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**Effects of ensiled mulberry leaves and sun-dried mulberry fruit pomace on the composition of bacteria in feces of finishing steers**Yan Li<sup>1,2</sup>, Qingxiang Meng<sup>1,2</sup>, Bo Zhou<sup>1,2</sup> and Zhenming Zhou<sup>1,2</sup><sup>1</sup>State Key Laboratory of Animal Nutrition, China<sup>2</sup>China Agricultural University, China

The objective of this study was to compare the effects of ensiled mulberry leaves (EML) and sun-dried mulberry fruit pomace (SMFP) on fecal bacterial communities in Simmental crossbred finishing steers fed the following 3 diets: A standard TMR diet, standard diet containing EML and standard diet containing SMFP and the diets had similar protein and energy levels. Bacterial communities in the fecal content were analyzed using Illumina Miseq sequencing of the V4 region of the 16S rRNA gene amplification. Quantitative real-time PCR was used to detect the selected bacterial species in the feces. Most of the sequences were assigned to phyla Firmicutes (56.67%) and Bacteroidetes (35.90%), followed by Proteobacteria (1.86%), Verrucomicrobia (1.80%) and Tenericutes (1.37%). And the predominant genera included the 5-7N15 (5.91%), CF231 (2.49%), *Oscillospira* (2.33%), *Paludibacter* (1.23%) and *Akkermansia* (1.11%). As for the treatments, no significant differences were observed in Firmicutes ( $p=0.28$ ), Bacteroidetes ( $p=0.63$ ), Proteobacteria ( $p=0.46$ ), Verrucomicrobia ( $p=0.17$ ) and Tenericutes ( $p=0.75$ ). On the genus level, classified genera with high abundance (more than 0.1%) mainly came from two phyla: Bacteroidetes and Firmicutes. Also no differences were observed in most genera level, 5-7N15 ( $p=0.21$ ), CF231 ( $p=0.62$ ), *Oscillospira* ( $p=0.9$ ), *Paludibacter* ( $p=0.33$ ) and *Akkermansia* ( $p=0.37$ ), except that rc4-4 were lower in the CON and SMFP groups compared to the EML animals ( $p=0.02$ ). Additionally, there were no differences in richness estimate and diversity indices ( $p>0.16$ ), and treatments had no significant effect on most selected bacterial species in the fecal ( $p>0.06$ ), except that *Ruminococcus albus* were higher in the EML group ( $p<0.01$ ) and *Streptococcus bovis* were lower in the CON group ( $p<0.01$ ). In conclusion, diets supplemented with EML and SMFP have little influence on fecal bacterial community composition in finishing steers.

394620205@qq.com