

Microbiome and metabolism impacted by dietary fiber

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The pig gastrointestinal tract harbors a diverse array of microorganisms. Dietary fiber plays a crucial role in influencing both the mucosal layer and the microbiota. High-fiber diets are known to promote the growth of beneficial bacteria, such as *Bifidobacterium* and *Lactobacillus* species, while low-fiber diets favor the proliferation of harmful bacteria, including *Clostridium perfringens* and *E. coli*. Thus, the inclusion of dietary fiber is essential for maintaining a healthy and well-functioning gut, earning it the designation of the “Seventh Category of Nutrients”.

Dietary fiber is primarily fermented in the hindgut, producing short-chain fatty acids (SCFAs) and other metabolites that play significant roles in body metabolism. These metabolites can affect the metabolism of the liver, brain, fat, and muscle tissues, ultimately influencing the overall nutrient and energy metabolism networks of the host, and consequently the health and performance of animals. However, the mechanisms underlying fiber-gut microbiome-host interactions require further investigation.

The effects of various structural fibers on the gut microbiota of sows, piglets, growing and finishing pigs have been reviewed, revealing that different types of structural fibers exert varying effects on gut microbiota. In summary, dietary fiber helps maintain the stability of the pig intestinal microbiota, promotes the growth of fibrolytic bacteria, and inhibits pathogenic bacteria. Diets supplemented with Eubiotic lignocellulose (OptiCell®) have been shown to reduce inflammation and enhance reproductive performance in sows and growth performance in piglets by modulating the intestinal microbiome.

Microbial metabolites, particularly SCFAs, serve as a crucial link between dietary fiber and gut health. Nonetheless, the specific effects of dietary fibers with different structures on the pig intestinal microbiome remain unclear.

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