

Methane emission has low genetic correlations to lamb growth traits in Norwegian White sheep

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Abstract

Selection for reduced methane (CH₄) emission is a mitigation option. Inclusion of liveweight adjusted CH₄ (CH_{4adj}) emissions as a trait in the breeding goal is expected to result in a cumulative and permanent reduction in sheep farms greenhouse gas emission. Fifty-minute CH₄ emissions were measured in portable accumulation chambers on 4,534 Norwegian White ewes from 44 breeding flocks and expressed as grams per hour. Ten years of observations for the lamb growth traits 42-day and 140-day weights were extracted from the database along with the corresponding pedigrees. Heritabilities and direct and maternal genetic correlations were estimated for CH_{4adj} and the lamb growth traits. The heritability for CH_{4adj} was 0.17, and heritabilities for the growth traits were in the range 0.07 to 0.13. The genetic correlation between CH_{4adj} and maternal genetic effect of 42-day weight was 0.32 and significantly different from zero, while other correlations between CH_{4adj} and growth were non-significant.

Introduction

In 2019, the Norwegian agriculture sector made an agreement with the Norwegian government to reduce its cumulated greenhouse gas (GHG) emissions over the 2020 to 2030 period by 11% from 45-million-ton to 40-million-ton (Regjeringen.no, 2021). The main source of GHG emission in lamb meat production comes from enteric methane (CH₄) emission produced as a by-product in the non-aerobic fermentation of feed. Other countries have shown that enteric CH₄ emission is heritable in sheep (Jonker *et al.*, 2018; Pinares-Patiño *et al.*, 2013) and in cattle (e.g., Lassen and Løvendahl, 2016; Pszczola *et al.*, 2017). Breeding is thus a mitigation option (Pickering *et al.*, 2015) and including CH₄ emission as a trait in the breeding goal will result in a cumulative and permanent reduction in the national GHG emission from lamb meat production. The aim of the current study was to investigate the heritability of CH₄ in Norwegian White sheep and compute the genetic correlations to direct and maternal genetic effect of 42-day and 140-day weights.

Materials & Methods

Selection of sheep and flocks

Methane measurements in portable accumulation chambers (PAC) were collected on 4,534 Norwegian White sheep ewes that have lambed at least once or were expecting their first lambing. These sheep belong to forty-four (44) breeding flocks from 12 ram circles (Gjerdrem, 1969). Flocks from ram circles were chosen as they circulate rams for natural mating within the ram circle and in addition are required to use artificial insemination. The use of common rams thus results in genetic connectedness between flocks (Kuehn *et al.*, 2008).

Methane emission measurements

CH₄ emission (ppm) was measured in lots of 10 animals at a time. A hand-held Eagle2 instrument was used to capture accumulated 50 min CH₄ emissions following a measurement

protocol developed in New Zealand (Jonker *et al.*, 2020). Sheep were either fed fresh grass or grass silage and were required to be off feed for at least one and less than four hours prior to entering the chamber and were in addition weighed prior to measurement. Fifty-minute CH₄ concentration was converted to CH₄ g/hr. Both CH₄ g/hr and ewe weights were scaled, they were divided by the mean of the lot and multiplied by the mean of all observations.

Growth traits in routine genetic evaluation

It is compulsory for the ram circle flocks to weigh lambs at birth and at weaning, while weighing during the main suckling period is voluntary. Weights for the main suckling period are recorded between 15 and 70 days of age and adjusted to a 42-day weight (42-d_{adj}), while weaning weights are recorded between 90 and 180 days of age and adjusted to 140 days (140-d_{adj}). Both 42-d_{adj} and 140-d_{adj} are expressed as weight gain from birth, and 42-d_{adj} thus represents a part of the growth period to weaning. The growth traits 42-d_{adj} and 140-d_{adj} are a part of the portfolio included for the routine genetic evaluations in Norwegian sheep.

Ten years of phenotypes of 42-d_{adj} and 140-d_{adj} were extracted for the 44 ram circle flocks with CH₄ emission measurements. Mean, standard deviation and number of observations of methane emission and weights are listed in Table 1.

Table 1. Mean (sd) and number of observations for CH_{4adj}, live weight at measurement (Weight_{adj}), 42-day weight (42-d_{adj}), and 140-day weight (140-d_{adj}), above the diagonal is the number of observations with both traits.

	Mean (sd)	CH _{4adj} , g/hr	Weight _{adj} , kg	42-d _{adj}	140-d _{adj}
CH _{4adj} , g/hr	1.37 (0.28)	4,534	4,534	3,986	4,253
Weight _{adj} , kg	79.70 (9.88)		4,534	3,986	4,253
42-d _{adj}	14.34 (3.31)			91,873	84,496
140-d _{adj}	40.01 (7.69)				93,669

Pedigree

Pedigree was extracted from the national sheep recording database and traced as far back as possible on animals with phenotypes. The pedigree included a total of 154,683 animals.

Genetic evaluation model

Data was analysed in a tri-variate animal model using the DMU-software (Madsen and Jensen, 2013).

The model for methane emission was:
$$Y_{ijk} = FL_i + A_j + b_1 * W_{ijk} + a_{ijk} + e_{ijk} \quad (1)$$

Where Y_{ijk} is scaled CH₄ emission measured on animal k in Flock*Lot i of Age class j . W_{ijk} is scaled weight at measurement, b_1 is regression coefficient on Weight, a_{ijk} is random additive genetic effect of animal k , and e_{ijk} is random residual corresponding to Y_{ijk} .

The model for 42-d and 140-d weight was:
$$Y_{ijkl} = FY_i + ABKW_j + a_{ijk} + m_{ijl} + pe_{ijl} + e_{ijkl} \quad (2)$$

Where Y_{ijkl} is weight observation on lamb k in Flock*Year i and in rearing type $ABKW_j$, a_{ijk} is random additive genetic effect of lamb k , m_{ijl} is random additive genetic effect of the fostering dam l , pe_{ijl} is permanent environment effect of the fostering dam, and e_{ijkl} is random residual corresponding to Y_{ijkl} .

Results

Genetic standard deviations, heritabilities and genetic correlations for CH_{4adj}, 42-d_{adj} and 140-d_{adj} weights are shown in Table 2 along with standard errors. The heritability estimate for liveweight adjusted PAC CH₄ emission is similar to previously published sheep estimates (Goopy *et al.*, 2015; Dominik *et al.*, 2017) and also similar to estimates where either feed intake or its proxies (liveweight, CO₂ emission, O₂ consumption) were used either as covariates or expressed in the denominator of a ratio of methane emission (Pinares-Patiño *et al.*, 2013; Jonker *et al.*, 2018). The only significant correlation between CH_{4adj} and growth traits was the maternal genetic effect of 42-day weight.

Table 2. Genetic standard deviation (σ_a), heritabilities (in diagonal) and genetic correlations for CH_{4adj}, and direct (dir.) and maternal (mat.) genetic effect of 42-d_{adj} and 140-d_{adj} weights.

	σ_a	CH _{4adj} , g/hr	42-d _{adj} (dir.)	42-d _{adj} (mat.)	140-d _{adj} (dir.)	140-d _{adj} (mat.)
CH _{4adj} , g/hr	0.112	0.17 (0.04)				
42-d _{adj} (dir.)	0.897	-0.07 (0.11)	0.11 (0.01)			
42-d _{adj} (mat.)	0.776	0.32 (0.09)	-0.19 (0.05)	0.08 (0.01)		
140-d _{adj} (dir.)	2.291	0.19 (0.10)	0.71 (0.03)	0.05 (0.05)	0.13 (0.01)	
140-d _{adj} (mat.)	1.703	0.11 (0.10)	-0.18 (0.06)	0.82 (0.03)	0.00 (0.06)	0.07(0.01)

Genetic trends for CH_{4adj} and maternal genetic effect of 42-day weight are shown in Figure 1 (Left) along with number of ewes with CH₄ observations. Both traits follow the same trend until 2018, where the curve seems to flatten for CH_{4adj}. Most CH₄ observations are from ewes born 2017 through 2020. This may be contributing to the trend change, which in earlier years is largely driven by the maternal genetic correlation with CH_{4adj}.

Phenotypic trends for average carcass weight and number of days to slaughter for all 763 ram circle flocks are shown in Figure 1 (Right) for the same time period. The figure shows a decreasing trend in number of days to slaughter of one day per year and a simultaneously slight increase in average carcass weight. The increasing trend in methane emission is thus related to an increase in lamb growth during the main suckling period where the rumen only is partly functioning.

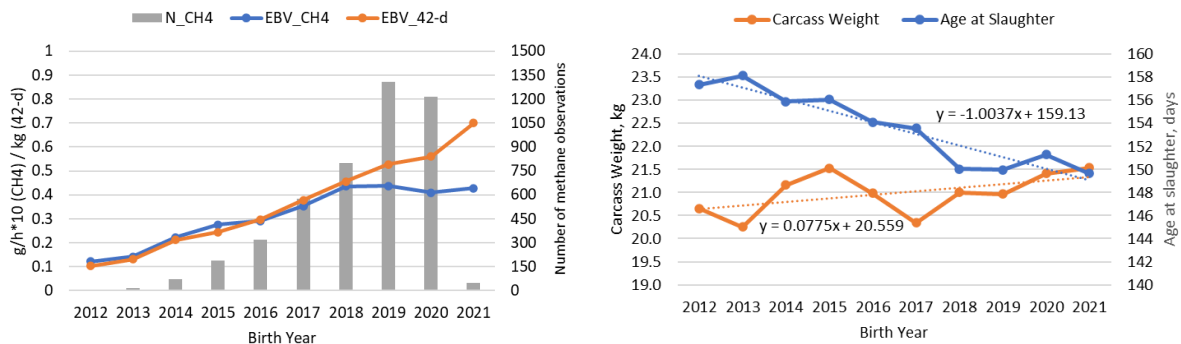


Figure 1. Left: Genetic trends for methane emission (g/hr *10), maternal genetic effect of 42-day weight, and number of animals with methane measurements by age class. Right: Phenotypic trends for carcass weight and age at slaughter.

Discussion

Based on this study, including liveweight adjusted PAC CH₄ emission into the breeding goal for Norwegian White sheep imply a reduction in the CH₄ conversion factor Y_m (% of gross energy intake partitioned into CH₄) Niu *et al.*, (2021) and as such also the national emissions, given no additional feed stuffs are grown or imported.

However, based on the correlations in Table 2, selection solely for reduced methane emission would result in a decrease in the maternal effect on lamb growth during main suckling period. This antagonistic relation should therefore be handled carefully when including methane emission in the breeding goal via appropriate weighting in the overall selection index.

Acknowledgement

This project has received funding from the European Union's Horizon 2020 research and innovation program under grant agreement No 772787 (SMARTER). The PAC chambers were designed and built by the Engineering Team at AgResearch New Zealand.

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