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Formation and Nutritional Modulation of the Porcine Gut Microbiota: Postprint

Authors: Liu Hong, Wang Qi, Liu Zuohua, Qi Renli

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Abstract

The establishment of porcine intestinal microbiota constitutes a highly complex process. Through long-term evolutionary processes, microorganisms and the host have established a microecological equilibrium characterized by mutual dependence and mutual constraint. Intestinal microorganisms play a vital role in host animal growth and development, organ function, nutrient metabolism, and immune function. The formation and dynamic balance of the microbiota are subject to influence and constraint by various internal and external factors, particularly different nutrients (carbohydrates, proteins, fats, etc.) that exert significant effects on the composition of porcine intestinal microbial communities. This review focuses on the establishment characteristics of porcine intestinal microbiota and the regulatory effects of major nutrients on its modulation.

Full Text

Formation of Intestinal Microflora in Pigs and Nutritional Regulation

LIU Hong, WANG Qi, LIU Zuohua, QI Renli*

(Chongqing Key Laboratory of Pig Industry Sciences, Key Laboratory of Pig Industry Sciences, Ministry of Agriculture, Chongqing Academy of Animal Sciences, Chongqing 402460, China)

Abstract: The establishment of intestinal microflora in pigs is a highly complex process. Through long-term co-evolution, microbes and their host have developed a mutually dependent yet restrictive microecological equilibrium. Intestinal microorganisms play crucial roles in host growth and development, organ function, nutritional metabolism, and immune function. The formation and dynamic balance of microbial communities are influenced by multiple internal and external factors, particularly dietary nutrients (carbohydrates, proteins, fats, etc.), which significantly affect the composition of porcine intestinal microbiota.

This review focuses on the characteristics of intestinal microflora formation and the regulatory effects of major nutrients.

Keywords: pigs; intestinal microflora; nutrients

1 Composition and Function of Intestinal Microorganisms

The digestive tract of monogastric animals harbors three main types of microorganisms: bacteria, archaea, and eukaryotic microbes, with bacteria being numerically dominant and primarily anaerobic [1-2]. Microbial composition varies across different gastrointestinal regions, with both diversity and density increasing from the stomach to the hindgut [3]. The cecum represents the most microbially diverse and abundant site in monogastric animals. In pigs, each gram of intestinal content contains 10^{12}-10^{13} CFU of microorganisms comprising 400–500 species, predominantly *Bacteroides* (8.5%-27.7%) and Firmicutes including *Clostridium* cluster XIVa (10.8%-29%) and *Clostridium* cluster IV (25.2%) [4-6].

Microbial communities form relatively stable consortia through utilization of specific nutritional environments in the gut and through interactions with the host and both inter- and intra-species microbial relationships. A stable intestinal microbiota establishes a bacterial barrier on the surface of intestinal epithelial cells, helping the host resist invasion by foreign pathogens and inhibiting colonization and proliferation of enteric pathogens through nutrient competition [7]. Additionally, stable gut microbiota participate in host nutrient metabolism through various mechanisms including fermentation, polysaccharide degradation, and vitamin synthesis [8-9]. Compared with conventional animals, germ-free animals exhibit delayed development of mucosal immune organs and reduced numbers of lymphocytes in the intestinal lamina propria, parameters that improve significantly when these animals are colonized with normal microbiota [10]. This demonstrates the critical relationship between intestinal microbiota and immune system development. Research in humans and animal models indicates that gut microbiota and their metabolites are closely associated with various cancers, metabolic diseases such as diabetes and obesity, and brain and neurological development [11].

2 Establishment of Intestinal Microflora in Pigs

Early studies suggested that piglets were sterile in the uterus and that microbial colonization began only after birth through exposure to maternal birth canal, fecal, and environmental microorganisms [12]. However, other research indicates that piglets may already harbor microorganisms such as *E. coli* and *Staphylococcus* in their intestines during embryonic development due to ingestion of amniotic fluid [13]. During the suckling period, *Lactobacillus* and *Streptococcus* dominate the piglet gut, which aligns with the physiological characteristics of the suckling piglet intestine and facilitates optimal utilization of milk nutrients. Weaning induces significant changes in diet and environment, resulting in corresponding shifts in gut microbial composition. As pigs age, the stability of intestinal microbiota gradually increases, with compositional differences among gut segments reflecting their distinct structural and functional adaptations. Eventually, a stable intestinal microflora dominated by *Bifidobacterium* and *Lactobacillus* becomes established.

Throughout this colonization process, the pig gut undergoes a successional transition from sterile → aerobic → facultative anaerobic → obligate anaerobic bacteria. The gut is initially oxygen-rich, but as aerobic and facultative anaerobic bacteria such as *Staphylococcus*, *Enterococcus*, and *Enterobacteriaceae* colonize and consume oxygen, intestinal pH and redox potential decrease, creating favorable conditions for obligate anaerobes. Consequently, although anaerobes colonize last, they ultimately account for over 99% of the microbial population, with facultative anaerobes and aerobes comprising less than 1%.

Different pig breeds and ages show high similarity in microbial species but substantial differences in distribution and abundance [14]. Comparative studies of colonic microbiota between Landrace and Meishan pigs revealed that Meishan pigs had significantly lower total bacteria, Firmicutes, and Bacteroidetes counts than Landrace pigs, but a higher proportion of Firmicutes relative to total bacteria. This may reflect the greater tolerance of Meishan pigs to roughage and their higher fiber digestibility, as major fiber-degrading bacteria belong to Firmicutes [15]. As pigs age, the abundance and quantity of dominant bacteria change markedly (Table 1) [16]. Research confirms that dietary fiber digestibility increases with body weight, with differences in fiber utilization across age stages primarily dependent on the fermentative capacity of gut microbiota—adult pigs harbor 6.7 times more fiber-degrading bacteria than growing pigs [17-18]. Additionally, studies demonstrate that gut microbial diversity is closely related to age (Figure 1 [Figure 1: see original paper]) [19].

3 Effects of Nutrients on Porcine Intestinal Microbial Composition

Dietary nutrients profoundly influence microbial colonization and dynamics in the host animal. Gut microorganisms utilize dietary components that the host cannot directly digest or absorb to support their own growth and reproduction, while reciprocally providing glucose, vitamins, fatty acids, and trace elements to the host. The composition of intestinal microbiota is intimately linked to the host’ s capacity for nutrient digestion and absorption [20]. Conversely, changes in dietary nutrients alter the substrates available for microbial fermentation, thereby significantly impacting microbial composition.

3.1 Effects of Carbohydrates on Porcine Intestinal Microbial Composition

Carbohydrates represent the primary energy source for pigs. Dietary crude fiber, a class of carbohydrates that cannot be directly digested or absorbed by the pig intestine, mainly comprises cellulose, hemicellulose, and lignin. Crude fiber significantly influences gut microbial composition. Freire et al. [21] compared the effects of four different fiber sources on cecal volatile fatty acid (VFA) content in weaned piglets, finding that soybean hulls increased VFA content by 11.2%, 30.5%, and 27.2% compared with wheat bran, beet pulp, and alfalfa meal, respectively. Additionally, pigs fed high-fiber diets showed significantly greater gastrointestinal microbial activity than those fed low-fiber diets [22]. These results demonstrate that fiber source and level differentially regulate gut microbial composition. Variations due to fiber source likely relate to solubility, lignification degree, and structure, as more soluble fiber is more readily fermented by gut microbes, increasing microbial activity. Differences due to fiber level may reflect distinct modes of action on gut microbiota. One study found that feeding high-level non-starch polysaccharide (NSP) diets initially decreased then increased colonic *E. coli* diversity, whereas low-level NSP diets produced the opposite effect [23].

Starch, another major carbohydrate, exists as amylose and amylopectin. Starch characteristics—including biological origin, amylose/amylopectin ratio, granule composition, and gelatinization degree—affect its biochemical properties, with the amylose/amylopectin ratio being a primary consideration in feed ingredient selection. Regmi et al. [24] fed piglets four starch-based diets (70% starch) containing <5%, 20%, 28%, and 63% amylose, respectively. The 63% amylose diet significantly increased fecal *Bifidobacterium* counts and total short-chain fatty acid (SCFA) and butyrate production compared with the other three groups. Amylose’ s stable structure and tendency to complex with lipids make it less digestible than amylopectin. Undegraded amylose escaping the small intestine enters the hindgut, where it serves as a substrate for anaerobic fermentation to produce SCFAs. Consequently, gut microbiota are more influenced by amylose than amylopectin.

Furthermore, various oligosaccharides uniquely regulate microbial balance. Studies demonstrate that fructooligosaccharides, xylooligosaccharides, soybean oligosaccharides, and inulin differentially promote gut health in pigs, primarily through varying degrees of utilization by gut microbiota, as reflected in differential proliferation of beneficial bacteria, inhibition of harmful bacteria, and variations in acid and gas production [25-26].

3.2 Effects of Protein on Porcine Intestinal Microbial Composition

Research indicates that as dietary protein level increases, unabsorbed protein entering the large intestine is hydrolyzed into peptides or amino acids that are fermented by microbes to synthesize microbial protein and metabolites such as volatile fatty acids. Branched-chain fatty acids (BCFAs) are exclusively generated by microbial metabolism of isoleucine, leucine, and valine, making them markers of microbial protein utilization [27]. Cho et al. [28] found that compared with a high-protein diet (20%), a low-protein diet (15%) reduced phenol, indole, SCFA, and BCFA contents in pig feces by 35%-40%, indicating that microbial protein utilization is closely related to dietary protein level. High-protein diets increase nitrogenous compounds in the hindgut, elevate intestinal pH, inhibit *Lactobacillus* growth, and promote proliferation of pathogenic microorganisms [29]. Luo et al. [30] reported that low-protein diets (10%) significantly affected microbial species in cecal digesta of finishing pigs compared with normal-protein diets (16%), but did not significantly alter dominant phyla such as Bacteroidetes and Firmicutes. Cecal mucosal microbiota remained largely unchanged, likely because mucosal communities are relatively stable and less susceptible to environmental influences. Moreover, host genetic factors may exert stronger selective pressure on mucosal microbiota than environmental factors [31].

Different protein sources selectively influence microbial composition and metabolism. Microbial synthesis of B vitamins is affected by dietary protein degradation rate, quantity, and the balance between degraded biological ammonia and microbially available substrates [32]. Yu et al. [33] investigated the effects of two types of fermented soybean protein replacing partial fish meal in weaned piglet diets on major intestinal bacterial groups. Both fermented soybean proteins promoted *Lactobacillus* proliferation and inhibited *E. coli* in the hindgut, but the product fermented primarily with *Bacillus subtilis*, lactic acid bacteria, and yeast was superior to that fermented with *B. subtilis*, yeast, and *Aspergillus*. This difference likely relates to content of soy globulin and β-conglycinin (allergenic proteins), which can trigger allergic reactions in piglet intestines.

Therefore, considering the anti-nutritional properties of plant proteins and safety concerns of animal proteins, careful selection of dietary protein sources is essential in pig production. Compared with high-protein diets, appropriately reduced protein levels (while meeting essential amino acid requirements) better support intestinal health and reduce nitrogenous emissions.

3.3 Effects of Fat on Porcine Intestinal Microbial Composition

Dietary lipids in pig diets primarily derive from plant oils such as soybean, coconut, and corn oil. Triglycerides consist of one glycerol molecule and three fatty acid molecules. Free fatty acids entering the digestive system can cross microbial cell membranes, affecting microbial survival. Boyen et al. [34] fed *Salmonella typhimurium*-infected piglets different fatty acids and found that coated butyrate reduced fecal *S. typhimurium* counts and intestinal colonization. Using a porcine cecal model to investigate medium-chain fatty acids (sodium acetate, caprylate, and caprate) on *S. typhimurium* and other bacteria, researchers found that 15 mmol/L sodium caprylate significantly reduced *E. coli* and *Salmonella* without affecting other bacterial populations [35]. These differential effects likely relate to chemical structure. Medium-chain fatty acids can cross microbial cell membranes, lower intracellular pH, and cause pH-sensitive pathogenic microbes to expend excessive energy maintaining homeostasis, ultimately leading to death [36]. Short-chain fatty acids, conversely, help maintain intestinal barrier integrity [37].

Dietary fat effects are also influenced by source and level. Li et al. [38] investigated soybean oil, coconut oil, and their combinations in weaned piglets, finding that a 1:1 mixture improved villus height and medium-chain fatty acid digestibility compared with either oil alone. Differential effects likely relate to fatty acid composition—coconut oil contains >50% saturated medium-chain fatty acids that resist rancidity. Medium- and short-chain fatty acids more readily interact with microbes than long-chain fatty acids.

Although appropriate dietary fat sources can promote proliferation of beneficial bacteria, inclusion levels require careful consideration. Human microbiota transplantation studies in mice demonstrated that high-fat diets damaged intestinal structure, reduced microbial diversity, and caused dysbiosis [39]. Hekmatdoost et al. [40] similarly found that high-fat diets increased fecal Bacteroidetes and decreased beneficial bacteria, possibly because excessive fat accelerates intestinal metabolic dysfunction, disrupts redox balance, induces oxidative stress, and destabilizes gut microbiota [41-42].

3.4 Effects of Minerals and Vitamins on Porcine Intestinal Microbial Composition

Minerals and vitamins are essential micronutrients for normal physiological function, but their effects on gut microbiota remain unclear. High dietary zinc shows significant anti-diarrheal effects in piglets, closely associated with reduced fecal *E. coli* counts, as zinc ions inhibit *E. coli* respiratory chains [43]. However, other research suggests high zinc increases *E. coli* and *Enterococcus* counts in weaned piglets, while high copper inhibits harmful bacteria [44]. Although organic zinc and copper have partially replaced inorganic forms in production, concerns persist regarding residues in animal products and environmental pollution from excessive mineral excretion. These uncertainties complicate definitive conclusions about mineral effects on microbial composition. Research on vitamin supplementation effects is scarce, possibly because gut microbes synthesize many vitamins, making it difficult to accurately assess exogenous vitamin impacts. However, vitamin D may improve piglet gut health by modulating the immune system [45], suggesting potential influences on microbial composition.

3.5 Effects of Microecological Preparations and Other Substances on Porcine Intestinal Microbial Composition

Antibiotic misuse has dramatically increased bacterial resistance and disrupted gut microbial balance. Microecological preparations, particularly probiotics, have become major antibiotic alternatives. Numerous studies demonstrate that single or combined use of *Lactobacillus*, *Bifidobacterium*, *Enterococcus faecium*, and *Bacillus* improves gastrointestinal health, optimizes microbial structure, inhibits pathogenic *E. coli* and *Salmonella*, and reduces diarrhea and enteritis [46]. However, practical challenges include inconsistent efficacy, uncertain dosing, and inter-strain antagonism. Other functional additives such as enzymes, acidifiers, and plant extracts also improve gut health and microbial balance but suffer from unstable effects and high production costs. Developing green, efficient additives remains an important ongoing challenge.

3.6 Effects of Nutrient Ratios on Porcine Intestinal Microbial Composition

Nutrients do not function independently but interact with each other, particularly among the three macronutrients. Jha et al. [47] found that the dietary crude protein to NSP ratio positively correlated with ammonia concentration but negatively correlated with SCFA content in growing pig colons, indicating interactive effects between protein and fiber levels. Similar research confirmed that high protein levels (20%) increased protein fermentation in piglet colons, while simultaneous fiber elevation reduced protein fermentation, decreased fecal Enterobacteriaceae, and enhanced carbohydrate fermentation [48]. Furthermore, as the dietary carbohydrate to plant fat energy ratio decreased, piglet cecal and colonic pH increased while VFA content and *Lactobacillus* and *Bifidobacterium* counts decreased, and *E. coli* counts increased [49]. Reduced carbohydrate energy decreased available substrates for microbes, causing cecal and colonic dysbiosis [50], while increased fat induced intestinal inflammation and promoted pro-inflammatory microbes [51]. These findings suggest that optimizing nutrient ratios during diet formulation, considering their interactive effects on gut microbiota, better promotes intestinal health.

3.7 Effects of Other Factors on Porcine Intestinal Microbial Composition

Gut microbiota are also affected by housing environment, feeding methods, and feed form. Weaning separates piglets from sows, changes their environment, and transitions them from milk to solid feed, altering feeding behavior and feed physical form. These environmental, psychological, and nutritional stressors increase pathogenic bacteria such as *E. coli* and can cause severe diarrhea. Compared with suckling piglets, weaned piglets show significantly reduced beneficial *Lactobacillus* and increased harmful *E. coli*, severely threatening gut health [52]. Therefore, enhanced management and smooth weaning transitions are critical in pig production.

4 Conclusion

Intestinal microbiota play vital roles in pig health and development but are susceptible to environmental, stress, disease, and nutritional factors that can cause dysbiosis. Nutrients are key determinants of microbial balance, and optimal intestinal environment and microbiota can only be achieved by comprehensively considering pig breed, age, and appropriate nutrient combinations (including sources, levels, and ratios). Given the similarities between porcine and human intestinal development, physiology, and metabolism, mechanistic studies on nutrient effects on porcine gut microbiota can not only improve pig production efficiency but also provide theoretical insights for human intestinal health and disease management.

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