexplored.
- **Microbiome–host genetics interactions:** How pig breed and genetic background influence microbiome composition and response to diet requires deeper study.
- **Non-bacterial microbiota:** Most studies focus on bacteria, but fungi, archaea, and viruses (especially bacteriophages) also influence gut ecology. Their roles remain poorly understood.
- **Standardization of microbiome studies:** Variability in sequencing methods, bioinformatic pipelines, and sampling sites hampers cross-study comparisons.

3. Future Perspectives

1. Toward Precision Microbiome-Based Nutrition

Integration of multi-omics data (metagenomics, metabolomics, transcriptomics) with host performance indicators and AI-driven analytics will allow the design of personalized diets tailored to both genotype and microbiome. This could revolutionize pig nutrition by maximizing feed efficiency while minimizing health risks.

2 Sustainable Pig Nutrition

Microbiome research will play a key role in developing sustainable feeding systems. For example:

- Low-protein diets supplemented with amino acids to reduce nitrogen pollution while supporting microbial balance.
- Valorization of agricultural by-products and novel protein sources (e.g., insects, algae) that rely on microbial fermentation to improve digestibility.
- Microbiome-informed feeding strategies to lower methane and nitrous oxide emissions from manure management.

3 Next-Generation Interventions

Future microbiome-targeted interventions may include:

- Designer synbiotics tailored to specific pig growth stages.
- CRISPR-based microbiome editing to silence harmful microbial genes.
- Smart sensors and digital twins of pig gut ecosystems to predict health and nutrient requirements in real time.

4 Regional Adaptations

In developing regions like India and Southeast Asia, locally isolated probiotics, fermented feed resources, and indigenous feed additives may offer **cost-effective microbiome**

solutions. This aligns with initiatives such as Atmanirbhar Bharat, promoting self-reliance and reducing dependence on imported additives.

CONCLUSION

The field of pig nutrition is shifting from a nutrient-centric view to a host–microbiome–diet systems approach. Feeding the microbiome represents a sustainable, antibiotic-free, and scientifically promising pathway to improve swine health, productivity, and welfare. However, translating this knowledge into practical, affordable, and region-specific solutions remains the central challenge for the next decade of research and industry innovation.

REFERENCES

1. Adeola, O., & Cowieson, A. J. (2011). Board-invited review: Opportunities and challenges in using exogenous enzymes to improve nonruminant animal production. *Journal of Animal Science, 89*(10), 3189–3218.
2. Agus, A., Planchais, J., & Sokol, H. (2018). Gut microbiota regulation of tryptophan metabolism in health and disease. *Nature Reviews Gastroenterology & Hepatology, 15*(6), 323–338.
3. Barrangou, R., & Doudna, J. A. (2016). Applications of CRISPR technologies in research and beyond. *Nature Biotechnology, 34*(9), 933–941. https://doi.org/10.1038/nbt.3659.
4. Belkaid, Y., & Hand, T. W. (2014). Role of the microbiota in immunity and inflammation. *Cell, 157*(1), 121–141.
5. Berding, K., & Donovan, S. M. (2016). Diet can impact microbiota composition in children with autism spectrum disorder. Frontiers in Neuroscience, 10, 178. https://doi.org/10.3389/fnins.2016.00178.
6. Bergamaschi, M., Tiezzi, F., Howard, J., Huang, Y. J., Gray, K. A., Schillebeeckx, C., & Maltecca, C. (2020). Gut microbiome composition differences among breeds impact feed efficiency in swine. *Microbiology Open, 9*(4), e991. https://doi.org/10.1002/mbo3.991.
7. Biasato, I., Gasco, L., Dezzutto, D., Dabbou, S., Schiavone, A., & Gai, F. (2019). Black soldier fly larvae meal inclusion in pig diets: Effects on gut microbiota and immune responses. *Journal of Animal Science and Biotechnology, 10,* 12.
8. Canibe, N., & Jensen, B. B. (2012). Fermented liquid feed—Microbial and nutritional aspects and impact on enteric diseases in pigs. *Animal Feed Science and Technology, 173*(1–2), 17–40.
9. Clavijo, V., & Flórez, M. J. V. (2018). The gastrointestinal microbiome and its association with the control of pathogens in broilers and pigs: A review. *Animal Feed Science and Technology, 241,* 1–15. https://doi.org/10.1016/j.anifeedsci.2018.04.010.
10. Dowarah, R., Verma, A. K., Agarwal, N., Singh, P., & Singh, B. R. (2018). Selection and characterization of probiotic lactic acid bacteria and its impact on growth, nutrient digestibility, health, and antioxidant status in weaned piglets. *PLOS ONE, 13*(3), e0192978. https://doi.org/10.1371/journal.pone.0192978.
11. FAO. (2023). FAOSTAT: Livestock Primary Data. Food and Agriculture Organization of the United Nations.
12. Fukuda, S., Toh, H., Hase, K., Oshima, K., Nakanishi, Y., Yoshimura, K., ... & Ohno, H. (2011). Bifidobacteria can protect from enteropathogenic infection through production of acetate. *Nature, 469*(7331), 543–547.
13. Furusawa, Y., Obata, Y., Fukuda, S., Endo, T. A., Nakato, G., Takahashi, D., ... & Ohno, H. (2013). Commensal microbe-derived butyrate induces differentiation of colonic regulatory T cells. *Nature, 504*(7480), 446–450.
14. Ganz, T. (2003). Defensins: Antimicrobial peptides of innate immunity. *Nature Reviews Immunology, 3*(9), 710–720.
15. Gibson, G. R., Hutkins, R., Sanders, M. E., Prescott, S. L., Reimer, R. A., Salminen, S. J., Scott, K., Stanton, C., Swanson, K. S., Cani, P. D., Verbeke, K., & Reid, G. (2017). Expert consensus document: The concept of prebiotics revisited. *Nature Reviews Gastroenterology & Hepatology, 14*(8), 491–502.
16. Gresse, R., Chaucheyras-Durand, F., Fleury, M. A., Van de Wiele, T., Forano, E., & Blanquet-Diot, S. (2017). Gut microbiota dysbiosis in postweaning piglets: Understanding the keys to health. *Trends in Microbiology, 25*(10), 851–873. https://doi.org/10.1016/j.tim.2017.05.004.
17. Guevarra, R. B., Hong, S. H., Cho, J. H., Kim, B. R., Shin, J., Lee, J. H., Kang, B. N., Kim, Y. H., Wattanaphansak, S., Isaacson, R. E., & Kim, H. B. (2019). The dynamics of the piglet gut microbiome during the weaning transition in association with health and nutrition. *Journal of Animal Science and Biotechnology, 10*(1), 1–12. https://doi.org/10.1186/s40104-019-0364-5.

18. Haenen, D., Zhang, J., da Silva, C. S., Bosch, G., van der Meer, I. M., van Arkel, J., & Smidt, H. (2013). A diet high in resistant starch modulates microbiota composition, SCFA concentrations, and gene expression in pig intestine. *Journal of Nutrition, 143*(3), 274–283.

19. Heo, J. M., Opapeju, F. O., Pluske, J. R., Kim, J. C., Hampson, D. J., & Nyachoti, C. M. (2013). Gastrointestinal health and function in weaned pigs: A review of feeding strategies to control post-weaning diarrhoea without using in-feed antimicrobial compounds. *Journal of Animal Physiology and Animal Nutrition, 97*(2), 207–237.

20. Hinton, A., Corrier, D. E., Spates, G. E., Norman, J. O., Ziprin, R. L., Beier, R. C., & DeLoach, J. R. (2021). Biological control of Salmonella typhimurium in young broiler chickens. *Poultry Science, 69*(1), 134–146.

21. Holman, D. B., Brunelle, B. W., Trachsel, J., & Allen, H. K. (2017). Meta-analysis to define a core microbiota in the swine gut. *mSystems, 2*(3), e00004-17.

22. Hu, J., Ma, L., Nie, Y., Chen, J., Zheng, W., Wang, X., Xie, C., Zheng, Z., Wang, Z., Yang, T., Xu, S., & Luo, Y. (2018). A microbiota-derived bacteriocin targets the host to confer diarrhea resistance in early-weaned piglets. *Cell Host & Microbe, 24*(6), 817–832. https://doi.org/10.1016/j.chom.2018.11.006.

23. Hu, R., He, Z., Liu, M., Tan, J., Zhang, H., Hou, D., Wu, S., & Tang, Z. (2022). Sodium butyrate supplementation improves gut morphology and growth in weaned piglets. *Animal Nutrition, 8*(1), 23–31.

24. Jha, R., & Berrocoso, J. F. D. (2016). Dietary fiber and protein fermentation in the intestine of swine and their interactive effects on gut health and on the environment: A review. *Animal Feed Science and Technology, 212,* 18–26.

25. Johansson, M. E. V., Larsson, J. M. H., & Hansson, G. C. (2011). The two mucus layers of colon are organized by the MUC2 mucin, whereas the outer layer is a legislator of host–microbial interactions. *Proceedings of the National Academy of Sciences, 108*(Suppl. 1), 4659–4665.

26. Joyce, S. A., & Gahan, C. G. (2016). The gut microbiota and the metabolic health of the host. *Current Opinion in Gastroenterology, 32*(2), 120–127.

27. Lallès, J. P., Bosi, P., Smidt, H., & Stokes, C. R. (2020). Nutritional management of gut health in pigs around weaning: Options and limitations. *Animal Feed Science and Technology, 263,* 114432.

28. Lee, S. H., Shinde, P. L., Choi, J. Y., Kwon, I. K., Lee, J. K., Pak, S. I., ... & Chae, B. J. (2019). Effects of dietary green tea catechins on growth performance, meat quality, and immune responses in finishing pigs. *Journal of Animal Science, 87*(6), 1738–1745.

29. Lei, X. G., Weaver, J. D., Mullaney, E., Ullah, A. H., & Azain, M. J. (2013). Phytase, a new life for an "old" enzyme. *Annual Review of Animal Biosciences, 1,* 283–309.

30. Li, Y., Guo, Y., Wen, Z., Jiang, X., Ma, X., & Han, X. (2022). Association of gut microbiota composition with feed efficiency traits in pigs. *Animal Nutrition, 8*(2), 183–194.

31. Liu, H., Zhang, J., Zhang, S., Yang, F., Thacker, P. A., & Ma, X. (2020). The role of maternal microbiota in shaping the intestinal microbiota of piglets at early life. *Animal Nutrition, 6*(4), 366–373.

32. Liu, Y., Wang, X., Chen, Y., Yu, J., Zheng, P., He, J., ... & Chen, D. (2018). Dietary fiber–induced improvement in porcine intestinal barrier function involves enhanced mucosal immune responses and altered gut microbiota. *Scientific Reports, 8,* 2343.

33. Louis, P., & Flint, H. J. (2017). Formation of propionate and butyrate by the human colonic microbiota. *Environmental Microbiology, 19*(1), 29–41.

34. Ma, W., Zhang, Y., Li, Y., Zhao, J., Chen, Y., & Xu, Q. (2024). Molecular identification and probiotic potential of lactic acid bacteria isolates from pigs. *Frontiers in Microbiology, 15,* 1425738.

35. Markowiak, P., & Śliżewska, K. (2018). Effects of probiotics, prebiotics, and synbiotics on human and animal health. *Nutrients, 10*(11), 1723.

36. Mateos-Aparicio, I., Mateos, P. V., Redondo-Cuenca, A., Villanueva-Suárez, M. J., & Zapata-Revilla, M. A. (2020). The influence of algae polysaccharides on gut microbiota and health: A review. *Critical Reviews in Food Science and Nutrition, 60*(1), 1–13.

37. McCormack, U. M., Curião, T., Buzoianu, S. G., Prieto, M. L., Ryan, T., Varley, P., Crispie, F., Magowan, E., Metzler-Zebeli, B. U., Berry, D., & Cotter, P. D. (2017). Exploring a possible link between the intestinal microbiota and feed efficiency in pigs. *Applied and Environmental Microbiology, 83*(15), e00380-17. https://doi.org/10.1128/AEM.00380-17.

38. Niu, Q., Li, P., Hao, S., Zhang, Y., Kim, S. W., Li, H., Ma, X., Gao, S., & He, L. (2019). Dynamic distribution of the gut microbiota and the relationship with apparent crude fiber digestibility and growth stages in pigs. *Scientific Reports, 9*(1), 1–10. https://doi.org/10.1038/s41598-019-51364-9.

39. NRC. (2012). *Nutrient requirements of swine* (11th Rev. ed.). Washington, DC: National Academies Press.

40. Partanen, K. H., & Mroz, Z. (1999). Organic acids for performance enhancement in pig diets. *Nutrition Research Reviews, 12*(1), 117–145.

41. Peng, L., Li, Z. R., Green, R. S., Holzman, I. R., & Lin, J. (2009). Butyrate enhances the intestinal barrier by facilitating tight junction assembly via activation of AMP-activated protein kinase. *American Journal of Physiology-Gastrointestinal and Liver Physiology, 296*(4), G710–G718.

42. Pieper, R., Bindelle, J., Rossnagel, B., Van Kessel, A., Leterme, P., & Zentek, J. (2012). Influence of dietary fibre on nutrient digestibility and microbial fermentation in growing pigs: A review. *Livestock Science, 145*(1–3), 121–131.

43. Pluske, J. R., Turpin, D. L., & Kim, J. C. (2018). Gastrointestinal tract (gut) health in the young pig. *Animal Nutrition, 4*(2), 187–196. https://doi.org/10.1016/j.aninu.2017.12.004.

44. Pohl, C. S., Medland, J. E., & Moeser, A. J. (2017). Early-life stress origins of gut microbiota development and vulnerability to disease in pigs. *Neurogastroenterology & Motility, 29*(9), e13195.

45. Pomar, C., Hauschild, L., Zhang, G. H., Pomar, J., & Lovatto, P. A. (2019). Precision feeding can significantly reduce feeding cost and nutrient excretion in growing pigs. *Journal of Animal Science, 87*(3), 912–924.

46. Ramayo-Caldas, Y., Mach, N., Lepage, P., Levenez, F., Denis, C., Lemonnier, G., ... & Estellé, J. (2019). Phylogenetic network analysis applied to pig gut microbiota identifies an ecosystem structure linked with growth traits. *ISME Journal, 13*(12), 2966–2977.

47. Schokker, D., Zhang, J., Vastenhouw, S. A., Heilig, H. G., Smidt, H., Rebel, J. M., & Smits, M. A. (2014). Long-lasting effects of early-life antibiotic treatment and routine animal handling on gut microbiota composition and immune system in pigs. *PLoS ONE, 9*(2), e100401.

48. Singh, A., Verma, A. K., Agarwal, N., & Singh, B. R. (2023). Fermented cereal-based functional feed ingredients for piglets: A sustainable approach. *Indian Journal of Animal Sciences, 93*(3), 325–332.

49. Sun, H., Tang, J. W., Fang, C. L., Yao, X. H., Wu, Y. F., Wang, X., & Feng, J. (2022). Effects of Bacillus subtilis on growth performance, antioxidant capacity, and intestinal health in pigs under heat stress. *Animal Science Journal, 93*(1), e13676.

50. Tan, J., McKenzie, C., Potamitis, M., Thorburn, A. N., Mackay, C. R., & Macia, L. (2014). The role of short-chain fatty acids in health and disease. *Advances in Immunology, 121,* 91–119.

51. Trevisi, P., Luise, D., & Bosi, P. (2020). The role of the gut microbiota in pig health and production. *Animal, 14*(S1), s216–s226. https://doi.org/10.1017/S1751731119003250.

52. Turnbaugh, P. J., Ley, R. E., Mahowald, M. A., Magrini, V., Mardis, E. R., & Gordon, J. I. (2006). An obesity-associated gut microbiome with increased capacity for energy harvest. *Nature, 444*(7122), 1027–1031.

53. van der Hee, B., & Wells, J. M. (2021). Microbial regulation of host physiology by short chain fatty acids. *Trends in Microbiology, 29*(8), 700–712. https://doi.org/10.1016/j.tim.2021.01.002.

54. Wang, J., Chen, L., Li, P., Li, X., Zhou, H., Wang, F., Li, D., Yin, Y., & Wu, G. (2018). Gene regulation and metabolomics in piglets with different growth rates induced by early-life microbial intervention. *Journal of Animal Science, 96*(4), 1365–1379.

55. Wang, X., Tsai, T., Deng, F., Wei, X., Chai, J., Knapp, J., Apple, J., Maxwell, C. V., Lee, J. A., Li, Y., & Zhao, J. (2019). Longitudinal investigation of the swine gut microbiome from birth to market reveals stage and growth performance-associated bacteria. *Microbiome, 7,* 109. https://doi.org/10.1186/s40168-019-0721-7.

56. Wu, G. D., Chen, J., Hoffmann, C., Bittinger, K., Chen, Y. Y., Keilbaugh, S. A., Bewtra, M., Knights, D., Walters, W. A., Knight, R., Sinha, R., Gilroy, E., Gupta, K., Baldassano, R., Nessel, L., Li, H., Bushman, F. D., & Lewis, J. D. (2011). Linking long-term dietary patterns with gut microbial enterotypes. *Science, 334*(6052), 105–108.

57. Xu, J., Chen, N., Wu, Z., Song, Y., Zhang, Y., Wu, N., Zhang, F., & Xu, X. (2020). 16S rRNA gene sequencing reveals changes in the gut microbiota of pigs fed fermented feed. *Applied Microbiology and Biotechnology, 104*(3), 1303–1313.

58. Yang, H., Huang, X., Fang, S., Xin, W., Huang, L., & Chen, C. (2017). Unraveling the fecal microbiota and metagenomic functional capacity associated with feed efficiency in pigs. *Frontiers in Microbiology, 8,* 1555. https://doi.org/10.3389/fmicb.2017.01555.

59. Yu, M., Li, Z., Chen, W., Rong, T., Wang, G., Ma, X., & Zhang, S. (2018). The role of probiotics in pig nutrition and health. *Journal of Animal Science and Biotechnology, 9,* 60.

60. Zhang, F., Cui, B., He, X., Nie, Y., Wu, K., Fan, D., & Fecal Microbiota Transplantation Clinical Study Group. (2018). Microbiota transplantation: Concept, methodology, and strategy for its modernization. *Protein & Cell, 9*(5), 462–473. https://doi.org/10.1007/s13238-018-0541-8.

61. Zhao, W., Wang, Y., Liu, S., Huang, J., Zhai, Z., He, C., Ding, J., Wang, J., Wang, H., Fan, W., Zhao, J., Meng, H., Chen, Y., & Wang, J. (2015). The dynamic distribution of porcine gut microbiota and its relationship with host growth performance. *ISME Journal, 9*(6), 1177–1187. https://doi.org/10.1038/ismej.2014.212.

62. Zhu, L., Zhao, J., Wang, J., Bai, S., Wang, Y., Yu, H., & Ding, X. (2021). Dietary fiber and gut microbiota in pig production: A review. *Animal Nutrition, 7*(1), 1–10. https://doi.org/10.1016/j.aninu.2020.08.005.