Understanding the Diversity and Roles of the Pig Gut Microbiome

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The pig gastrointestinal tract (GIT) harbors a complex, dynamic, and dense microbial ecosystem, collectively known as the gut microbiome, which plays a foundational role in host health, metabolic homeostasis, and overall swine production efficiency. Phylogenetically, the pig gut is heavily dominated by the phyla Firmicutes and Bacteroidota, though its composition shifts drastically along the longitudinal axis of the GIT, dictated by local physiological gradients such as pH, digesta transit time, and oxygen availability. Temporal successions are equally pronounced. The transition during the weaning period represents a critical developmental window characterized by sharp microbial dysbiosis, making piglets highly susceptible to post-weaving diarrhea caused by pathogens like enterotoxigenic *Escherichia coli*. Functionally, the swine microbiome acts as a critical metabolic organ. It breaks down non-digestible dietary carbohydrates via fermentation to produce short-chain fatty acids (SCFAs), principally acetate, propionate, and butyrate, which serve as primary energy sources for colonocytes and modulate systemic energy metabolism. Beyond nutrition, the microbiota is indispensable for the structural maturation of gut-associated lymphoid tissue (GALT), the regulation of mucosal immunity, and the maintenance of intestinal barrier integrity through the competitive exclusion of pathogens. Ultimately, a deeper mechanistic understanding of these host-microbiota interactions provides a roadmap for precision nutrition.