Mitigation of Methane in Dairy Cows by Nitrate Feed and Yea-Sacc Supplementation

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Dairy cattle are responsible for approximately 128 kg CH4/head compared with swine and beef (1.5 and 53 kg CH4/head, respectively). The aim was to feed nitrate to dairy cows to mitigate ruminal methane production by competing with methanogens for H2 produced during fermentation. Selenemonas species are stimulated by yeast, so Yea-Sacc was added to encourage selenomonads to drive DMI and propionate production from lactate. Three squares consisting of 4 lactating Jersey cows each were fed either a diet containing urea or calcium nitrate. Cows were given TMR twice daily with 50 g of a ground corn control or Yea-Sacc topdress. After a transition period, the cows were on a final diet of 1.5% nitrate on a DM basis. On the fourth week, rumen, blood, milk, and methane samples were collected. Each period was at least 4 weeks. Rumen samples were collected at 0, 3, 6, and 9 h post feeding, and 6 N HCl was added to stop fermentation for subsequent VFA and ammonia concentrations. Methane sampling was taken 8 times over a 3-day period. Blood samples were taken prior to, and 3 h following, feeding for subsequent methemoglobin analysis. Ammonia concentration increased from 10.3 to 12.2 mg/dL of NH3N ($p=0.11$) when fed nitrate, which supported proof of concept. Methane production decreased ($p<0.01$) when cows were fed nitrate. An interaction of nitrate and Yea-Sacc ($p=0.01$) was explained by Yea-Sacc decreasing acetate:propionate without nitrate but increasing it with nitrate. Total protozoa numbers increased ($p=0.02$), probably explaining the increased butyrate ($p<0.01$). Methemoglobin increased ($p=0.01$) slightly from 0.55 to 1.53%; however, being below 30%, this was not a concern. Future research should focus on increasing DMI. Lower dosages or other nitrate forms might improve palatability. Determination of bacterial DNA results would help explain if Selenemonas species increased when nitrate and Yea-Sacc were fed.