



Editorial: Gut Microbial Response to Host Metabolic Phenotypes

Jie Yin¹, Yong Su^{2*} and Hui Han^{3*}

¹ College of Animal Science and Technology, Hunan Agricultural University, Changsha, China, ² College of Animal Science and Technology, Nanjing Agricultural University, Nanjing, China, ³ State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China

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Editorial on the Research Topic

Gut Microbial Response to Host Metabolic Phenotypes

It is increasingly apparent that gut microbiota perform functions crucial to the host, such as regulating host physiology and influencing host health (1–3). Using fecal bacteria transplantation technology, Wu et al. found that fecal microbiota from obese Jinhua pigs and lean Landrace pigs exert different lipid metabolic phenotypes. Zheng et al. also witnessed gut microbial alterations in high fat diet-fed mice, with a high ratio of Firmicutes to Bacteroidetes and abundance of *Allobaculum*. Although this Research Topic failed to receive any papers about the role of gut microbiota in amino acid metabolism, nucleic acid metabolism, and carbohydrate metabolism, other reports have confirmed these functions (4, 5).

Currently, the gut microbiota is attracting much interest due to its role in maintaining host health and its association with all aspects of health and diseases. In this Research Topic, gut microbial disorders are screened in persistent atrial fibrillation patients (Xu et al.) renal cell carcinoma metastasis patients (Dai et al.), and a spinal cord injury animal model (Rong et al.). Xu et al. thoroughly discussed the taxonomic and functional characteristics of the gastrointestinal microbiota and demonstrated the profound relationship between gastrointestinal microbiota and metabolic disorders in ruminants. Together, these results further confirmed the role of gut microbiota in disease occurrence and development and manipulation of gut microbiota might, therefore, be considered a potential target for treating diseases.

Indeed, various disease treatment measures include gut microbial improvement, such as dietary probiotics (6). For example, Zhang et al. reported that dietary *Lactobacillus acidophilus* ATCC 4356 improved gut microbiota distribution and alleviated renal ischemia–reperfusion injury. Similarly, beneficial effects of *Lactobacillus* have been identified in lumbar disc herniation (Wang et al.), hypercholesterolemic golden hamsters (Yang et al.), asthma, and *Clostridium perfringens* infection (Wang et al.). In animal production, the gut is generally disturbed by weaning stress, dietary toxins, and pathogen infections, thus dietary probiotics have been widely introduced to maintain a healthy gut and guarantee higher production performance (7). *Lactococcus lactis*, in this Research Topic, has been identified to improve gut function in piglets (Yu et al.). However, probiotics are not limited to *Lactobacillus*, some species of *Bifidobacterium*, *Escherichia coli*, *Enterococcus*, and *Saccharomyces* have long been used as probiotics to alleviate various diseases by changing gut microbiota compositions.

Gut microbiota diversity and compositions are highly associated with dietary fluctuations. Thus, dietary manipulation has also been used to target gut microbiota to regulate host physiology and metabolism. In this Research Topic, Qian et al. found that dietary dried citrus peel (Chenpi) improved gut microbiota compositions in high fat diet-fed mice. Li et al. concluded that maternal fiber nutrition during pregnancy regulated the health of offspring, and the response of the maternal

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Christophe Lacroix,
ETH Zürich, Switzerland

*Correspondence:

Yong Su
yong.su@njau.edu.cn
Hui Han
hanhui16@mailsucas.ac.cn

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intestinal microbes played an important role in intervening in the phenotype of sows and neonatal piglets. Dietary protein and amino acids are the main factors shaping gut microbiota (8), Fu et al. also reported a role of tryptophan in gut microbiota. Besides, vitamin K2 (Liu et al.), β -carotene (Yuan et al.), olive fruit extracts (Wang et al.), bovine lactoferrin (Wang et al.), and β -sitosterol (Yu et al.) have been reported to shape gut microbiota compositions in this Research Topic.

How does gut microbiota affect host physiology and metabolism? Hou et al. showed that the gut–liver FXR–FGF19 axis is involved in *Lactobacillus delbrueckii*-promoted ileal bile acid deconjugation. In our previous studies, we found that gut microbiota-derived metabolites are highly associated with host metabolic reprogramming (9–12). Furthermore, bacterial microRNA, bacteriocin, and microbiota sensing pathways have also been identified to be involved in the relationship between gut microbiota and host metabolism (13, 14). However, with the focus on the detailed mechanism by which gut microbiota influence host metabolism, much still needs to be elucidated.

In summary, papers from the current Research Topic screened the gut microbiota dysbiosis in various diseases and reported the beneficial roles of dietary probiotics and other active components in the improvement of gut microbiota. Despite the progress made in understanding the relationship between gut microbiota and host metabolism, there are a number of prominent research avenues that remain to be explored. For example, what are the

molecular and physiological links between the gut microbiota and host metabolism at the epigenetic, transcriptome, and proteome levels? Gut microbiota is changed in various pathologic conditions and microbial biomarkers need to be screened in specific metabolic diseases. Additionally, dietary manipulation is widely used to maintain a healthy gut microbiota composition, and the interaction between diets, gut microbiota, and host metabolism will be an important area of future research.

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All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

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