

## IMPLEMENTING GENETIC TOOLS TO REDUCE METHANE EMISSIONS IN NZ SHEEP FLOCKS

J.A. Archer<sup>1</sup>, M.D. Aspin<sup>1</sup>, D.E. Brier<sup>1</sup>, S-J. H. Powdrell<sup>1</sup>, D. Campbell<sup>1</sup>, C.L. Winkworth-Lawrence, S.J. Rowe<sup>2</sup>, J.C. McEwan<sup>2</sup> and M. Lee

<sup>1</sup>Beef + Lamb NZ, Wellington, New Zealand.

<sup>2</sup>AgResearch Ltd, Mosgiel, New Zealand.

### SUMMARY

Genetics is a tool which can reduce methane emissions, and a concerted effort is required to make this technology available to ram breeders and commercial sheep producers. As a technically demanding trait to measure there is a need for a combination of cheaper and more scalable proxy measures coupled with a genomic selection strategy. Roll out will require some technical challenges within the evaluation to be addressed, particularly around genomic evaluations in multi-breed populations when phenotype records are limited. Incentives to address methane emissions using genetic selection will require different approaches to many other traits as methane is an externality to sheep production business and not directly observable. Consequently, approaches to indirectly quantify genetic reduction in methane emissions, and to incorporate these reductions into assessments of farm level methane emissions will be required to incentivise uptake.

### INTRODUCTION

Methane emissions from ruminant livestock form a significant proportion of greenhouse gas emissions (GHG) in New Zealand, and so research to identify ways to reduce GHG without significant reductions in productivity has been undertaken in New Zealand and elsewhere for approximately two decades. Genetic selection of sheep to reduce methane output has been shown to be feasible, and to generate real reductions in methane with few antagonisms apparent with production and health traits (Rowe *et al.* 2019). The challenge is to implement this selection opportunity on an industry-wide scale to achieve verified reductions in the national GHG inventory. Some of the opportunities, approaches and challenges to achieving this are outlined.

### CHALLENGES IN PHENOTYPING, GENOTYPING AND EVALUATIONS

Methane is, at least with current technology, a “hard to measure” trait requiring both significant expertise and capital equipment for phenotype collection. This limits the scale at which phenotyping can be applied, and a strategy (breeding scheme design) utilising genomics is the obvious mechanism to maximise the benefits from the phenotypes collected to the wider breeding population.

**Phenotyping.** There are multiple ways of measuring methane emissions, but many are not scalable or portable, and so not well suited to on-farm measurement of methane in industry breeding flocks. The method that has been chosen and developed with industry in New Zealand is to use Portable Accumulation Chambers (PAC) mounted on a trailer that is shifted between properties (Goopy *et al.* 2011, Jonker *et al.* 2018). In New Zealand this method as currently configured has capacity to measure 12 animals concurrently for a 30-minute period. The protocol requires animals to be fully fed prior to measurement and it is feasible to measure approximately 168 animals over 1.5 days per property. It has been successfully used for the past 10 years, and the total number of animals phenotyped per year has been more than 7,000 up to 2016 in research and resource flocks and 2,328, 3,029, and 5,574 from 2020 to 2022 respectively and the capacity is effectively fully utilised currently. A second trailer will effectively double the capacity for PAC phenotypes to be collected, and the potential will exist to collect approximately 10,000 phenotypes per year in the

future. Notwithstanding the success of the PAC phenotype approach, it is logistically challenging, requires specialised technical expertise, has limited capacity, and costs NZ\$40 per animal.

The challenges around PAC measurements mean that a proxy measure would have significant benefits. Ideally the proxy measure would be cheaper, able to be scaled to many more animals and utilise more widely available expertise while maintaining a high genetic correlation with the target trait. Currently the use of a metagenomics approach based on a rumen sample looks promising (Bilton *et al.* 2022). It requires expertise to sample animals while maintaining welfare requirements, but this is widely available in the veterinary and animal technician community (and readily trainable). The throughput of animals is determined mainly by the time taken to sample (approximately 2 minutes per animal) and laboratory capacity, and so can be scaled to a significantly greater number of animals than the PAC measurement. The genetic correlation with the PAC measurement is  $0.76 \pm 0.14$  (Bilton *et al.* 2002) so is sufficiently high as to be a useful indirect criterion. The estimated cost is currently around \$50/sample, which will likely limit implementation unless technology can drive cost down (or alternative ways of funding the proxy phenotype are developed). Rumen microbiome samples have not yet been used in routine genetic evaluations.

A related approach might be to undertake a similar rumen microbial meta-biome analysis based on buccal swab samples (Kittlemann *et al.* 2015). This could further reduce the welfare cost to the animal (via less invasive sampling procedure relative to rumen fluid sampling) and make it feasible as an on-farm test without requiring highly trained technicians for sample collection. The cheaper and easier sampling could encourage further scale-up for phenotype measurement. However, currently there are several technical challenges implementing the preferred rumen metagenomics approach on buccal samples and this is under active development.

**Genotyping.** The challenge around genotyping is firstly to ensure that the methane phenotypes are matched with genotypes so that they contribute to methane genomic predictions, and then secondly to enhance the wider adoption of genotyping. The latter is not a methane-specific challenge, although demand for predictions on methane could conceivably assist with genomic technology uptake. Currently approximately 55,000 sheep are genotyped annually from a total of approximately 343,000 new animal identities loaded onto the national sheep genetic evaluation (nProve) database (averages per year born over 2020-2022 period). To date, all lambs with methane phenotypes collected are also genotyped, as industry subsidies for methane phenotype collection are conditional on the animal also having a genotype available in the analysis.

**Evaluations.** Currently research genomic breeding values (gBVs) for methane are produced in a single-step genomic BLUP (ssGBLUP) analysis, with the trait defined as absolute emissions. To make gBVs available widely across industry, key evaluation challenges will need solutions.

Firstly, a strategy will be required to enable gBV calculations across as many maternal breeds of sheep (and then Terminal breeds as the next priority) as possible. At present the NZ Genetic Evaluation (NZGE) for maternal worth uses genotypes for Romney, Perendale, Coopworth, Texel, and composites containing significant proportions of these breeds (being the most widely used maternal breeds in the NZ sheep flock), while genotypes from other breeds are excluded. A terminal evaluation is planned which will use genotypes from Suffolk, Texel and some other meat-oriented breeds. However, the NZ sheep flock is increasing in breed diversity, including moving towards fine-wool composites or shedding breeds. A strategy relying on genomics to select for methane across the wide range of breeds will require a solution which allows genotypes from multiple breeds to be used. This will depend on sufficient animals in these other breeds having both methane phenotypes and genotypes, and an evaluation solution which allows these genotypes to be incorporated and used to predict phenotypes for animals with genotypes only. This may require additional custom evaluations using genotypes from specific sets of breeds not currently included in the standard runs. In the long-term it would be desirable to include all breeds into a single analysis, but this may be more aspirational than realistic with available analysis techniques.

The ratio of phenotypes to genotypes is important to achieve stable evaluations using ssGBLUP analyses with current software. Methane will have a relatively low number of phenotypes relative to the number of animals currently genotyped, and within the current evaluation pipeline this leads to challenges in producing stable analyses with good convergence properties. Genotyping is likely to increase relative to methane phenotypes. Consequently, a different approach to evaluating methane and other sparsely recorded traits is required. One option to explore restricting the genotypes going into the ssGBLUP evaluation to animals from flocks actively recording methane phenotypes, and using a SNP co-efficients based approach to calculate gBVs for methane on animals whose genotypes are not included in the ssGBLUP.

**Methane EBV definition and indexes.** At present the research version of a methane BV is being calculated based on the absolute value of methane in nProve. In contrast, methane per kg dry matter intake, calculated from the same information, has been used to successfully create high and low methane selection lines in an experimental setting. However, it is still an open question as to how the methane BV should be formatted and expressed for use in industry, and the overall direction of the breeding program needs to account for the desired goals, regulatory environment and likely farmer responses. Regulatory authorities either want absolute values of methane per animal or preferably methane emitted per kilogram of dry matter ingested to be compatible with IPCC reporting conventions. In practice counting sheep and their classification is currently easier than estimating the dry matter production per farm. If the overall effect of the breeding program is mainly to improve the efficiency of production relative to methane emissions (i.e.. reduce emissions intensity), absolute methane emissions will only be reduced if production is capped and efficiency gains are used decrease the total feed consumed. Alternatively, a breeding objective which focusses on reducing the methane produced per kg of dry matter consumed could result in reduced absolute methane emissions without reducing the feed base or productivity. The latter approach is more desirable as drivers for financial sustainability of farm businesses tend to be directed towards maximising quantity of feed grown and utilised.

While the ultimate outcome of a breeding program is determined by the actual selection decisions, the format of BVs and indexes used can influence the direction substantially. Different formats of BVs can result in equivalent outcomes providing the index is generated consistently with the BV format, but a format which is easily understood and best aligns to the desired selection outcome will enhance uptake and utility. Different BV format options exist, including using the absolute value, using a percentage reduction relative to contemporary group mean, or using a residual approach (analogous to residual feed intake) by adjusting methane (on either a genetic or phenotypic basis) for another trait (e.g. total respiration, feed intake or weight) to lower the correlation between methane and size or production. Factors to consider include the ability of users to understand the trait definition and intuitively assess trait relationships, availability and accuracy of the trait data used in adjustments, and the suitability of the EBVs for use in GHG calculators.

#### **INCENTIVISING UPTAKE**

As an expensive and technically demanding trait, GHG measurement will only be sustained in the long-term if a commercial model emerges where breeders can extract sufficient additional revenue (or non-financial benefits) to cover measurement costs. This requires demand for improved rams in terms of methane production from commercial farmers. For most traits where genetic improvement results in better financial performance in the business (either cost savings, improved production or market premiums) the demand for improvement occurs from within the business. However, GHG emissions are an externality to farm businesses, and are not directly measured or observable, so improvement is unlikely to occur without other interventions.

The New Zealand government has proposed to levy agricultural businesses based on their methane emissions, which effectively converts methane emissions from an externality to having a

direct financial impact on farm businesses. Industry has expressed a strong preference for this to occur at the individual farm level based on a specific farm's emissions profile calculated using models and farm performance levels as inputs to an approved emissions calculator. To incentivise using genetics as a mitigation, it will be important to develop a mechanism where genetic reduction in emissions from sheep can be accounted for and reduce the emissions levy payable for farm businesses using methane improved rams. An estimate of the flock level genetic merit for methane emissions would be required as an input to the calculator.

Calculation of improvement at the national and individual flock level might use information on ram sales/purchases over time and a gene flow model. This will need to be backed by some sort of verification system to ensure information making its way into both the individual farm level calculator (for levy calculation purposes) and the national GHG inventory (to meet international reporting obligations) is accurate. Direct measurement of methane for verification is unlikely to be viable, but there is likely to be a role for genomics in the verification processes. Genomics could be used to directly estimate flock level methane emissions from co-efficient-based predictions, or could be used to estimate the genetic contribution of rams with methane EBVs to the flock (to verify claims based on gene flow models). Both approaches would utilise information held in the national sheep genetics database (nProve). Investment in information systems to implement this will be required.

With a strong government/public interest in climate mitigation, and a real need to accelerate the uptake of genetic improvement of methane emissions, there have been joint industry/government programs to offset 50 to 100% of methane recording costs. This has led to significant uptake of phenotyping, and also removes much of the "freeloader" objection to phenotyping when competitors benefit via genomics. However, once methane phenotyping becomes routine and not subsidised longer-term strategies will be required. Much of the further work described here will be incorporated into a new "Cool Sheep" program funded by Beef + Lamb NZ and the NZ government to accelerate the application of this proven GHG mitigation technology.

## **CONCLUSION**

Implementation and uptake of selection to improve methane emissions is a priority within the New Zealand sheep industry and is supported by Government. Challenges in improving methane are similar to other difficult to measure traits, but with additional issues which are unique to methane. These unique challenges revolve around the fact that methane is an externality to the business, while the societal and governmental drive to address greenhouse gas emissions provides opportunity to take different approaches to implementing selection to reduce methane emissions.

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