



Seasonal Differences in Fecal Microbial Community Structure and Metabolism of House-Feeding Chinese Merino Fine-Wool Sheep

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The digestive tract microorganisms play a very important role in the host's nutrient intake, environmental suitability, and affect the host's physiological mechanism. Previous studies showed that in different seasons, mammalian gut microbes would be different. However, most of them are concentrated in wild animals. It remains unclear how seasonal change affects the gut microbes of Chinese merino fine-wool Sheep. Therefore, in this experiment, we continuously collected blood and feces samples of 50 Chinese merino fine-wool sheep in different seasons, measured the physiological indicators of blood, and passed 16S rRNA amplicon sequencing, determined the microbial community structure of fecal microorganisms and predicted flora function by PICRUSt. The results of blood physiological indicators showed that WBC, Neu and Bas in spring were significantly higher than those of other seasons. Fecal microbial sequencing revealed seasonal changes in gut microbial diversity and richness. Among them, Chinese merino fine-wool sheep had the highest gut microbes in summer. Firmicutes and Bacteroidetes were the dominant phyla, and they were unaffected by seasonal fluctuations. LEfSE analysis was used to analyze representative microorganisms in different seasons. The Lachnospiraceae and its genera (Lachnospiraceae NK4A136 group, Lachnospiraceae AC2044 group, g_unclassified_f_ Lachnospiraceae) were representative microorganisms in the three seasons of spring, summer and winter with harsh environmental conditions; while in autumn with better environmental conditions, the Ruminococcaceae and its genus (Ruminococcaceae_UCG-009 and Ruminococcaceae_UCG-005) were the representative microorganism. In autumn, the ABC transporter and the pyruvate metabolic pathway were significantly higher than other seasons. Correlation analysis results showed that Lachnospiraceae participated in the ABC transporters metabolic pathway, which caused changes in the blood physiological indicators. Overall, our results showed that, in response to seasonal changes, Chinese merino fine-wool sheep under house-feeding have adjusted their own gut microbial community structure, causing