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Article

Genetic evaluation for growth traits in Mexican Pelibuey sheep

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Abstract:

The objective of this study was to estimate genetic parameters for weight traits for the Pelibuey sheep. The traits analysed were birth weight (BWT), weaning weight (WWT), weight at 120 d (W120), weight at 150 d (W150), and weight at 210 d (W210). Data set with records from 51,382 lambs, progeny of 1,440 sires, and 14,715 dams were used to conduct genetic analyses, using an animal model. Six models varying the random effects were fitted including genetic, maternal and maternal permanent environmental effects. Then, the same base models were fitted with the additional random effect of sire by flock interaction. Direct heritability estimates for the base models ranged from 0.13 to 0.18 and reduced across all traits when the sire by flock was fitted in the model (0.03 to 0.11). Additive genetic correlations ranged from 0.49 to 0.96 and 0.81 to 1.00 for the base models and sire by flock models, respectively. Validation analyses were performed to study the predictability of sire EBVs on progeny performance, with a cross-validation procedure developed for W120. Fitting sire by flock improved predictability, with values for all sires at 0.22, and for link sires at 0.43, close to the expected value of 0.50. The estimated annual genetic trends were 0.011, 0.051, 0.060, 0.068 and 0.045 kg/yr for BWT, WWT, W120, W150 and W210, respectively, for the period between 2010 and 2017. Overall, the results indicate that an across-flock genetic evaluation for Pelibuey sheep in Mexico is possible.

Keywords: Genetic evaluation, Pelibuey sheep, Heritability, Genetic correlation, Validation study, Cross-validation.

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Introduction

Sheep production in Mexico incorporates a great diversity of breeds, which are distributed according their productive potential and the environmental conditions(1). Currently, the hair sheep represent an important genetic resource for diversifying small ruminant production, demonstrating environmental adaptation advantages in tropical conditions(2). One of the first hair sheep breeds introduced in Mexico was the Pelibuey, which today is a fundamental feature of the diverse production systems in the Mexican sheep industry(3). The Pelibuey breed is desired by producers due to their high adaptability to both tropical and temperate territories of Mexico(4,5). The Pelibuey breed is known for its high fertility and prolificacy, absence of seasonality, tolerant to internal parasites, and good adaptation a wide range of environmental conditions (rain, heat, cold)(5,6), making it an ideal breed as the maternal breed in a prime lamb crossbreeding program(7,8). Mexican Pelibuey sheep are small to medium-sized (35-80 kg), with high fertility (> 80 %) and prolificacy ranging from 1.51 to 1.80 lambs per birth and often produce lower growth rates than wool breeds, where a combination of several environmental and genetics factors contributed to the productive and reproductive performance(9,10,11).

Genetic technology is changing the livestock sector across the globe(12) and the implementation of breeding programmes based on estimated breeding values (EBVs) using performance and pedigree data has been the key to increasing productivity and profitability in the sheep industry(13,14). However, conducting a breeding program requires a good design and a clear definition of a breeding objective(15). Accurate pedigree and performance recording are the basis of a successful breeding program, and improvements in data quality and effectiveness strengthen the accuracy of EBVs(16). In animal breeding, estimating the genetic parameters for the breeding objective traits is a prerequisite in establishing a selection program(17). Accurate estimation of these genetic parameters and in particular genetic correlations between traits requires large across-generation data sets for each relevant population which are not always available(18).

Sheep production in Mexico has made an important contribution to addressing rural poverty, providing significant income for many farmers(19). However, over a long period, flock management has followed traditional practices without the adoption of modern genetic improvement programs(20), which in combination with other factors such as a wide range in production systems and poor definition of breeding objectives(21), has resulted in low productivity in the sector(22). In this way, is highly recommendable the establishment of genetic improvement programs, which have been key in increasing the profitability of sheep farmers throughout the world. However, the success of these programs depends on the use of genetic tools available to conduct genetic evaluations; including sensible evaluation models, good data quality, and a series of effective strategies to increase the adoption and dissemination of estimated breeding values(23).

In the case of the Mexican sheep industry, there is a knowledge gap on the benefits of using modern genetic tools, and performance recording for economically important traits, and this has affected the development of systematic breeding programs to improve the breed. The Mexican sheep industry, after the establishment of the data recording systems, has been able to conduct genetic evaluation mainly for growth traits, which are relatively easy to collect while being economically important(24). However, these evaluations have been approached irregularly, and there is a lack of information about genetic parameters for growth and reproductive traits, which are important and could be used to estimate breeding values to conduct breeding programs(25).

Currently, the Pelibuey breed is the third most prevalent breed in the national studbook registrations, with 51,382 animals in the data set of the Mexican Sheep Producers Association (UNO) as of 2018. Historically this breed have led the studbook registrations, and similarly to the other breeds have attempt to establish an official genetic evaluation for growth and reproduction traits(26). However, to date there has been no effort to establish a genetic evaluation for this breed. Consequently, understanding and interest in genetic tools within Pelibuey breeders has lagged behind other breeds and countries.

The objectives of this study were to develop an analysis to estimate breeding values for weight traits using Pelibuey industry data, and to validate the analysis by testing aspects including a linkage between flocks and contemporary grouping strategies, which could inform the development of routine evaluations for the breed.

Material and methods

Pelibuey growth data

Data and pedigree information were provided by UNO for the period from 2000 to 2018. Records of growth traits from birth to 210 d of age were collected from 127 flocks distributed across eight environmental regions of México: North West, North Central, North East, Pacific Central, Central, Gulf Central, Pacific South, and South East. The highest number of the records was for the Pacific Central region (15,306) and the lowest was for the North Central (1,201). Climatic information including annual average temperature and rainfall for the different regions in Mexico are shown in Table 1.

Table 1: Climatic information for different regions in Mexico

Region	**States**	**Weather**	**T° (⁰C)**	**Pp (mm)**	**Pelibuey contrib. (%)¹**
North West	Sinaloa	Subhumid, Semi-dry	25	790	5.59
North Central	Aguascalientes, Chihuahua, Zacatecas	Semi-dry, Subhumid, very dry	17	512	2.68
North East	Nuevo León, San Luis Potosí, Tamaulipas	Semi-warm humid, Sub-humid, Temperate dry, Warm semi-dry	21.5	793	6.35
Pacific Central	Jalisco, Michoacán	Semi-warm subhumid, warm subhumid	20	850	34.10
Central	Tlaxcala, Hidalgo, Estado de México, Querétaro, Guanajuato	Temperate, Temperate subhumid, Semi-warm semi dry, Semi-cold	16	728	11.30
Gulf Central	Tabasco, Veracruz	Warm humid and subhumid	25	2,025	12.76
Pacific South	Chiapas, Guerrero	Sub-humid and sub humid tropical, warm semi-dry	25	1,585	11.80
South East	Yucatán	Warm sub-humid, semi-dry very warm	26	1,100	15.42

Source of information(27).

T°= temperature; Pp= precipitation. ¹ Contribution to Pelibuey national studbook registrations.

The final data set comprised information from 51,382 lambs, the progeny of 1,440 sires, and 14,715 dams with a total pedigree of 53,235 over 12 generations. Data cleaning and descriptive statistics were performed in R statistical programming language(28). Data for all traits were filtered for missing sires, dams, birth and rearing type and age at measurement. Also, the data set was filtered to remove contemporary groups where only 1 sire was represented and less than 3 animals were recorded. A summary of descriptive statistics and the number of records, sires, dams, flocks, and the number of contemporary groups is shown in Table 2.

Table 2: Data structure and summary of descriptive statistics for growth traits

Component	BWT	WWT	W120	W150	W210
Number of records	21,102	17,517	12,054	11,649	4,294
Mean	3.02	16.6	27.63	33.63	39.45
Standard deviation	0.66	3.86	6.82	8.08	9.73
Coefficient of variation	21.85	23.25	24.68	24.03	24.66
Number of sires	988	892	589	576	359
Number of dams	9,215	7,892	5,249	5,118	2,549
Number of flocks	127	122	70	68	50
Number of Contemporary groups	1,084	1,007	679	668	357

BWT= birth weight (kg); WWT= weaning weight (kg); W120= weight at 120 d (kg); W150= weight at 150 d (kg); W210= weight at 210 d of age (kg).

Genetic linkage between Pelibuey flocks

Genetic linkage between flocks is important to increase accuracy in the estimation of the breeding values of animals in a genetic evaluation(29). The Pelibuey breed in Mexico presented moderate levels of linkage across the flocks (Table 3). Of the 992 sires in the Pelibuey data set, 87 % are represented in only one flock. Sires with progeny across flocks (132) had 5,507 progeny accounting for 26 % of total offspring.

Table 3: Summary of linkage for all population, for progeny born from 2000 onwards

Sires represented in one flock	860 (87 %)
Progeny of sires represented in one flock	15,695 (74 %)
Link sires represented in multiple flocks	132 (13 %)
Progeny of link sires	5,507 (26 %)

Estimation of genetic parameters

Genetic parameters were estimated from an animal model, using the ASReml 4.1 software(30) in a series of univariate and multivariate analyses between weight traits. The traits analysed were birth weight (BWT), weaning weight (WWT), weight at 120 d (W120), weight at 150 d

(W150), and weight at 210 d (W210). Contemporary groups (CG) were defined by the flock of birth, year of birth, and season. The seasons were winter (December to February), spring (March to May), summer (June to August), and autumn (September to November). For animals born in the winter season that crossed over from December to February, December-born animals were assigned to the next year.

Fixed effects included sex, birth type, rearing type, age of dam, and age of the animal at measurement. Sex was fitted as a factor with two levels (male and female). Birth type and rearing type were fitted independently and coded with three levels, defined as single, twin, and triplet (3+). The frequency of quadruplet or greater litters was very low, and so these were grouped with the triplet class. The age of the dam was fitted as a factor with eight categories, which included ages greater than 8+ yr grouped into the 8-yr-old subclass, and 5.4 % assigned to an “unknown” subclass.

Model selection of significant random effects for each weight trait was conducted by comparing a series of univariate analyses using Likelihood Ratio Test (LRT), Akaike Information Criterion (AIC), and Bayesian Information Criterion (BIC). Six base models were tested with a combination of the random effects including direct effects, maternal effects, correlated direct-maternal genetic effects and maternal permanent environmental effects, followed by the same models with the additional random effect of the sire by flock. Also, the contemporary group effect was fitted as random which can be beneficial when contemporary groups are small(31). The final model selection was a balance between these three criteria with qualitative aspects; also considered discounting analyses with extreme negative estimates of the correlation between direct and maternal genetic effects. The variance components from the univariate analyses for the most informative base models and sire by flock models were used in validation analyses.

The random effects tested included an additive genetic direct effect ($var(a) = A\sigma_a^2$), an additive genetic maternal effect ($var(m) = A\sigma_m^2$), a maternal permanent environment effect ($var(pe) = I\sigma_{pe}^2$), and a sire by flock effect ($var(sf) = I\sigma_{sf}^2$). Where both direct and maternal genetic effects were fitted, the merit of fitting a genetic covariance ($cov(a,m) = A\sigma_{am}$) was also explored.

Total phenotypic variance from univariate models was calculated as the sum of the variance components fitted in each model (e.g., for Model 12: $\sigma_p^2 = \sigma_a^2 + \sigma_m^2 + \sigma_{am} + \sigma_{pe}^2 + \sigma_{sf}^2 + \sigma_e^2$, where σ_e^2 is the residual variance component). Heritability for the direct genetic effect was estimated as $h_a^2 = \sigma_a^2 / \sigma_p^2$, heritability for the maternal genetic effect as $h_m^2 = \sigma_m^2 / \sigma_p^2$, the genetic correlation between direct-maternal genetic effects as $r_{am} = \sigma_{am} / \sigma_a \, \sigma_m$, the ratio of maternal permanent environmental effects as $pe^2 = \sigma_{pe}^2 / \sigma_p^2$, the ratio of phenotypic variance due to sire by flock variance as $s^2 = \sigma_{sf}^2 / \sigma_p^2$.

Preferred models defined by this model selection process were then used in pairwise bivariate analyses to estimate covariances and correlations between traits.

Considering all possible effects, the general multivariate form of the variance structures was:

$$\text{Var}\begin{bmatrix} a \\ m \\ pe \\ sf \\ cg \\ e \end{bmatrix} = \begin{bmatrix} G_{aa} \otimes A & G_{am} \otimes A & 0 & 0 & 0 & 0 \\ G_{ma} \otimes A & G_{mm} \otimes A & 0 & 0 & 0 & 0 \\ 0 & 0 & P \otimes I & 0 & 0 & 0 \\ 0 & 0 & 0 & S \otimes I & 0 & 0 \\ 0 & 0 & 0 & 0 & CG \otimes I & 0 \\ 0 & 0 & 0 & 0 & 0 & R \otimes I \end{bmatrix}$$

where $\boldsymbol{G_{aa}}$ is a matrix of direct genetic covariances between traits, $\boldsymbol{G_{mm}}$ is a matrix of maternal genetic covariances and $\boldsymbol{G_{am}}$ is a matrix of covariances between direct and maternal genetic effects. $\boldsymbol{A}$ is the numerator relationship matrix for all animals in the pedigree and $\otimes$ represents the Kronecker product matrix operation. $\boldsymbol{P}$ is a matrix of covariances between permanent maternal environment effects of the traits, $\boldsymbol{S}$ is a diagonal matrix of sire by flock interaction variances, $\boldsymbol{CG}$ is a diagonal matrix of contemporary group variances, $\boldsymbol{R}$ is a matrix of residual covariances between traits, and $\boldsymbol{I}$ represents identity matrixes of appropriate order for each random effect.

Estimation of breeding values

Multi-Trait BLUP

Breeding values (EBV) were estimated from a multi-trait BLUP model using all five traits in ASReml 4.1(30), with and without (base models) sire by flock interaction. The BLUPs were developed using the genetic parameters from the univariate analysis of the most statistically sensible model selection. The genetic correlations to construct the **G**, **P**, and **R** matrixes were taken from the bivariate analysis. The R statistical programming language(28) was used to ensure the multi-trait covariance matrixes $\mathbf{G_{aa}}$, **P**, and **R** were positive definite.

Single trait BLUP

The breeding values were estimated from a single trait animal model (BLUP) only for 120-d weight using ASReml 4.1 software(30). That trait for this study was chosen due to high genetic correlations between growth traits, particularly between later growth traits (W120, W150 and W210), as well as the higher number of records at this age. The BLUPs were developed using variance components from the univariate analysis using the most informative models including and excluding sire by flock interaction. Cross-validation procedure of the data set at 120-d weight was used to develop the single trait BLUPs.

Validation analyses of breeding values

Validation analyses were performed to study the predictability of the sire EBVs in progeny performance. A cross-validation procedure was used, where the data set was split into 5 folds based on random allocation of the total flocks (70), replicated 5 times in a bootstrapping procedure. Sequentially, each fold was defined as the "Validation" data, and then the estimation of the breeding values was from the "Training" data combining phenotypes from the other four-folds, using a single-trait animal model with base models and with sire by flock interaction. Then, the adjusted progeny performance in the validation data was regressed on sire EBVs from the training data for all sires, link sires between training and validation data sets, and sires only in the validation data (non-link sires). The regressions of offspring performance on sire breeding values were calculated from linear models in R statistical programming language(28), where the expected value of this regression is 0.5. The linear model included the fixed effects of sex, birth type, rearing type, age of the dam, age at measurement at the 120-d weight and the sire's EBVs. Five-fold validations were performed in three data sets of 120-d weight with varying levels of data quality. Data set Q1 was the full data set for the trait, while Q2 was filtered from Q1 to consider only flocks with sires represented in at least two flocks (linked flocks), and Q3 was filtered from Q2 to remove contemporary groups when only 1 sire was represented and less than 10 animals recorded. The same random allocation of flocks to folds was used across data sets. A summary of the three data sets for 120-d weight used in the validation analyses is presented in Table 4.

Table 4: Summary of 120-day weight data sets in the Pelibuey sheep

Data set	**Animals recorded**	**Number of**		**Number of flocks**	**Contemporary groups**	
		Sires	**Dams**		**Number**	**Av. size**
Q1	12,054	589	5,249	70	679	17.75
Q2	9,433	441	3,781	36	527	17.89
Q3	8,072	362	3,265	29	311	25.95

Q1= full data set; Q2= filtered from Q1, considered only flocks with sires represented in at least two flocks (linked flocks), Q3= filtered from Q2, removing contemporary groups when only 1 sire was represented and less than 10 animals recorded.

Analysis of genetic trends

Estimated breeding values to predict genetic trends were derived from multi-trait BLUP including all data set between 2000 and 2018. Yearly means of EBVs were computed for BWT, WWT, W120, W150, and W210. Lastly, genetic trends were generated by plotting all the weight traits over time.

Results and discussion

Genetic parameters

A summary of estimates of variance components and genetic parameters for the selected models for both base and sire by flock interaction models are shown in Table 5. Direct effects, maternal additive effects and maternal permanent environmental effects were fitted for BWT; while for WWT, W120, W150 and W210, direct additive effects and maternal permanent environmental effects were fitted.

The phenotypic variance for both base models (range, 0.27 to 16.15) and sire by flock interaction (0.28 to 17.02) of growth traits increased from BWT to W210 (Table 5). Direct heritability estimates for the base models ranged from 0.13 to 0.18 and were reduced across all traits when the sire by flock interaction term was fitted in the model (0.03 to 0.11). The estimate of maternal heritability for BWT was similar for both the base model (0.03) and the model incorporating the sire by flock term (0.02). The ratio of maternal permanent environmental effects fluctuated between 0.10 and 0.07 in both the base models and sire by flock from BWT to W150, but for W210 the ratio was 0.17. The ratio of the sire by flock term ranged from 0.06 to 0.14.

The estimated heritability for BWT was 0.13 and 0.11 for the base model and sire by flock (Table 5). These estimates are in agreement with previous findings in multi-breed Australian meat sheep and the Suffolk breed(32,33). Other higher estimates were reported in Merino sheep and Iranian Afshari sheep(34,35). However, lower heritabilities were reported in Pelibuey (0.01) and Blackbelly breeds (0.05)(36).

The estimated heritability for WWT in the base model was higher (0.18) than the heritability from the sire by flock model (0.11). Similar heritability of 0.20 was estimated using a standard model in a genetic evaluation of the Mexican Pelibuey(26). However, a higher estimate (0.39) with sire by flock fitted was observed in a study in Australian Merino sheep(37).

The direct heritability for W120 for the base model was 0.13. Slightly higher heritability estimates were reported from a genetic evaluation in Mexican Pelibuey (0.17)(26) and in Katahdin (0.18)(38).

Direct heritabilities for W150 were 0.14 and 0.08 respectively for the base and sire by flock interaction models. The estimates from base models in this study were slightly lower than others reported at 6 mo of age in multi-breed Australian sheep(39), in Suffolk and Charollais breeds(33), which ranged between 0.16 and 0.32.

The heritability for a W210 was 0.15 and 0.03 for the base and sire by flock models, respectively. However, higher estimates were reported in wool (0.30), dual-purpose (0.28) and meat breeds (0.22)(40).

The maternal heritability for BWT was the same for the base models and sire by flock interaction model (Table 5). This estimate is in agreement with literature estimates in Suffolk, Texel and Charollais meat breeds, ranging from 0.02 to 0.06(33). The maternal permanent environmental effects were similar for both the base models and sire by flock interaction ranging between 0.10 and 0.07 across traits from BWT to W150. In both cases, maternal permanent environmental effects become less important with age. However, the estimates for W210 increased in base and sire by flock models with the same value of 0.17, which may be due to low numbers of records and poor data structure. To investigate this further, an analysis was conducted to better separate direct from maternal effects, by filtering the data set to include only progeny of dams with more than one offspring. However, the ratio of maternal permanent environmental effects for both the base and sire by flock models was not significantly different (0.13). These estimates of the maternal permanent environmental effects are similar to literature estimates, of 0.08 for BWT in Iranian Afshari sheep(35), 0.07 for WWT in Australian Merino sheep(40), and 0.04 for W120 in Mexican Katahdin sheep(38).

The inclusion of sire by flock interaction in the models has shown a significant improvement in the genetic evaluation(37,41,42). This interaction is important overall in across flock evaluation, because the performance of the sires across flocks and years tends to be different can vary due genotype by environment interaction, and preferential treatment of progeny of artificial insemination sires. Fitting the interaction can help to improve the fit of the model resulting in breeding values representing average performance across environments, but can lead to removal of genetic variation for traits with maternal effects(41,43). The estimates of sire by flock interaction in this study ranged from 0.06 to 0.12 across the growth traits. Lower ratios were estimated in Australian Poll Dorset sheep (2–4 %)(41), and in Merino sheep (4 %)(37). The estimates of sire by flock variance in this study indicate a large variation in sire performance across farms. This indicates the data set presents issues related to structure and into the future, sire linkage needs to be improved.

Genetic correlations

Estimated correlations between the five weight traits from the base models and the sire by flock term are presented in Table 6. Both additive genetic correlations from the base models and sire by flock models were positive and moderate to strong, ranging from 0.47 to 0.96 and 0.81 to 1.00, respectively.

Estimates of genetic correlations in both the base models and sire by flock between BWT and WWT were 0.63 and 0.97, respectively. From W120 onwards genetic correlations with BWT declined, but not significantly (Table 6). Lower genetic correlations have been reported between BWT and later growth traits in multi-breed Australian sheep(39) and Merinos(34).

Estimated genetic correlations between WWT, W120, W150 and W210 for both the base and sire by flock interaction models ranged from 0.65 to 0.95 (Table 6). Similar estimates of additive genetic correlations between WWT and post-weaning weight at 6 months of age were reported in other studies. For instance, Irish meat breeds ranged from 0.77 to 0.99(33), in Merino and multi-breed Australian sheep estimates were 0.78 and 0.74, respectively(34,39).

Phenotypic correlations from the base models and sire by flock were positive ranging from 0.21 to 0.89 (Table 6). In both, base models (0.21 - 0.30) and sire by flock models (0.22 - 0.31), BWT had low phenotypic genetic correlations with WWT, W120, W150 and W210. These estimates are in agreement with other findings in Australian breeds (0.09)(34) and (0.32)(39). Phenotypic correlations between WWT and later body growth traits in both the base and sire by flock models were moderate, ranging from 0.47 to 0.53. Estimates from studies in other breeds and different production systems range from 0.52 to 0.90 in Merino and Australian meat sheep(34,39).

Table 6: Estimated correlations from the base models (above diagonal) and sire by flock interaction (below diagonal) between growth traits in Pelibuey sheep

Trait	**BWT**	**WWT**	**W120**	**W150**	**W210**
Additive genetic correlation					
BWT		0.63 ± 0.06	0.49 ± 0.09	0.51 ± 0.09	0.47 ± 0.12
WWT	0.97 ± 0.09		0.80 ± 0.04	0.66 ± 0.06	0.65 ± 0.09
W120	0.81 ± 0.13	0.95 ± 0.05		0.96 ± 0.01	0.89 ± 0.04
W150	0.83 ± 0.14	0.86 ± 0.08	1.00 ± 0.01		0.92 ± 0.03
W210	0.94 ± 0.25	0.93 ± 0.15	0.97 ± 0.39	1.00 ± 0.04	
Phenotypic correlation					
BWT		0.30 ± 0.01	0.23 ± 0.01	0.21 ± 0.01	0.21 ± 0.02
WWT	0.31 ± 0.01		0.52 ± 0.01	0.47 ± 0.01	0.48 ± 0.01
W120	0.23 ± 0.01	0.53 ± 0.01		0.88 ± 0.00	0.77 ± 0.01
W150	0.22 ± 0.01	0.48 ± 0.01	0.89 ± 0.00		0.86 ± 0.00
W210	0.23 ± 0.02	0.50 ± 0.01	0.77 ± 0.01	0.86 ± 0.00	
Maternal permanent environmental correlation					
BWT		0.38 ± 0.06	0.35 ± 0.08	0.30 ± 0.09	0.50 ± 0.10
WWT	0.32 ± 0.06		0.50 ± 0.07	0.48 ± 0.08	0.60 ± 0.08
W120	0.30 ± 0.08	0.45 ± 0.07		0.83 ± 0.04	0.70 ± 0.07
W150	0.25 ± 0.09	0.44 ± 0.08	0.81 ± 0.04		0.75 ± 0.06
W210	0.45 ± 0.10	0.56 ± 0.09	0.80 ± 0.06	0.73 ± 0.06	

BWT= birth weight (kg); WWT= weaning weight (kg); W120= weight at 120 d (kg); W150= weight at 150 d (kg); W210= weight at 210 d of age (kg).

Estimates of maternal permanent environmental correlations were similar for both base models (0.30 to 0.83) and sire by flock models (0.25 to 0.81) (Table 6). Low estimates of maternal permanent environmental correlations were found between BWT and WWT, W120 and W150, ranged for the base models (0.30 - 0.38) and sire by flock interaction models (0.25 - 0.32). The estimates of maternal permanent environmental correlations between BWT and W210 were similar and increased to 0.50 in the base model and 0.45 in the sire by flock model. Estimates of maternal permanent environmental correlations for the base models and sire by flock models between WWT and later growth traits (0.44 - 0.60).

Validation of breeding values

The objective of the validation analyses was to study the predictability of the sire EBVs in progeny performance. However, due to low levels of sire linkage across flocks, the validation study was complemented using a cross-validation procedure in which the quality of the data set was improved by restricting the minimum size of contemporary groups and selecting flocks with higher linkage, which may be more suitable for accurate genetic evaluations.

Means and standard deviations of the sire-offspring regression coefficients at W120 for the base models and sire by flock interaction in the Mexican Pelibuey breed are shown in Table 7. The average regression of offspring performance on sire breeding values in the Data sets Q1, Q2 and Q3 showed low predictability for the base models with all sires (0.15), link sires (0.26) and non-link sires (-0.03) between training and validation data sets, and in all cases deviation below the expected value of 0.5 demonstrated over-prediction. However, when sire by flock was fitted the predictability was improved with all sires (0.22) and link sires (0.43), but lower for non-link sires (-0.21).

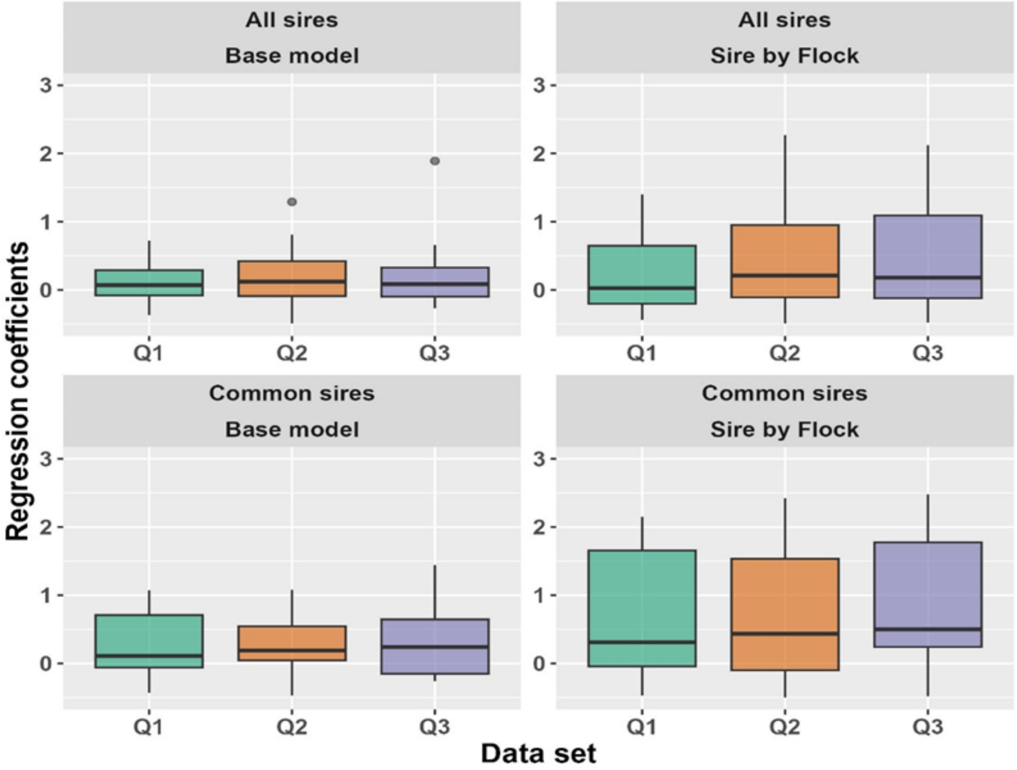
Table 7: Regression coefficients *(b)* and their standard deviations of progeny performance on sire estimated breeding values for 120-day weight trait for the base model and sire by flock interaction in Pelibuey sheep

Model	**Data set**	**All sires**	**Common sires**	**Non-link sires**
		Regression coefficients		
Base model				
	Q1	0.12 (0.27)	0.27 (0.45)	0.07 (0.25)
	Q2	0.18 (0.39)	0.25 (0.45)	-0.07 (0.73)
	Q3	0.15 (0.46)	0.28 (0.51)	-0.11 (0.60)
Average		0.15	0.26	-0.03
Sire by flock				
	Q1	0.21 (0.57)	0.50 (0.96)	0.04 (0.46)
	Q2	0.24 (0.80)	0.35 (1.07)	-0.33 (1.21)
	Q3	0.21 (0.82)	0.45 (1.10)	-0.35 (1.03)
Average		0.22	0.43	-0.21

Q1= full data set; Q2= filtered from Q1, considered only flocks with sires represented in at least two flocks (linked flocks); Q3= Filtered from Q2, removing contemporary groups when only 1 sire was represented and less than 10 animals recorded.

Figure 1 is provided in support of Table 7, and presents the mean values of the regression coefficients of progeny performance on sire EBV estimated in three data sets for all sires and link sires in the base and sire by flock interaction models. The regression coefficients for non-link sires are not included in the figure.

Figure 1. Mean values of the regression coefficients of progeny performance on sire EBVs

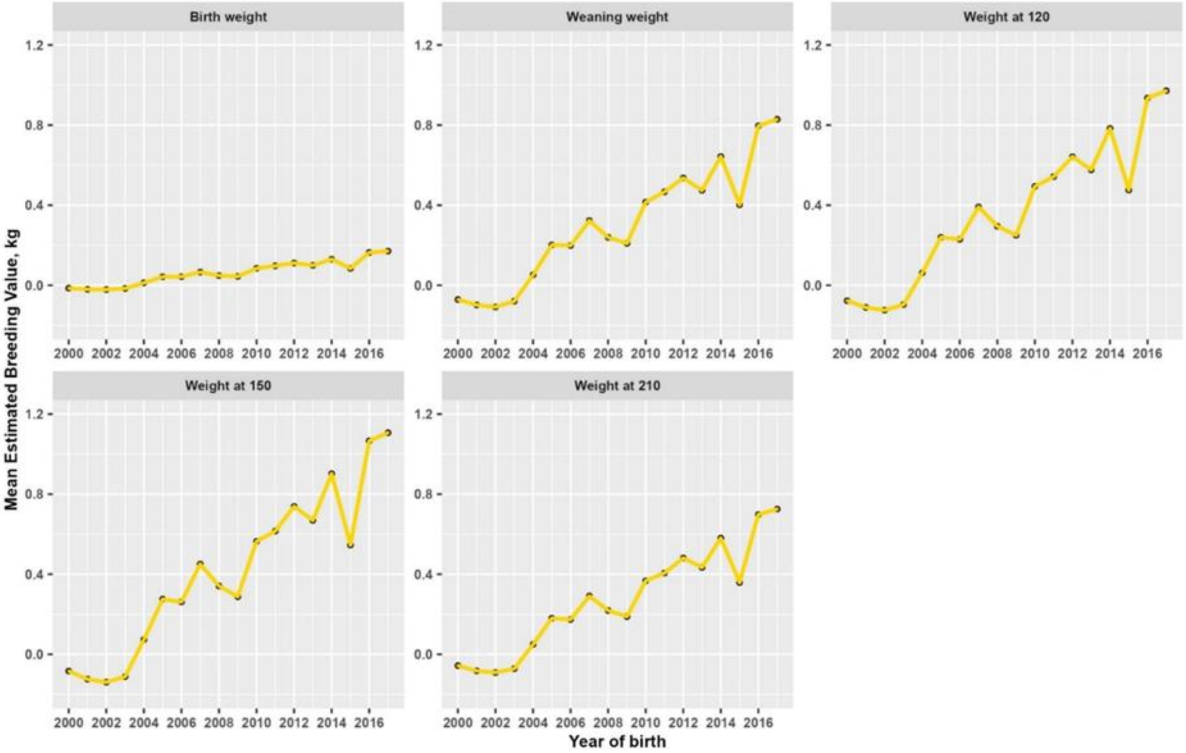


Encouragingly, these results demonstrate there is real potential to develop a national genetic evaluation, even though the data set showed some issues with structure and poor linkage across the flocks, reasonable predictability was still achieved for the common sires across the flocks.

Predicted genetic trends

Predicted genetic trends between 2000 and 2017 for BWT, WWT, W120, W150 and W210, respectively, are shown in Figure 2. The genetic trends from 2000 to 2003 were slightly negative, but between 2004 and 2017, the mean breeding values increased. This means that the selection has been consistent in this period of evaluation.

Figure 2: Genetic trends for growth traits in the Pelibuey sheep from 2000 to 2017



The estimated annual genetic trends were 0.011, 0.051. 0.060, 0.068 and 0.045 kg/yr for BWT, WWT, W120, W150 and W210, respectively, for the period between 2010 and 2017. These estimates were slightly higher than previous findings in other breeds, ranging from 0.04 to 0.12(44-47).

The Mexican sheep industry has made a moderate effort over the last decade to increase the adoption and dissemination of genetic tools. EBVs as a product of genetic evaluations are currently not being used by ram breeders or ram buyers, and when they have been available(26,38,48) in the past users have found them confusing and have had limited confidence in their ability to predict progeny performance. The results presented in this study go some way to growing industry engagement in breeding values. It is noted that the data in this study has its limitations in both volume and quality and yet the validation results show favourable predictivity for growth traits. The analysis and resulting breeding values will provide an important cornerstone for industry adoption. Being able to benchmark genetic gain and publicising trait leader sires, even for only a small number of traits, provides the industry with a tangible outcome for their efforts to capture pedigree and performance records. As the database grows to include more animals, traits and potentially genomic information the findings and models presented herein will require reviewing.

Conclusions and implications

The estimates of heritability in this study were reasonably consistent with estimates presented in a range of previous findings, albeit slightly lower. Estimates of genetic and phenotypic correlation were positive and moderate to strong, in agreement with estimates in previous studies. The validation study of the sire EBVs in the progeny of the offspring showed good predictability when sire by flock interactions were fitted in the models, with link sires between training and validation data sets; indicating that an across-flock genetic evaluation is possible when the sire by flock term was included in the models. Predicted genetic trends in this genetic evaluation showed reasonable genetic progress for growth traits in the Mexican Pelibuey population. The Pelibuey sheep in Mexico has played an important role in the industry and has demonstrated good adaptation to different environmental conditions. This adaptability is crucial for the future sustainability of sheep production. To develop an effective genetic evaluation system for the Pelibuey breed, an intensive artificial insemination program to strengthen genetic linkage across flocks will be necessary. This will allow the investigation of genotype by environment interactions (G by E), which may be present because the breed is located across Mexico in a wide range of environmental conditions. A further step is to explore genetic evaluation for reproductive traits, which will be economically important for this maternal sheep breed.

Acknowledgements and conflict of interest

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Table 5: Estimates of contemporary group variance (σ^2_{cg}), phenotypic variance (σ^2_{p}), additive variance (σ^2_{a}), maternal variance (σ^2_{m}), maternal permanent environmental variance (σ^2_{pe}), sire by flock variance (σ^2_{s}), residual variance (σ^2_{e}), heritability (h^2_{a}), maternal heritability (h^2_{m}), maternal permanent environmental effects (m^2) and sire by flock effects (s^2) without and with sire by flock interaction for growth traits in Pelibuey sheep

Trait	σ^2_{cg}	σ^2_{p}	σ^2_{a}	σ^2_{m}	σ^2_{pe}	σ^2_{s}	σ^2_{e}	h^2_{a}	h^2_{m}	m^2	s^2
Base models:											
BWT	0.12 ± 0.01	0.27 ± 0.00	0.03 ± 0.00	0.01 ± 0.00	0.02 ± 0.00	n.f.	0.20 ± 0.00	0.13 ± 0.02	0.03 ± 0.01	0.09 ± 0.01	n.f.
WWT	7.18 ± 0.37	5.97 ± 0.08	1.07 ± 0.12	n.f.	0.60 ± 0.06	n.f.	4.31 ± 0.09	0.18 ± 0.02	n.f.	0.10 ± 0.01	n.f.
W120	29.03 ± 1.70	11.40 ± 0.17	1.46 ± 0.25	n.f.	0.90 ± 0.13	n.f.	9.05 ± 0.20	0.13 ± 0.02	n.f.	0.08 ± 0.01	n.f.
W150	40.41 ± 2.31	15.26 ± 0.23	2.21 ± 0.34	n.f.	1.06 ± 0.17	n.f.	11.99 ± 0.28	0.14 ± 0.02	n.f.	0.07 ± 0.01	n.f.
W210	75.88 ± 6.01	16.15 ± 0.41	2.40 ± 0.66	n.f.	2.75 ± 0.43	n.f.	11.01 ± 0.54	0.15 ± 0.04	n.f.	0.17 ± 0.03	n.f.
Sire by flock:											
BWT	0.11 ± 0.01	0.28 ± 0.00	0.03 ± 0.01	0.00 ± 0.00	0.02 ± 0.00	0.02 ± 0.00	0.20 ± 0.00	0.11 ± 0.02	0.02 ± 0.01	0.09 ± 0.01	0.06 ± 0.01
WWT	5.97 ± 0.34	6.54 ± 0.12	0.69 ± 0.13	n.f.	0.60 ± 0.06	0.90 ± 0.10	4.35 ± 0.09	0.11 ± 0.02	n.f.	0.09 ± 0.01	0.14 ± 0.01
W120	27.07 ± 1.63	11.83 ± 0.21	0.89 ± 0.27	n.f.	0.87 ± 0.13	0.88 ± 0.15	9.19 ± 0.21	0.08 ± 0.02	n.f.	0.07 ± 0.01	0.07 ± 0.01
W150	37.49 ± 2.28	15.91 ± 0.29	1.34 ± 0.37	n.f.	1.06 ± 0.17	1.31 ± 0.22	12.20 ± 0.28	0.08 ± 0.02	n.f.	0.07 ± 0.01	0.08 ± 0.01
W210	73.55 ± 5.91	17.02 ± 0.52	0.52 ± 0.77	n.f.	2.92 ± 0.44	2.06 ± 0.46	11.53 ± 0.55	0.03 ± 0.04	n.f.	0.17 ± 0.03	0.12 ± 0.02

BWT= birth weight (kg); WWT= weaning weight (kg); W120= weight at 120 d (kg); W150= weight at 150 d (kg); W210= weight at 210 d of age (kg); n.f.= random effect not fitted.

Literature cited:

1. Herrera HJG, Álvarez FG, Bárcena GR, Núñez AJM. Characterization of sheep flocks in the south of the Ciudad de México, México. Acta Universitaria 2019;29. https://doi.org/10.15174/au.2019.2022.

2. Wildeus S. Hair sheep genetic resources and their contribution to diversified small ruminant production in the United States. J Anim Sci 1997;75(3):630-640. https://doi.org/10.2527/1997.753630x...

3. Macedo-Barragán RJ, Arredondo-Ruiz V, Cervantes-Lechuga A. Head and tail morphology of Pelibuey, Katahdin and Blackbelly rams in Colima, México. Vet México OA 2016;3(3). https://doi.org/10.21753/vmoa.3.3.375.

4. Gutiérrez J, Rubio MS, Méndez RD. Effects of crossbreeding Mexican Pelibuey sheep with Rambouillet and Suffolk on carcass traits. Meat Sci 2005;70(1):1-5. https://doi.org/10.1016/j.meatsci.2004.10.017.

5. Aguilar-Martínez CU, Berruecos-Villalobos JM, Espinoza-Gutiérrez B, Segura-Correa JC, Valencia-Méndez J, Roldán-Roldán A. Origen, historia y situación actual de la oveja Pelibuey en México. Trop Subtrop Agroecosyst 2017;20(3):429-439.

6. Macías C, Álvarez V, Olguín A, Molina R, Avendaño R. Ovejas Pelibuey sincronizadas con progestágenos y apareadas con machos de razas Dorper y Katahdin bajo condiciones estabuladas: producción de la oveja y crecimiento de los corderos durante el período predestete. Arch Med Vet 2012;44(1):29-37.

7. Pineda J, Palma JM, Haenlein GFW, Galina MA. Fattening of Pelibuey hair sheep and crossbreds (Rambouillet-Dorset × Pelibuey) in the Mexican tropics. Small Ruminant Res 1998;27(3):263-266. https://doi.org/10.1016/S0921-4488(97)00021-7.

8. Hinojosa-Cuellar JA, Oliva-Hernández J, Torres-Hernández G, Segura-Corra JC, González-Garduño R. Productividad de ovejas F1 Pelibuey x Blackbelly y sus cruces con Dorper y Katahdin en un sistema de producción del trópico húmedo de Tabasco, México. Archiv Med Vet 2005;47(2):167-174. https://scielo.conicyt.cl/pdf/amv/v47n2/art07.pdf.

9. Arroyo LJ, Gallegos SJ, Villa GA, Berruecos JM, Perera G, Valencia J. Reproductive activity of Pelibuey and Suffolk ewes at 19 north latitude. Anim Reprod Sci 2007;102(1-2):24-30. https://doi.org/10.1016/j.anireprosci.2006.09.025.

10. Segura JC, Sarmiento L, Rojas O. Productivity of Pelibuey and Blackbelly ewes in Mexico under extensive management. Small Ruminant Res 1996;21(1):57-62. https://doi.org/10.1016/0921-4488(95)00814-4.

11. García-Chávez CA, Luna-Palomera C, Macías-Cruz U, Segura-Correa JC, Ojeda-Robertos NF, Peralta-Torres JA, *et al*. Crecimiento de corderos y productividad en ovejas Pelibuey mantenidas bajo condiciones tropicales de producción. Rev Mex Cienc Pecu 2020;11(3): 884-893. https://doi.org/10.22319/rmcp.v11i3.5157.

12. Georges M, Charlier C, Hayes B. Harnessing genomic information for livestock improvement. Nature Reviews Genetics 2019;20(3):135-156. doi:https://doi.org/10.1038/s41576-018-0082-2.

13. Amer P, Byrne T, Fennessy P, Jenkins G, Martin D, Berry D. Review of the genetic improvement of beef cattle and sheep in the UK with special reference to the potential for genomics. 2015. Retrieved from https://signetdata.com/media/2553/review-of-the-genetic-improvement-of-beef-cattle-and-sheep-in-the-uk-final-report-140515.pdf.

14. Swan A, Banks R, Brown D, Chandler H. An update on genetic progress in the Australian sheep industry. Paper presented at the Proc Assoc Advmt Anim Breed Genet, Queensland. 2017.

15. van der Werf J. Sustainable animal genetic improvement. E3S Web of Conferences, 2022;335, doi:https://doi.org/10.1051/e3sconf/202233500001.

16. Brown D, Huisman A, Swan A, Graser H, Woolaston R, Ball A, *et al*. Genetic evaluation for the Australian sheep industry. Proc Assoc Advmt Anim Breed Genet. Armidale, Australia. 2007.

17. Meyer K. Estimation of genetic parameters. Evolution Anim Breeding 1989:161-167.

18. Safari E, Fogarty N, Gilmour A. A review of genetic parameter estimates for wool, growth, meat and reproduction traits in sheep. Livestock Prod Sci 2005;92(3):271-289. doi:https://doi.org/10.1016/j.livprodsci.2004.09.003.

19. Martínez G, Muñoz R, García M, Santoyo C, Altamirano C, Romero M. El fomento de la ovinocultura familiar en México mediante subsidios en activos: lecciones aprendidas. Agronom Mesoamericana 2011;22(2):367-377. https://www.scielo.sa.cr/scielo.php?script=sci_arttext&pid=S1659-3212011000200013.

20. Galaviz R, Ramírez B, Vargas L, Zaragoza R, Guerrero R, Mellado B, *et al*. Effect of three production systems of central Mexico on growth performance of five lamb genotypes. J Anim Plant Sci 2014;24:1303-1308. Retrieved from http://www.thejaps.org.pk/docs/v-24-5/05.pdf.

21. Vélez IA, Espinosa JA, De la Cruz CL, Rangel J, Espinoza I, Barba C. Caracterización de la producción de ovino de carne del estado de Hidalgo, Mexico. Archiv Zoot 2016;65(251), 425-428. doi:https://doi.org/10.21071/az.v65i251.708.

22. Bobadilla S, Ochoa A, Perea P. Dinámica de la producción y consumo de carne ovina en México 1970 a 2019. Agronom Mesoamericana 2021;963-982. https://revistas.ucr.ac.cr/index.php/agromeso/article/download/44473/47878?inline=1.

23. Collison C, Brown D, Gill J, Chandler H, Apps R, Swan A, *et al*. A decade of sheep genetics: what have we achieved?. Proc 11th World Congress on Genetics Applied to Livestock Production. Auckland, New Zealand. 2018.

24. Larios S, Domínguez VJ, Ramírez V, Núñez DR, Rodríguez A, García M. Tendencias geneticas de poblaciones ovinas de pelo en Mexico. Trop Subtrop Agroecosyst 2109;22:315-329. https://repositorio.chapingo.edu.mx/server/api/core/bitstreams/711f9b3a-926f-496a-9e0f-f163ecffc115/content#page=65.

25. Brown D, Bunter K, Swan A. Genetic correlations between production traits and components of reproduction in Merino sheep. Proc Assoc Advmt Anim Breed Genet. Townsville, Queensland. 2017.

26. UNO. Evaluaciones geneticas en ovinos. Catálogo de sementales de alto valor genetico. 2015. https://www.uno.org.mx/catalogos/catalogoovinosunoenero2016.pdf.

27. Zepeda V. Las regiones climáticas de México. Universidad Nacional Autónoma de México. 2005(2).

28. R Core Team R: A language and environment for statistical computing. R Foundation for Statistical Computing. Vienna, Austria. 2021. https://www.R-project.org/.

29. Brown D, Ball A, Huisman A, Swan A, Atkins K, Graser H, *et al*. Sheep genetics Australia: A national genetic evaluation system for Australian sheep. Proc 8th World Cong Genetics Applied to Livestock Production. Belo Horizonte, Brazil. 2006.

30. Gilmour AR, Gogel BJ, Cullis BR, Welham SJ, Thompson R. ASReml user guide release 4.1 Functional Specification. VSN International Ltd, Hemel Hempstead, HP1 1ES, UK. 2015.

31. Schaeffer LR. Contemporary groups are always random. 2009; Generic In: Guelph: APS. 1:6.

32. Brown DJ, Swan AA, Gill JS, Ball AJ, Banks RG. Genetic parameters for liveweight, wool and worm resistance traits in multi-breed Australian meat sheep. 1. Description of traits, fixed effects, variance components and their ratios. Anim Production Sci 2016;56(9):1442-1448. https://doi.org/10.1071/AN14787.

33. Fitzmaurice S, Conington J, Fetherstone N, Pabiou T, McDermott K, Wall E, *et al*. Genetic analyses of live weight and carcass composition traits in purebred Texel, Suffolk and Charollais lambs. Animal 2020;14(15):899-909. https://doi.org/10.1017/S1751731119002908.

34. Huisman AE, Brown DJ. Genetic parameters for bodyweight, wool, and disease resistance and reproduction traits in Merino sheep. 2. Genetic relationships between bodyweight traits and other traits. Australian J Exp Agr 2008;48(9):1186-1193. https://doi.org/10.1071/EA08120.

35. Latifi M, Mohammadi A. Analysis of genetic parameters and genetic trends for early growth traits in Iranian Afshari sheep. Biotech Anim Husbandry 2018;34(3):289-301. https://doi.org/10.2298/BAH1801001G.

36. Rodriguez HV, Vega MV, Germano CR, Parraguirre LC, Valencia de Ita MDLA, Romero AO. Evaluation of genetic parameters of growth of Pelibuey and Blackbelly sheep through pedigree in Mexico. Animals 2022;12(6):691. https://doi.org/10.3390/ani12060691.

37. Swan AA, Brown DJ. A simple bootstrapping procedure to validate the MERINOSELECT model for weaning weight. Paper presented at the Proc Assoc Advmt Anim Breed Genet 2007;17:24-26.

38. Manzanilla PCIV, Torres VJA, Borrayo ZA, Ríos UA, Baeza RJJ, Martínez VG, Vega MV, Montaño BM. Estimación de parámetros genéticos para características de crecimiento en borregos Katahdin usando diferentes modelos. Rev Mex Cienc Pecu 2012;3(4):487-500.

39. Brown DJ, Swan AA. Genetic parameters for liveweight, wool and worm resistance traits in multi-breed Australian meat sheep. 2. Genetic relationships between traits. Anim Prod Sci 2016;56(9):1449-1453. https://doi.org/10.1071/AN14788.

40. Safari E, Fogarty NM, Gilmour AR. A review of genetic parameter estimates for wool, growth, meat and reproduction traits in sheep. Livestock Prod Sci 2005;92(3):271-289. https://doi.org/10.1016/j.livprodsci.2004.09.003.

41. Brown DJ, Swan AA, Johnston JD, Graser UH. Sire by flock-year interactions for body weight in Poll Dorset sheep. Proc Assoc Advmt Anim Breed Genet 2009;18:48-51.

42. Li L, Swan AA, Brown DJ, van der Werf JHJ. Genotype by environment interaction in Australian maternal and terminal sheep. Proc Assoc Advmt Anim Breed Genet 2019;23:234-237.

43. Meyer K. Estimates of genetic parameters for weaning weight of beef cattle accounting for direct-maternal environmental covariances. Livestock Prod Sci 1997;52(3):187-200. https://doi.org/10.1016/S0301-6226(97)00144-9.

44. Baneh H, Ahmadpanah J. Genetic evaluation of body weight traits in Iranian native Ghezel sheep. Genetika 2018;50(1):275-284. https://doi.org/10.2298/GENSR1801275B.

45. Hossein NG. Bayesian estimates of genetic changes for body weight traits of Moghani sheep using Gibbs sampling. Trop Anim Health Prod 2012;44(3):531-536.

46. Mohammadi H, Moradi SM, Moradi SH. Genetic analysis of ewe productivity traits in Makooei sheep. Small Ruminant Res 2012;107(2-3):105-110. https://doi.org/10.1016/j.smallrumres.2012.04.019.

47. Mokhtari MS, Rashidi A. Genetic trends estimation for body weights of Kermani sheep at different ages using multivariate animal models. Small Ruminant Res 2010;88(1):23-26. https://doi.org/10.1016/j.smallrumres.2009.11.003.

48. De La Cruz CL, Gutierrez, GJ. Evaluacion genetica en ovinos de la raza Hampshire, mediante un esquema de sementales de referencia. Folleto Tecnico No. 7. Pachuca de Soto, Hidalgo: Instituto Nacional de Investigaciones Forestales, Agricolas y Pecuarias. 2009:98.