

29. Genetic selection of feed efficiency and methane emissions in sheep and cattle in Uruguay: progress and limitations

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Abstract

Residual feed intake (RFI) and methane (CH₄) emissions are potential new selection objectives in beef and sheep breeding programmes to assist reaching greenhouse gas mitigation targets and to support economic, social, and environmental sustainability. Phenotyping platforms in both species are in place in Uruguay, linked with the genetically evaluated populations of main breeds (Hereford, Merino, Corriedale, Dohne and Texel), being the basis of the reference populations for genomic selection. Current progress and main findings are described here. New selection indexes and selection criteria, as residual CH₄, are needed given the potential unfavourable associations between CH₄ and performance. Larger reference populations imply higher genomic prediction accuracies, accurate estimations of genetic correlations among feed intake, RFI, CH₄ and performance and a comprehensive understanding of these associations. On-going rumen metagenomics and metatranscriptomics will also provide information about its value as predictor of genetic merit of these traits.

Introduction

Global concerns regarding mitigation of greenhouse gas (GHG) emissions and efficient use of limiting resources is intensifying, as well as pressures to achieve national targets in the context of international environmental agreements. The identification of alternatives to support sustainable development is particularly relevant for countries whose economy rely on sheep and cattle production, such as Uruguay. The incidence of enteric methane (CH₄) in the total GHG emissions tend to be high in these countries (i.e. 46%, Uruguay) and drastic alternatives, such as reducing national flocks and herds to decrease total CH₄ would have significant unfavourable economic and social implications. Emission intensity (CH₄ per unit of product) is one of the indicators proposed to assess progress of GHG mitigation keeping the balance among environmental, economic, and social sustainability.

Genetic selection can contribute to both components of emission intensity. Uruguay have had breeding programmes in beef cattle and sheep for 30 years, and genetic progress have been reported for individual traits and selection indexes in both species. Although this looks promising in terms of enhancing the contribution of genetic selection to reduce emission intensity, improving production accompanied with higher feed intake may jeopardise the expected progress (Barwick *et al.*, 2019). Feed intake, feed efficiency and GHG emissions are recorded in new phenotyping platforms with the aim of evaluating strategies to incorporate these traits into the national breeding programmes supporting sustainable development (Phocas *et al.*, 2016). Here we describe the research approach carried out in cattle and sheep in Uruguay since 2014, in connection with breeding programmes, results and limitations.

Feed intake and efficiency

Feed efficiency measurements rely on feed intake records (adjusted by dry matter, DMI), which is a difficult-to-measure trait in large number of animals. Commercial availability of automated feed intake recording systems contributed to partially overcome this limitation. Post-weaning feed efficiency tests of Hereford bulls and steers started in 2014 at the Central de Prueba Kiyú of the Hereford Breeders Society of

Uruguay, with the aim of implementing genomic selection of residual feed intake (RFI) (Ravagnolo *et al.*, 2018). Nowadays, the national database includes post-weaning feed efficiency information of 960 pedigree bulls and 560 steers. More recently, RFI at finishing (feedlot) is also evaluated in steers immediately after the postweaning test. A similar initiative is carried out in the main sheep breeds in Uruguay in INIA Experimental Station La Magnolia, with 981 Merino, 300 Corriedale, 367 Dohne and 77 Texel lambs recorded at the end of 2021. These animals belong to Selection Nucleus (Merino), Information Nucleus (Corriedale, Dohne) and Central Progeny Testing (Texel) and are strongly connected with population in the genetic evaluation (performance recorded).

Koch *et al.* (1963) defined RFI as the difference between actual and predicted DMI, based on average daily gain (ADG) and metabolic body weight (MBW). Improving feed efficiency by selecting for RFI is an appealing breeding objective because of the associated increase of farmers net income by reducing feed costs without compromising animal performance. At a production system or national level, improving RFI could also be interpreted as a contribution to optimise the use of limiting resource, such as land in grazing-based systems. The final impact will depend on its genetic variability and covariance with other breeding objectives.

Heritability of RFI and association with production traits

As previously reported in the literature, RFI is a moderately heritable trait in Uruguayan Hereford and Merino breeds, with estimates of 0.25 (Pravia *et al.*, 2022, unpublished) and 0.27 (Marques *et al.*, WCGALP 2022), respectively. The genetic correlations (r_G) of RFI and the traits used for its estimation in Hereford were similar to the phenotypic associations (r_p): positive correlations with DMI ($r_p=0.63$; $r_G=0.40$) and very low or zero with ADG ($r_G=0.07$; $r_p=-0.003$) and MBW ($r_G=-0.12$; $r_p=-0.001$).

Accurate estimations of genetic parameters depend on large databases, principally for genetic correlations, which is challenging for difficult-to-measure traits. Consequently, many of the first studies rely on phenotypic associations and comparisons between animals with extreme values for the traits of interest, particularly when aiming to establish the associations of RFI with other difficult-to-measure traits, such as carcass and meat quality. In agreement with other studies, no significant differences were found in pasture-based finishing performance, carcass quality, meat production and quality between high- and low-RFI steers, based on their post-weaning RFI (Pravia *et al.*, 2018). The analysis of post-weaning RFI and feedlot RFI in 100 Hereford steers indicated that both feed efficiencies were strongly correlated (0.72), whilst AGD and MBW at finishing were independent of post-weaning and feedlot RFI ($P>0.05$) (Silveira *et al.*, 2022, unpublished data). Although there is evidence indicating that low RFI (high feed efficiency) was associated with lower fatness, we did not find unfavourable phenotypic associations between RFI and fatness measured *in vivo* or post-slaughter, or in terms of genetic correlations ($r_p=0.08$; $r_G=0.01$, Pravia *et al.*, 2022, unpublished). This may be explained by the incorporation of subcutaneous fat depth in the multiple regression model used for RFI estimation, as proposed by Basarab *et al.* (2003).

Studies in Corriedale lambs also indicated that RFI tends to be independent of growth, wool production, and genetic resistance to gastrointestinal parasites (Navajas *et al.*, WCGALP 2022, Ferreira *et al.*, 2021), whilst r_p and r_G between RFI and fleece weight in Australian Merino sheep were not significantly different from zero (Marques *et al.*, WCGALP 2022).

Genetics of GHG emissions in beef cattle and sheep

Methane and carbon dioxide (CO₂) emissions are being measured in all lambs with feed intake and efficiency records using Portable Accumulation Chambers (PAC) (Paganoni *et al.*, 2017), leading to a very interesting database that is used to investigate the association between current breeding objectives and

potentially new ones, such as RFI with GHG emissions. Similarly, GreenFeed stations are now installed and recording CH₄ during the feed efficiency tests in Hereford.

The first analysis in Corriedale and Merino lambs showed no-significant phenotypic association between RFI and CH₄ and CO₂ (Navajas *et al.*, WCGALP 2022), although a favourable positive genetic correlation was estimated in Merino which indicates that less efficient lambs are also higher emitters (Marques *et al.*, WCGALP 2022). This is in agreement with other studies in sheep (Paganoni *et al.*, 2017) and beef cattle (Fitzsimons *et al.*, 2013), reinforcing the possibility of using RFI as an indirect selection criterion for reducing GHG emissions. The lack of consistency among studies relies on different factors as discussed by Cantalapiedra-Hijar *et al.* (2018).

A consistent result across studies is the positive association of DMI with RFI, CH₄, as well as with animal productive performance. As mentioned before, several studies indicates that RFI tend to be independent of productive trait (null or low correlation) and moderate to highly correlated with DMI. Associations of similar magnitude have been reported between CH₄ and performance traits, suggesting a potential antagonism that could limit the scope of GHG mitigation strategies. Nonetheless, new CH₄-derived traits such as residual methane emissions and the development of multi-trait selection including DMI and CH₄ are promising alternatives to reduce CH₄ emissions while maintaining animal production (Manzanilla-Pech *et al.*, 2021; Smith *et al.*, 2021).

As DMI is a main driver of animal productivity and CH₄ emissions, disentangling the relationships among these traits is key, and requires considering not only animal genetics but also the role of rumen microbiota. On-going characterization of rumen microbial community and metabolic pathways by metagenomics and metatranscriptomics will contribute to a better understanding of these associations. These analysis in the Uruguayan reference populations will also provide information about its value as predictor of genetic merit.

Improving feed efficiency and methane emission by genetic selection

The complexity of measuring GHG emission and DMI to estimate RFI, clearly indicates the benefits of implementing genomic selection. Because of this, RFI and GHG emissions phenotyping platforms in sheep and beef cattle in Uruguay were designed as the initial reference populations for genomic selection based on national and international research funding. DNA samples are stored at INIA animal DNA bank and have been genotyped mainly with medium density (50k) single nucleotide polymorphism (SNP) panels. An initial binational reference population of 731 Uruguayan Hereford bulls and steers and 1168 Canadian bulls was the basis for the estimation of genomic expected breeding values (GEPD) published since 2017 (Ravagnolo *et al.*, 2018). Research GEPD for RFI and CH₄ have also been estimated in 2021 for Australian Merino, as a first step before incorporating these traits in the breeding programme. Larger reference populations have favourable impact on high accuracies of genomic predictions, which also represent an incentive for breeders to invest in genotyping and RFI and CH₄ phenotyping that accelerates the growth of reference population (Berry *et al.*, 2016). Although the expected benefits of genomic selection are more relevant in difficult-to-measure traits, phenotyping costs and complexity are the main challenges for building the corresponding references populations. Successful implementation and uptake of genomic selection will increase the number of animals in the national genetic evaluation with GEBV for RFI and CH₄, with favourable implications in terms of the applicability of selection indices including these new traits and balancing potential antagonisms between productivity and GHG emissions.

In summary, improving feed efficiency and reducing CH₄ emission by animal selection is achievable as both traits are heritable and phenotyping larger number of animals is now possible, although still costly and limited to experimental research farms or nucleus herds/flocks. Further research is needed for a

more comprehensive understanding of the genetic and phenotypic relationships not only between these groups of traits, but also with productivity in order to optimise genetic progress supporting environmental, economic, and social sustainability. Expanding regional and international collaborations is one of the alternatives to build larger reference population for genomic selection with increased genomic accuracies.

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References

- Barwick S.A., Henzell A.L., Herd R.M., Walmsley B.J and Arthur P.F. (2019) *Genet. Sel. Evol.* 51(18) <https://doi.org/10.1186/s12711-019-0459-5>
- Basarab J.A., Price M.A., Aalhus J.L., Okine E.K., Snelling W.M. *et al.* (2003). *Can. J. Anim. Sci.* 83(2):189-204. <https://doi.org/10.4141/A02-065>
- Berry D.P., Garcia J.F and Garrick D.J. (2016) *Anim. Front.* 6(1):32-38.
- Cantalapiedra-Hijar G., Abo-Ismael M., Carstens G.E., Guan, L.L., Hegarty R. *et al.* (2018). *Animal* 12:s321- s335 <https://doi.org/10.1017/S1751731118001489>
- Fitzsimons C., Kenny D.A., Deighton M.H., Fahey A.G., and McGee, M. (2013) *J. Anim. Sci.* 91(12): 5789–5800. <https://doi.org/10.2527/jas2013-695>
- Koch R., Swiger L., Chambers D., and Gregory K. (1963) *J. Anim. Sci.* 22(2):486–494.
- Manzanilla-Pech C.I.V., Lövendahl, P., Mansan Gordo, D., Difford G.F., Pryce J.E., *et al.* (2021) *J. Dairy Sci.* 104(8): 8983-9001 <https://doi.org/10.3168/jds.2020-19889>
- Paganoni B., Rose G., Macleay C., Jones C., Brown D.J., *et al.* (2017). *J. Anim. Sci.* 95(9): 3839–3850. <https://doi.org/10.2527/jas.2017.1499>
- Pravia M.I., Navajas E.A., Macedo F.L., Clariget J., and Luzardo S. (2018). Proc. of the 11th WCGALP, Auckland, New Zealand.
- Phocas F., Belloc C., Bidanel J., Delaby L., Dourmad J., *et al.* (2016). *Animal* 10(11):1749-1759. <https://doi.org/10.1017/S1751731116000926>
- Ravagnolo O., Aguilar I., Crowley J.J., Pravia M.I., Lema M., *et al.* (2018) Proc. of the 11th WCGALP, Auckland, New Zealand.
- Smith P.E., Waters S.M, Kenny D.A., Kirwan S.F., Conroy S. *et al.* (2021) *J. Anim. Sci.* 99(11)