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Differences in the rumen methanogen population exist between Jerseys and Holsteins

Holstein and Jersey breeds account for the vast majority of cows within the dairy industry. While the population of rumen methanogens has been sequenced and analyzed in the Holstein, to our knowledge, a direct comparison has not yet been done between Holsteins and Jerseys. The molecular diversity of rumen methanogens in Holstein and Jersey dairy cows were investigated using 16S rRNA gene libraries prepared from pooled PCR products from the rumens of 9 Holsteins and 10 Jersey cows from Vermont. A total of 365 clones were generated, 180 clones from the Holsteins and 185 clones from the Jerseys. Approximately 99% of all clones identified belonged to the genus Methanobrevibacter, with 43% of these clones closely related to Methanobrevibacter ruminantium. Based upon 98% sequence identity, these 365 clones were assigned to 55 different OTU's. Twenty OTU's (85% of the clones) were common in both breeds. However, the Holstein cows revealed 23 OTU's not found in the Jersey cows, and the Jersey cows revealed 12 OTU's not found in the Holsteins. Shannon index and Libshuff analysis indicate that significant differences exist between the composition ($p=0.01$) and diversity ($p<0.05$) of the methanogen libraries constructed from these two dairy breeds. These results suggest that breed and differences in feed utilization efficiency may account for the different rumen methanogen populations from these two dairy breeds.