Carracelas, B., De Barbieri, I., Navajas, E., Guillenea, A., Aguilar, I., Ciappesoni, G. (2026) Single-step GWAS identifies candidate genes associated with feed efficiency in Corriedale sheep, *Proceedings 13th World Congress on Genetics Applied to Livestock Production* 23992: https://doi.org/10.31274/wcgalp.23992 ©2026 Carracelas, et al. CC BY-NC-ND

Single-step GWAS identifies candidate genes associated with feed efficiency in Corriedale sheep

B. Carracelas[1]*, I. De Barbieri[2], E.A. Navajas[1], A. Guillenea[4], I. Aguilar[1,3], and G. Ciappesoni[1]

*[1]Sistema Ganadero Extensivo, INIA, Las Brujas, Uruguay; [2]Sistema Ganadero Extensivo, INIA, Tacuarembó, Uruguay; [3]Sistema Lechero, INIA, Las Brujas, Uruguay; [4]Secretariado Uruguayo de la Lana, Montevideo, Uruguay; *Corresponding author: bcarracelas@inia.org.uy*

Introduction

Corriedale sheep represent one of the most important breeds in Uruguay, accounting for approximately 42% of the national flock (MGAP, 2018). As a dual-purpose breed in pasture-based systems, improving feed efficiency is key to enhancing productivity and sustainability. In recent years, increasing emphasis has been placed on improving feed efficiency and reducing methane emissions; however, the genetic architecture of these traits remains poorly characterized in Corriedale sheep.

This study aimed to identify genomic regions and positional candidate genes associated with dry matter intake (DMI), residual feed intake (RFI), feed conversion ratio (FCR), average daily gain (ADG), metabolic body weight (MBW), and methane emissions (ME) in Corriedale sheep.

Materials & Methods

Animals and phenotypes. Phenotypic data were collected from Corriedale sheep evaluated in 10 feed intake trials conducted between 2017 and 2025. Records were available for 581 animals for DMI, FCR, ADG, and MBW; 569 animals for RFI; and 522 animals for ME. All trials were conducted at INIA's La Magnolia Experimental Station following the protocols described by Amarilho-Silveira *et al.* (2022). RFI was calculated as the residual from the linear regression of DMI on ADG and MBW, according to Koch *et al.* (1963). ME were measured using portable accumulation chambers (PACs) as previously described (Goopy *et al*., 2011; Paganoni *et al*., 2017; De Barbieri *et al.,* 2024).

Genotypes and quality control. Genotypes from 511–522 animals (depending on the trait) were obtained using the Applied Biosystems™ Axiom™ Ovine Genotyping Array 50K. Quality control was performed with preGSf90 (Aguilar *et al*., 2014), removing SNPs with call rate <90% or MAF <1%, and animals with call rate <90%. After QC, 38,473 SNPs and all samples were retained for analysis.

Statistical analysis. Single-step genome-wide association studies (ssGWAS) were performed using the BLUPF90 software suite (Lourenco *et al.,* 2022). For each trait, a univariate animal model was fitted:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e} \quad (1)$$

where b is the vector of fixed effects, including contemporary group (CG), type of birth, age of dam, and animal age at test start (covariate); X and Z are incidence matrices relating observations to fixed and additive genetic effects, respectively; u is the vector of additive genetic effects, assumed $u \sim N(0, H\sigma_u^2)$, with H combining pedigree (A) and genomic (G) information; and e is the vector of residuals, assumed $e \sim N(0, I\sigma_e^2)$, with σ_u^2 and σ_e^2 representing the additive genetic and residual variances, respectively. CG were defined as the combination of trial, birth year, sex, flock, and management group.

SNP effects were estimated by back-solving genomic estimated breeding values (GEBVs) from single-step genomic BLUP (ssGBLUP), as described in Wang *et al.* (2012), using a single-marker approach. Genome-wide significance for all traits was determined with a Bonferroni-corrected threshold ($p < 0.05$) based on the total number of SNPs retained after quality control.

Candidate gene identification and functional analysis. Linkage disequilibrium (LD) decay was estimated in the study population using an r^2 threshold of 0.2, yielding an average LD extent of approximately 50.6 kb. Based on this result, a ±50 kb window around significant SNPs was used to identify positional candidate genes using the Oar_v4.0 genome assembly and NCBI Genome Data Viewer annotations (https://www.ncbi.nlm.nih.gov/gdv/?org=ovis-aries). Genes identified within this interval were considered positional candidates. Functional enrichment analysis was conducted with the gprofiler2 package in R (Kolberg *et al.,* 2020).

Results & Discussion

Significant genomic regions for RFI, FCR, and ADG were identified by ssGWAS, whereas no genome-wide significant associations were found for DMI, MBW, or ME (Figure 1). After Bonferroni correction, 22 SNPs were significantly associated with RFI, one SNP with FCR, and 21 SNPs with ADG.

RFI showed the strongest genomic signal. The 22 significant SNPs were distributed across multiple chromosomes, each explaining a small proportion of the phenotypic variance, consistent with a polygenic architecture. Twenty-six positional candidate genes were identified within ±50 kb of significant SNPs (Table 1, selected candidate genes shown). However, given the marker density of the 50K SNP array and potential variation in LD across the genome, these associations may represent broader genomic regions rather than precise loci. Functional enrichment revealed a single Gene Ontology term (GO:0110016, B-WICH complex), involving *MYBBP1A* (MYB binding protein 1a) and *ERCC6* (ERCC excision repair 6, chromatin remodeling factor), suggesting a potential role for chromatin remodeling and transcriptional regulation in feed efficiency. In addition, *ERCC6* has been previously associated with RFI in water buffalo (Sikka *et al*., 2023). Other nearby genes, such as *RORA* (RAR-related orphan receptor A) and *SPNS2* (SPNS lysolipid transporter 2, sphingosine-1-phosphate), are involved in metabolic regulation and lipid signaling, and may represent biologically plausible positional candidates. Notably, *SPNS2* and *MYBBP1A* have also been associated with methane yield in beef cattle (Arikawa *et al.,* 2025), suggesting potential shared biological pathways. Nevertheless, these findings should be interpreted with caution, and further validation is required to confirm the underlying causal genes.

For FCR, only one SNP reached genome-wide significance, with *GALNT3* (polypeptide N-acetylgalactosaminyltransferase 3) located within the defined window as a positional candidate gene. The limited number of associations may reflect the composite nature of FCR, which integrates feed intake and growth and typically exhibits lower heritability than its component traits (Polizel *et al.,* 2018). However, given that this signal is supported by a single marker without clear neighboring SNPs, it should be interpreted cautiously, as it may reflect limited marker density rather than a well-resolved association. *GALNT3* encodes a glycosyltransferase involved in protein modification and metabolic regulation, suggesting a potential role in nutrient utilization efficiency, although no direct association with FCR has been previously reported.

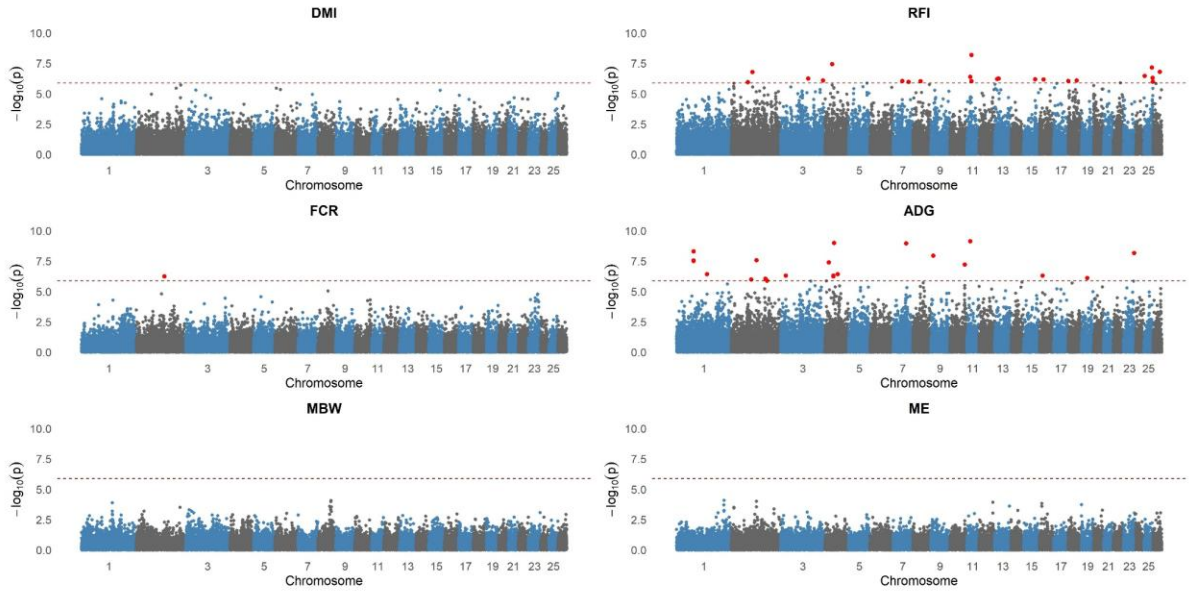

Figure 1. Manhattan plots for dry matter intake (DMI), residual feed intake (RFI), feed conversion ratio (FCR), average daily gain (ADG), metabolic body weight (MBW), and methane emissions (ME). The *x*-axis shows chromosome number and the *y*-axis -$\log_{10}$(*p*-values) for each SNP. The red dashed line indicates the Bonferroni-corrected genome-wide significance threshold ($p = 1.3 \times 10^{-6}$).

ADG was associated with 21 significant SNPs mapping to 16 positional candidate genes, including *SORT1* (sortilin 1), involved in intracellular protein trafficking; *PCCA* (propionyl-CoA carboxylase subunit alpha), involved in energy metabolism; *PDE1C* (phosphodiesterase 1C), involved in cyclic nucleotide signaling; and *MAGI2* (membrane-associated guanylate kinase, WW and PDZ domain containing 2), involved in signal transduction (Table 1, selected

Table 1. Selected positional candidate genes identified for residual feed intake (RFI), feed conversion ratio (FCR), and average daily gain (ADG)*.

Trait	SNP_ID	Chr	BP	p-value	Positional candidate gene
RFI	s10340.1	11	24588035	6.5×10^{-9}	*SPNS2, MYBBP1A*
	s41985.1	25	43068716	5.1×10^{-7}	*ERCC6*
	OAR7_51300745.1	7	46510322	9.1×10^{-7}	*RORA*
FCR	OAR2_151635110.1	2	142668484	5.8×10^{-7}	*GALNT3*
ADG	250506CS3900464100001_519.1	1	85655170	4.9×10^{-9}	*SORT1*
	s18739.1	10	76439829	6.2×10^{-8}	*PCCA*
	OAR4_68231479.1	4	64454295	3.8×10^{-7}	*PDE1C*
	OAR4_44580873.1	4	42297895	5.1×10^{-7}	*MAGI2*

*Due to space limitations, only selected candidate genes are shown.

candidate genes shown). *SORT1* has been shown to regulate lipid metabolism and triacylglycerol accumulation in the liver of dairy cows, suggesting a role in fat deposition–related traits (Yang *et al.,* 2022). However, similar to RFI, several associations were driven by

isolated SNPs without consistent support from neighboring markers, which may reflect the limited SNP density of the 50K SNP array. No enriched pathways were detected, and none of these genes have been previously reported as associated with ADG, highlighting the complex and polygenic nature of this trait.

No significant associations were detected for DMI, MBW, or ME, likely reflecting both the limited sample size and the highly polygenic nature of these traits. In addition, the marker density of the 50K SNP array may have limited the power to detect and resolve associations, particularly for traits influenced by many loci of small effect. Methane emissions, in particular, are influenced by complex interactions between host genetics and rumen microbiota composition (Difford *et al.,* 2018), which may require larger datasets and higher-density genotyping arrays to detect significant associations.

Conclusions

This study identified genomic regions associated with RFI, FCR, and ADG in Corriedale sheep. RFI showed the strongest signal, supporting its relevance as a key feed efficiency trait. Identified genes represent positional candidates involved in regulatory and metabolic processes. These findings improve understanding of the genetic architecture of feed efficiency, although further validation is required.

Acknowledgements

This study was part of the Global Methane Genetics initiative, which is led by Wageningen University and Research and in partnership with the Bezos Earth Fund and the Global Methane Hub. Funding was provided by the Green ERA-Hub program under the EU's Horizon Europe research and innovation programme (grant no. 101056828).

References

Aguilar I., Misztal I., Tsuruta S., *et al*. (2014) Proc. 10th WCGALP, Vancouver, Canada.

Amarilho-Silveira F., De Barbieri I., Cobuci J.A., *et al*. (2022) Livest Sci 258:104889. doi.org/10.1016/j.livsci.2022.104889

Arikawa L.M., Mota L.F.M., Fonseca L.F.S., *et al*. (2025) Sci Rep 16, 2961. doi.org/10.1038/s41598-025-32815-z

De Barbieri I., Navajas E.A., Ramos Z., *et al*. (2024) Front Anim Sci 5. doi.org/10.3389/fanim.2024.1480928

Difford G. F., Plichta D. R., Løvendahl P., *et al*. (2018) PLoS Genet 14(10):e1007580. doi.org/10.1371/journal.pgen.1007580

Goopy J.P., Woodgate R., Donaldson A., *et al*. (2011) Anim Feed Sci Technol 166–167:219–226. doi.org/10.1016/j.anifeedsci.2011.04.012

Koch R., Swiger L., Chambers D., *et al*. (1963) J Anim Sci 22:486–494. doi.org/10.2527/jas1963.222486x

Kolberg L., Raudvere U., Kuzmin I., *et al*. (2020) F1000Res 9(ELIXIR):709. doi.org/10.12688/f1000research.24956.2

Lourenco D., Tsuruta S., Aguilar I., *et al*. (2022) Proc. 12th WCGALP, Rotterdam, The Netherlands.

Ministerio de Ganadería, Agricultura y Pesca (2018) Encuesta Ganadera Nacional 2016. Available at: www.gub.uy/ministerio-ganaderia-agricultura-pesca/datos-y-estadisticas/estadisticas/resultados-encuesta-ganadera-nacional-2016, visited on: 30-11-2025.

Paganoni B., Rose G., Macleay C., *et al*. (2017) J Anim Sci 95(9):3839–3850. doi.org/10.2527/jas.2017.1499

Polizel G.H.G., Grigoletto L., Carvalho M.E., *et al*. (2018) Livest Sci 214:209-210. doi.org/10.1016/j.livsci.2018.06.013

Sikka P., Paul S.S., Jerome A., *et al*. (2023) Adv. Biosci. Biotechnol. 14:210-236. doi.org/10.4236/abb.2023.144014

Wang H., Misztal I., Aguilar I., *et al*. (2012) Genet Res 94(2):73–83. doi.org/10.1017/S0016672312000274

Yang W., Wang S., Loor J.J., *et al*. (2022) J. of Dairy Sci.105(6):5420-5434. doi-org.proxy.timbo.org.uy/10.3168/jds.2021-21607