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Ruminal pH, VFA, microbiota, and performance of high-yield dairy cows supplemented with *saccharomyces cerevisiae* culture

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Dramatic increases in milk yields in recent decades have created challenges in terms of rumen pH and microbial health which ultimately impact on dairy cow health. The objective of this study was to assess effects on ruminal pH, Volatile Fatty Acid (VFA), microbiota, and performance of high-yield dairy cows by supplementing *saccharomyces cerevisiae* culture (SCC). Forty Holstein cows were divided into two groups based on their milk yield, days of milk, and parity, were fed the same basal ration diet that did or did not contain 100 g of SCC /cow per d. Individual dry matter intake (DMI) and milk yield were recorded each day. Rumen fluid and milk samples were collected after 2 hours of morning feeding at intervals of 15 days during the experiment period. The data showed that average rumen pH was increased by 0.19 ($P=0.09$) when SCC was supplemented than when no SCC was provided. Supplemented cow consumed 0.28 kg ($P<0.05$) extra DM/d during the trial period. Those supplemented with SCC produced 1.36 kg ($P<0.05$) more milk/cow per d than did non-supplemented cows. Milk fat percentage was higher (4.11 vs. 3.96%) for cows receiving SCC. There were no differences in milk protein percentage. Rumen fluid VFA concentration was not statistically affected by SCC, but was numerically higher acetic and lower propionic for supplemented cows. SCC-supplemented cows had a greater relative abundance of *prevotellaceae, Succinivibrionaceae, Burkholderiaceae, Fibrobacteraceae, Lactobacillaceae*, and lower relative abundance of *Spirochaetaceae, Methanobacteriaceae, Enterobacteriaceae* than the unsupplemented cows. It had greater functions on xylanolysis, fermentation, cellulolysis in rumen in terms of the KEGG function prediction analysis. This study demonstrated that high-yield lactation cows receiving supplemental SCC produced more milk and consumed more DM. Cows consuming SCC potentially enhanced rumen good bacteria and depressed maleficent bacteria.