

GWAS FOR METHANE YIELD, RESIDUAL FEED INTAKE AND LIVEWEIGHT IN NEW ZEALAND SHEEP

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SUMMARY

Identification of genomic regions associated with environmentally important traits, such as methane yield and residual feed intake, has the potential to improve genomic selection models for these traits, which are typically difficult and/or expensive to measure. Methane Yield, Residual Feed Intake and Liveweight phenotypes were available on 965 composite ewe lambs that had gone through an individual feed intake facility between 5 and 10 months of age. Our aim was to estimate heritabilities and identify genomic regions associated with these traits. Bayesian genomic models showed moderate heritability estimates between 0.38 and 0.44 for all traits. A genome wide association study failed to identify any large-effect QTL for any of the traits, consistent with these being highly polygenic traits. Future studies will explore the relationships between these environmentally important traits and other production traits and assess prediction accuracies.

INTRODUCTION

Animals that have a lower environmental footprint will be a vital part of future livestock production. Methane Yield and Residual Feed Intake (RFI) are environmentally important traits that are typically difficult and expensive to measure on large numbers of animals, therefore identifying causative mutations or indicator traits may facilitate selection on these traits. Genomic selection is a promising approach (Rowe *et al.* 2014) and incorporation of QTL or their tagging SNPs into current selection models may further improve the potential of using genomics in these traits.

Dual-purpose composite ewe lambs (Dodds *et al.* 2014) were put through an individual feed intake facility between 5 and 10 months of age, and gas emissions, including methane, were measured using portable accumulation chambers (PAC). Bayesian Genome Wide Association Studies were run for RFI, Methane Yield (CH₄Yield) and Liveweight at 8 months (Liveweight) to identify genomic regions that are associated with these environmentally important traits.

MATERIALS AND METHODS

This study utilises a series of feed intake trials at AgResearch's Invermay campus (Elmes *et al.* 2014; Johnson *et al.* 2016; Johnson *et al.* 2018). Five cohorts of approximately 200 lambs were put through an individual feed intake facility for ~42 consecutive days between 5 and 10 months of age, where they were fed a Lucerne pellet diet. Gas emissions, including methane, were measured twice for each individual using PAC, ~14 days apart, as described in Jonker *et al.* (2018). The 965 lambs in this study came from 102 sires (range = 1-27 offspring per sire, median = 8).

Traits. Methane Yields, expressed as methane volume divided by total gas volume, were averaged for each individual to get the phenotype of CH₄Yield. RFI was calculated as described in Johnson *et al.* (2018), whereby energy intake was corrected for metabolic mid-weight, average daily gain, trial, cohort, and pen. Liveweight was recorded when the lamb was 8 months of age.

Genotypes. Animals were genotyped on a variety of sheep SNP chips, ranging in density from 6,000 to over 500,000 markers. These SNPs were imputed to ~48,000 SNPs present on the 50,000

SNP panel using a reference population of 16,320 New Zealand sheep using FImpute (Sargolzaei *et al.* 2014).

Statistical Analyses. Univariate Bayesian selection models for CH4Yield, RFI, and Liveweight were run using GenSel v4.90 (Fernando and Garrick 2009) with a chain length of 51,000, including burn-in of 1,000. Model equations were:

$$y = \mu + \text{brr} + \text{aod} + \text{bdev} + \text{cg} + \text{SNPs}$$

where y is the trait of interest: CH4Yield ($n=959$), RFI ($n=962$) or Liveweight ($n=963$); brr and aod are the fixed class effects for birth rear rank and age of dam, respectively; bdev is the fixed covariate for birth date deviation; cg is the contemporary group: flock*birthYear for CH4Yield and RFI, and flock.rbyrmx for Liveweight. Heritability estimates were obtained by fitting SNPs in a BayesC model assuming all SNPs were associated with the trait ($\pi = 0$). GWAS were performed by fitting SNPs in a BayesB model assuming ~5% of SNPs are associated with the trait ($\pi = 0.95$).

RESULTS AND DISCUSSION

Heritabilities. Moderate heritability estimates were obtained for all traits (Table 1). These estimates are consistent with other estimates for these traits in the same population (Pickering *et al.* 2012; Pinares-Patiño *et al.* 2013; Johnson *et al.* 2018; Jonker *et al.* 2018). The heritability for methane yield is a little higher than has previously been published in an expanded New Zealand dataset (Jonker *et al.* 2018), however this could be due to averaging the two measurements for CH4Yield rather than fitting a repeatability model. The two measurements were averaged because GenSel cannot fit random effects apart from SNP effects (Fernando & Garrick 2009).

Table 1. Genetic and phenotypic variance and heritability estimates for Methane Yield, Residual Feed Intake and Liveweight in ewe lambs

Trait	Genetic Variance	Phenotypic Variance	Heritability
Methane Yield	0.004	0.009	0.41
Residual Feed Intake	0.65	1.71	0.38
Liveweight (kg)	9.2	20.8	0.44

Genome wide association studies. All traits were found to be highly polygenic and the highest peak explained less than 0.6% of the total genetic variance (Figure 1). Within the 15 windows that explained the most variation in each trait, there was at least one window with a high posterior probability of inclusion in the model (>90%; larger points in Figure 1), suggesting that there may be causal mutations in these genomic regions that have a small impact on these phenotypes.

Selection for environmentally important traits. Although no large QTL were identified for CH4Yield or RFI, it is still possible to make genetic progress in these traits, due to their moderately high heritability estimates. 181 sheep were from the Methane Yield selection lines, which have been successfully bred for high and low Methane Yield using pedigree-based selection (Rowe *et al.* 2019). This flock is a valuable resource for uncovering relationships between Methane Yield and environmentally and economically important traits. Incorporation of additional information into evaluations, such as rumen microbial community profiles; has the potential to further improve our ability to select elite animals for these traits (Kittelmann *et al.* 2014).

CONCLUSIONS

This study confirms that both methane yield and residual feed intake are heritable but polygenic traits in New Zealand sheep; therefore, marker assisted selection for a limited number of markers is unlikely to be as successful as genomic selection for making genetic progress in these traits. Future studies will evaluate genetic and phenotypic relationships between these environmentally important traits and production traits, including carcass quality. Ongoing research is assessing prediction accuracy for these traits and evaluating the impact of including rumen microbial profiles.

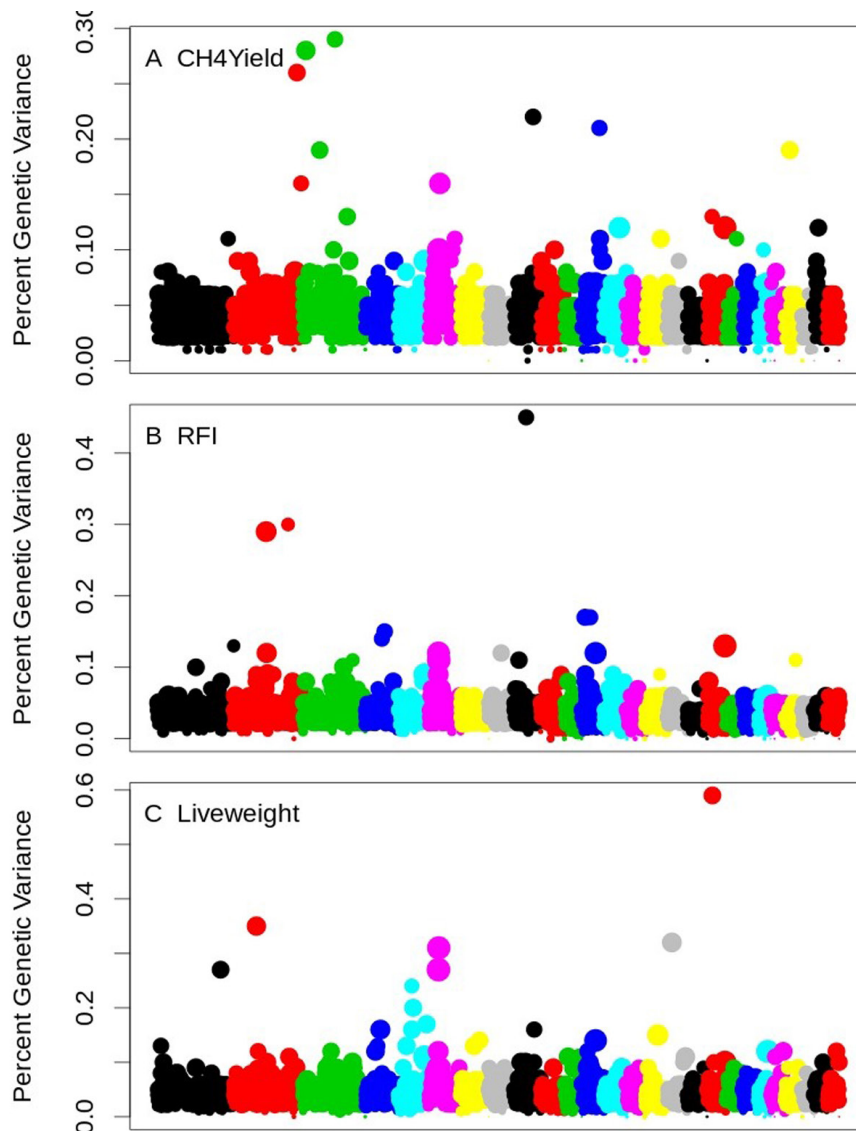


Figure 1. Genome wide association study of Methane Yield (A), Residual Feed Intake (B) and Liveweight (C) in ewe lambs whereby the size of the point is relative to the proportion of iterations in which the 1 Mb window explains some of the overall genetic variance

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