SMARTER

SMAll RuminanTs breeding for Efficiency and Resilience

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Report on genetic correlations of feed efficiency and other economically important traits

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About the SMARTER research project

SMARTER will develop and deploy innovative strategies to improve Resilience and Efficiency (R&E) related traits in sheep and goats. SMARTER will find these strategies by: i) generating and validating novel R&E related traits at a phenotypic and genetic level ii) improving and developing new genome-based solutions and tools relevant for the data structure and size of small ruminant populations, iii) establishing new breeding and selection strategies for various breeds and environments that consider R&E traits.

SMARTER with help from stakeholders chose several key R&E traits including feed efficiency, health (resistance to disease, survival) and welfare. Experimental populations will be used to identify and dissect new predictors of these R&E traits and the trade-off between animal ability to overcome external challenges. SMARTER will estimate the underlying genetic and genomic variability governing these R&E related traits. This variability will be related to performance in different environments including genotype-by-environment interactions (conventional, agro-ecological and organic systems) in commercial populations. The outcome will be accurate genomic predictions for R&E traits in different environments across different breeds and populations. SMARTER will also create a new cooperative European and international initiative that will use genomic selection across countries. This initiative will make selection for R&E traits faster and more efficient. SMARTER will also characterize the phenotype and genome of traditional and underutilized breeds. Finally, SMARTER will propose new breeding strategies that utilise R&E traits and trade-offs and balance economic, social and environmental challenges.

The overall impact of the multi-actor SMARTER project will be ready-to-use effective and efficient tools to make small ruminant production resilient through improved profitability and efficiency.

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Summary

Deliverable 1.2 is a report on genetic and phenotypic correlations of feed efficiency and other economically important traits. These in turn provide information regarding the relevance or otherwise of including them into breeding programmes for sheep and goats. Due to the requirement for large numbers of records to ensure statistically-significant results, the majority of the data are from industry with some from experimental herds and flocks. Some of the traits reported here are direct estimations of feed intake and other are proxy measurements (e.g. live weight).

Overall, the difficulty of generating individual animal feed intake records should be recognised as it requires specialist (expensive) feed intake measuring equipment which is prohibitive for use in large-scale breeding programmes. Notwithstanding this difficulty, new estimations of residual feed intake taken from automated data capture of feed consumption and corrected for body weight and milk yield provide novel insight into the biological relationships amongst these traits (in UK dairy goats). The use of lactose content as a proxy for production efficiency in Greek sheep is also considered here as well as other milk composition traits. Novel feed efficiency estimations estimated for Lacaune ewes are both strongly genetically associated with milk yield. These include milk ratio (NEICMR, as described in D1.1 P.19-20, and feed efficiency 'residual energy intake (REI)'. They could be proposed as proxies for efficiency without having to directly measure actual feed or nutritional intakes. Phenotypic relationships between residual feed intake (RFI) and other traits including methane yield were reported for 3 Uruguayan sheep breeds which showed that in all cases, the more efficient animals (low RFI) had higher methane yields than less efficient (high RFI) ones. More efficient animals tended to emit 10% less methane per kg of body weight gain and in the case of CO_2, more efficient animals had lower emissions in Dohne and Merino breeds ($p<0.05$), 6.8 and 4.8%, respectively. Additionally, genetic correlations were estimated for Merino breed. Some additional (novel) 'type' traits for 3 French meat breeds (P27) are reported in relation to body weight showing promising possibilities as proxy traits. In Norwegian White Sheep (NWS) genetic correlations between weight corrected methane emission and feed intake proxy corrected feed intake, respectively, were correlated to other traits in the total merit index. While weight corrected methane emission was antagonistically correlated to maternal genetic effects of lamb growth traits, the corresponding correlations for feed intake proxy corrected feed intake was close to zero.

Introduction

A previous SMARTER report (D1.1) summarised new phenotypes associated with Feed efficiency (FE) as a key trait to improve in small ruminants. This is not only to improve animal efficiency and reduce costs in the farming system, but also to reduce greenhouse gas emissions from agriculture.

The rationale for the identification of more efficient animals for feed intake is because feed makes up a high proportion of costs associated with animal production.

Feed efficiency (FE, residual feed intake, RFI) and different proxy measurements for these (e.g. lamb growth) are included in this report where the number of animals, records and structure of the populations has enabled the estimation of genetic and phenotypic parameters. Specifically, this report includes data from industry populations of animals where feed efficiency or their proxy measurements have been recorded, as well as data collected in experimental animal populations.

The populations of animals used for this report are:

1. Chios and Frizarta dairy sheep (Greece)
2. Lacaune dairy sheep (France)
3. Yorkshire Dairy goats (UK)
4. Alpine and Saanen goats (France)
5. Merino, Dohne Merino and Corriedale sheep (Uruguay)
6. Texel, Suffolk, Charollais (UK)
7. Texel, Suffolk, Charollais, (Ireland)
8. Blanche du Massif Central, Mouton Vendéen, Rouge de l’Ouest (France)
9. Norwegian White Sheep (Norway)

The overall aim of this report is to report the estimation of genetic parameters for resource use efficiency, notably those associated with utilisation of feed resources and growth and with other aspects of production. Where possible, the estimates of genetic and phenotypic correlations of feed resource efficiency with other economically important traits are documented and implications for their use in small ruminants.

As a proxy measurement for feed efficiency, parameters for animal growth and body composition are reported for some breeds. As the measurements and traits are not replicated across all countries, individual country reports are summarised and then brought together in the conclusion.

Dairy Sheep and Goats

1.1 Greece

Frizarta and Chios sheep were used for this study reared in commercial populations in Greece. The feed resource use efficiency indicators identified in Task 1.1 (of milk fat – FC, and lactose content – LC) were used for this study and parameters estimated together with daily milk yield (DMY).

1.1.1 Farms and animals

A total of 838 dairy ewes of two local Greek breeds, Chios (n=369) and Frizarta (n=469), were used. Ewes were randomly selected from four farms, two per breed, located in Northern and Western Greece. Two of the selected farms (one per breed) were managed intensively and the other two semi-intensively, representing the most common sheep farming systems in Greece. In intensive farms, animals were housed year-round and their diet comprised of roughage (alfalfa hay and wheat straw) and a concentrate mix. In semi-intensive farms, animals were grazing daily during spring and summer months. All selected farms participated in two cooperatives (Chios farms: Agricultural Cooperative of Chios Sheep Breeders "Makedonia", Frizarta farms: Agricultural Cooperative of Western Greece) that were involved in the national programmes for the genetic improvement of the two breeds and were responsible for pedigree and phenotypic data collection and record keeping. Based on pedigree data, predetermined individual or group matings were performed. Furthermore, selected Frizarta ewes were artificially inseminated with fresh semen.

1.1.2 Available phenotypic data

Due to Covid-19 restrictions that hindered data sampling, available data were used for this study to guarantee a sufficient sample size for genetic parameters estimation. Specifically, historical data of Chios sheep, collected during iSAGE project (Innovation for Sustainable Sheep and Goat Production in Europe, Grant Agreement No: 679302, EU Horizon 2020, 2016-2020) and available data of Frizarta ewes from the regular milk recordings and analyses performed by the Agricultural Cooperative of Western Greece (2019-2020) were used.

Milk recordings were performed monthly for two consecutive milking periods on each farm and individual milk samples were collected. Specifically, milk produced from each ewe in a single milking was collected in volumetric tubes; following mixing, approximately 50ml of milk were collected in sampling vials of 70ml capacity. Samples were immediately stored in portable coolers (approximately 4°C) and transferred to the nearest national analytical laboratory (Hellenic Agricultural Organization

DIMITRA). Milk FC and LC were determined using special automated devices for milk sample analysis (MilkoScan™ FT 6000, Foss).

1.1.3 Pedigree data, genotypes and quality control

Available pedigree and lambing (date of lambing, parity) data of Chios and Frizarta ewes were obtained from the cooperatives. Pedigree pruning was performed with R programming language (software version 4.1.2 – R core team, 2021) and statistical package "FamAgg" (Rainer et al., 2016). Information regarding ancestors of the last ten generations were used for the estimation of genetic parameters and correlations of the studied traits. Pruned pedigree included 878 Chios and 1,136 Frizarta sheep.

For the above dairy ewes, available Chios genotypes from iSAGE project (n=317, Illumina OvineSNP50 Genotyping Beadchip) and newly generated Frizarta genotypes (n=346, Illumina OvineSNP50 Genotyping Beadchip v2) were matched with the respective phenotypes under study and used to estimate genomic heritability of FC and LC. Genotype quality control was performed with PLINK 1.9 software (Chang et al., 2015). All SNPs on non-autosomal regions were removed. Furthermore, SNPs with minor allele frequency (MAF) lower than 2%, call rate lower than 97% or deviating from Hardy-Weinberg equilibrium (HWE, P-value=10^{-6}) were filtered out. Sample call rate threshold was set at 90%. Chromosomal coordinates were allocated to SNPs based on the Oar_v4.0 genome assembly. The final datasets included 43,998 and 47,451 SNPs for Chios and Frizarta sheep, respectively, spread across 26 ovine autosomes. No samples were removed due to low call rate.

1.1.4 Phenotypic data handling

Based on the date of lambing, the stage of lactation in each sampling occasion was determined and expressed in days from lambing. Individual DMY on each sampling occasion were calculated from test yields (TY), that corresponded to one milking. In two of the selected farms, three milkings were performed daily in the beginning of lactation, whereas in any other case two milkings per day were the norm. Hence, the standard methods of DMY calculation suggested by the International Committee for Animal Recording (ICAR) could not be implemented, since they assume two milkings daily throughout lactation. To allow for a common calculation method among all farms, an alternative to the above was used. Specifically, the method used herein is implemented by Agricultural Cooperative of Chios Sheep Breeders "Makedonia" and is independent of the number of milkings performed within a day. Specifically, DMY is calculated based on the following formula:

$$DMY = \frac{TY}{\Delta t} * 1440$$

Where:

DMY = Daily milk yield (in grams)
TY = Recorded test yield that corresponds to one milking (in grams)
Δt = Time interval between the recorded and the previous milking (in min)

The number 1440 represents the total number of minutes within a day.

Descriptive statistics of DMY, FC and LC of Chios and Frizarta ewes of the present study are presented in Table 1.

Table 1. Mean values and standard deviations (in parentheses) of daily milk yield (DMY), daily milk fat (FC) and lactosecontent (LC) of Chios and Frizarta ewes.

	DMY (g)	**FC (%)**	**LC (%)**
Chios	1548.9 (702.09)	5.4 (1.56)	4.9 (0.34)
Frizarta	1600.4 (763.33)	6.6 (1.30)	5.0 (0.19)

DMY = daily milk yield; FC = fat content; LC = lactose content

Individual repeated measurements of FC, LC and DMY were used to estimate genetic parameters and correlations based on pedigree data. For the estimation of genomic heritability, individual mean values of FC and LC for each year of the study weighted over the respective DMY were calculated based on the following formula:

$$\bar{y} = \frac{\sum_{i=0}^{n} DMYi * yi}{\sum_{i=0}^{n} DMYi}$$

where $\bar{\mathbf{y}}$ is the annual weighted mean of the studied trait (FC or LC), $\mathbf{DMY_i}$ is the daily milk yield in the ith milk recording occasion and $\mathbf{y_i}$ is the respective value of the studied trait. The average of the individual weighted means of FC and LC for the two years of the study was considered for genomic analyses.

1.1.5 Statistical analyses

Regarding the estimation of genetic parameters and correlations based on pedigree data, environmental factors with significant effects on daily FC and LC were identified in preliminary analyses. The effects of farm, year of the study (1st or 2nd), parity (1st – 9th), days from lambing (representing the stageof lactation), and lambing date (capturing the year-month of lambing interaction) were tested. For Frizarta sheep data analyses, effects of total number of milkings per day (2 or 3) and time of milking (morning, noon, evening) were considered, as well. Univariate animal models were used for each breed separately to estimate variance components for FC and LC, which were used to estimate heritability and repeatability for each trait. Bivariate analyses were then performed to estimate the genetic, phenotypic, permanent environmental and residual correlations between studied traits and DMY. All models included the fixed effects of farm, year, lambing date and the regression coefficient on days from lambing. Furthermore, the fixed effect of parity was used in the Chios sheep analyses. The LC model for Frizarta sheep also included the effects of parity and time of milking, whereas time of milking and total number of milkings per day were included in the FC model. Random effect of ewe including the pedigree relationship matrix was fitted in the models. The ASReml software version 4.2 (Gilmour et al., 2021; Gilmour and Thompson, 2021) was used for all analyses.

In a separate series of analyses, genomic heritability was estimated for the annual weighted means of FC and LC. Prior to estimating genomic heritability, a centered genomic relatedness matrix for each breed was created from post quality control genomic data with GEMMA software version 0.98.1 (Zhou and Stevens, 2012). Further formatting and inversion of the matrices was completed with R version 4.1.2 (R core team, 2021) and package "AGHmatrix" (Amadeu et al., 2016). Furthermore, within breed Principal Component Analysis (PCA) of animal genotypes was performed with GEMMA 0.98.1 to investigate possible population structures for subsequent analyses. Population structure associated with farm was revealed in both populations. The first three principal components (PCs) for Chios and the first PC for Frizarta were considered as fixed effects for genomic analyses. Other environmental factors tested in preliminary analyses for possible effects on the studied traits included farm, parity (in the first year of the study – 6 levels, 1st – 5th and ≥6th), recording years (2 levels, representing ewes with records in one or both years of the study), lambing season (3 levels – representing ewes lambing in 1: Summer-Autumn i.e. first lambing group of each year; 2: Winter-Spring i.e. second lambing group of each year; or 3: either first or second lambing group depending on the year) and the average prolificacy for both years of the study. Only variables with a statistically significant effect ($P<0.05$) on each studied trait were retained in the final models of statistical analyses. Variance components of FC and LC were estimated within breed by residual maximum likelihood (REML) using the genomic relatedness matrix with the following single-trait animal linear mixed model:

$$y = X\tau + Zu + \varepsilon$$

where **y** is the phenotypes vector, **τ** is the vector of fixed effects, **u** is the vector of random effects, **X** and **Z** are the design matrices that associate phenotypes with fixed and random effects, respectively, whereas **ε** is the vector of random residual errors. The random additive genetic effect of ewe and residual effect were included in all models. In the Chios analyses, the model for FC included parity, lambing season and the 1st and 3rd PCs as fixed effects, whereas the model for LC included farm, lambing season and average prolificacy. In the Frizarta analyses, farm, parity and lambing season were included as fixed effects in both models, whereas the LC model included also the fixed effect of average prolificacy. Analyses were performed with ASReml software version 4.2 (Gilmour et al., 2021; Gilmour and Thompson, 2021).

1.1.6 Results

Estimates of heritability and repeatability of the studied traits, and correlations between them are presented in Tables 2 (a and b) and 3 (a and b), respectively. Statistically significant (P<0.05) moderate to high repeatability estimates were reported for all traits. The highest repeatability for both breeds was that of daily LC (Table 2). Heritability estimates based on pedigree data (Table 2a), were low to moderate and that of daily milk LC of Chios sheep and DMY of both breeds were not significant (P>0.05). Significant (P<0.05) negative genetic, phenotypic, permanent environmental and residual correlations of DMY with daily FC were reported; the only exceptionwas the permanent environmental correlation in the case of Frizarta sheep, which was non- significantly different from zero. Negative correlations were also reported between daily LC and FC. Significant (P>0.05) positive phenotypic, permanent environmental and residual correlations were estimated between DMY and daily LC (Tables 3a, 3b, 4a and 4b). Genetic correlations involving daily LC of Chios sheep generated extremely high standard errors indicating that their estimation was impossible basedon the present data.

Genomic heritability estimates for annual weighted means of FC and LC (Table 2b) were higher (h^2 ranging from 0.34 to 0.57) compared to the ones for daily FC and LC that were estimated based on pedigree data. However, heritability of LC of Frizarta ewes (h^2 = 0.34) was not statistically different from zero.

Table 2a. Heritability (h^2), repeatability (r) and respective standard errors in parentheses of daily milk yield (DMY), milk fat (FC) and lactose content (LC).

	Frizarta		**Chios**	
	h^2	**r**	**h^2**	**r**
DMY	0.05 (0.05)	0.26 (0.03)	0.11 (0.07)	0.44 (0.03)
FC	0.15 (0.07)	0.28 (0.03)	0.13 (0.07)	0.29 (0.03)
LC	0.14 (0.07)	0.47 (0.03)	0.01 (0.06)	0.45 (0.03)

DMY = daily milk yield; FC = fat content; LC = lactose content

Table 2b. Heritability estimates and respective standard errors in parentheses of annual weighted means of milk fat (FC) and lactose content (LC).

	Frizarta	**Chios**
FC	0.44 (0.216)	0.47 (0.193)
LC	0.34 (0.203)	0.57 (0.149)

FC = fat content; LC = lactose content

Table 3a. Genetic (above diagonal) and phenotypic (below diagonal) correlations (and standard errors in parentheses) for daily milk yield (DMY), milk fat (FC) and lactose content (LC) of Frizarta sheep.

Trait	**DMY**	**FC**	**LC**
DMY		-0.81 (0.25)	0.50 (0.52)
FC	-0.26 (0.03)		-0.53 (0.31)
LC	0.23 (0.03)	-0.39 (0.02)	

DMY = daily milk yield; FC = fat content; LC = lactose content

Table 3b. Genetic (above diagonal) and phenotypic (below diagonal) correlations (and standard errors in parentheses) for daily milk yield (DMY), milk fat (FC) and lactose content (LC) of Chios sheep.

Trait	DMY	FC	LC
DMY		-0.66 (0.28)	NA
FC	-0.43 (0.03)		NA
LC	0.22 (0.03)	-0.21 (0.03)	

*NA: Data not available – Non-estimable parameters
DMY = daily milk yield; FC = fat content; LC = lactose content

Table 4a. Permanent environmental (above diagonal) and residual (below diagonal) correlations (and standard errors in parentheses) for daily milk yield (DMY), milk fat (FC) and lactose content (LC) of Frizarta sheep.

Trait	DMY	FC	LC
DMY		-0.20 (0.23)	0.33 (0.14)
FC	-0.18 (0.03)		-0.44 (0.14)
LC	0.17 (0.03)	-0.36 (0.02)	

DMY = daily milk yield; FC = fat content; LC = lactose content

Table 4b. Permanent environmental (above diagonal) and residual (below diagonal) correlations (and standard errors in parentheses) for daily milk yield (DMY), milk fat (FC) and lactose content (LC) of Chios sheep.

Trait	DMY	FC	LC
DMY		-0.46 (0.16)	0.46 (0.12)
FC	-0.39 (0.02)		-0.08 (0.17)
LC	0.15 (0.02)	-0.28 (0.02)	

DMY = daily milk yield; FC = fat content; LC = lactose content

1.1.7 Conclusions

Results of the present study suggest that selection for higher feed efficiency using FC as proxy trait might unfavorably affect milk yield. In the case of Frizarta sheep, LC could be used to select for improved feed efficiency without compromising milk yield since no significant genetic correlations were reported. Nevertheless, it is recommended that the relevant results be validated on a larger dataset, involving more flocks. Further investigation for a possible way to integrate FC and LC in a single proxy trait may also be of interest. Limitations of the present Chios sheep data regarding the estimation of correlations involving LC may be attributed to limited genetic links between the two studied flocks, which are expected due to the lack of AI and the use of flock-specific sires that are products of within flock reproduction. In accordance with present results, higher heritability estimates are expected with genomic data compared to pedigree-based approaches, since genomic relatedness matrices more accurately capture family structure and relationships between animals. Use of genomic data in future studies may improve accuracy of estimations.

1.1.8 References

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1.2 France, Lacaune ewes

1.2.1 Method

In deliverable D1.1, phenotypic results for one feed efficiency trait were reported for the 4 French dairy sheep breeds over one lactation (milk year 2019-2020). Genetic studies were extended to a second feed efficiency trait, data of a second lactation (milk years 2019-2020 and 2020-2021) and focused on the Lacaune breed. To date, 4,680 Lacaune dairy ewes were phenotyped for feed efficiency over the two milk dairy years with a total of 30,854 records used to estimate genetic parameters. Milk quantity and quality from ewes were individually measured at monthly intervals with a target of six test-days over the lactation period. The first milk test-day (TD) was performed approximately 50 days after lambing. For each test-day, milk yield, protein and fat content were measured.

1.2.2 Feed efficiency traits

The first feed efficiency trait, 'net energy intake' is converted into a ratio trait, milk ratio (NEICMR), as described in D1.1. (P.19-20 and included below in Appendix 1). The second feed efficiency trait, named residual energy intake (REI), was estimated as the residual of multiple linear regression of approximated daily energy intake (DEI) on daily milk yield (DMY), fat content (FC), protein content (PC) to account for production requirements, difference of body condition score (BCSΔ) to account energy from body reserves and body weight to account for maintenance requirements. At each six-monthly TD, NEICMR and REI were calculated and considered as lactation net energy feed efficiency traits. Based on the NEICMR and REI definitions, efficient animals had high NEICMR and low REI values.

The individual DEI in UFL/d was calculated multiplying individual dry matter intake by energy density of the feed in the diet at each TD. Individual animal dry matter intake was calculated from the estimated average amounts of feed distributed collectively per ewe (pasture, forages and concentrates) with a refusal rate of 10% (De Boissieu et al., 2019), plus individual concentrates distributed individually in the milking parlour. For the grazing part, an estimation of the ingestion at pasture was calculated according to the time of presence per ewe (De Boissieu et al., 2019). Depending on the test day, Body Condition Scores are defined differently. For TD1, BCSΔ1 was evaluated between end of suckling and TD1, for TD2 to TD5, BCSΔ2 was evaluated betweenTD1 and before mating and for TD6, BCSΔ3 was evaluated between before and after mating.

1.2.3 Results - genetic parameters

On average, Lacaune ewes had a DMY of 2.04 ± 0.81 L/d, with a fat content (FC) of 73.6 ± 13.9 g/L and a protein content of 60.1 ± 8.6 g/L. Their feed efficiency was on average 0.93 ± 0.29 for NEICMR and 0.00 ± 0.31 UFL/d for REI.

Calculated feed efficiency related traits and recorded milk production traits at each TD were linked to a month of lactation. Only data from month 2 to month 7 were kept, i.e. the exclusive milking period, and extreme months (1 and 8) were not analysed due to the low number of data. In order to determine environmental factors affecting NEICMR and REI, analyses of variance were performed with the packages car, lme4 and lmerTest implemented in the R software. First, at each lactation month, fixed environmental effects and interaction terms were included into a linear model and selected using Fisher's tests (P-value < 0.05). To analyse the effect of the lactation stage, all lactation month data were merged anda linear mixed model was applied to these data. The environmental factors thus selected were retained as fixed effects for the genetic analyses.

Heritabilities of DMY, FC, PC, NEICMR and REI on one hand, and genetic correlations between each pair of traits on the other hand were estimated with univariate and bivariate analyses respectively with WOMBAT software (Meyer, 2007) using AI-REML method. A data set of 30,854 phenotypes for 4,680 Lacaune ewes and a six-generation pedigree including 17,267 animals were used. A single trait animal model with repeatability was used for the estimation of heritabilities. This model was the same for each trait and included the fixed effects of: parity (1/2/3/4+) interacting with lactation month (2/3/4/5/6/7), litter size (single/multiple) interacting with lactation month, lambing period (start/end) according to parity interacting with lactation month, mating mode (animal insemination/return/natural breeding) interacting with lactation month, and herd (n=8) interacting with dairy years (2019-2020/2020-2021) and lactation month. It also included random animal genetic and permanent environment effects. The model used for bivariate analysis between each pair of traits for DMY, FC, PC, NEICMR and REI included the same effects with a covariance component for random and environmental effects.

Heritabilities of feed efficiency related traits and milk production traits, and genetic correlations between traits are presented in table 5. Estimated heritability for DMY is moderate (0.16 ± 0.02) and higher for FC (0.36 ± 0.02) and PC (0.43 ± 0.02). DMY is negatively highly correlated with FC (-0.50 ± 0.05) and PC (-0.62 ± 0.05), and the two contents are positively highly correlated (0.65 ± 0.03). Heritabilities of feed efficiency related traits over the lactation are low (0.10 ± 0.01 for NEICMR, 0.11 ± 0.01 for REI). The two feed efficiency traits are genetically highly correlated (-0.63 ± 0.06). They are also highly correlated with milk yield (0.74 ± 0.04 for NEICMR and -0.79 ± 0.04 for REI). However, they show contrasted genetic correlations with milk contents: low for NEICMR (0.11 ± 0.07 with FC, -0.18 ± 0.07 with PC) and higher for REI (0.46 ± 0.06 with FC and 0.75 ± 0.04 with PC).

Table 5 Estimates of heritabilities ± standard error (diagonal) and genetic correlations ± standard error (below diagonal) among feed efficiency and dairy traits in Lacaune dairy ewes.

	DMY	FC	PC	NEICMR	REI
DMY	0.16 ± 0.02				
FC	-0.50 ± 0.05	0.36 ± 0.02			
PC	-0.62 ± 0.05	0.65 ± 0.03	0.43 ± 0.02		
NEICMR	0.74 ± 0.04	0.11 ± 0.07	-0.18 ± 0.07	0.10 ± 0.01	
REI	-0.79 ± 0.04	0.46 ± 0.06	0.75 ± 0.04	-0.63 ± 0.06	0.11 ± 0.01

DMY = daily milk yield; FC = fat content; PC = protein content; NEICMR *= net energy intake converted in milk ratio; REI = residual energy intake.*

This study was the subject of a recently published scientific article (Machefert et al., 2023; https://doi.org/10.1016/j.animal.2023.100951)

1.2.4 References

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1.3 Dairy Goats UK

1.3.1 Methods

The data consisted of 42,434 test day records for feed intake (kg) and body weight (kg) from 3,421 multiparous, mixed-breed composite Yorkshire Dairy Goats (YDG) (originally made up from Saanen, Alpine, and Toggenburg) were used for univariate analyses this study. First lactation animals only (n=1146) were used to estimate the genetic correlations amongst the traits. Animals were zero-grazed year-round across 2 farm sites and had continuous access to water and hay. Animals were fed a digestible fibre-based blended feed ad libitum for the first 150 days of lactation, after which feed was restricted based on MY. Feed was provided in the milking parlour and automatically dispensed, while body weights were recorded as the animals exited the milking parlour. Records were related to individuals via electronic identification devices. Animals were the progeny of 180 sires and 2,212 dams, and the pedigree contained 8,068 animals.

Fixed effects for feed intake and body weight included milk yield, year-season of kidding, age at kidding, herd test day, and fixed lactation curves using third order Legendre polynomials nested withinlactation number. Feeding regime (*ad libitum* vs restricted feeding) was included as a fixed effect for feed intake, but not body weight, as this did not significantly contribute to the variance in this trait, asdetermined by Wald F statistics (P > 0.05). In addition, body weight was included as a fixed effect for feed intake, and vice versa. By including body weight and milk yield as fixed effects for feed intake, an approximation of feed efficiency was obtained. Additive genetic and permanent environment effects were modelled using second order Legendre polynomials across days in milk.

1.3.2 Results

Descriptive statistics of the test day records for goat body weight, feed intake and milk yield are presented in Table 6.

Table 6: Summary statistics for body weight, feed intake and milk yield.

Trait	*n*	Lactation	Min	Max	Mean	SD
Body weight (kg)	20,390	1	36.00	106.40	62.46	9.94
	12,729	2	35.50	121.80	78.73	10.49
	9,315	≥3	38.00	123.50	79.23	10.57
Feed intake (kg)	20,390	1	0.28	4.51	1.83	0.55
	12,729	2	0.22	5.07	1.81	0.60
	9,315	≥3	0.14	4.53	1.54	0.62
Milk yield (kg)	20,390	1	0.21	9.25	4.36	1.13
	12,729	2	0.20	9.49	4.70	1.35
	9,315	≥3	0.21	10.55	4.16	1.45

1.3.3 Heritability estimates

Figures 1-3 show heritabilities up to 520d of lactation for daily feed intake, body weight and milk yield.

Figure 1: Heritabilities for daily feed intake

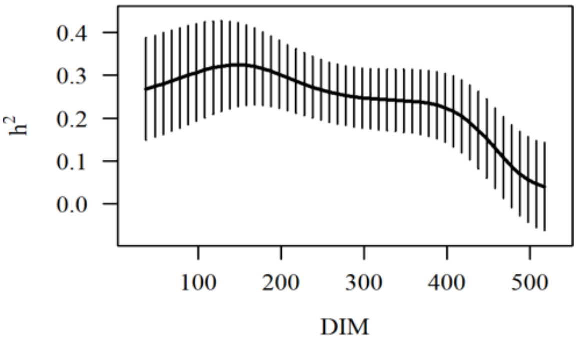


Figure 2: Heritabilities for Body weight

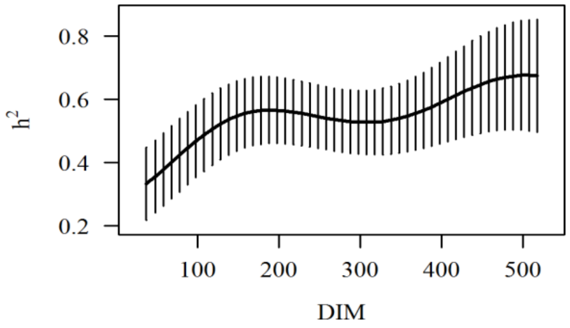
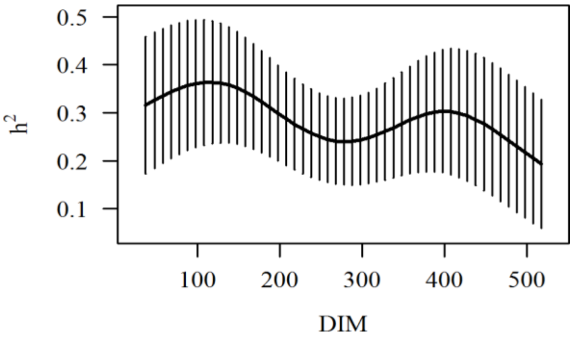
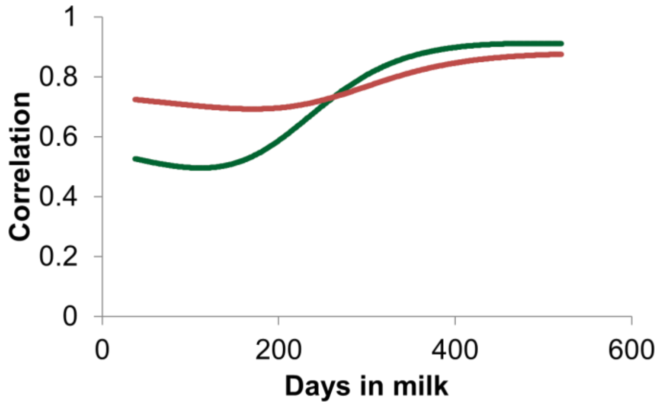


Figure 3: Heritabilities for milk yield



Figures 4-6 show genetic and phenotypic correlations between the traits. Lines in **RED** are phenotypic correlations and lines in **GREEN** are genetic correlations.

Figure 4: Correlations between feed intake and milk yield



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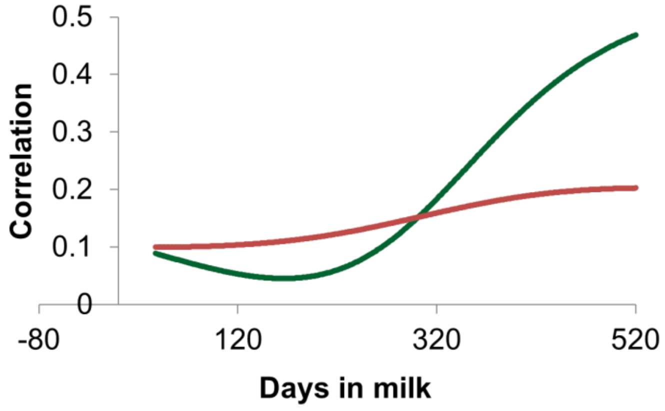
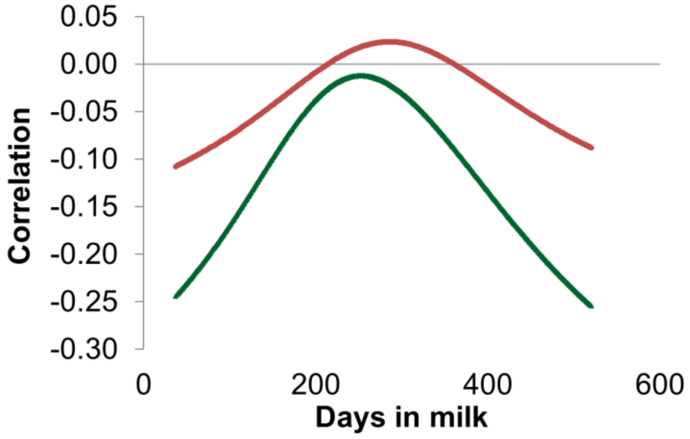


Figure 6: Correlations between milk yield and live weight



Results show that selection for increased milk yield will result in a rise in feed intake and that there is sufficient genetic variation to select for feed efficiency in goats. Due to the positive correlation of feed intake with body weight, all 3 traits should be included together into breeding programmes to breed more efficient goats.

1.4 Alpine and Saanen, France

1.4.1 Aim

This study has been conducted as part of this project and aims to estimate the genetics parameters of feed efficiency under commercial conditions, for a large diversity of breeding systems in two breeds of dairy goats (Alpine and Saanen).

1.4.2 Methods

Animals and housing: The experiment was performed in 14 commercial farms and at the Experimental Farm of La Sapinière (INRAE, Bourges), between 2019 and 2021. To date, 1,636 (663 Alpine and 973 Saanen) primiparous dairy goats were phenotyped for feed efficiency. Feed intake was recorded 4 times during the lactation: 2 times at the beginning of the lactation (between 0 and 60 DIM and between 60 and 90 DIM), around the reproduction (between 210 and 260 DIM) and at the end of the lactation (between 240 and 280 DIM). A total of 4,827 records (1,879 and 2,948 for Alpine and Saanen, respectively) were included in the dataset.

Animals were fed with different forages and concentrates, depending on the breeder. At each test day, feed intake was determined by weighing the total ration distributed and that wasted, by trained staff from the milk recording organisms. The forage quantity was determined at the batch or farm level (not individually). For concentrates, the quantity was measured either individually with automatic feeders or manually in milking parlour, or at the batch level by weighing all the offered concentrates, depending on the farm. Thus, for farms without individual distribution of concentrates, the individual feed intake was the average feed intake of the batch to which the animal belongs (83% of the dataset). For farms with individual distribution of concentrates, the individual feed intake was the average feed intake of the batch to witch the animal belongs for forage plus the individual intake of concentrates (17%). Dry matter intake (DMI) was thus estimated for each animal and each test day. Energy Intake (EI) was estimated by multiplying DMI and energy concentration. Nutritional feed quality was recorded for each forage and each concentrate and energy content was given by INRAE (2010). Test day milk recording data (milk yield, fat and protein contents) were also measured, at the same time than the feed intake control.

The chest width (CW) was used as a proxy of the body weight and was measured one time during the lactation (about 150 DIM). No body condition scores were performed.

REI estimation: To estimate feed efficiency, **Residual Energy Intake (REI),** was estimated as the residual of a linear regression model (1):

$$EI = \beta0 + \beta1 \times MY + \beta2 \times FC + \beta3 \times PC + \beta4 \times CW + REI \qquad (1)$$

Where, EI is the energy intake (expressed in Unité Fourragère Lait unit (UFL), 1 UFL=1.7 Mcal), β0 is the intercept, β1 is the regression coefficient for MY (milk yield), β2 and β3 are the regression coefficients of FC and PC (fat and protein contents) and β4 is the regression coefficient for CW (chest width). We classified the animals in 3 groups of REI, using standard deviation (sd_REI): inefficient (REI >0.5 x sd_REI), intermediate (-05 x sd_REI ≤ REI≤ 0.5 X sd_REI), efficient (REI<-0.5 x sd_REI).

Estimation of genetic parameters: The traits analysed were the REI and MY. The genetic parameters were estimated, for each breed separately, using WOMBAT software (Mayer, 2007), with the following animal linear models:

Y=Flock + Camp + Htd + PhSt + an + permp + e (2)

Y=Age + Camp + Htd + PhSt + an + permp + e (3)

Where, Y is the observation vector for REI (1) or MY (3), Flock is the fixed effect of the flock, Age is the effect of the age at kidding, Camp is the fixed effect of the lactation campaign, Htd is the fixed effect of the herd test day, PhSt is the fixe effect of the physiological stage. The random effects included in the model were, the additive genetic effect of the animal (an), the permanent environmental effect (permp) and the residual (e).

Only animals with 2 or more test day records are kept. The final data set was comprised 1,331 and 2,414 test day records of 455 and 785 Alpine and Saanen goats, respectively. Animals were the progeny of 74 and 94 sires and 355 and 576 dams and the pedigree contained 7,484 and 8,652 animals for Alpine and Saanen breeds, respectively.

1.4.3 Results and Discussion

A general description of the data is presented in Table 7. DMI was on average 2.7 kg with a standard deviation of 310 g and 280 g in Alpine and Saanen breed, respectively. EI was on average 2.5 UFL for both breeds, with a moderate variability (CV of 13% and 11%). The residual energy intake (REI) was zero on average by definition. The milk yield was on average 3.40 L in Alpine breed and 3.04 L in Saanen breed with a standard deviation of 940 mL and 770 mL respectively. The mean chest width was 88 cm in the two breeds, with a low variability (CV of 5% for both breeds).

Table 7. Descriptive statistics of REI (Residual Energy Intake), DMI (Dry Matter Intake), Energy Intake (EI), Milk Yield (MY) and Chest Width (CW) per goat breed.

Breed	Trait	N	Min	Mean	Max	Sd[1]	CV[2]
Alpine	REI	1879	-1.02	0.00	0.71	0.27	11%
	DMI (kg)	1879	2.01	2.68	3.63	0.31	12%
	EI (UFL)	1879	1.66	2.48	3.41	0.31	13%
	MY (L)	1879	0.90	3.40	6.50	0.94	28%
	CW (cm)	1879	76.00	88.24	103.00	4.29	5%
	REI	2948	-0.87	0.00	1.01	0.28	11%

Saanen	DMI (kg)	2948	2.02	2.82	3.78	0.28	10%
	EI (UFL)	2948	1.78	2.62	3.85	0.29	11%
	MY (L)	2948	0.30	3.04	6.60	0.77	25%
	CW (cm)	2948	76.00	88.51	103.00	4.64	5%

[1]Standard deviation; [2]Coefficients of variation

Dry matter intake (DMI) was higher in the inefficient group, and lower in the efficient group, with a difference of 0.49 kg of DMI per day in Alpine breed and 0.57 kg in Saanen breed between both groups. (Table 8). This difference was explained both by a lower CDMI (concentrates DMI) and a lower FDMI (forage DMI) for the inefficient group. The ratio of milk output to DMI (DMI/MY) is lower for the efficient group. MY (results not shown) is the same in the three groups. These results show that we are able to roughly but correctly classify goats: efficient vs inefficient. Despite, the lack of precision due to on-farm measurements, this classification could be useful for breeders.

Table 8. Descriptive statistics of DMI (Dry Matter Intake), Energy Intake (EI), ratio of milk output to DMI (DMI/MY), concentrates DMI (CDMI) and forage DMI (FDMI) per group of REI and per goat breed.

	Mean (sd)					
	Inefficient		**Intermediate**		**Efficient**	
Trait	Alpine (n=526)	Saanen (n=724)	Alpine (n=879)	Saanen (n=1317)	Alpine (n=474)	Saanen (n=907)
DMI (kg)	2.86 (0.26)	3.11 (0.15)	2.73 (0.26)	2.86 (0.16)	2.37 (0.20)	2.54 (0.21)
EI (UFL)	2.71 (0.15)	2.98 (0.16)	2.55 (0.15)	2.64 (0.11)	2.08 (0.26)	2.32 (0.21)
DMI/MY	0.95 (0.25)	1.13 (0.44)	0.79 (0.23)	0.99 (0.25)	0.83 (0.30)	0.89 (0.37)
CDMI (kg)	1.29 (0.17)	1.02 (0.22)	1.24 (0.17)	0.95 (0.09)	1.03 (0.17)	0.79 (0.19)
FDMI (kg)	1.57 (0.38)	2.08 (0.19)	1.47 (0.36)	1.89 (0.14)	1.33 (0.20)	1.74 (0.21)

Variance components, heritabilities and repeatability of the traits analysed are shown in Table 9. The heritability of test day milk yield was 0.19 and 0.20 in Alpine and Saanen breeds, respectively. Arnal et al. (2019) found higher heritabilities of 0.27 and 0.28 on test day milk yield for the same breeds. Estimated heritabilities for REI, in both breeds, were moderate (0.18 and 0.20), with higher repeatability for Alpine breed (0.31) than Saanen breed (0.12). The estimated heritability of REI was slightly lower than the feed efficiency heritability reported by Desire et al. (2017) in mixed-breed (Saanen, Alpine and Toggenburg) population (around 0.25). Köck et al. (2018) reported a lower heritability (0.11) for energy efficiency which is the ratio of milk energy output to total energy intake (LE/ INEL, where LE = energy in milk and INEL= energy intake in DM), in Austrian dairy cattle. Köck et al. (2018) reported a lower heritability (0.11) for energy efficiency which is the ratio of milk energy output to total energy intake (LE/ INEL, where LE = energy in milk and INEL= energy intake in DM), in Austrian dairy cattle. According to Berry and Crowley (2013), heritability varies between studies depending on the type of model used to estimate feed efficiency (ratio traits or regression/residual traits) and on the type of animal involved (the range for growing animals is between 0.14 and 0.62, this falls to between 0.00 and 0.38 in adult cows).

Moreover, one of the greatest challenges in our caseis our large diversity of feeding systems due to the collect of feed intake information in commercial farms and the lack of individual feed intake due to the expensive cost of automatic feeders for breeders. The use of feed efficiency group can allow breeders to know in which categories their goatsare, and to adapt their feed system.

Table 9. Variance components: additive genetic variance (V_A), permanent environmental variance (V_E) and residual variance (V_R), heritabilities (h^2) and repeatability (r) for residual energy intake (REI) and milk yield (MY), with SEs in brackets.

Breed	Trait	V_A	V_E	V_R	h^2	R
Alpine	REI	0.004 (0.001)	0.006 (0.002)	0.009 (0.001)	0.18 (0.08)	0.31 (0.08)
	MY	0.096 (0.049)	0.186 (0.044)	0.227 (0.011)	0.19 (0.09)	0.37 (0.09)
Saanen	REI	0.003 (0.001)	0.002 (0.001)	0.011 (0.0001)	0.20 (0.07)	0.13 (0.06)
	MY	0.097 (0.036)	0.185 (0.031)	0.202 (0.007)	0.20 (0.07)	0.38 (0.07)

Meat Sheep

1.5 Dohne Merino, Corriedale, Merino, Uruguay

1.5.1 Descriptive statistics

Descriptive statistics of the traits recorded during feed intake trials are presented in Table 10. Corriedales were the youngest animals at the moment of the test, while Dohnes were the oldest and Merinos intermediate. While only females are evaluated for Corriedale and Dohne, in Merino, both sexes were considered. Independently of the age and BW at the moment of the test, the three breeds presented a feed intake from 3 to 3.5% of BW and ADG between 160 to 200 g/d. Data were recorded at informative nucleus from INIA (Corriedale, Dohne and Merino) and Uruguayan Wool Secretariat (SUL-CIEDAG) in Corriedale.

Table 10: Descriptive statistics (number of animals, mean, standard deviation) for traits related to efficiency by breed (INIA progeny 2018-2021 and CIEDAG-SUL 2017 for Corriedale).

	Corriedale			Dohne			Merino		
Trait	**N**	**Mean**	**sd**	**N**	**Mean**	**sd**	**N**	**Mean**	**sd**
age at test (days)	371	214.2	52.94	357	419.4	8.23	1193	293.2	43.28
ADG (kg/d)	371	0.16	0.05	357	0.16	0.06	1193	0.19	0.07
R^2 ADG	371	0.88	0.13	357	0.79	0.19	1193	0.85	0.16
N° of meals	371	53.63	16.54	357	83.75	16.91	1193	60.63	17.99
Feed intake (kgDM/d)	371	1.21	0.29	357	1.52	0.28	1193	1.36	0.28
Feed Intake (MjME/d)	371	2.87	0.73	357	3.68	0.73	1193	3.29	0.69
Feed conversion ratio (FI/ADG)	371	7.92	3.2	357	11.14	11.5	1193	8.21	6.96
Feed conversion ratio (ME/ADG)	371	18.72	7.4	357	26.86	26.99	1193	19.74	16.28
Mid FI test BW (kg)	371	32.75	4.97	357	50.17	5.46	1193	40.91	6.4
Metabolic BW (kg)	371	13.66	1.56	357	18.83	1.55	1193	16.14	1.89
BW gain on trial (kg)	367	6.43	2.05	352	6.97	2.6	1187	7.36	2.86
Methane (g/d)	312	16.41	4.24	349	26.83	5.68	1162	22.27	5.59
CO_2 (g/d)	312	843	170.28	349	1425.73	322.46	1162	1095.6	241.02
O_2 (g/d)	312	842.71	154.73	349	1260.86	291.15	1162	989.03	195.61
Methane intensity (g/kg ADG)	312	0.1	0.04	349	0.2	0.21	1162	0.13	0.1
Methane yield (g/kgDM)	312	13.02	3.18	349	18.03	4.22	1162	16.54	3.67
Staple length trial (mm)	147	19.38	5.89	250	17.73	3.19	678	18.63	7.13
RFI (breed)	371	0	0.13	357	0	0.17	1193	0	0.14
age at weaning (days)	700	109.34	8.89	1031	118.87	25.3	1513	122.46	16.89
Weaning BW (kg)	700	25.35	4.53	1031	27.85	5.27	1513	24.23	4.69
age at FEC (days)	385	251.02	36.7	929	232.43	45.35	1403	220.51	38.48
FEC 1	385	1089.87	1726.32	929	3323.47	3357.39	1403	1837.78	1655.85
Ln FEC1 (log e FEC)	385	6.32	1.23	929	7.48	1.35	1403	7.26	0.81
FAMACHA 1	319	1.61	0.68	713	1.97	0.8	987	1.98	0.88
Body condition score at FEC1	322	3.02	0.33	725	3.01	0.54	987	2.81	0.39
Temperament (points)	327	40.85	24.37	473	62.99	30.87	1452	66.21	33.38
age at Shearing (days)	543	365.04	53.35	863	367.61	42.11	1440	403.59	16.29
Yearling BW (kg)	542	33.53	5.22	979	44.01	5.01	1436	46.72	12.15
Greasy Fleece Weight (kg)	376	2.82	0.75	977	2.46	0.55	1431	3.89	0.77
Clean Fleece Weight (kg)	372	2.12	0.54	965	1.84	0.44	1421	2.96	0.57
Fiber diameter (µ)	373	22.62	1.87	968	17.95	1.22	1433	14.8	0.95
Staple length (cm)	373	12.09	2.24	968	9.57	1.95	1433	11.19	1.34
Rib eye area (cm^2)	245	5.98	1.43	631	9.41	1.71	1433	8.05	2.34
Backfat depth (mm)	245	1.14	0.41	631	1.83	1.04	1433	1.91	1.04

1.5.2 Models

The results indicated that the basic model (sex-pen-trial, ADG, MW) is the most parsimonious for both analyses; the other fixed effects, body composition, and fleece growth traits were not significant (p>0.05) (AIC difference >2). Furthermore, RFI values estimated with the basic and alternative models were highly correlated (r=0.99). In conclusion, it might not be necessary to include estimations of wool growth during 42-day tests in RFI models when evaluating Merino sheep (Marques et al., 2021).

Pearson and Spearman correlations between RFI linear and weekly 42-days models were 0.93 and 0.92, respectively. The 35-days length models (linear and weekly) presented Pearson and Spearman correlations greater than 0.98 with the 42-days models. The RFI models with 35 days allowed to decrease seven days the FI test maintaining accuracy and explaining 75.3% and 63.6% of the FI by the linear and weekly models, respectively (Amarilho-Silveira et al., 2022).

Genetic parameters estimation in Merino breed:

Preliminary results were presented at 12th WCGALP (Marques et al. 2022). These new analyses include one more generation 2018-2021. Multivariate analyses were conducted using the entire population dataset of Merino breed. The dataset included animals that have records of FD, CFW and BW. The total dataset consisted of 64,480 records with a total pedigree of 88,839 animals. The feed intake and methane data were recorded in 11 trials in years 2018 to 2022, recording 270, 316, 341, 211 animals from progeny 2018, 2019, 2020 and 2021, respectively (total n=1,138). A Bayesian analysis of variance and covariance components using GIBBSF90 computer package (Misztal *et al.,* 2002) was performed. The number of iterations after burn-in used for posterior inferences was 300,000 with the model:

$$\mathbf{yijklm = CGi + BTj + DAk + agel + am + eijklm}$$

where:

yijklm…m-th performance record of animal l,

CGi…fixed effect of the contemporary group i (year-management group-sex-pen-trial, 134 levels),

BTj … fixed effect of birth type j (2 levels),

DAk… fixed effect of dam age k (3 levels),

age… age at m measurement of animal l as a co-variable,

al …random additive genetic effect of animal l (1,962 animals),

and eijklm …random residual.

1.5.3 RFI Contrasting groups

The association between Predicted and Observed Feed Intake (kg DM/day) by breed is presented in figure 7. High, medium, and low RFI animals are present at any observed intakes (low, medium, or high).

Figure 7: Predicted Feed Intake vs Observed Feed Intake (kgDM/day) by RFI group for Corriedale, Merino and Dohne breeds.

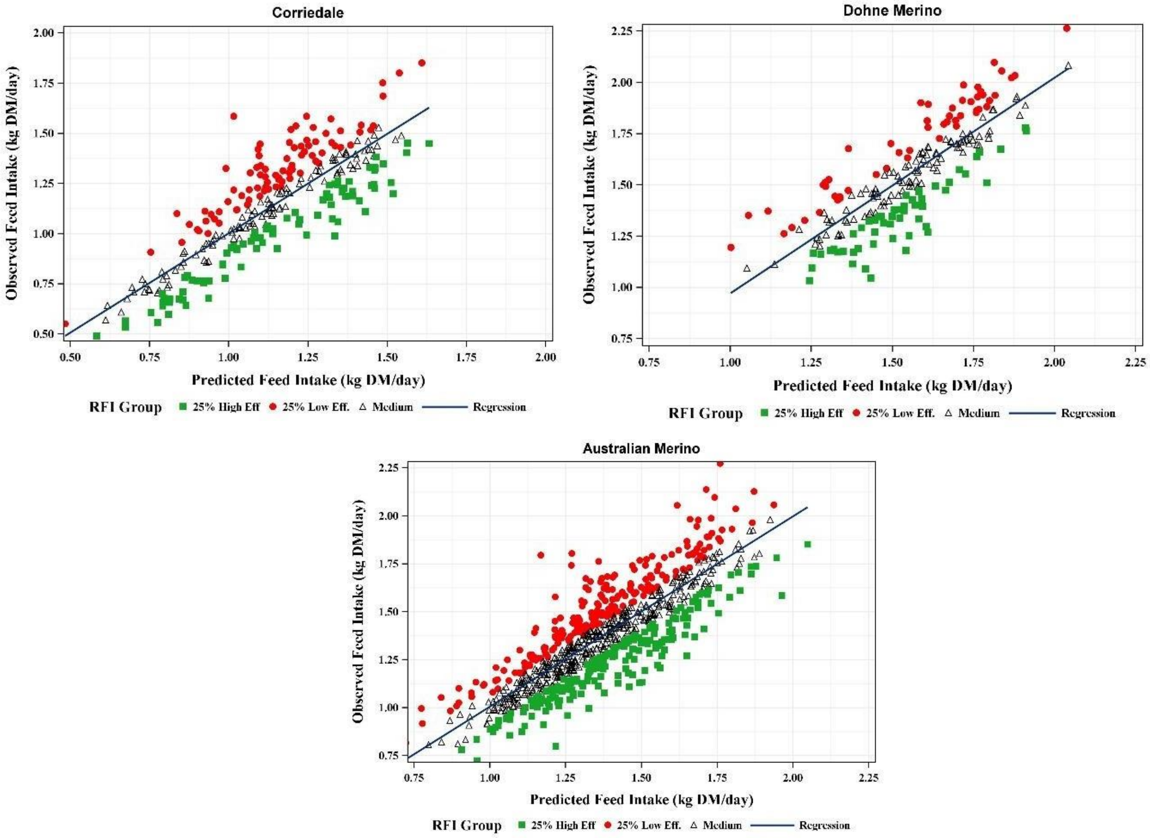


Table 11: RFI group effect on feed intake, feed conversion ratio, RFI and behaviour for all breeds (all p<0.05) (means±sd)

Breed	**Corriedale**			**Dohne**			**Merino**		
RFI group	High	Medium	Low	High	Medium	Low	High	Medium	Low
FI (kgDM)	0.97±0.02	1.12±0.01	1.27±0.02	1.34±0.02	1.52±0.01	1.70±0.02	1.18±0.01	1.33±0.01	1.50±0.01
FCR (MJEM)	14.8±0.54	16.4±0.47	19.7±0.62	19.9±0.79	22.2±0.55	24.5±0.79	15.5±0.27	18.0±0.18	20.7±0.26
FCR (kgDM)	6.2±0.23	6.9±0.20	8.3±0.26	8.1±0.32	9.1±0.22	10.0±0.32	6.4±0.11	7.4±0.08	8.5±0.11
RFI	-0.14±0.01	0.00±0.01	0.16±0.01	-0.18±0.01	-0.01±0.01	0.16±0.01	-0.16±0.00	-0.01±0.00	0.15±0.00
N° Meals	44.1±1.65	56.3±1.46	66.9±1.91	73.9±1.90	81.6±1.33	91.5±1.92	52.9±1.00	60.4±0.69	72.5±0.98

In terms of GHG emissions (Table 12), the RFI group affected the total methane only in the Merino breed ($p<0.05$), where the less efficient animals emitted 6.6% more methane. Alternatively, the RFI group affected the methane emission corrected by feed intake in the model (methane g/d FI 24-48-72 hours) or as precorrection (methane g/DMI 24hs). In all cases, the more efficient animals had higher methane yields than less efficient ones. Only in the Merino breed were observed a tendency in methane intensity ($p=0.0538$) affected by the RFI group. More efficient animals tended to emit 10% less methane by kg of body weight gain (21 days before each methane record). In the case of CO_2, more efficient animals had lower emissions in Dohne and Merino breeds ($p<0.05$), 6.8 and 4.8%, respectively.

Table 12: RFI group effect on GHG emissions reported as total methane, methane yield, methane intensity, and CO_2 for Corriedale, Dohne, and Merino breeds

Breed	**Corriedale**			**Dohne**			**Merino**		
RFI group	High	Medium	Low	High	Medium	Low	High	Medium	Low
Methane (g/d)	16.3^{a}	16.2^{a}	16.7^{a}	26.6^{a}	28.2^{a}	27.8^{a}	22.6	22.9	24.1
Methane yield (g/d) (by FI 24-48-72hs)	17.2	16.2	15.7	28.7	28.5	26.9	24.8	23.3	22.6
Methane yield (g/kgDM 24hs)	5.7	5.0	4.3	7.5	6.8	6.0	7.0	6.4	5.9
Methane intensity (g/kgBWG)	4.6^{a}	4.4^{a}	4.9^{a}	9.6^{a}	8.8^{a}	9.2^{a}	6.9	7.1	7.5
CO_2 (g/d)	830.9^{a}	831.7^{a}	851.2^{a}	1354.8	1438.4	1446.5	1056.7	1063.6	1107.1

In the Corriedale breed, the RFI group also significantly affected the staple length where the less efficient animals have longer wool. In Merino, more efficient animals were slightly leaner than the low efficient group (Table 13).

Table 13: Contrast by RFI group for Corriedale and Merino breeds

	RFI group				
	High	Medium	Low	Breed	P
Staple length (cm)	11.9±0.37	12.8±0.33	12.8±0.34	Corriedale	<0.05
Staple length (cm)	10.8±0.10	10.9±0.07	11.1±0.09	Merino	0.0801
Backfat (g/kgBWG)	2.01±0.04	2.08±0.03	2.19±0.04	Merino	<0.05
Fiber diameter (µ)	22.4±0.41	23.1±0.36	23.4±0.37	Corriedale	0.535

1.5.4 Phenotypic correlations

Moderate correlations were estimated between FI and RFI in the three studied breeds (Tables 14, 15 and 16). The correlation between GHG emissions and FI also presented moderated correlations, being CO_2 the trait with higher correlations with FI within each breed. In relation to RFI, the number of meals and CH4 yield were the most correlated traits, again within each breed.

Table 14: Phenotypic correlations for traits related to efficiency for the Corriedale breed.

Corriedale	RFI	FCR	Nmeals	SL	Backfat	CH_4	CO_2	O_2	CH_4 intensity	CH_4 yield
Feed intake (kg/d)	0.74	0.23	0.55	0.40	0.16	0.60	0.65	0.56	0.35	-0.39
RFI (breed)		0.42	0.53	0.28	-0.03	0.28	0.22	0.15	0.27	-0.52
Feed CR (FI/ADG)			0.25	0.16	0.01	0.11	-0.03	-0.15	0.08	-0.12
N° of meals				0.20	0.05	0.32	0.43	0.41	0.25	-0.23
Staple Length (cm)					-0.06	0.43	0.27	0.27	0.39	-0.11
Backfat depth (mm)						-0.08	0.20	0.11	-0.25	-0.04
Methane (g/d)							0.72	0.61	0.88	0.23
CO_2 (g/d)								0.84	0.49	0.11
O_2 (g/d)									0.42	0.11
CH_4 intensity (g/kgBW)										0.26

Table 15: Phenotypic correlations for traits related to efficiency for the Dohne breed.

Dohne	RFI	FCR	Nmeals	SL	Backfat	CH_4	CO_2	O_2	CH_4 intensity	CH_4 yield
Feed intake (kg/d)	0.61	0.02	0.38	-0.09	0.39	0.38	0.70	0.64	-0.01	-0.43
RFI (breed)		0.30	0.44	0.03	0.09	-0.02	0.16	0.15	-0.04	-0.51
Feed CR (FI/ADG)			-0.13	-0.05	-0.05	-0.05	-0.04	-0.03	-0.03	0.03
N° of meals				0.13	0.09	0.02	0.08	0.08	0.00	-0.31
Staple Length (cm)					-0.20	-0.02	-0.31	-0.34	0.06	0.11
Backfat depth (mm)						0.07	0.45	0.45	-0.19	-0.24
Methane (g/d)							0.52	0.42	0.85	0.49
CO_2 (g/d)								0.96	0.13	-0.16
O_2 (g/d)									0.05	-0.20
CH_4 intensity (g/kgBW)										0.63

Table 16: Phenotypic correlations for traits related to efficiency for the Merino breed.

Merino	RFI	FCR	Nmeals	SL	Backfat	CH_4	CO_2	O_2	CH_4 intensity	CH_4 yield
Feed intake (kg/d)	0.57	-0.22	0.29	0.32	0.24	0.64	0.80	0.74	0.19	-0.23
RFI (breed)		0.20	0.30	0.13	-0.02	0.18	0.28	0.22	0.21	-0.42
Feed CR (FI/ADG)			0.24	-0.19	0.07	-0.15	-0.34	-0.35	-0.15	0.09
N° of meals				-0.02	0.17	0.23	0.13	0.11	0.03	-0.04
Staple Length (cm)					-0.07	0.25	0.30	0.35	0.16	-0.05
Backfat depth (mm)						0.16	0.17	0.11	-0.16	0.06
Methane (g/d)							0.71	0.66	0.75	0.41
CO_2 (g/d)								0.93	0.37	-0.03
O_2 (g/d)									0.32	-0.01
CH_4 intensity (g/kgBW)										0.43

1.5.5 Principal component analysis for Feed Intake

Descriptive statistics of the traits involved in the PCA are presented in Table 17.

Table 17: Descriptive Statistics for the traits analysed for PCA by breed.

Breed	Trait	N	Mean	sd	min	max
Corriedale	Metabolic BW (kg)	281	13.9	1.6	9.6	18.3
	ADG (kg)	281	0.166	0.046	0.030	0.274
	Methane (g/d)	218	16.4	4.8	5.7	28.5
	CO_2 (g/d)	218	828.9	183.8	404.3	1447.7
	O_2 (g/d)	218	847.0	160.0	445.8	1315.8
Dohne	Metabolic BW (kg)	214	18.8	1.6	13.8	22.9
	ADG (kg)	214	0.181	0.050	0.079	0.325
	Methane (g/d)	208	28.1	5.7	15.7	50.6
	CO_2 (g/d)	208	1483.6	344.0	850.2	2537.8
	O_2 (g/d)	208	1321.5	325.5	774.1	2734.0
Merino	Metabolic BW (kg)	811	16.1	1.8	11.7	23.2
	ADG (kg)	811	0.202	0.068	0.055	0.469
	Methane (g/d)	784	23.4	5.4	8.9	44.7
	CO_2 (g/d)	784	1086.2	232.5	533.9	2269.6
	O_2 (g/d)	784	1000.3	189.4	560.9	2114.7

The PCA 1 explains 68.54% of the total variance. The correlation between PCA 1 and the observed FI was 0.82 for Australian Merino (figure 8). Therefore, with two estimates of GHG emission in portable accumulation chambers, in addition to measures of BW and ADG, it would be possible to have an estimation of feed intake.

Figure 8: PCA 1 vs. observed feed intake for Australian Merino (r= 0.82).

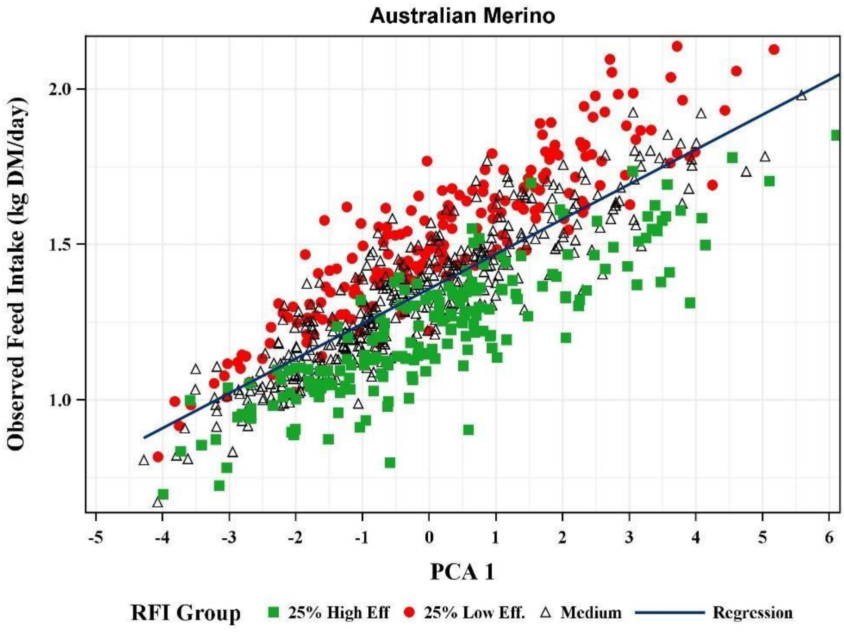
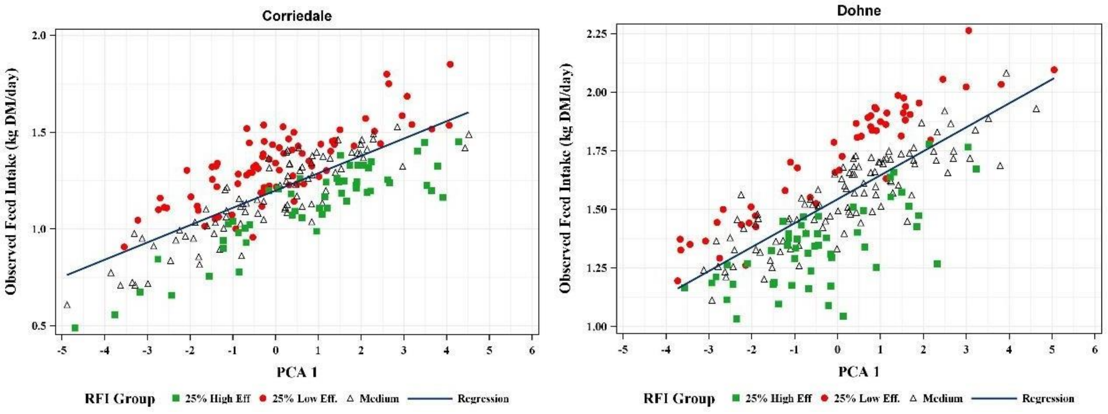


Table 18: Eigenvectors for the five principal components.

	PCA 1	PCA 2	PCA 3	PCA 4	PCA 5
Metabolic BW	0.405	0.594	-0.360	0.594	0.023
ADG (kg)	0.396	-0.644	0.321	0.569	-0.037
Methane (g/d)	0.421	0.419	0.764	-0.245	0.064
CO_2 (g/d)	0.505	-0.112	-0.275	-0.371	-0.720
O_2 (g/d)	0.497	-0.211	-0.330	-0.354	0.689

To validate the results obtained with Merino, the eigenvectors of PCA 1 obtained (Table 18) were multiplied by the standardized values of the five analysed traits of Corriedale and Dohne breeds to calculate a PCA 1 estimated for each breed. The correlation between these estimated PCA 1 vs observed feed intake was 0.7341 and 0.7338 for Corriedale, Dohne, and Merino, respectively (figure 9).

Figure 9: PCA 1 estimated from Merino data vs. observed feed intake for Corriedale and Dohne breeds.



Animals were classified based on percentiles from PCA 1 (from PCA analysis for Merino and estimated for Corriedale and Dohne) into three classes: High (>25%), Medium, and Low PCA (<25). A confusion matrix between these classes and observed FI is presented in Table 19. In conclusion, the PCA estimated class can help to predict if an animal has high or low feed intake based on traits that can be recorded under field conditions. The false-negative and positive rates were almost zero.

Table 19. Confusion matrix: percentage of animal classified by observed feed intake and PCA

		1. High PCA	2. Medium PCA	3. Low PCA
Corriedale n=218	**1. High FI**	53.7	46.3	0.0
	2. Medium FI	22.9	61.5	15.6
	3. Low FI	0.0	32.7	67.3
- Dohne n=208	**1. High FI**	61.5	38.5	0.0
	2. Medium FI	18.3	62.5	19.2
	3. Low FI	1.9	36.5	61.5
Merino n=784	**1. High FI**	73.5	26.0	0.5
	2. Medium FI	13.3	73.2	13.5
	3. Low FI	0.0	27.6	72.5

1.5.6 Genetic parameter estimation for Australian Merino

The descriptive statistics are presented in Table 20. Average age of lambs at FEC, feed intake trial and shearing were 374±41, 272±73 and 294±43 days, respectively.

Table 20. Descriptive statistics for clean fleece weight (CFW, kg), fibre diameter (FD, microns), bodyweight at shearing (BW, kg), postweaning faecal egg count (FEC, Log e), daily methane emissions (CH4, g/day), feed intake (FI, kgDM/day), residual feed intake (RFI kgDM/day), rib eye area (REA, cm2), backfat thickness (BF, mm) traits in Australian Merino breed

TRAIT	N	mean	sd	min	max
CFW (kg)	64,480	2.41	0.68	0.5	10.03
FD (microns)	64,480	16.2	1.6	11.6	24.9
BW (kg)	64,480	37.17	9.85	13	98
FEC (count)	28,174	1311.21	1905.34	0	36800
Ln FEC (log e FEC)	28,174	6.64	1.14	4.61	10.52
CH4 (g/day)	1,107	22.29	5.6	8.9	44.7
FI (kgDM/day)	1,138	1.36	0.28	0.67	3.16
RFI(kgDM/day)	1,120	-0.01	0.12	-0.38	0.41
REA (cm^2)	3,073	9.3	2.72	3	19.26
BF (mm)	3,061	2.38	1.07	0.3	6.9

Heritabilities, genetic and phenotypic correlations estimated are shown in Table 21. Moderate The heritabilities for all examined traits fell within the range of 0.20 to 0.41, indicating a moderate genetic basis for these characteristics. Notably, fiber diameter consistently exhibited higher heritability estimates compared to other traits. Correlation values presented in italic means that zero were included in the HPD97 interval. The strong correlations observed between FI and BW along with CH4 are remarkable. These correlations suggest that BW and CH4 can potentially serve as proxies for FI selection. Given that field body weighing is a simpler and more practical task, and that the implementation of a methane recording system using portable chambers (PAC) is relatively straightforward, these variables present feasible alternatives for estimating FI. On the other hand, no unfavorable genetic correlations were observed between FI or RFI and the other analyzed traits. This suggests the possibility of selecting for efficiency either directly based on RFI or by incorporating FI into the selection objective alongside body weights.

Table 21. Genetic and phenotypic parameters for clean fleece weight (CFW, kg), fibre diameter (FD, microns), bodyweight at shearing (BW, kg), postweaning faecal egg count (FEC, Log e), daily methane emissions (CH4, g/day), feed intake (FI, kgDM/day), residual feed intake (RFI kgDM/day), rib eye area (REA, cm2), backfat thickness (BF, mm) traits in Australian Merino breed [1,2]

	CFW	FD	BW	FEC	CH4	FI	RFI	REA	BF
CFW	**0.30 (0.01)**	0.35 (0.02)	0.29 (0.02)	*0.03* (0.05)	*0.17* (0.15)	*0.18* (0.12)	*0.02* (0.15)	*0.07* (0.08)	*0.15* (0.11)
FD	0.13	**0.64 (0.01)**	0.25 (0.02)	-0.08 (0.04)	*0.17* (0.17)	*0.20* (0.14)	*0.15* (0.15)	*0.13* (0.08)	0.40 (0.08)
BW	0.45	0.13	**0.41 (0.01)**	*-0.07* (0.04)	0.58 (0.15)	0.68 (0.09)	*-0.22* (0.14)	0.50 (0.06)	0.44 (0.08)
FEC	*-0.02*	-0.05	-0.07	**0.20 (0.01)**	*-0.20* (0.20)	*-0.06* (0.22)	*0.13* (0.19)	*-0.21* (0.11)	*-0.02* (0.15)
CH4	0.15	*0.09*	0.30	*0.08*	**0.34 (0.09)**	0.75 (0.12)	0.43 (0.19)	0.37 (0.17)	0.36 (0.15)
FI	0.34	*0.14*	0.48	*-0.04*	0.29	**0.41 (0.08)**	0.79 (0.09)	0.39 (0.14)	0.34 (0.12)
RFI	*0.00*	*-0.01*	*-0.02*	*-0.08*	*-0.02*	0.63	**0.37 (0.08)**	*-0.15* (0.20)	*-0.17* (0.16)
REA	0.23	0.18	0.47	*-0.02*	0.13	0.30	*-0.02*	**0.39 (0.04)**	0.53 (0.10)
BF	0.10	*0.03*	0.24	-0.09	*0.04*	0.11	*0.01*	0.21	**0.32 (0.04)**

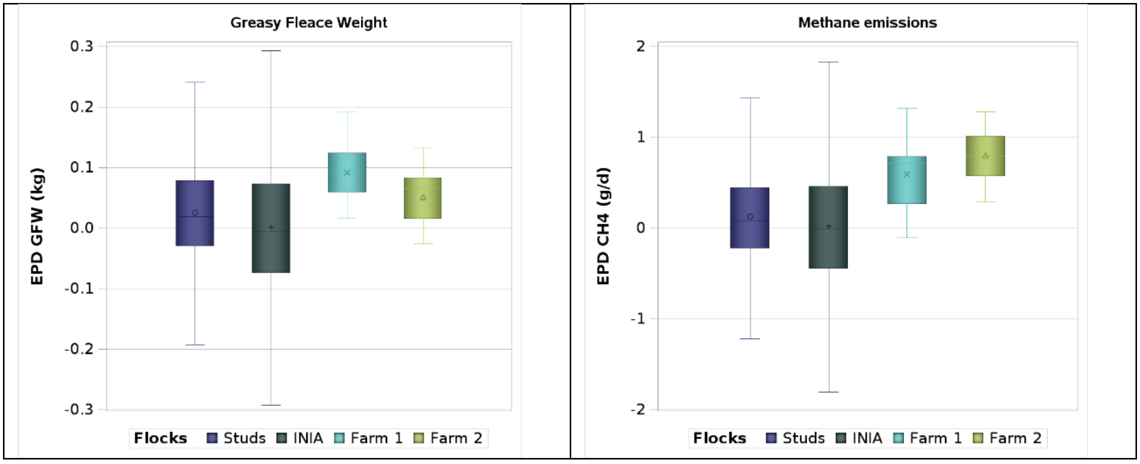
[1] Heritabilities (in bold) on the diagonal, phenotypic and genetic correlations below and above the diagonal, respectively, posterior standard deviation in parenthesis.

[2] Correlation values presented in italic means that zero were included in the HPD95 interval.

Based on these parameters, genomic predictions were carried out on two commercial farms, each comprising 20 rams. A multivariate analysis (6 traits CFW, BW, FEC, FI, RFI, CH4) was conducted, incorporating genomics data from 2,544 animals genotyped with various SNP panels, (9,304 SNPs in common). For these animals, which lacked both phenotypic and genealogical information, estimates for different traits were obtained with an average accuracy of 0.51, 0.48, 0.45, 0.39, 0.39, and 0.29 for BW (Body Weight), CFW (Clean Fleece Weight), FEC (Fecal Egg Count), FI (Feed Intake), CH4 (Methane), and RFI (Residual Feed Intake), respectively.

Figure 10 presents expected progeny difference (EPD) for GFW and methane emissions for these two Australian Merino commercial farms and their comparison with the stud flocks (under genetic evaluation) and the INIA´s informative nucleus.

Figure 10. Expected progeny difference (EPD) for greasy fleece weight (kg) and methane emissions (g/day) for animals from stud flocks under genetic evaluation (Studs n=36,500), from INIA-CRILU nucleus of «Glencoe» Experimental Unit (INIA n=6,500) and two commercial farms (Farm 1 and 2, n=20).



This study was incorporated as one of the components within the framework of parameters contributing to the vision of regenerative livestock farming in Uruguay. This vision has been presented for the sale of wool to international companies such as Chargeurs and GUCCI.

Regenerative livestock farming in Uruguay:

http://www.ainfo.inia.uy/digital/bitstream/item/17283/1/Ganaderia-regenerativa-2023.pdf

Presentation to Chargeurs and GUCCI teams:

https://youtu.be/up9gSOCFIHI

1.5.7 References

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Marques, C.B, De Barbieri, I., Velazco, J., Navajas, E.A. and Ciappesoni, G. Genetic parameters for feed efficiency, gas emissions, oxygen consumption and wool traits in Australian Merino. In: Proceedings of the World Congress on Genetics Applied to Livestock Production (WCGALP), 12., Rotterdam, the Netherlands, 3-8 July 2022. pp. 160 – 163. https://doi.org/10.3920/978-90-8686-940-4_28

1.6 Texel, Suffolk, Charollais sheep - UK

Proxy measures of feed efficiency such as lamb growth and body composition (e.g. fat and muscle) have been estimated for 3 breeds in the UK and Ireland

All available data were extracted from the National Sheepbreeder Database (AHDB) and subsequently edits were performed to provide a more informative data set. Three breeds were considered for analysis, namely Texel, Suffolk and Charollais and only purebred animals from these three breeds were retained.

Lamb live body weights were recorded at early life and scanning in the UK using weigh-scales and carcass composition traits were recorded at the same time point as scan weight, post weaning using ultrasound scanning. Early life weight was defined as live weight measured between 40 and 85 days of age and weighing between 12 and 45 kg. Scan weight was defined as live weight taken between 121 and 180 days; only lambs weighing between 25 and 75 kg were retained for further analysis. Muscle depth and fat depth traits were recorded at the same time point as scan weight. Muscle depth had to measure between 10 and 44 mm to be retained for further analysis. Only fat depth records measuring between 0.5 and 8.0 mm were included in further analyses. For both live body weight traits, average daily gain (ADG) was calculated for all lambs; only lambs with ADG between 100 and 650 g/day were retained.

Additional lamb records were discarded if they had an unknown sire, dam, maternal grandsire or flock of birth. In order for a lamb record to be retained both their sire and maternal grandsire were required to have at least five progeny each. Dams with no known age or aged >9 years had their lamb records discarded; dam age number was then categorised as 1,2,3,4, or ≥5 years. Age at first lambing was defined as the age of the dam at her first lambing and this ranged from 1 to 3 years. Birth type was defined as the number of lambs born per lambing event per ewe. Only lambs with a birth type between 1 (single) and 4 (quadruplets) were included in subsequent analysis. Rearing type was defined as the number of lambs reared per litter per ewe; only lambs with a rearing type of between 1 and 3 were retained. Lambs that were born as a result of embryo transfer, lambs that were artificially reared or not reared by their biological dam were not used as part of the present study. Sires were required to have progeny in more than one flock to be included in further analysis. After all previously mentioned edits were performed, lambs were allocated to a contemporary group of breed-by-flock-by-week of weighing. Only contemporary groups with at least five records were retained for further analysis.

After all data edits were completed a total of 132,490 live weight and carcass composition records from 55,155 animals across 374 flocks between the years 2010 and 2017 remained.

1.6.1 Genetic Analysis

A linear animal mixed model was built for the genetic analysis, which was performed using the ASReml software (Gilmour et al., 2009); each studied trait was analysed separately within breed. The model fitted was:

$$Y_{inhdkljzm} = CG_i + AFL_n + Dam\ age_h + Gender_d * Age + Birth\ type_k * Rearing\ type_l + Animal_j + Dam_z + Litter_m + e_{inhdkljzm}$$

Where Yinhdkljzm = lamb record, CGi=fixed effect of the ith contemporary group (i=1 to 871), AFLn = fixed effect of nth age of the dam at first lambing (1 to 3), Dam ageh = fixed effect of the hth age of the dam at lambing (1 to 5), Genderd*Age = the interaction between the dth (1 to 2) gender of the lamb and age of the lamb at record, Birth typek*Rearing typel = the interaction between the birth typek (1 to 4) and rearing type l of the lamb (1 to 3), Animalj = random additive genetic effect of jth animal(lamb) including all pedigree available, Damz = random maternal effect of zth dam of animal j, Litterm = random common environmental effect among lambs in the mth litter, and einhdkljzm = random residual effect.

The above model was built up for each trait and breed separately. Significance of random effects was examined using the log-likelihood ratio test (Ferreira et al., 1999). The random dam maternal effect was an overall collective maternal effect including both a genetic and permanent environment effect of the dam. Early life weight was the only trait to include all random effects included in the model above. All other traits only included additive genetic and common environmental random effects as no significant dam effect was observed for these traits.

Heritability of each trait was calculated as the proportion of the total phenotypic variance accounted for by the additive genetic effect. The ratios of the maternal and common environmental variances to the total phenotypic variance were also derived. Genetic correlations between traits were estimated using the same model in a series of bivariate analyses of all traits studied.

1.6.2 Results

a) Descriptive Statistics

Data after edits used for further genetic analysis is shown in Table 22. The Texel breed had the highest number of records by far across all traits studied. They also proved to have the highest number of sires, dams, maternal grandsires, flocks and contemporary groups. The coefficient of variation was lowest in the Charollais breed for all traits indicating that this breed may be more uniform for the traits studied.

Table 22. Number of lambs (n), trait mean (µ) and standard deviation (SD), coefficient of variation (CV), corresponding mean lamb age, and number of sires, dams, maternal grandsires (MGS), flocks and contemporary groups (CGs) by trait and breed.

Trait (unit of measurement)	Breed	n	µ (SD)	Age	CV	Sires	Dams	MGS	Flocks	CGs
Early life weight (kg)	Texel	21,480	27.16 (6.48)	65.53	23.86%	300	10,399	1,475	199	871
	Suffolk	12,302	28.86 (6.95)	66.85	24.08%	132	5,206	606	73	408
	Charollais	16,452	27.45 (6.20)	66.43	22.59%	186	6,233	651	81	513
Scan weight (kg)	Texel	13,219	49.00 (9.24)	146.7	18.86%	192	6,986	1,171	179	627
	Suffolk	7,736	50.14 (11.27)	144.8	22.48%	95	3,827	498	62	265
	Charollais	7,778	52.01 (9.52)	146.6	18.30%	120	3,797	463	71	312
Muscle depth (mm)	Texel	12,619	28.69 (4.05)	146.8	14.12%	180	6,680	1,134	174	594
	Suffolk	7,519	29.62 (5.17)	144.2	17.45%	88	3,701	486	58	249
	Charollais	6,971	29.43 (3.53)	146.6	11.99%	105	3,493	445	69	287
Fat depth (mm)	Texel	12,527	2.45 (1.26)	146.8	51.43%	180	6,650	1,130	174	593
	Suffolk	7,383	3.31 (1.66)	144.2	50.15%	87	3,649	480	58	244
	Charollais	6,504	4.15 (1.73)	146.6	41.69%	101	3,317	426	66	274

b) Genetic Parameters

Statistically greater than zero (P<0.05) heritability estimates were found for all breeds and traits in Table 23. Heritability estimates for the live body weight traits increased as lambs got older for all breeds. The maternal effect was significant (P<0.05) for all breeds for the early life weight trait. The litter common environmental effect accounted for a high proportion of total phenotypic variance for all traits particularly within the Texel breed, where it accounted for up to 22% of total variance. Heritability estimates differed between breeds for the carcass composition traits. The Suffolk breed had a higher heritability estimate (P<0.05) for muscle depth compared to all other breeds and Charollais had a significantly higher heritability estimate than the Texel breed for fat depth (P<0.05).

Table 23. Lamb heritability (h2), and proportion of the phenotypic variance due to the maternal (m2) and common environmental (C^2) effect; model of analyses of scan weight, muscle and fat depth did not include a maternal effect; SE=standard error of estimate.

	Breed	h^2 (SE)	m^2 (SE)	C^2 (SE)
Early life weight	Texel	0.18 (0.03)	0.09 (0.01)	0.20 (0.02)
	Suffolk	0.14 (0.03)	0.08 (0.02)	0.17 (0.02)
	Charollais	0.12 (0.02)	0.08 (0.01)	0.19 (0.01)
Scan weight	Texel	0.22 (0.03)		0.22 (0.02)
	Suffolk	0.30 (0.04)		0.14 (0.02)
	Charollais	0.21 (0.03)		0.10 (0.02)
Muscle depth	Texel	0.19 (0.03)		0.17 (0.02)
	Suffolk	0.42 (0.04)		0.08 (0.02)
	Charollais	0.28 (0.04)		0.07 (0.02)
Fat depth	Texel	0.18 (0.03)		0.18 (0.02)
	Suffolk	0.29 (0.04)		0.16 (0.02)
	Charollais	0.32 (0.04)		0.09 (0.02)

Positive genetic correlations were calculated between the additive genetic effects for all traits in all breeds (Table 24). All pairwise correlations were significantly (P<0.05) different from zero, except between muscle depth and fat depth for the Charollais breed. Genetic correlations were strongest between the two live body weight traits reaching a maximum of 0.92 (± 0.02) between early life weight and scan weight in the Texel breed. These strongly positive correlations between the live body weight traits indicate that lambs that grow well early in life will also perform better during subsequent growth phases.

Table 24. Correlations (standard error in parentheses) between the additive genetic effects for the studied traits by breed

Breed	Trait	Early life weight	Scan weight	Muscle depth
Texel	Early life weight			
	Scan weight	0.92 (0.02)		
	Muscle depth	0.50 (0.05)	0.50 (0.05)	
	Fat depth	0.49 (0.06)	0.50 (0.06)	0.35 (0.07)
Suffolk	Early life weight			
	Scan weight	0.90 (0.03)		
	Muscle depth	0.65 (0.05)	0.65 (0.05)	
	Fat depth	0.46 (0.08)	0.39 (0.07)	0.43 (0.06)
Charollais	Early life weight			
	Scan weight	0.81 (0.04)		
	Muscle depth	0.43 (0.08)	0.43 (0.08)	
	Fat depth	0.34 (0.09)	0.38 (0.08)	0.03 (0.10)

1.7 Texel, Suffolk, Charollais sheep Ireland

A similar analysis was performed for Irish sheep of the same breeds as above. A full database was extracted across three breeds, namely Texel, Suffolk and Charollais, from Sheep Ireland, the Irish national database (http://www.sheep.ie). Only purebred lambs (as defined by the data records) of Texel, Suffolk and Charollais were considered in this study.

1.7.1 Traits

In Ireland lamb live weights are recorded at three time points post lambing by Irish producers using weigh-scales: pre weaning, at weaning and post weaning, the latter coinciding with muscle and fat ultrasound scanning. Based on the editing criteria used for the national genetic evaluations pre weaning weight was defined as live weight taken between 20 and 65 days of age; only records of lambs weighing between 12.00 and 32.00 kg were retained in the present study. Weaning weight was defined as the live weight recorded between 66 and 120 days of age and weighing between 20.00 and 55.00 kg. Post weaning weight was defined as live weight measured between 121 and 180 days of age; only lambs with live weight records between 25.00 and 75.00 kg were considered for further analysis. Across all live weight measurements average daily gain was calculated for each lamb with a known birth and weigh date at either of the three weight points; only average daily gains between 100 and 650 g/d were retained for each live weight measurement (261 lambs with an erroneous average daily gain were omitted from subsequent analyses). Muscle and fat depth traits were recorded on the same day as post weaning weight in all lambs. Only muscle depth measurements within the range of 10 to 44 mm and fat depth measurements ranging within 1 to 23 mm were retained.

Live weight and carcass composition measurement records were discarded if flock of birth, sire, dam or maternal grandsire were unknown. Dams with no known parity number or a parity number >10 were discarded; parity number was subsequently categorised as 1, 2, 3, 4, or ≥ 5. Age at first lambing was defined based on the age of the ewe at first lambing; ewes were either defined as lambing for the first time as ewe lambs (between 8 and 18 months of age) or those that lambed for the first time as hoggets (between ≥18 and 28 months of age). Birth type was defined as the number of lambs born per lambing event; only birth types between 1 (singles) and 4 (quadruplets) were retained. Rearing type was defined as the number of lambs reared per litter; only rearing type between 1 and 3 were retained for analysis. Lambs that were recorded as artificially reared or reared by a non-genetic dam were discarded.

For all traits, each lamb was allocated to a contemporary group of breed-by-flock-by-week of weighing. Only contemporary groups containing at least 5 records were retained for analysis.

Following all edits described above, 33 721 pre weaning weight records, 32 623 weaning weight records, 28 140 post weaning weight records, 21 468 muscle depth records and 21 442 fat depth records were retained for genetic analysis; the breakdown of records per breed is shown in Table 25.

Table 25. Number of lambs (n), trait mean (µ), standard deviation (SD), coefficient of variation (CV), corresponding mean lamb age, and number of sires, dams, maternal grandsires (MGS), flocks and contemporary groups (CGs) by trait and breed.

Trait (units of measurement)	Breed	*n*	*µ* (SD)	Age	CV (%)	Sires	Dams	MGS	Flocks	CGs
Pre-weaning weight (kg)	Texel	11 891	20.86 (4.70)	46.59	22.53	804	5359	1093	162	480
	Suffolk	8783	22.32 (4.85)	45.12	21.73	541	3816	759	110	329
	Charollais	13 047	20.58 (4.58)	46.20	22.25	602	4965	919	139	456
Weaning weight (kg)	Texel	12 388	36.69 (7.63)	96.92	20.80	847	5688	1176	161	508
	Suffolk	7839	40.93 (7.87)	96.31	19.23	542	3625	774	107	308
	Charollais	12 396	37.09 (7.40)	96.65	19.95	607	4820	913	139	449
Post-weaning weight (kg)	Texel	12 074	48.70 (9.47)	144.76	19.45	847	5746	1179	161	422
	Suffolk	6819	56.42 (10.79)	147.24	19.12	508	3411	753	96	281
	Charollais	9247	51.92 (9.91)	148.99	19.09	567	4106	844	129	354
Muscle depth (mm)	Texel	8810	32.59 (4.09)	146.57	12.55	662	4259	916	108	280
	Suffolk	5589	34.11 (5.01)	151.28	14.69	402	2792	621	69	204
	Charollais	7094	33.23 (3.97)	151.81	11.95	455	3344	714	96	252
Fat depth (mm)	Texel	8782	6.10 (2.70)	146.63	44.26	661	4250	916	108	281
	Suffolk	5556	8.50 (4.00)	151.42	47.06	399	2784	618	69	205
	Charollais	7087	8.10 (3.80)	151.82	46.91	455	3346	712	97	253

1.7.2 Genetic Analysis

Variance components were estimated for each lamb live weight trait (i.e., pre weaning, weaning and post weaning weight) and each carcass composition trait (i.e., muscle depth and fat depth) using linear mixed animal models in ASReml (Gilmour *et al.,* 2009) separately for each breed. The model employed was:

$$Y = CG + AFL + Parity + Gender * Age + Birth\ type * Rearing\ type + Animal + Dam + DamPE + Litter + e$$

where Y = lamb live weight or carcass composition record, CG = contemporary group, AFL = age at first lambing of the dam, Parity = parity of the dam, Gender*Age = the interaction between the gender and age of the lamb, Birth type*Rearing type = the interaction between the birth type and rearing type of the lamb, Animal = random animal direct additive genetic effect, Dam = random maternal genetic effect, DamPE = random dam permanent environmental effect associated with multiple lambing records of the same dam, Litter = common environmental effect reflecting the non-genetic covariance among members of the same litter, and e = random residual effect.

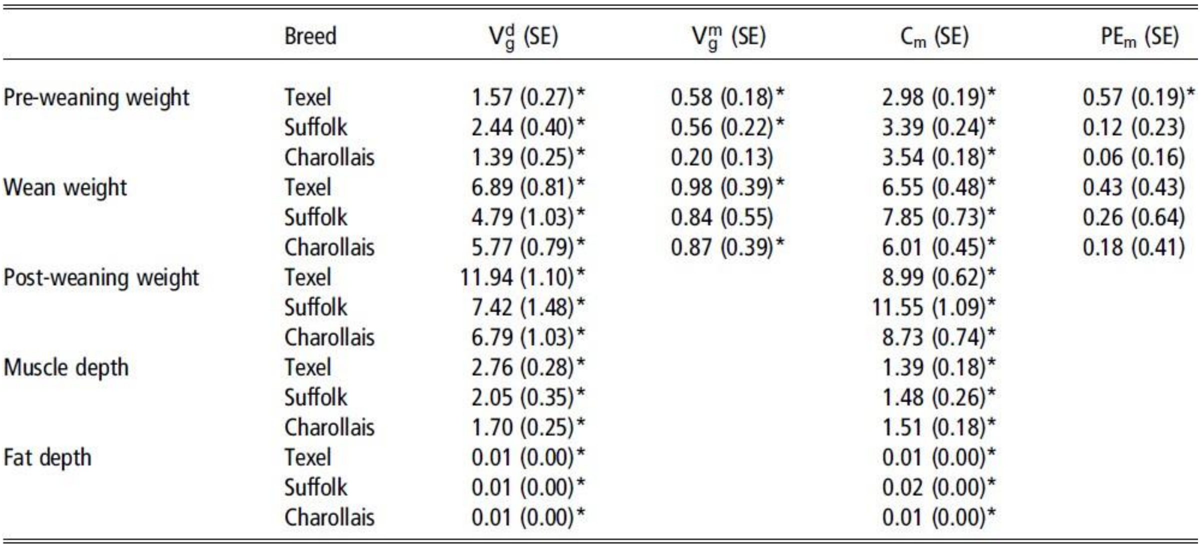
Each model was progressively built up from including just a residual effect to include a direct genetic, maternal genetic, dam permanent environmental and litter common environmental effect. In the case of post weaning weight, muscle and fat depth the model included a direct genetic and a litter common environmental effect only as there was no significant dam effect. A log likelihood ratio test was used to determine if the additional random terms improved the fit of the data (Ferreira *et al.,* 1999).

Direct heritability was calculated as the ratio of the direct additive genetic variance to the observed total phenotypic variance. Maternal heritability was estimated as the ratio of the maternal genetic variance to the total phenotypic variance. Common environmental effect was calculated as the ratio of the litter variance to the total phenotypic variance. Dam repeatability was calculated as the ratio of maternal genetic variance plus permanent environment to the total phenotypic variance. Genetic correlations between the studied traits were estimated pairwise using the model previously described in a series of bivariate analyses.

1.7.3 Results

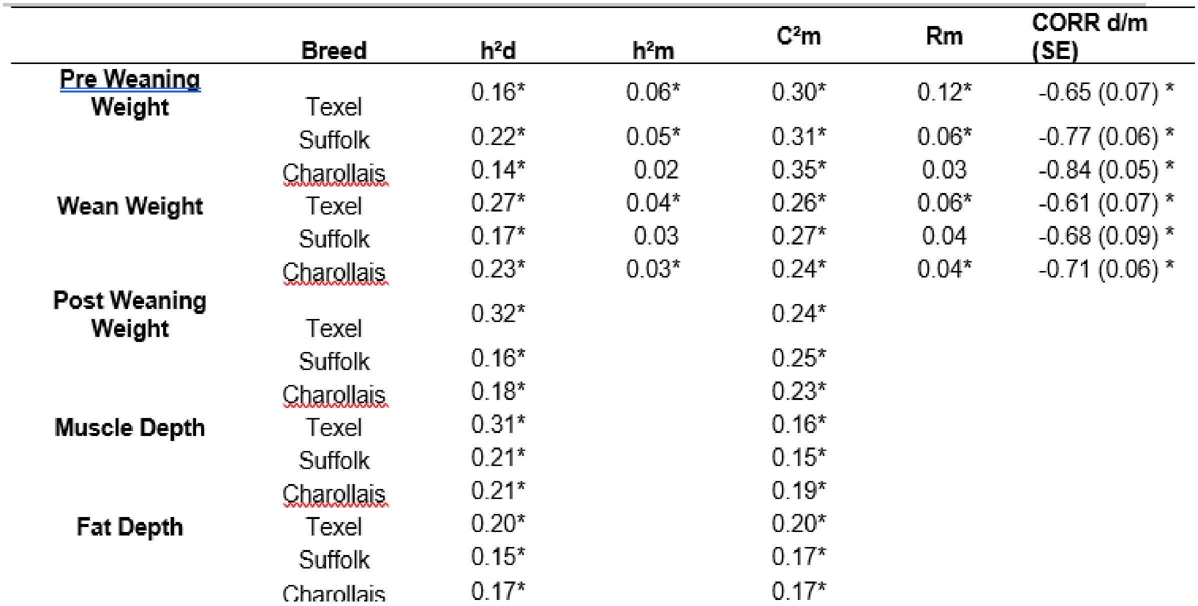
The parameter estimations for these breeds are shown in Tables 26 - 27 below.

Table 26. Direct genetic variance (Vgd), maternal genetic variance (Vgm), variance due to common environmental effect (Cm) and variance due to maternal repeatability (PEm) per trait and breed; model of analyses of post weaning weight, muscle and fat depth did not include a maternal effect; SE=standard error of estimate.



	Breed	V_g^d (SE)	V_g^m (SE)	C_m (SE)	PE_m (SE)
Pre-weaning weight	Texel	1.57 (0.27)*	0.58 (0.18)*	2.98 (0.19)*	0.57 (0.19)*
	Suffolk	2.44 (0.40)*	0.56 (0.22)*	3.39 (0.24)*	0.12 (0.23)
	Charollais	1.39 (0.25)*	0.20 (0.13)	3.54 (0.18)*	0.06 (0.16)
Wean weight	Texel	6.89 (0.81)*	0.98 (0.39)*	6.55 (0.48)*	0.43 (0.43)
	Suffolk	4.79 (1.03)*	0.84 (0.55)	7.85 (0.73)*	0.26 (0.64)
	Charollais	5.77 (0.79)*	0.87 (0.39)*	6.01 (0.45)*	0.18 (0.41)
Post-weaning weight	Texel	11.94 (1.10)*		8.99 (0.62)*	
	Suffolk	7.42 (1.48)*		11.55 (1.09)*	
	Charollais	6.79 (1.03)*		8.73 (0.74)*	
Muscle depth	Texel	2.76 (0.28)*		1.39 (0.18)*	
	Suffolk	2.05 (0.35)*		1.48 (0.26)*	
	Charollais	1.70 (0.25)*		1.51 (0.18)*	
Fat depth	Texel	0.01 (0.00)*		0.01 (0.00)*	
	Suffolk	0.01 (0.00)*		0.02 (0.00)*	
	Charollais	0.01 (0.00)*		0.01 (0.00)*	

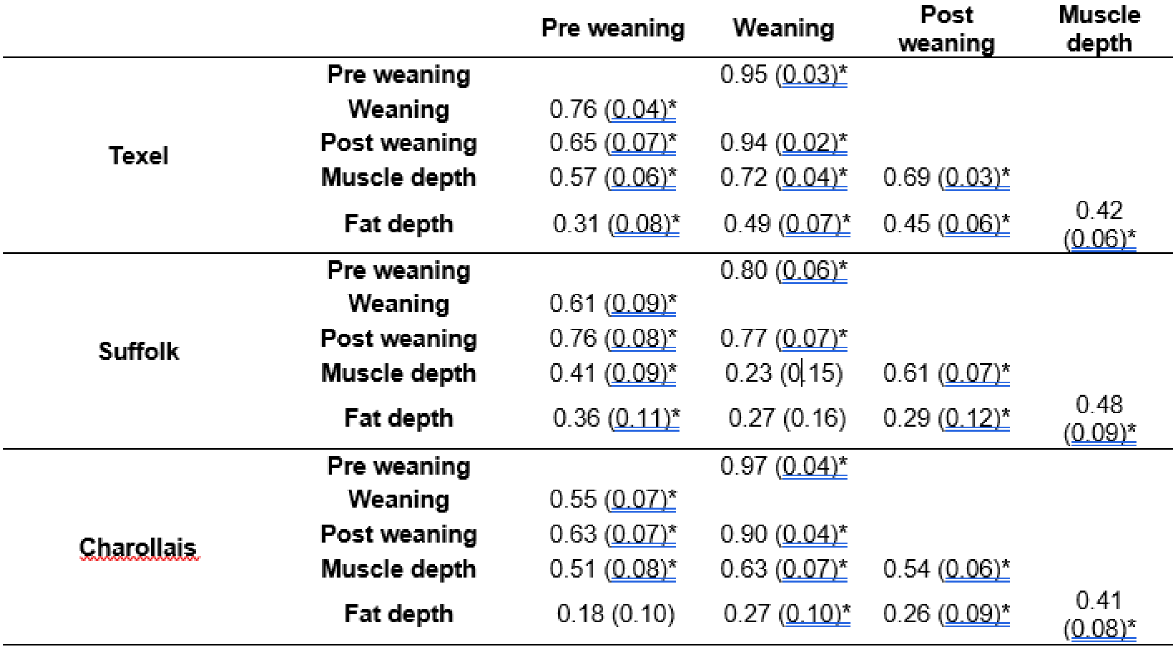
Table 27: Direct heritability (h^2_d), maternal heritability (h^2_m), proportion of phenotypic variance due to the common environmental effect (C^2m), maternal repeatability (R_m), and the correlation between direct and maternal genetic effects (CORR d/m) per trait and breed; model of analyses of post weaning weight, muscle and fat depth did not include a maternal effect; SE=standard error of estimate.



	Breed	h^2d	h^2m	C^2m	Rm	CORR d/m (SE)
Pre Weaning Weight	Texel	0.16*	0.06*	0.30*	0.12*	-0.65 (0.07) *
	Suffolk	0.22*	0.05*	0.31*	0.06*	-0.77 (0.06) *
	Charollais	0.14*	0.02	0.35*	0.03	-0.84 (0.05) *
Wean Weight	Texel	0.27*	0.04*	0.26*	0.06*	-0.61 (0.07) *
	Suffolk	0.17*	0.03	0.27*	0.04	-0.68 (0.09) *
	Charollais	0.23*	0.03*	0.24*	0.04*	-0.71 (0.06) *
Post Weaning Weight	Texel	0.32*		0.24*		
	Suffolk	0.16*		0.25*		
	Charollais	0.18*		0.23*		
Muscle Depth	Texel	0.31*		0.16*		
	Suffolk	0.21*		0.15*		
	Charollais	0.21*		0.19*		
Fat Depth	Texel	0.20*		0.20*		
	Suffolk	0.15*		0.17*		
	Charollais	0.17*		0.17*		

Genetic correlations amongst the traits for the 3 Irish breeds are shown below in Table 28.

Table 28. Genetic correlations (standard error in parentheses) between the direct additive genetic effects for each trait (below the diagonal) and the maternal genetic effects for each trait (above the diagonal) by breed; model of analyses of post weaning weight, muscle and fat depth did not include a maternal effect.



		Pre weaning	Weaning	Post weaning	Muscle depth
Texel	**Pre weaning**		0.95 (0.03)*		
	Weaning	0.76 (0.04)*			
	Post weaning	0.65 (0.07)*	0.94 (0.02)*		
	Muscle depth	0.57 (0.06)*	0.72 (0.04)*	0.69 (0.03)*	
	Fat depth	0.31 (0.08)*	0.49 (0.07)*	0.45 (0.06)*	0.42 (0.06)*
Suffolk	**Pre weaning**		0.80 (0.06)*		
	Weaning	0.61 (0.09)*			
	Post weaning	0.76 (0.08)*	0.77 (0.07)*		
	Muscle depth	0.41 (0.09)*	0.23 (0.15)	0.61 (0.07)*	
	Fat depth	0.36 (0.11)*	0.27 (0.16)	0.29 (0.12)*	0.48 (0.09)*
Charollais	**Pre weaning**		0.97 (0.04)*		
	Weaning	0.55 (0.07)*			
	Post weaning	0.63 (0.07)*	0.90 (0.04)*		
	Muscle depth	0.51 (0.08)*	0.63 (0.07)*	0.54 (0.06)*	
	Fat depth	0.18 (0.10)	0.27 (0.10)*	0.26 (0.09)*	0.41 (0.08)*

All estimates of genetic standard deviation and direct heritability were statistically greater than zero (P<0.05) and all traits studied apart from pre weaning weight were most heritable in the Texel breed. Pre weaning weight was most heritable in the Suffolk breed. Direct heritability estimates differed significantly (P<0.05) between the Texel and all other breeds studied for both post weaning weight and muscle depth. Significant differences were also observed between direct heritability estimates in the Texel and Suffolk breed for weaning weight. Maternal heritability was significantly greater than zero for all weight traits in the Texel breed, pre weaning weight in Suffolks and weaning weight in Charollais'. The litter common environmental effect accounted for the majority of the total phenotypic variance for most live weight traits. Direct heritability estimates differed significantly between breeds (P<0.05) in weaning weight, post weaning weight and muscle depth traits.

Negative correlations were estimated between direct additive and maternal genetic effects within trait for all breeds. This is an antagonistic correlation suggesting that animals with genetically superior direct additive genetic effect are expected to be maternally inferior.

Significant (P<0.05) positive genetic correlations between the direct additive genetic effects on pre weaning and subsequent weights for each of the three breeds were calculated. Direct genetic correlations between post weaning weight and the two carcass composition traits were also strongly positive reaching a maximum of 0.69 (±0.03) with muscle depth for the Texel breed.

1.7.4 Results

In conclusion, Variance components and genetic parameters derived in the present study for five live weight and carcass traits may be used to support the breeding programme of sheep in Ireland. Considerable differences in genetic analysis results were found between the Texel, Suffolk and Charollais breeds for each of the five traits examined. Differences were observed in both heritability and genetic correlation estimates suggesting that current genetic improvement systems may benefit by considering these breeds separately in future genetic evaluations.

1.8 Blanche du Massif Central, Mouton Vendéen, Rouge de l’Ouest - France

1.8.1 Report other economically important traits.

Eleven phenotypes have been recorded for three French meat sheep breeds in commercial flocks: Blanche du Massif Central (BMC), Mouton Vendéen (MV), Rouge de l’Ouest (RO). The phenotypes andcorresponding number of records are reported in the Tables 29, 30, and 31. Two additional phenotypes(Chest size and Efficiency) have been computed from NEC, Chest depth and chest width.

Phenotypic correlations between traits are provided in Table 32.

1.8.2 Methods and models

Genetic parameters have been estimated for main traits as a minimum number of records are needed:Body Condition Score (BS), Chest Depth (CD), Chest Width (CW) and Height at Wither (HW). All analyseshave been done within breed as there is no genetic structure among breeds. First, variance components and fix effects have been evaluated through general linear mixed models. Then genetic parameters have been estimated using the wombat software.

Two uni-traits model have been used:

A simple uni-trait model for height (wither).

Fix effects: flock, season (+ technician for BMC breed)Random effect: additive genetic effect (animal model)

A uni-trait model with repeated data for body score, chest depth and width. Fix effects: flock, season (+ technician for BMC breed), physiological stage. Covariate: weight

Random effect: additive genetic effect (animal model) and permanent environmental effect

1.8.3 Results

Results (heritability h^2 and repeatability rep are provided in Table 33).

To evaluate genetic correlations between traits we used six muti-traits models (two traits models). Thegenetic correlations we estimated were quite high. For example, for BMC breed they were ranged between 0.802 to 0.903. For computing reasons, we had to remove the weight as a covariate from the model. This can lead to the overestimation of genetic correlations between traits. In addition, the estimates are not very accurate because of partial convergence of the analysis models and the high sensitivity of the result to the starting values. increasing the number of observations could improve the ability to estimate correctly the genetic correlations through multi traits model.

Table 29. Traits description for the BMC Breed.

	N	Mean	std
body condition score	9087	2.33047	0.66995
weight	7860	66.49569	10.31979
Chest depth	13969	31.47122	2.25125
Chest width	13969	25.01718	2.43875
height (withers)	9480	60.50575	3.87513
Chest size	13969	89.37879	6.47283
Efficiency	7860	1.37142	0.1767
wool extent	2828	2.49328	0.97163
wool defect	383	0.89556	0.49028
wool appreciation	171	1.71345	0.99102
teeth	2700	0.33111	0.64533
foot	13	1	0
udder	75	1.09333	0.57359

Table 30. Traits description for the MV Breed.

	N	Mean	Std
body condition score	5141	2.90673	0.81809
weight	3039	58.21369	9.94213
Chest depth	5285	31.97553	2.16525
Chest width	5285	24.88682	2.84524
height (withers)	4337	58.87941	3.81088
Chest size	5285	90.12417	6.5282
Efficiency	2990	1.57435	0.22659
Fat	99	4.12727	1.52106
Muscle	99	24.21414	3.36923
wool extent	508	2.04921	0.34335
wool defect	489	1.16564	0.43321
wool appreciation	511	2.10763	0.72366
teeth	839	0.08343	0.37231

Table 31. Traits description for the RO breed.

	N	Mean	Std
body condition score	3213	3.15002	0.83867
weight	3143	64.33945	18.15449
Chest depth	3235	32.29594	1.98364
Chest width	3207	26.69212	3.21401
height (withers)	3011	62.03434	3.57334
Chest size	3207	93.20591	6.87264
Efficiency	3114	1.49021	0.22575
Fat	278	4.70558	1.31281
Muscle	278	26.64065	3.19178
wool extent	298	2.62416	0.76521
wool defect	33	1	0
wool appreciation	940	2.63617	0.95677
teeth	1455	0.10034	0.38126

Table 32. Phenotypic correlations between traits in the BMC, MV and RO breeds.

		weight	**Chest depth**	**Chest width**	**height (withers)**	**Chest size**	**Efficiency**
BMC (n= 4094)	body score	0.31	0.31	0.44	-0.05	0.43	-0.14
	weight		0.51	0.49	0.28	0.57	-0.88
	Chest depth			0.51	0.11	0.88	-0.13
	Chest width				NS	0.86	-0.11
	height (withers)					0.06	-0.30
	Chest size						-0.14
MV (N=2405)	body score	0.37	0.09	0.15	NS	0.14	-0.37
	weight		0.48	0.47	0.37	0.56	-0.88
	Chest depth			0.45	0.31	0.82	-0.15
	Chest width				0.25	0.88	-0.08
	height (withers)					0.33	-0.27
	Chest size						-0.13
RO	body score	0.18	0.18	0.33	NS	0.31	-0.19
	weight		0.43	0.41	0.20	0.48	-0.65
	Chest depth			0.48	0.36	0.80	-0.45
	Chest width				0.17	0.91	-0.31
	height (withers)					0.29	-0.27
	Chest size						-0.42

Table 33. Heritabilities and repeatabilities for Body Condition Score (BCS), Chest Depth (CD), Chest Width (CW) and Height at Wither (HW) in the BMC, MV and RO breeds.

	BMC				MV				RO			
	Nobs	Newe	h^2	rep	Nobs	Newe	h^2	rep	Nobs	Newe	h^2	rep
BS	5571	2508	0.062	0.242	2848	1332	0.296	0.298	3116	1244	0.161	0.176
CD	7859	2609	0.177	0.395	2990	1318	0.245	0.377	3138	1244	0.273	0.343
CW	7859	2609	0.129	0.260	2990	1318	0.180	0.189	3110	1216	0.060	0.093
HW	1601	1601	0.176		1044	1044	0.321		1067	1067	0.320	

Heritability and repeatability based on uni-trait model.

1.9 Norwegian White Sheep – Norway

1.9.1 Selection of sheep and flocks for PAC measurements

Methane measurements in portable accumulation chambers (PAC) were collected on 6,002 Norwegian White sheep ewes that have lambed at least once or were expecting their first lambing. These sheep belong to fifty-seven (57) breeding flocks from 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).

1.9.2 Methane emission measurements

Methane measurements in portable accumulation chambers (PAC) were collected on 6,002 Norwegian White sheep ewes that have lambed at least once or were expecting their first lambing. These sheep belong to fifty-seven (57) breeding flocks from 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).

CH_4 emission (ppm) was measured in lots of 10 animals at a time. A hand-held Eagle2 instrument was used to capture accumulated 50 min CH_4 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 CH_4 concentration was converted to CH_4 g/hr. Both CH_4 g/hr and ewe weights were scaled, they were divided by the mean of the lot and multiplied by the mean of all observations.

1.9.3 Traits in the genetic evaluation of Norwegian White Sheep

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 ($42\text{-}d_{adj}$), while weaning weights are recorded between 90 and 180 days of age and adjusted to 140 days ($140\text{-}d_{adj}$). Both $42\text{-}d_{adj}$ and $140\text{-}d_{adj}$ are expressed as weight gain from birth, and $42\text{-}d_{adj}$ thus represents a part of the growth period to weaning. The growth traits $42\text{-}d_{adj}$ and $140\text{-}d_{adj}$ are a part of the portfolio included for the routine genetic evaluations in Norwegian sheep. Lamb carcass weight, EUROP grading of fat and carcass as well as fleece weight and fleece grade are loaded to the sheep recording system (SRS) from the abattoir. Lamb carcass weight is adjusted to 154 days of age (154-d$_{adj}$), while grading of fat and carcass is adjusted to 20 kg carcass weight (20-kg$_{adj}$) for the routine genetic evaluations.

Phenotypic traits

Ten years of selected phenotypes included in the routine genetic evaluation were extracted for the 57 ram circle flocks with CH_4 emission measurements. Number of observations, mean, and standard deviation of the traits are listed in Table 34.

Table 34. Traits included in the analyses, number of records (N), phenotypic mean and standard deviation (SD)

Trait	N	Mean (SD)
CH_{4adj}, g/hr	6,002	1.34 (0.27)
Ewe weight$_{adj}$, kg	6,002	83.08 (9.87)
(mol CH_4 /mol CH_4 + mol CO_2)adj	6,002	0.05 (0.01)
Birth Weight, kg	172,006	4.91 (1.06)
42-day$_{adj}$	145,296	14.61 (3.31)
Weaning weight, adj 140 days	153,371	40.61 (7.62)
Carcass Weight, adj 154 days	111,028	18.78 (3.92)
Carcass Classification, adj 20 kg carcass	111,028	8.97 (0.89)
Fat Grading, adj 20 kg carcass	111,028	5.70 (1.26)
Fleece weight	71,037	0.81 (0.21)
Fleece grade	71,151	0.90 (0.30)

1.9.4 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 255,166 animals.

1.9.5 Genetic evaluation model

Variance components were obtained using the Apex linear models software licensed by GHPC PTY. LTD., Armidale, Australia.

The model for weight corrected methane emission was:

$$Y_{ijk} = FL_i + A_j + b_1 * W_{ijk} + a_{ijk} + e_{ijk} \quad (1)$$

Where Y_{ijk} is scaled CH_4 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 feed intake proxy corrected methane emission was:

$$Y_{ijk} = FL_i + A_j + b_1 * W_{ijk} + a_{ijk} + e_{ijk} \quad (2)$$

Where Y_{ijk} is scaled feed intake proxy corrected CH_4 emission measured on animal k in Flock*Lot i of Age class j. a_{ijk} is random additive genetic effect of animal k, and e_{ijk} is random residual corresponding to Y_{ijk}.

The model for birth weight was: $Y_{ijklm} = FY_i + ABKF_j + a_{ijk} + m_{ijl} + pe_{ijl} + pel_{ijlm} + e_{ijklm}$ (3)

Where Y_{ijkl} is birth weight observation on lamb *k* in Flock*Year *i* and in rearing type $ABKF_j$, a_{ijk} is random additive genetic effect of lamb *k*, m_{ijl} is random additive genetic effect of the biological dam *l*, pe_{ijl} is permanent environment effect of the biological dam across litters, pel_{ijl} is within litter

permanent environment effect and e_{ijklm} is random residual corresponding to Y_{ijklm} .

The model for 42-d weight, 140-d weight, carcass weight, carcass classification og fat carcass grading was: $Y_{ijkl} = FY_i + ABKW_j + a_{ijk} + m_{ijl} + pe_{ijl} + e_{ijkl}$ (4)

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}

The model for lamb fleece weight and lamb fleece grade was:

$Y_{ijkl} = FY_i + ABKW_j + b_1 * W_{ijk} + a_{ijkl} + pe_{ijl} + e_{ijkl}$ (5)

Where Y_{ijkl} is fleece observation on lamb *k* in Flock*Year *i* and in rearing type $ABKW_j$, W_{ijk} is age at slaughter, b_1 is regression coefficient on age at slaughter, a_{ijk} is random additive genetic effect of lamb *k*, pe_{ijl} is permanent environment effect of the fostering dam, and e_{ijkl} is random residual corresponding to Y_{ijkl} .

1.9.6 Heritabilities

Heritabilities of weight corrected methane emission (CH_{4adj}), and feed intake proxy corrected methane emission (mol CH_4 /mol CH_4 + mol $CO_2)_{adj}$ are shown in Table 35. The heritability of feed intake proxy corrected methane was 0.34 compared to 0.18 for weight corrected methane.

Table 35. Heritabilities for weight corrected methane emission and for feed intake proxy corrected methane

Trait	**Heritability**
CH_{4adj}, g/hr (weight corrected methane emission)	0.18
(mol CH_4 /mol CH_4 + mol $CO_2)_{adj}$ (feed intake proxy corrected methane)	0.34

1.9.7 Genetic correlations between methane traits and traits in the breeding goal

The Norwegian Total Merit Index is composed of direct genetic effects of: birth weight, carcass weight, EUROP carcass classification, EUROP fat score; maternal genetic effects of: birth weight, 42-day weight, and carcass weight, and genetic effects of fleece weigh, fleece grade, litter size and teat size. Litter size and teat size were not included in the genetic analysis presented in this study. Genetic correlations between weight corrected methane and feed intake proxy corrected methane and traits in the total merit index included for this analysis are shown in Table 36.

Apart from the correlation between feed intake proxy corrected methane and direct genetic effect of carcass weight, all correlations between traits included in the total merit index and feed intake proxy corrected methane were closer to zero compared to weight corrected methane. This result reveals the opportunity of selecting for feed intake proxy corrected methane without an undesirable effect on traits under selection. However, feed intake corrected methane emission is a ratio trait and care should be taken in inclusion of such trait in the index.

Table 36. Genetic correlations between weight corrected methane and feed intake corrected methane and traits from the analyses included in the total merit index.

Trait	**Birth Weight**	**Carcass Weight**	**EUROP carcass**	**EUROP fat**	**Birth Weight (mat)**	**42-day Weight (mat.)**	**Carcass Weight (mat.)**	**Fleece Weight**	**Fleece Grade**
CH_4, corr. weight	-0.11	0.02	-0.08	-0.27	0.23	0.32	0.25	0.04	0.07
CH_4 corr. “feed”	-0.08	-0.18	0.04	0.00	0.00	0.16	0.18	0.05	0.05

1.9.8 Conclusion

PAC methane emission is heritable in Norwegian White sheep and correlations to other traits in the breeding goal are low. However, while correlations between breeding goal traits of maternal genetic effects and weight corrected methane emission are slightly antagonistic the corresponding correlations are close to zero for feed intake proxy corrected methane. Feed intake proxy corrected methane is however as ratio trait and inclusion of the trait into the index should be done with caution.

These results pave the way todefining the most appropriate methane trait to be included in the breeding goal.

Part of this work was presented at the WCGALP in Rotterdam in 2022 (Jakobsen et al, 2022).

1.9.9 References

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Conclusion

The results from this report highlight the variability that exists amongst the relationships of feed efficiency with other production traits, including the methodologies to estimate these and the definitions of the traits. Regardless, the results show conclusively that genetic variation exists for feed intake and feed efficiency with moderate heritabilities. Therefore, the inclusion of feed intake into breeding programmes is likely to lead to enhanced efficiency and cost savings for farmers. It is difficult to generalise about the relationships amongst feed intake, efficiency and other traits. Nevertheless, for French Lacaune sheep, we see strong genetic correlations between the efficiency definitions (see Appendix A) and milk yield, but lower for protein and fat content. In dairy goats (UK) the genetic correlations for feed intake (adjusted for body size) across 520d lactation with milk yield are also moderate to strong. Phenotypic correlations are reported for 3 Greek, 3 Uruguayan and 3 additional French meat breeds amongst aspects of feed efficiency and with other traits. The results from these studies can be used in the decision-making for the development of new breeding goals for future sheep breed improvement programmes.

Appendix A: French definition of efficiency

Computation of feed efficiency-related traits:

Feed efficiency calculations were applied to the ewes having at least one BCS recorded. No individual total feed intake neither body weights were recorded, so RFI could not be calculated.

We calculated the Net Energy Intake Converted in Milk Ratio (NEICMR) that had been proposed (P. Hassoun personal communication) to take into account that the total energy intake is not only for production but also for maintenance requirements and that energy could be stored or mobilized in the body reserves.:

Net Energy Intake Converted in Milk Ratio (NEICMR)=

$$\frac{\text{Lactation requirements}}{\text{Feed intake} - \text{Maintenance requirements} + \text{variation in body condition}}$$

=0.71 x [MY x (0.0071 x FC + 0.0043 x PC + 0.224)]

$=0.033 \times BW^{0.75}$

=(-0.43 × BW × Δ BCS / duration) × 0.956

$=\sum_{i=1}^{n}(amount\ feed_i\ x\ feed\ value\ _i)$

With Δ BCS the difference between two BCS and duration being the time step between two BCS.

Feed value is expressed in net energy/g

For NEICMR at the first milk recording, the difference between BCS at suckling and BCS at first milk test-day was used. For the last milk test-day (6), the difference between BCS before mating and BCS after mating was used.

A NEICMR value lower than 1 means that the ewe is not efficient, the intake of the ration consumed for milk production (in net energy/d) is higher than the lactation needs of the animal (in net energy/d). Conversely, a value higher than 1 means that the ewe has not consumed more than necessary to cover her lac