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THE EFFECT OF INTESTINAL MICROFLORA ON FAT DEPOSITION IN PIGS

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Porcine gastrointestinal tract harbors a vast and complex microbial community that plays fundamental roles in many essential processes, such as energy harvest and carbohydrate metabolism. Here we performed a comparative survey on gut microbiota and metagenomics among jejunum, ileum and cecum in Jinhua pigs with distinct fatness by 16S rRNA gene and metagenomic sequencing. Furthermore, we investigated the effects of host genetics and environmental factors on porcine gut microbial composition, and particularly focused on the identification of microbes associated with porcine FCR in a large scale of Jinhua pigs pig population. The major results are as follows:

1. We performed a comparative survey of the phylogenetic composition and diversity of gut microbiota among jejunum, ileum and cecum in Jinhua pigs by 16S rRNA gene sequencing, and found dramatic differences of microbial composition between small intestine (including jejunum and ileum)and cecum. Compared to the small intestine, the alpha diversity was greater in the cecum, while similar alpha-diversity was observed between jejunum and ileum. Clostridium and SMB53 were significantly enriched in the small intestine, while Prevotella, Treponema, Ruminococcus and Faecalibacterium showed a higher abundance in the cecum. Functional capacity analysis of gut microbiome revealed that the microbiome of small intestine plays important roles in the metabolism of small molecule nutrients, while the microbiome of cecum has stronger ability to degrade xylan, pectin and cellulose.

2. Jinhua pigs exhibit the characteristic of strong ability of fat deposition. We identified 42 fatness associated-bacterial species including Escherichia spp. that showed a notable increase of relative abundance in all three gut locations of high fatness pigs. By metegenomic sequencing analysis, we found genes related to pyruvate metabolism, and cysteine and methionine metabolism were significantly enriched in the jejunal metagenome of high fatness pigs; antigen processing and presentation, MAPK signaling pathway and endocrtosis were significantly enriched in the ileal microbiome of high fatness pigs; two-component system and bacterial chemotaxis were significantly enriched in the cecal metagenome of high fatness pigs. We suggested that the potential pathogens, inflammation process, and microbial metabolism and nutrient sensing are involved in the high fatness of pigs. Furthermore, the higher abundances of Bacteroides-Prevotella may inhibit the fat mass development and inflammation in the low fatness pigs.

3. A total of 550 Jinhua pigs with detailed feed intake records from two pig farms were used for 16S rRNA gene sequencing analysis. The results revealed significant effects of gender, farm and host genetics on porcine gut microbial community. The average FCR value of gilts was significantly higher than that of boars, and gilts also showed significantly higher alpha-diversity of gut microbiota than boars. In addition, pigs reared III in the same pen showed significantly higher similarity of beta-diversity than pigs in different pens. Full-siblings had a higher similarity of bacterial community structure than half-siblings and unrelated individuals. We further compared the relative abundance of bacteria between males and females, and identified 8 bacterial families that showed distinct abundances between gilts and boars in both populations, including Veillonellaceae, Prevotellaceae and Spirochaetaceae. Furthermore, at the genus level, 62.5% of FCR-associated genera are sex-different in their abundances. Functional prediction and meta-

genomic sequencing analysis demonstrated significant difference of gut microbiome between boars and gilts. Most of these differential functional profiles are related to digestion and metabolism. We then suggested that sex-biased microbes and metagenomics might play important effects on porcine feed efficiency.