SMARTER

SMAll RuminanTs breeding for Efficiency and Resilience

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New breeding goals for lifetime resilience for maternal sheep breeding programmes

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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.

Table des matières

Preamble

Large data sets from industry were used to quantify new traits for lifetime resilience (longevity, lambing interval, age at 1st lambing, lamb survival) in the Scottish Blackface, Dorset, Lleyn and Texel sheep breeds in the UK and with additional traits (e.g. barren rate) in multiple-breed analyses in Ireland. Some of these new traits have now already been incorporated into new breeding goals in the UK and for most breeds (Ireland) that were reported in the earlier years of the project and included in the 18 month report to the EU for T2.2 and T2.4. For these traits to be analysed, a requirement is to have the dates of culling /death from the flocks which are held by the national genetic evaluations in the respective countries (AHDB, UK, Sheep Ireland in Ireland). For example, 173,895 records from 70 Scottish

Blackface flocks, 51,174 records from 47 Lleyn flocks, 15,433 records from 20 Dorset and 48,995 from 108 Texel flocks were analysed. Also reported in 18 mth SMARTER report, INRAE quantified a new breeding goal for length of productive life in French dairy goat industry data to quantify and identify bucks with high and low breeding values for longevity which have been used in the SMARTER project to create divergent lines for longevity that have been reported throughout the lifespan of SMARTER. This was also reported at the World Congress on Genetics Applied to Livestock Production 2018 by Palhiere, I., Oget, C., & Rupp, R. (2018). 'Functional longevity is heritable and controlled by a major gene in French dairy goats'. Proc 10th World Congr Genet App Livest Prod, 165.

In Ireland, (also reported in the 18 mth SMARTER report), data on 199,338 lambing records across 1,828 industry flocks between the years 2010 and 2019, inclusive were analysed for ewe and lamb survival, and other traits associated with resilience (e.g. number of productive days post 1st lambing). The new traits derived have now been incorporated into the national sheep evaluations with genomic data to derive genomic breeding values for these traits (in Ireland).

A recent study investigating the genomic regions for reproduction in prolific Chios dairy sheep in Greece is now included in this deliverable and a paper was published in Animal journal this year ' Novel genomic markers and genes related to reproduction in prolific Chios dairy sheep: a genome-wide association study' V. Tsartsianidoua, A. Pavlidisa, E. Tosioua, G. Arsenosc, G. Banos and A. Triantafyllidis https://doi.org/10.1016/j.animal.2023.100723 . A summary of that paper is below.

Genetic architecture of sheep reproduction is increasingly gaining scientific interest due to the major impact on sheep production systems. In the present study, we conducted pedigree-based analyses and genome-wide association studies using the Illumina Ovine SNP50K BeadChip to explore the genetic mechanisms underlying the reproduction of the highly prolific Chios dairy sheep. First lambing age, total prolificacy and maternal lamb survival were selected as representative reproductive traits and estimated as significantly heritable ($h2 = 0.07–0.21$) with no evident genetic antagonism among traits. We identified novel genome-wide and suggestive significant single-nucleotide polymorphisms (SNPs) on chromosomes 2 and 12 associated with age at first lambing. The new variants detected on chromosome 2 span a region of 357.79 kb with high pairwise linkage disequilibrium estimates (r2 = 0.8–0.9). Functional annotation analysis revealed candidate genes, such as the collagen-type genes and the Myostatin gene, that participate in osteogenesis, myogenesis, skeletal and muscle mass development resembling the functionality of major genes affecting the ovulation rate and prolificacy. Additional functional enrichment analysis associated the collagen-type genes with multiple uterine-related disfunctions, such as cervical insufficiency, uterine prolapse and abnormalities of the uterine cervix. Several genes (e.g., KAZN, PRDM2, PDPN, LRRC28) localised close to the SNP marker on chromosome 12 were grouped in annotation enrichment clusters majorly involved in developmental and biosynthetic pathways, apoptosis, and nucleic acid-templated transcription. Our findings may further contribute to unravel the genomic regions that are important for sheep reproduction and could be incorporated into future selective breeding programmes.

The rest of this report describes in detail a long-term experimental data set of Scottish Blackface sheep that was used to quantify body tissue mobilisation and lamb deaths linked to ewe fertility which is now a paper by McLaren A, Lambe, N R and Conington J. 2023. 'Genetic associations of ewe body condition score and lamb rearing performance in extensively managed sheep' which is in press to Livestock Science journal.

Summary

Sheep managed in harsh conditions need not only to be robust to deal with short-term challenges, but also be sufficiently resilient to allow them to survive and remain productive in the medium to longer term. Lifetime breeding ewe performance of 8,355 ewes from 2 extensively-reared hill sheep flocks, collected over a 20 year period, were used to quantify the genetic and phenotypic relationships for Body Condition Score (BCS) linked to ewe reproductive and lamb rearing success. Using between 14,000 and 25,000 data records per trait for 11 defined traits measured across the annual sheep reproductive cycle, results for the genetic and phenotypic parameters among all traits were quantified, and the implications for their use in breeding programmes discussed. The pedigree file used for the analyses included sire and dam information for 50,207 animals.

The direct heritability estimates for most BCS, and their changes, were significantly different from zero and low, ranging between 0.07 and 0.17; the repeatability for these were higher at between 0.11 and 0.32. The direct heritability estimates (s.e) for the no. lambs at pregnancy scan was 0.09(0.01) with a repeatability of 0.15(0.01). Heritabilities for foetal loss from pregnancy to lambing, lamb loss from lambing to weaning and number of lambs weaned were 0.02 (0.005), 0.02 (0.01) and 0.06(0.01) respectively. Repeatability estimates for the same traits were 0.02(0.01), 0.02(0.01) and 0.07(0.01). These estimates indicate that genetic control over these reproductive and lamb survival traits (expressed as a trait of the dam), are lower than that for body condition score (and their changes) over the reproductive cycle although all can be considered for use in sheep breeding programmes. The genetic relationships amongst the BCS of ewes at premating, pregnancy scan and at pre-lambing, with litter size at pregnancy scan and number of lambs weaned, are consistent. They indicate that ewes of high body condition score conceive and rear, fewer lambs with genetic correlations of between -0.18(0.05) and -0.58(0.04). However, post-partum, animals with higher BCS gain from lambing to mid-lactation and from weaning to pre-mating have higher litter sizes and rear more lambs. Foetal loss from pregnancy scanning to lambing was higher for ewes that had low gains in BCS between pre-mating and pregnancy scanning, and between pregnancy scanning and lambing. The results paint a complex picture that should be interpreted in the context of specific management practises for hill sheep at critical times in their reproductive cycle.

Introduction

Many small ruminant production systems are relatively low input and rely heavily on animals grazing pastures often in extensive and harsh environmental conditions, unsuitable for any other type of agriculture. With agriculture facing numerous challenges, including those associated with climate change and the rising costs of inputs, production from these grazing environments is predicted to become increasingly important in the future.

The challenges that the sector faces to improve its sustainability are numerous. Genetic breeding programmes associated with UK hill sheep production in these environments are already available to farmers with improved productivity and financial gains having been observed. However, future breeding strategies may benefit from identifying robust and resilient animals to improve the sustainability of these systems further.

Ewes require a level of robustness, to deal with short-term challenges, but also a degree of resilience, to allow them to survive and remain productive in the more medium to longer term. Hill ewes must often deal with limited food availability and poor weather conditions for several months each year, particularly during periods of high energy demand (pregnancy and early lactation). The extensive nature of these environments means there is less opportunity for farmers to make changes in management to reduce the impact of poor environmental conditions, therefore it is important that ewes are robust and resilient to face these challenges. To do this, many will mobilise body tissue reserves to meet the nutritional requirements of both her own needs and the demands of reproduction.

A simple and low-cost method of assessing these changes is body condition scoring (BCS), a subjective measure of fat and muscle cover in the loin region, based on a scale of 0 - 5 . Whilst traditionally used as a flock management tool for nutritional management, BCS has been found to be heritable at specific time points throughout the year and over time but the number of studies reporting genetic parameters remains relatively low and, to date, none have been investigated in UK hill sheep breeds. The influence that the ewe’s BCS has on lamb survival and the number of lambs she successfully rears are also important relationships to consider, in terms welfare and productivity.

Aims of the study

The main objectives of this study were to a) investigate genetic parameters for ewe body condition score traits, collected throughout the annual production cycle, b) assess genetic parameters for traits associated with ewe rearing performance, and c) investigate the genetic and phenotypic relationships between body condition score traits and ewe rearing performance, to help assess the potential for body condition related traits to be included in future hill sheep breeding programmes.

Materials and methods

Animals and Data Collection

All procedures involving animals for data collection were approved by an animal ethics committee at Scotland's Rural College (SRUC) and were performed under the United Kingdom Home Office licence following the regulations of the Animals Act 1986.

Data used were from 8,335 individual Scottish Blackface ewes reared on two extensively managed hill farms between 1999 and 2019. The ewes were reared under typical hill farm conditions on either Castlelaw farm, in the Pentland hills, in Midlothian (n = 4,635 individual ewes) or on Kirkton farm, in the West Highlands, in Perthshire (n = 3,700 individual ewes). Both flocks have been performance recorded as part of a genetic improvement scheme since 1991 and 1996 respectively. The flocks are genetically linked through the use of common sires.

Ewe body condition score traits

Body condition score (BCS) data were collected on ewes at each farm at pre-mating (PBCS) in November; pregnancy scanning (SBCS) in February; pre-lambing (LBCS) in April; mid-lactation (MBCS) in June; and weaning (WBCS) in August. BCS was assessed on a 0-5 scale, as described by Russel et al. (1969), by different scorers on each farm. The data collected at each event was also used to assess the change in body condition between events. The traits investigated were the gain between pre-mating and pregnancy scanning (PSGain); between pregnancy scanning and pre-lambing (SLGain); between pre-lambing and mid-lactation (LMGain); between lambing and weaning (LWGain); and between weaning and the next pre-mating (WPGain). An additional period, between pre-mating and pre-lambing (PLGain) was also considered. Although the BCS change traits were referred to as "gains", in practice ewes could lose or gain BCS during these periods, but this defines the direction of the BCS changes being considered. There were no LBCS or MBCS data collected at Kirkton farm after 2006, with the exception of LBCS data collected in 2015.

Ewe maternal performance

The traits relating to ewe maternal performance included those associated with the number of foetuses the ewe was carrying at pregnancy scanning (PScan); the number of foetuses lost between pregnancy scanning and lambing (FLoss); the number of lambs lost between lambing and mid-lactation (LLoss) and the number of lambs reared to weaning (LWean). All barren and triplet-rearing ewes were removed from the Loss trait analyses.

Genetic analysis

The pedigree file used in the analyses had sire and dam information for 50,207 animals with X sires and Y dams Using ASReml 3.0 (Gilmour et al., 2009) variance components (genetic and phenotypic variances and heritability) for each trait were estimated using univariate analyses. Analyses were based on the following model:

$y = Xb + Za + Wpe + e$

Where y is the vector of phenotypic observations; b is the vector fixed effects, consisting of ewe age, farm, year, lambs carried/reared, plus the interactions between farm and year and between farm and eweage; a is the vector of random animal effects; pe is the vector of permanent environment effects; e is the vector of random residual effects, and X, Z and W are incidence matrices relating observations to their respective effects. Ewe age was the age of the ewe, in years (6 levels: 2 to >7) and farm was where the ewes were based (2 levels: Castlelaw and Kirkton). Number of lambs carried/reared was the number of feotuses the ewe was carrying from pregnancy scanning to lambing (4 levels: 0 to 3) or the number of lambs reared from lambing (3 levels: 0 lambs to 2 lambs). Number of lambs carried/reared was not fitted in the PBCS model. Year was the year in which the data was collected (21 levels: 1999 to 2019). Interactions between farm and year and farm and ewe age were also fitted. For the Gain traits, a similar model was used with BCS at the initial event also included as a covariate. Each fixed effect was significant for the majority of traits and to remain consistent, the same models were fitted across the different traits. However, to allow convergence, no pe random effect was fitted for WBCS or LWGain. Additionaly, the interaction between farm and ewe age was removed from the model used to analyse WPGain. Summary statistics for each BCS trait and covariates are given in Table 1.

Genetic and phenotypic correlations were then estimated between each BCS trait and the traits associated with ewe rearing performance (PScan, FLoss, LLoss and LWean), using bivariate models in ASReml 3.0 (Gilmour et al., 2009). The animal models used for the BCS traits were the same as described above. Analyses of the ewe rearing performance traits were based on the following model:

$y = Xb + Za + Wpe + e$

Where y is the vector of phenotypic observations; b is the vector fixed effects, consisting of ewe age, farm, year, initial lamb number, plus the interactions between farm and year and between farm and eweage; a is the vector of random animal effects; pe is the vector of permanent environment effects; e is the vector of random residual effects, and X, Z and W are incidence matrices relating observations to their respective effects. All of the fixed effects were the same as those described previously for the BCS associated traits, with the exception of the initial lamb number, which was the number of lambs the ewe originaly had (e.g. number of feotuses at pregnancy scanning for FLoss and the number of lambs born for for LLoss) (2 levels: 1 lamb or 2 lambs). The models for PScan and LWean did not include initial lamb number. The PScan model included the ewe's pre-mating weight and PBCS as covariates. (Summary statistics are given in Table 1).

Results

Data summaries

Summaries of the data analysed, and the relevant covariates fitted in the models, are given in Table 1. The highest average condition score recorded across the flocks was at PBCS recording event (2.91). The average fell to the lowest point at LBCS (2.66) before increasing towards the next pre-mating BCS (2.83) (Figure 1). The period between pregnancy scanning and pre-lambing had the lowest level of condition score gain (SLGain = -0.14), with the most condition gained during the period between weaning and the next pre-mating (WPGain = 0.15). The overall averages for PSCAN and LWEAN were 1.28 and l.09 lambs respectively.

Figure 1. Average body condition score (BCS), across both farms, at each recording event

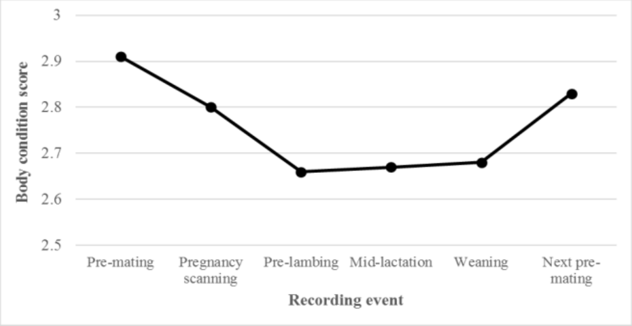

Table 1 Summary of the body condition score (BCS) and ewe maternal performance traits included in the analyses.

Trait	Description	Count	Min.	Max.	Mean	S.D.
Body condition score						
PBCS	Pre-mating (score)	23,903	2.0	5.0	2.91	0.37
SBCS	Pregnancy scan (score)	20,691	1.25	5.0	2.80	0.33
LBCS	Pre-lambing (score)	14,936	1.0	4.0	2.66	0.34
MBCS	Mid-lactation (score)	14,895	1.25	4.5	2.67	0.43
WBCS	Weaning (score)	23,031	1.0	5.0	2.68	0.48
Body condition score gain						
PSGain	Pre-mating to Pregnancy scan (score)	20,590	-2.0	2.0	-0.12	0.35
SLGain	Pregnancy scan to Pre-lambing (score)	14,265	-2.25	1.0	-0.14	0.32
PLGain	Pre-mating to Pre-lambing (score)	14,865	-2.25	1.5	-0.28	0.42
LMGain	Pre-lambing to Mid-lactation (score)	14,105	-1.50	2.0	-0.05	0.39
LWGain	Pre-lambing to Weaning (score)	14,343	-2.25	2.75	0.04	0.55
WNPGain	Weaning to next Pre-mating (score)	13,827	-2.75	3.0	0.15	0.57
Ewe maternal performance traits						
PScan	Pregnancy scan result (count)	25,068	0	3	1.28	0.66
FLoss	Foetal loss: Pregnancy scan to lambing (count)	22,293	0	2	0.07	0.31
LLoss	Lamb loss: Lambing to Mid-lactation (count)	22,105	0	2	0.17	0.41
LWean	Lambs reared to weaning (count)	23.938	0	2	1.09	0.67
Additional covariates						
PMWT	Pre-mating live weight	24,051	29.0	83.0	52.04	7.12

Genetic parameters

The univariate heritabilities for the BCS and maternal performance traits are given in Table 2. With the exception of WBCS and LWGain (which had heritability estimates close to zero), low heritability estimates were observed for the remaining BCS traits ranging from 0.07 to 0.17 and which were associated with permanent environment effects ranging from 0.04 to 0.16. The highest heritability estimates were associated with SBCS and WPGain (both 0.16). The heritabilities for the ewe maternal performance traits were also low, ranging from 0.02 to 0.09.

Table 2 Univariate heritabilities (h^2), permanent environment effects (pe), phenotypic variances (σ^2_p) and repeatability (rep) for each trait investigated (SE in parentheses)

Trait	Description	h^2	*pe*	σ^2_p	*rep*
PBCS	Pre-mating BCS	0.14 (0.01)	0.08 (0.01)	0.10 (0.001)	0.22 (0.01)
SBCS	Pregnancy scan BCS	0.17 (0.01)	0.09 (0.01)	0.08 (0.001)	0.27 (0.01)
LBCS	Pre-lambing BCS	0.16 (0.02)	0.12 (0.01)	0.08 (0.001)	0.27 (0.01)
MBCS	Mid-lactation BCS	0.10 (0.01)	0.13 (0.02)	0.11 (0.001)	0.23 (0.01)
WBCS	Weaning BCS	0.002 (0.002)	-	0.18 (0.002)	-
PSGain	Pre-mating to Pregnancy scan	0.11 (0.01)	0.04 (0.01)	0.06 (0.001)	0.15 (0.01)
SLGain	Preg. Scan to Pre-lambing	0.07 (0.01)	0.05 (0.01)	0.06 (0.001)	0.11 (0.01)
PLGain	Pre-mating to Pre-lambing	0.12 (0.01)	0.07 (0.01)	0.07 (0.001)	0.19 (0.01)
LMGain	Pre-lambing to Mid-lactation	0.07 (0.01)	0.04 (0.01)	0.09 (0.001)	0.12 (0.01)
LWGain	Pre-lambing to Weaning	0.004 (0.004)	-	0.19 (0.002)	-
WPGain	Weaning to Pre-mating	0.16 (0.02)	0.16 (0.02)	0.10 (0.001)	0.32 (0.01)
PScan	Pregnancy scan result	0.09 (0.01)	0.06 (0.01)	0.39 (0.004)	0.15 (0.01)
FLoss	Foetal loss (P. Scan to lambing)	0.02 (0.005)	0.003 (0.01)	0.09 (0.001)	0.02 (0.01)
LLoss	Lamb loss (lambing to weaning)	0.02 (0.01)	0.01 (0.01)	0.14 (0.001)	0.02 (0.01)
LWean	Number of lambs weaned	0.06 (0.01)	0.01 (0.01)	0.42 (0.004)	0.07 (0.01)

Relationships between body condition scores recorded at each event

Genetic correlations estimated between each BCS event are given in Table 3. High genetic correlations (>0.88) were observed between each event, apart from those associated with WBCS which were low and associated with high standard errors. The highest genetic correlation was observed between SBCS and LBCS (0.98). Phenotypic correlations were low to moderate (0.30 to 0.54), again with the exception of those associated with WBCS (which were all 0.01).

Table 3 Genetic (above diagonal) and phenotypic (below diagonal) correlations estimated between each Body Condition Score recorded at Pre-mating (PBCS), Pregnancy Scanning (SBCS), Pre-lambing (LBCS), Mid-lactation (MBCS) and Weaning (WBCS). (SE in parentheses)

Trait	PBCS	SBCS	LBCS	MBCS	WBCS
PBCS		0.91 (0.01)	0.88 (0.02)	0.92 (0.02)	0.16 (0.22)
SBCS	0.50 (0.01)		0.98 (0.01)	0.92 (0.02)	0.23 (0.21)
LBCS	0.41 (0.01)	0.54 (0.01)		0.93 (0.01)	0.06 (0.24)
MBCS	0.30 (0.01)	0.37 (0.01)	0.44 (0.01)		0.36 (0.21)
WBCS	0.01 (0.01)	0.01 (0.01)	0.01 (0.01)	0.01 (0.01)	

Relationships between body condition score traits and ewe maternal performance

The genetic and phenotypic correlations estimated between the BCS and ewe maternal performance traits are given in Table 4. Genetic correlations observed with PScan were low to moderate with the strongest relationships observed between PScan and LBCS (-0.48), PBCS (-0.45) or WPGain (0.42). The lowest genetic correlations with PScan were associated with PSGain and PLGain (0.02). The phenotypic relationships between PScan and the BCS traits were low ranging from -0.38 (LBCS) to 0.10 (PBCS). The strongest genetic correlation between BCS and FLoss was associated with PBCS (0.40). Most of the remaining genetic correlations were low and negative, ranging from -0.10 to -0.28. The correlations of Floss with SBCS and WBCS were positive but associated with high standard errors. Phenotypic correlations ranged from -0.08 to 0.09, with the negative correlations associated with BCS data collected from PBSC through to LMGain. The genetic correlations estimated with LLoss were all positive (ranging from 0.03 to 0.34) apart from the negative correlation observed with WPGain (-0.25). The highest correlation with LLoss was associated with PBCS (0.34). Phenotypic correlations were all close to zero, ranging form -0.01 to 0.05. The strongest genetic correlations estimated for LWEAN were with PBCS (-0.58) and WPGain (0.30). The strongest phenotypic correlations was observed with WPGain (-0.31), with the remaining estimates ranging from -0.09 to 0.09.

Table 4: Genetic and phenotypic correlations estimated between the BCS and ewe maternal performance traits

Trait	PScan		FLoss		LLoss		LWean	
	r_g	r_p	r_g	r_p	r_g	r_p	r_g	r_p
PBCS	-0.45 (0.05)	0.10 (0.01)	0.40 (0.08)	-0.03 (0.01)	0.34 (0.09)	-0.01 (0.01)	-0.58 (0.04)	0.09 (0.01)
SBCS	-0.18 (0.05)	0.03 (0.01)	0.04 (0.09)	-0.04 (0.01)	0.14 (0.09)	-0.02 (0.01)	-0.26 (0.05)	0.03 (0.01)
LBCS	-0.48 (0.05)	-0.38 (0.01)	-0.11 (0.11)	-0.08 (0.01)	0.22 (0.10)	-0.03 (0.01)	-0.18 (0.06)	0.03 (0.01)
MBCS	0.05 (0.07)	-0.05 (0.01)	-0.23 (0.12)	0.09 (0.01)	0.08 (0.12)	0.04 (0.01)	0.12 (0.08)	-0.09 (0.01)
WBCS	0.37 (0.29)	-0.01 (0.01)	0.11 (0.38)	0.00 (0.01)	0.46 (0.47)	-0.01 (0.01)	0.19 (0.28)	-0.03 (0.01)
PSGain	0.02 (0.06)	-0.01 (0.01)	-0.20 (0.10)	-0.03 (0.01)	0.03 (0.11)	-0.01 (0.01)	0.07 (0.01)	0.03 (0.01)
SLGain	-0.14 (0.08)	-0.14 (0.01)	-0.13 (0.13)	-0.02 (0.01)	0.20 (0.14)	-0.02 (0.01)	-0.03 (0.08)	0.03 (0.01)
PLGain	0.02 (0.06)	-0.13 (0.01)	-0.28 (0.11)	-0.03 (0.01)	0.17 (0.11)	-0.03 (0.01)	0.14 (0.07)	0.05 (0.01)
LMGain	0.22 (0.07)	0.02 (0.01)	-0.21 (0.13)	-0.05 (0.01)	0.06 (0.13)	0.05 (0.01)	0.23 (0.08)	-0.08 (0.01)
LWGain	0.41 (0.27)	0.00 (0.01)	0.29 (0.40)	0.00 (0.01)	0.25 (0.40)	-0.01 (0.01)	0.35 (0.29)	-0.01 (0.01)
WPGain	0.42 (0.05)	-0.01 (0.01)	-0.19 (0.10)	0.04 (0.01)	-0.25 (0.11)	-0.01 (0.01)	0.30 (0.07)	-0.31 (0.01)

PBCS = Pre-mating BCS; SBCS = Pregnancy scan BCS; LBCS = Pre-lambing BCS; MBCS = Mid-lactation BCS; WBCS = Weaning BCS; PSGain = Pre-mating to Pregnancy scan Gain; SLGain = Pregnancy scan to Pre-lambing Gain; PLGain = Pre-mating to Pre-lambing Gain; LMGain = Pre-lambing to Mid-lactation Gain; WPGain = Weaning to Pre-mating Gain; PScan = Pregnancy Scan result; FLoss = Foetal loss (Pregnancy scan to Lambing); LLoss = Lamb loss (Lambing to Weaning); LWean = Number of lambs weaned

Discussion

Parameters

The results from this study have confirmed that many of the traits associated with body condition score, in Scottish Blackface ewes, were heritable. Notable exceptions were those associated with WBCS and LWGain, which were found to have no significant genetic component with heritability estimates close to zero. This suggests that any phenotypic variation in these traits was not due to genetics, but influenced by other environmental factors. The heritabilities of the remaining BCS scores collected at each recording event ranged from 0.10 to 0.17). The genetic correlations estimated between each BCS event were all >0.88, with the highest estimate between SBCS and LBCS (0.98). The high genetic correlations suggest the different BCS traits are under similar genetic control. The BCS Gain traits range of heritabilities were also low (0.07 to 0.16) The heritability estimates observed for LLoss and LWean were very similar to those previously estimated by Conington et al. (2001) and Lambe et al. (2008), using earlier data recorded from the same population. Those associated with PScan and Floss have not been estimated before for this population, but the estimates are in close agreement with those reported from Australia.

Relationships between body condition and rearing performance

When assessing the relationships between the BCS traits and PScan, the genetic correlations indicated that ewes that gain more condition between weaning and pre-mating had higher pregnancy scan results. However, the negative genetic correlations estimated between PScan and PBCS suggest higher pregnancy scan results are associated with ewe with lower condition scores at pre-mating. Even though this appears to be counter-intuitive, it does suggest that within the constraints of acceptable BCS levels for management of hill sheep (ie with the majority of animals having >BCS 2+), at the genetic level, more prolific ewes have the genetic propensity to be leaner. This means that careful management of over- fat animals at pre-mating is required otherwise lower lamb numbers will persist.