Rumination and Methane Emissions in Pasture-Based Dairy Cows

L. J. Watt1, S. A. Utsumi2, C. Clark3, G. Krebs1, C. Petzel1

1 Charles Sturt University, Wagga Wagga, NSW, Australia, 2678
2 Michigan State University, W.K. Kellogg Biological Station, Hickory Corners, MI, USA, 49060 and
3 FutureDairy, Camden, NSW, Australia, 2006

Introduction and Background

• Growing global demand for milk, cost of milk production, and the added consequence of milk intensification on the environment is a significant issue facing dairy producers globally.
• Enteric methane from ruminant livestock, including dairy cows, accounts for approximately 17% of global methane emissions per year (Knapp et al. 2014).
• High consumption of fibre, associated with pasture-based diets, increases rumination patterns (Mendes et al. 2013) and methane (Knapp et al. 2014). But the potential association between rumination patterns and methane emissions has been largely unexplored.
• Manipulation of rumination patterns may offer opportunities to reduce methane production per unit of milk (i.e. residual methane).
• The objective of this case study is to investigate the variation of rumination patterns in pasture-based dairy cows overtime, and to establish if a relationship exists between rumination patterns and methane emissions.

Hypothesis

• We expect temporal consistency of rumination patterns in high and low ruminating cows.
• We expect an association between rumination patterns and methane emissions, with the prediction that high rumination cows will also be high methane emitting cows.
• We additionally predict that rumination will be associated with production traits, and that increasing milk production will reduce the residual methane.

Materials & Methods

• Animals: A herd of 156 lactating Holstein-Friesian cows including 90% US Holstein and 20% NZ Friesian (DIM: 174; 20.4, parity; 2.15, liveweight; kg; 609.91 and milk production; kg/d; 29.39).
• Treatments:
  - Rumination collars for collection of rumination and activity data (Right).
  - Rumination collars for collection of rumination and activity data (Right).

Results

• Analysis: Comparison between high and low rumination groups was conducted with a mixed model for a completely randomized design and structural equation modelling for path analysis of residual methane production using SAS 9.3v (Statistical Analysis Software, Cary, NC).

Conclusions

• As expected, temporal rumination patterns were shown in this case study to be consistent overtime.
• Cows previously classified high ruminators remained as high ruminators whereas low ruminators remained as low ruminators overtime.
• High ruminating cows were also high methane emitting cows. This response is largely associated with high milk production and thus higher feed intake in the high ruminating group.
• Insufficient evidence from the case study to support the prediction of a direct association between rumination and methane production as no direct or indirect association was detected.
• High ruminating cows were detected as high milk producing cows, thus their residual methane production was lower than the low rumination group.
• Potential strategies to decrease residual methane production could include increasing milk production (conversion efficiency), decreasing methane emissions (dietary and rumen manipulation), or some combination of both.
• Findings support the importance of increasing individual cow production to reduce residual methane.

Dilution of fibre diets, to alter rumination patterns could be a more promising methane mitigation strategy, with the hypothesis that high ruminating cows will be more sensitive to diet manipulations, for example changing concentrate levels.

References


Acknowledgements:

The authors would like to thank the W. K. Kellogg Biological Station, and KBS dairy staff Howard Straub III, Paul Greenway, Cheyenne Ryzena and Shannon Kimbure for their assistance during the study. Authors also want to thank the financial support to Lucy Watt from The Royal Agricultural Society Foundation and FutureDairy and partial funding from the WK Kellogg Foundation and AgBioResearch-MSU.