

ABSTRACT

458 Impact of Rumen Bacteria on Marbling in Wagyu Cattle.

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The objective of this study was to investigate the influence of the rumen bacterial community composition and abundance on marbling grade and breed in Wagyu cattle. Wagyu cattle are known for highly marbled and tender meat with unique flavor. This taste comes from the mono-unsaturated fatty acids, mainly oleic acid (18:1 n-9) which makes Wagyu fat more soft and palatable. It is believed that stearic acid (18:0) is responsible for fat hardness and its desaturation by a Delta -9 desaturase in Wagyu to oleic acid results in the tenderness. In the rumen, the microbial community plays important role in saturation and desaturation of fatty acids by biohydrogenation and in providing energy to the host animal through volatile fatty acids. In this study, we have analyzed the rumen bacterial community structure in 85 Wagyu animals from rumen samples collected at harvesting. Phenotypes of carcass traits were also collected from all animals at harvest. The animals in this study were either crossbred (F1) or full blood (FB) animals and came from 14 different producers which utilized different dietary and management conditions. The V4 region of the 16S rRNA gene was sequenced using the Illumina MiSeq platform to evaluate the microbial community composition in Wagyu cattle. The sequencing data were processed by using custom pipelines. All statistical analysis performed was adjusted to account for producer variation before analyzing for carcass traits. Alpha diversity metrics, Chao1 and observed OTUs, displayed higher ($P= 0.001$) bacterial richness in F1 than FB and displayed no difference ($P >0.4$) in bacterial community richness due to marbling grade. The principal coordinate analysis displayed distinct clustering of bacterial communities for FB and F1 which suggested that breed has an effect on the bacterial community composition. Further, these observations were confirmed by PERMANOVA which displayed different ($P<0.001$) bacterial communities between breeds (FB and F1) and producers while no difference ($P>0.05$) for marbling grade. Furthermore, we performed analysis to identify differential OTUs between marbling grades and to identify OTUs that were correlated with increased marbling scores. The differential OTUs ($P<0.001$) identified in the highest marbling grade predominately belonged to families Mogibacteriaceae, Lachnospiraceae and Clostridiaceae. Additionally, several differential OTUs ($P<0.001$) were also associated with FB, predominantly from bacterial families Spirochaetaceae, Mogibacteriaceae, Lachnospiraceae, Fibrobacteraceae, Ruminococcaceae and Prevotellaceae. The results from this preliminary study demonstrate that the rumen microbial community composition may influence marbling and manipulating the rumen microbial community may lead to increased marbling.

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