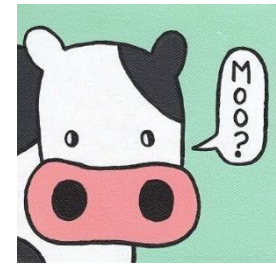


Enteric Fermentation Flagship Project

RUMEN MICROBIOME TO PREDICT METHANE EMISSIONS FROM CATTLE



WHY?

- Between animal variation for CH₄ production is known and heritable
- Breeding for low emitters offers permanent and cumulative changes over generations
- Cattle responsible for 62% of livestock greenhouse gas emissions worldwide
- Rumen microbial profile can be used as a proxy for CH₄ production

HOW?

- Methodology developed by Hess et al. (2018)* with sheep rumen samples has been validated with dairy cattle rumen samples from New Zealand
- High quality DNA produced that can be used to generate rumen microbial community profiles
- Genotyping by Sequencing (GBS) to optimise processing time and cost

THE PROJECT

- Develop microbial and genomic predictors for differences in CH₄ production among different large ruminant species (*Bos taurus*, *Bos indicus*, buffaloes, ...)
- Open to different production systems (grazing, confinement, dairy, beef, ...)
- 1,000 samples fully funded by Global Research Alliance (GRA)
- Allowance for sequencing costs for developing countries



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*Hess MK, Rowe SJ, Van Stijn TC, Brauning R, Hess AS, Kirk MR, Attwood GT, Janssen PH, McEwan JC (2018) High-throughput rumen microbial profiling using genotyping-by-sequencing. Paper presented at the World Congress for Genetics Applied to Livestock Production, Auckland, New Zealand