Biggins, A., McGovern, F., O' Connor, E., Boland, T., Walsh, H., McHugh, N. (2026) Are we breeding more efficient sheep? The role of maternal genetics in feed intake and methane emissions, *Proceedings 13th World Congress on Genetics Applied to Livestock Production* 23751: https://doi.org/10.31274/wcgalp.23751 ©2026 Biggins, et al. CC BY-NC-ND

Are we breeding more efficient sheep? The role of maternal genetics in feed intake and methane emissions

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Introduction

Genetic selection through maternal breeding indexes is an effective tool for enhancing reproductive efficiency, lamb survival and thereby flock productivity, with previous research demonstrating improvements in ewe productivity with concurrent reductions in production costs (Farrell *et al.,* 2022; Fetherstone *et al.,* 2023). Maternal breeding indexes typically combine female reproductive, survival and lamb growth traits into a single breeding index, with index structures reflecting country specific production systems (Conington *et al.,* 2004; Santos *et al.,* 2015). The comparison of similar international breeding indexes across comparable systems of production can help to elucidate the strengths and weakness of individual indexes by highlighting differences in index composition and trait emphasis (Fetherstone *et al.*, 2023). This presents an opportunity to assess trait inclusion as production goals evolve. Currently most maternal breeding indexes do not directly incorporate dry matter intake (DMI) or environmental traits such as methane emissions. However, given the mounting global pressure on agricultural systems to reduce enteric methane emissions, without a detrimental impact on productivity or farm system profitability, the effect of current maternal sheep breeding indexes on such traits warrants investigation. The objective of this project was to evaluate the impact of contrasting maternal genetic groups on a range of ewe efficiency and environmental traits.

Materials & Methods

This experiment was carried out at the Teagasc Animal and Grassland Research Centre, Mellows Campus, Athenry, Co. Galway, Ireland, across four production years. All procedures were approved by the Teagasc Animal Ethics Committee and the Health Products Regulatory Authority. Four distinct ewe genetic groups selected on maternal indexes were evaluated: elite maternal Irish ewes (Elite Irish), elite maternal New Zealand ewes (NZ), a cross between elite Irish and elite NZ ewes (Elite Irish×NZ), and low maternal Irish ewes (Low Irish). Each genetic group consisted of 50 animals, with breed balanced within group (25 purebred Suffolk and 25 purebred Texel ewes), balanced for age. All Irish ewes were selected based on their within breed rankings within the Irish maternal index; with the elite representing the top 20% and the low representing the bottom 20% of animals on the Irish maternal index. The NZ group originated from animals imported from New Zealand to Ireland in 2014 and 2015 that ranked in the top 40% of the New Zealand Maternal Worth Index (Fetherstone *et al.,* 2023). The NZ ewes evaluated in the current study also represented the top 20% of ewes evaluated within breed in the current Irish maternal index. Ewes were mated annually within genetic group, with reproductive management standardised across each genetic group. Following lambing, ewes and lambs grazed uniform pastures but remained within their genetic group. All groups were

stocked at a rate of 11 ewes/ha. A maximum of two lambs were reared per ewe; surplus lambs were artificially reared or fostered within genetic group. Ewe and lamb live weights were recorded at key timepoints throughout the production cycle which enabled the calculation of an annual ewe efficiency metric, as the ratio of total litter weaning weight of all lambs reared per ewe relative to the ewe pre-mating live weight.

Feed intake. Dry matter intake was estimated on a subset of ewes (n=18) within each genetic group at three time points annually (twice in lactation and once in the dry period) using the *n*-alkane technique as described by McGovern *et al.* (2021). Approximately 70% and 27% of ewes had repeated intake records within and across years, respectively. Dry matter intake was reported per kilogram of dry matter (DM) and was also expressed per kilogram of ewe live weight (DMI/ kg live weight) coinciding with DMI measurement. Dry matter intake measurements were conducted within (±3 days) of corresponding methane measurement.

Enteric methane emissions. Methane, oxygen, and carbon dioxide measurements were taken annually on all ewes within each of the four genetic groups using portable accumulation chambers (PAC) as described by O'Connor *et al.* (2021). Ewes were removed from pasture at least 1 hour before PAC measurement, and live weight was recorded using a Prattley weighing scales. Gaseous measurements were carried out in lots of 12 randomly selected ewes across all genetic groups, each allocated to 1 of 12 chambers. Concentrations of methane (ppm), O_2 (%), and CO_2 (%) were measured at 0 and 50 minutes using an RKI Eagle 2 gas analyser. Methane concentrations obtained were reported expressed as grams per day (g/day) using equations described by O' Connor *et al.* (2021). Methane emissions were also expressed per kilogram of ewe live weight coinciding with methane measurement (g methane /kg live weight) and per kilogram of litter weaning weight (g methane /kg litter weaning weight). Methane yield was calculated as the daily methane divided by the ewes' DMI (g methane /kg DMI).

Statistical analysis. The effect of genetic group on methane (methane (g/day), methane/kg live weight, methane/kg litter weaning weight), DMI (DMI (kg DM/day) and DMI/kg live weight) and ewe efficiency metrics was analysed using a linear model in SAS (SAS Institute Inc., Cary, NC). For all models, the fixed effects included genetic group (Elite Irish, NZ, Elite Irish×NZ and Low Irish), ewe breed (Texel or Suffolk), ewe lactation number (1, 2, 3, 4, or ≥5) and year of lambing (2022 to 2025). Additional fixed effects for methane and DMI related traits were days since lambing and the interaction between number of lambs born (1, 2 or ≥3) and rearing type (1, 2). Contemporary group (defined as measurement date–lot) and chamber number (1 to 12) were included as fixed effects when methane traits were the dependent variables, date of DMI measurement was included as a fixed effect when DMI traits were the dependent variable. In all models, ewe was included as a repeated effect and sire of the ewe was included as a random effect.

Results

The effect of ewe genetic group on methane emissions, DMI and ewe efficiency are shown in Table 1. The NZ genetic group exhibited a lower DMI (1.92 kg DM/day) compared to all other genetic groups ($P<0.05$), which did not differ from each other ($P>0.05$). When DMI was expressed relative to ewe live weight, a similar trend was observed with the NZ genetic group having the lowest DMI per kg live weight ($P<0.05$). Methane output did not differ between the NZ, Elite Irish×NZ and Low Irish genetic groups ($P>0.05$), however, methane output measured in the Elite Irish genetic group was lower compared to NZ and Low Irish genetic groups ($P<0.05$).When methane was expressed per kg live weight, Elite Irish genetic group had a lower methane per kg live weight compared to the Low Irish genetic group ($P<0.05$). Methane

expressed per kg litter weaning weight differed by genetic group (P<0.05), with the Low and Elite Irish having the highest values; the Elite Irish did not differ from the NZ or Elite Irish×NZ genetic groups (P>0.05). Methane yield followed the same trend as methane expressed per kg litter weaning weight (P<0.05). Ewe live weight at mating ranged from 76 (Low Irish) to 79 kg (Elite Irish) and did not differ between genetic groups (P>0.05). Ewe efficiency differed between genetic groups (P<0.05), with NZ and Elite Irish×NZ weaning the highest proportion of their live weight compared to Elite Irish and Low Irish genetic group (P<0.05).

Table 1. Predicted marginal means and standard error of the mean (SEM) for genetic group (Elite Irish, NZ, Elite Irish×NZ and Low Irish) on dry matter intake (DMI) , methane and ewe efficiency traits.

	Ewe maternal genetic group				
Trait[1]	Elite Irish	NZ	Elite Irish×NZ	Low Irish	SEM
DMI	2.22 [a]	1.92 [b]	2.16 [a]	2.32 [a]	0.082
DMI/ kg live weight	0.029 [ac]	0.025 [b]	0.027 [a]	0.030 [c]	0.001
Methane	24.01 [a]	25.70 [b]	25.11 [ab]	25.78[b]	0.841
Methane/kg live weight	0.308 [a]	0.337 [bc]	0.317 [ab]	0.341 [c]	0.010
Methane/litter weaning weight	0.630 [ab]	0.572 [a]	0.561 [a]	0.698 [b]	0.036
Ewe efficiency	0.576 [a]	0.690 [b]	0.699 [b]	0.527 [a]	0.027

[a to c] Values within rows with different superscript differ (P < 0.05) from each other.

[1] DMI (kg DM/day), DMI/ kg live weight (kg DM/kg live weight), methane (g/day), methane/kg live weight (g methane/kg live weight), methane/litter weaning weight (g methane/kg litter weaning weight), ewe efficiency metric (kg live weight/kg litter weaning weight).

Discussion

The validation of breeding indexes is crucial to ensure that predictions of genetic merit are accurate and unbiased which underpins farmer confidence and adoption of the indexes (Fetherstone *et al.*, 2021). This experiment formed part of a larger study, with the primary aim of validating production traits currently included in the national maternal index. However, there is an increasing necessity to reduce the environmental impact of sheep production systems (Boix-Fayos and de Vente, 2023), therefore, this study quantified difficult to measure traits including methane and DMI, which are not currently included in the index. Although neither the New Zealand nor the Irish breeding objective contain such environmental or feed related traits, ewe mature weight has been shown to explain a large proportion of the variation in both feed intake (Lewis and Emmans, 2010) and methane emissions (Robinson *et al.*, 2014), therefore, the question remains are such traits required within the breeding objectives or are the current indexes indirectly selecting for greater production and environmental efficiency. Results from the current study suggest that future breeding strategies will require the incorporation of methane and feed related traits to help achieve environmental targets without compromising performance.

The present study demonstrated that lower DMI was associated with the NZ genetic group; however, this did not translate to lower daily methane emissions or methane per kg live weight (or methane yield). This is in contrast to previously reported findings which showed a strong relationship between DMI and methane (Herd *et al.,* 2014), albeit most studies report DMI in an indoor setting rather than at pasture. Collectively, these results indicate that further investigation into the relationship between DMI and methane is warranted, especially at pasture. Both genetic groups that contained (any) Elite Irish genetics had the lowest (in the case of the Elite Irish) or numerically lower (in the case of the Elite Irish×NZ) methane values. A similar pattern was observed when methane was expressed per kg of live weight, indicating

that the differences in methane emissions were not solely driven by differences in live weight and corroborates previous findings (Moorby *et al.,* 2015). Methane yield followed a similar trend to DMI; however, the absolute methane yield values for the genetic groups were not reported directly in this study as PAC are predominantly a ranking tool for methane, thus providing a ranking estimate of the genetic groups for methane yield rather than absolute values. New Zealand Suffolk and Texel breeds have been shown to be genomically diverse compared to their Irish counterparts (O'Brien *et al.,* 2020) indicating that hybrid vigour may be present in the Elite Irish×NZ genetic group. However, in all instances the Elite Irish×NZ didn't differ from at least one of the parent genetic groups suggesting that no heterosis effect was observed in the present study. Ewe efficiency was highest in genetic groups containing NZ bloodlines, which is not unexpected given the similarities in ewe live weight across the genetic groups but the superiority in number of lambs weaned from the NZ genetic group (Fetherstone *et al.*, 2021).

Conclusions

Overall, although significant differences among genetic groups were observed for individual traits, the results indicate that no single group was consistently superior across the combination of environmental traits and DMI. These findings suggest that the incorporation of such traits into breeding objectives may warrant consideration in the future, however further investigation is required to establish specific trait definitions before they can be integrated into national breeding objectives.

Acknowledgements

Funding from the Irish Department of Agriculture, Food and Marine RumenVentory (2023RP908) and Sustain Sheep (2023GEH253) projects are gratefully acknowledged.

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