Egyptian J. Anim. Prod. (2025) 62(3):179-187

VARIANCE COMPONENTS ESTIMATE USING BAYESIAN METHODS FOR LITTER SIZE AND TOTAL LITTER WEIGHT AT BIRTH IN SOHAGI SHEEP

A. Elnahas[1] and Reda Elsaid[2]

1- Animal Production Department, Faculty of Agriculture, Sohag University, Egypt. 2-Department of Sustainable Development, Environmental Studies and Research Institute (ESRI), University of Sadat City, Menofyia, Egypt
Corresponding author: reda.elsaid@esri.usc.edu.eg

Article History: Received: 16/6/2025; Accepted: 11/8/2025; Published: 21/9/2025
DOI: 10.21608/ejap.2025.394473.1115

SUMMARY

This study aimed to estimate variance components for litter size (LS) and total litter weight at birth (TLW) in Sohagi sheep using Bayesian methods. Data were collected from 2003 to 2022 at the experimental farm of Sohag University, which included records from 1,464 ewes, the offspring of 51 sires and 325 dams, to assess the influence of various environmental factors on these traits. The average LS and TLW were 1.25 ± 0.01 lambs and 3.74 ± 0.03 kg per ewe, respectively. To estimate the posterior means and standard deviations of genetic parameters for LS and TLW, univariate linear, univariate threshold, bivariate linear, and bivariate threshold linear models were employed using GIBBSF90+. For LS, heritability estimates ranged from 0.10 (univariate linear model) to 0.21 (univariate threshold model), while repeatability ranged from 0.13 to 0.26, following a similar pattern. For TLW, heritability estimates varied from 0.04 (univariate linear model) to 0.07 (bivariate threshold linear model), with repeatability estimates also showing a similar trend, ranging from 0.10 and 0.13. The bivariate threshold linear model indicated a high genetic correlation of 0.98 and a phenotypic correlation of 0.94. Additionally, the bivariate linear model showed strong positive correlations, with genetic and phenotypic values of 0.99 and 0.87, respectively. For LS, Spearman rank correlations between breeding values obtained from four models demonstrated consistent animal rankings across different statistical approaches. Based on these findings, we propose a selection index that incorporates both LS and TLW traits to enhance genetic evaluation strategies in Sohagi sheep.

Keywords: Sohagi sheep, Litter size and total litter weight at birth, Linear and threshold models, Genetic parameters

INTRODUCTION

The Sohagi sheep is one of the prominent indigenous sheep breeds in Egypt, especially well-adapted to the environmental conditions of Upper Egypt. These sheep are highly tolerant of heat stress, limited food availability, and extensive management systems (Elnahas and Elsaid, 2022). A key factor influencing their productivity and economic value is reproductive performance, particularly litter size and total litter weight at birth.Litter size, refers to the number of lambs of a ewe produces in a single lambing, and it significantly impacts the overall reproductive performance of the flock and making it an essential aspect of meat production. Similarly, total litter weight at birth, which is the combined weight of all lambs born in a single parturition, reflects the overall health and development potential growth of the newborns. A high litter size accompanied by appropriate birth weight increases survival rates, promotes efficient growth, and higher profitability for farmers (Ptáček *et al*., 2017, and Santos *et al*., 2023).

Enhancing the reproductive efficiency and productivity of Sohagi sheep can be achieved through genetic selection and effective management practices. Community-based breeding programs have demonstrated success in improving reproductive traits and decreasing pre-weaning mortality (Habtegiorgis *et al*., 2022). Consequently, these indicators are crucial not only for evaluating flock performance but also for developing sustainable breeding programs aimed at enhancing local genetic resources.

Litter size is considered a categorical trait that is measured on a discrete scale. This classification makes it more appropriate to treat it as a quasi-continuous or a threshold characteristic. When analyzed using linear models, the discrete and non-normally distributed nature of litter size is not adequately addressed, which can lead to less accurate results. Therefore, threshold models are generally more suitable to analyze categorical traits. Supporting this, Mekkawy *et al*. (2010) and Ziadi *et al*. (2024) recommended the use of threshold models for studying litter size in sheep. Their analyses, based on these models, produced higher heritability estimates compared to those obtained from linear models. However Moreno, (1993) and Ødegard *et al*. (2010) reported that threshold models can provide biased variance component estimates.

Recent applications of Bayesian threshold models in sheep have demonstrated their effectiveness in estimating genetic parameters for litter size while accounting for environmental effects and the categorical structure of the data (Fathallah *et al*., 2016, and Ziadi *et al*., 2024). However, the genetic improvement of reproductive performance can be further enhanced by leveraging information from genetically correlated traits such as total litter weight. Multivariate analyses, which integrate litter size with related continuous traits, can leverage these genetic correlations to improve the accuracy of breeding values estimates (Ziadi *et al*., 2024).To date, neither bivariate threshold linear models combining litter size and total litter weight, nor univariate threshold models, have been applied to the Sohagi sheep breed. Therefore, this study aims to estimate variance components using Bayesian univariate models and Bayesian threshold models for litter size and total litter weight at birth in Sohagi sheep.

MATERIAL AND METHODS

Farm location and management:

This study was conducted in accordance with the guidelines of the Sohag Institutional Animal Care and Use Committee (Sohag-IACUC), with approval number 6-12-5/2025-01. The data were gathered from a Sohagi sheep flock maintained at the experimental farm of the Faculty of Agriculture, Sohag University, spanning the year from 2003 to 2022. The flock was managed under a breeding system designed to produce three lamb crops within a two-year cycle, with mating seasons scheduled for January, May, and September. During the winter months, the animals' diet consisted of green fodder *(Trifolium alexandrinum)* supplemented with concentrated feeds including soybeans and corn.

Data and studied traits:

This study evaluated two traits: litter size (LS) and total litter weight at birth (TLW), using a data set of 1,464 ewe records from 51 sires and 325 dams.

Statistical analysis:

A common analytical framework was adopted for both traits, LS and TLW, using SAS (version 9.1, 2003). The fixed effects that were tested included type of birth (T), ewe parity (P), season of birth (S), lambing year (L), and age of the ewe at lambing (Age as a covariate term). All two-way interactions among fixed effects were included; however non-significant interactions (P>0.05) were subsequently removed. The final models were:

$$LS_{ijklm}=\mu+T_i+P_j+S_k+L_l+b(X_{ijklm} - \bar{X})+e_{ijklm} \quad (1)$$

$$TLW_{ijklm}=\mu+T_i+P_j+S_k+L_l+(S*L)_{kl}+b(X_{ijklm}- \bar{X}+e_{ijklm} \quad (2)$$

Where, Y_{ijklm}=observed litter size or total litter weight at birth trait; μ is the overall mean; T_i=Fixed effect of the *i^th^* type of birth (single, twins and triplet);P_j = Fixed effect of the j^{th} parity of ewe (1, 2,..,5);S_k =Fixed effect of the k^{th} season of birth (Winte, Summer, and Autumn);L_l= Fixed effect of the l^{th} lambing year (2003 to 2022); S*L= interaction between season of birth and lambing year; b= linear partial regression coefficient of the studied trait on the age of ewe (x); $\bar{X}$ = the average of ewe age, and e_{ijklm} is the random residual error assuming to be NID $(0,\sigma^2 e)$.

Four animal model variants were applied to analyze litter size (LS) and total litter weight at birth (TLW). A univariate linear model was applied to each trait separately, while a univariate threshold model was used to accommodate the categorical nature of LS. To estimate the genetic correlation between traits and to compare the genetic parameter estimates obtained from the univariate models, both a bivariate linear model (treating LS and TLW as continuous traits) and a bivariate threshold linear model (modeling LS as a categorical trait and TLW as a continuous trait) were implemented. The general form of the linear animal model used is as follows:

$$y = X\beta + Za + Wp + e \quad (3)$$

where y is the vector of observations or liabilities; X, Z, and W are incidence matrices relating observations to the fixed effects (β), random additive genetic effects (a), and permanent environmental effects (p), respectively. The random effects are assumed distributed as $\sim aN(0, A\sigma^2 a) \sim \mathrm{p}N(0,\mathrm{I}\sigma^2 p)$ and residual errors $\sim \mathrm{e}N(0,\mathrm{I}\sigma^2 e)$ a is the numerator relationship matrix and I is an identity matrix.

All models were fitted using GIBBSF90+(Misztal *et al*., 2024). Each Markov chain was run for a total of 100000 iterations; the first 20000 iterations were served as burn-in, and every 10th remaining draw was retained to thin the chain (lag=10). The convergence of the posterior samples was evaluated using Geweke's z-score diagnostic which tests the equality of early- and late-chain means (Geweke, 1992).

The Spearman's rank correlation coefficients were calculated to evaluate the degree of similarity between the rankings of estimated breeding values (EBVs) obtained from four animal models using Bayesian analysis. The SAS program (version 9.1, 2003) was used to compute these coefficients of rank correlation.

RESULTS AND DISCUSSION

The analysis of variance for the fixed effects affecting the studied traits is presented in Table 1. The results revealed that, for the LS trait, only parity and lambing year had statistically significant effects (P<0.01), while type of birth, season of birth, ewe age, and the interaction showed no significant effects (P>0.05).Similarly, in the TLW trait, parity, season of birth and lambing year were significant factors (P<0.05)as was the interaction between season of birth and lambing year (P<0.05).However, birth type and ewe age remained non-significant (P>0.05). Recent studies have corroborated the significant influence of parity, lambing year, and season of birth on reproductive traits in sheep. Balogun *et al*. (2021) found that parity and lambing year significantly affected litter size in Yankasa sheep.

Table 1. Analysis of variance for litter size at birth (LS) and total litter weight at birth (TLW) in Sohagi sheep

Source of variation	**LS**		**TLW**	
	Df	**MS**	**Df**	**MS**
Total	1463		1463	
Type of birth	2	0.079^{NS}	2	1.693^{NS}
Parity	4	0.672^{**}	4	5.317^{*}
Season of birth	2	0.580^{NS}	2	5.993^{*}
Lambing year	19	0.397^{**}	19	3.588^{**}
Season of birth*Lambing year			38	2.484^{*}
Age of ewe	1	0.381^{NS}	1	5.138^{NS}
Residual	1435	0.22	1397	5.79
C.V.%	35.63		33.65	

*= significant at 0.05, **= significant at 0.01, NS= non significant and C.V. = coefficient of variation.

Table 2, displays the least square means and standard errors for litter size (LS) and total litter weight at birth (TLW) in Sohagi sheep. The average LS and TLW at birth were found to be 1.25 ± 0.01 lambs and 3.74 ± 0.03 kg per ewe, respectively. Comparative studies by Doloksaribu *et al.* (2000) and Habtegiorgis *et al.* (2022) reported higher average values, with 1.52 ± 0.04 for LS in Sumatra thin-tailed sheep and 1.57 ± 0.02 for LS and 5.24±0.09 for TLW at birth in Doyogena sheep. These figures exceed the average observed in the current study. However, the current results are higher than those previously reported by Taye *et al.* (2010), who found average LS values of 1.19 in Washera sheep.

Ewes delivering triplets showed significantly higher LS and TLW, compared to those that delivered twins and singles. These results align with Gbangboche *et al.* (2006), which found that Karayaka and indigenous ewe breeds with multiple births had higher productivity than those with singlebirths. In terms of parity, both LS and TLW were lowest during the first and second parities, indicating lower reproductive efficiency in the early stages of ewe maturity. The highest LS and TLW values were observed in the fourth parity (1.38 ± 0.05 and 4.18 ± 0.14 kg, respectively).This support the findings of Mandal *et al.* (2012), who noted that improved reproductive performance of Muzaffarnagari lambs with increasing parity up to a certain threshold.

During the winter and summer months both LS and TLW were higher compared to autumn. This trend may be attributed to improved nutritional availability during these periods. These results are consistent with those of Habtegiorgis *et al.* (2022), who reported seasonal variations in reproductive traits among Doyogena sheep, noting better outcomes in cooler and moderately warm seasons. In contrast, results by Al-Dahl *et al.* (2022) indicated minimal seasonal effects on the Awassi sheep flock, emphasizing the role of management practices alongside environmental factors.

There was significant variation in litter size (LS) and total litter weight at birth (TLW) across different lambing years. The highest values were recorded in 2007, with LS and TLW averaging 1.53 ± 0.08 and 4.56 ± 0.24 kg, respectively. In contrast, the lowest LS was observed in 2010 (1.10 ± 0.07), while the lowest TLW was recorded in 2022 (3.19 ± 0.33 kg).

Year-to-year fluctuations in performance are often attributed to changes in environmental conditions, nutritional status, and management practices that influence both dam and lamb. These findings are consistent with those of Boujenane *et al.* (2013) demonstrated a significant effect of lambing year on LS in D'man ewes, attributing this variation to management and environmental factors.

The posterior means and standard deviations of the genetic parameters for LS and TLW at birth were evaluated using different models, including univariate linear model, univariate threshold model, bivariate linear model, and bivariate threshold linear model. The results are presented in Table 3. For LS, the univariate threshold model consistently produced higher estimates for additive genetic, permanent environmental, and residual variances (0.092 ± 0.037, 0.020 ± 0.016, and 0.317 ± 0.043, respectively).In contrast, the univariate linear model yielded lower estimates (0.021 ± 0.008, 0.006 ± 0.004, and 0.178 ± 0.008, respectively). When applying abivariate threshold linear model significantly reduced these estimates to 0.029 ± 0.012 for additive genetic, 0.010 ± 0.007 for permanent environmental, and 0.149 ± 0.014 for residual variance. This noticeable decrease in residual variance demonstrates the bivariate model's effectiveness in partitioning shared variance across correlated traits. It highlights the advantages of multivariate approaches which more refined estimates by incorporating additional sources of variation. These findings align with those of Ziadi et al. (2024), who reported a decrease in the residual variance for litter size from 0.21±0.008 under the bivariate linear model to 0.14±0.009 when using the bivariate threshold linear model.

Table 2. Least Square Means (LSM) and their standard error (± SE) for litter size at birth (LS) and total litter weight at birth (TLW) according to type of birth, parity, season of birth and lambing year

	N	LS	TLW
		LSM±SE	LSM±SE
Overall	1464	1.25±0.01	3.74±0.03
Type of Birth			
Single	965	1.27^{a}±0.02	3.78^{a}±0.05
Twins	469	1.29^{a}±0.02	3.81^{a}±0.07
Triple	30	1.33^{a}±0.08	4.12^{a}±0.24
Parity			
1	578	1.22^{c}±0.03	3.73^{c}±0.10
2	371	1.27^{bc}±0.03	3.82^{bc}±0.10
3	231	1.33^{ab}±0.04	3.99^{ab}±0.12
4	134	1.38^{a}±0.05	4.18^{a}±0.14
5	150	1.28^{ab}±0.05	3.82^{b}±0.15
Season of birth			
Winter	468	1.31^{ab}±0.04	4.02^{ab}±0.10
Summer	500	1.32^{a}±0.03	3.95^{a}±0.10
Autumn	496	1.26^{b}±0.04	3.75^{b}±0.11
Lambing year			
2003	71	1.38^{bcd}±0.06	4.12^{bc}±0.21
2004	88	1.27^{bcd}±0.06	3.72^{c}±0.16
2005	85	1.35^{bc}±0.06	4.05^{bc}±0.16
2006	80	1.37^{b}±0.06	4.19^{b}±0.17
2007	38	1.53^{a}±0.08	4.56^{a}±0.24
2008	84	1.32^{bcd}±0.06	4.22^{b}±0.17
2009	81	1.22^{bcd}±0.06	3.62^{c}±0.16
2010	49	1.10^{d}±0.07	3.59^{bc}±0.26
2011	100	1.28^{bcd}±0.06	3.80^{bc}±0.16
2012	48	1.28^{bcd}±0.07	4.04^{bc}±0.21
2013	75	1.33^{bcd}±0.06	4.28^{b}±0.18
2014	84	1.25^{bcd}±0.06	3.95^{bc}±0.17
2015	55	1.26^{bcd}±0.07	3.62^{c}±0.19
2016	73	1.33^{bcd}±0.06	3.90^{bc}±0.18
2017	114	1.34^{bc}±0.05	3.86^{bc}±0.14
2018	105	1.36^{b}±0.05	4.04^{bc}±0.15
2019	55	1.26^{bcd}±0.07	3.78^{bc}±0.19
2020	52	1.28^{bcd}±0.07	3.87^{bc}±0.19
2021	69	1.25^{bcd}±0.06	3.78^{c}±0.18
2022	58	1.16^{cd}±0.07	3.19^{d}±0.33

Different letters a, b and c in the same column are significantly different ($P<0.05$).

The bivariate linear model yielded slightly higher estimates of additive (0.024 ± 0.008) and permanent environmental (0.007 ± 0.004) variances compared to the univariate linear model, while the residual variance remained virtually unchanged (0.177 ± 0.008). Although these differences were minimal, the bivariate linear model provided more accurate estimates for genetic and environmental variances due to its better captures of the covariance structure between traits. This approach is particularly valuable when the traits are biologically correlated, as it improves estimation accuracy and genetic evaluation. These findings are in agreement with those of Casellas *et al.* (2007), Roshamfekr *et al.* (2015), and Yavarifard *et al.* (2015), who reported that the bivariate linear model often provides a more comprehensive understanding of reproductive traits compared to the univariate approach. These studies, which analyzed genetic parameters for reproductive traits in sheep breeds such as Arabi, Ripollesa, and Mehraban sheep, emphasize the importance of considering both genetic and phenotypic correlations between reproductive characteristics. Overall, the results suggest that bivariate models are effective in capturing the complex interrelationships among these traits, leading to more insightful conclusions than when each trait is analyzed in isolation.

The bivariate threshold linear model yielded slightly higher additive genetic and permanent environmental variance estimates for LS (0.029±0.012 and 0.010±0.007, respectively).In contrast, the bivariate linear model yielded lower estimates of 0.024±0.008 and 0.007±0.004, respectively for the same variances**.** Lower estimate for residual variance was obtained using bivariate threshold linear model with value of 0.149±0.014. These findings suggest that the threshold linear model may be better suited for traits like litter size, which are often expressed as discrete counts and may not follow a normal distribution. Several studies have emphasized the advantages of using threshold models for such traits. For example, de Villemereuil *et al.* (2016) highlighted the value of threshold-based methods for traits with non-linear or categorical distributions, while Mrode (2014) emphasized their importance in improving accuracy when modeling traits deviating from normality.

Table 3. Posterior means and standard deviations of genetic parameters for litter size at birth (LS) and total litter weight at birth (TLW) using univariate linear model, univariate threshold model, a bivariate linear model and a bivariate threshold linear model

Parameter	LS^{ul}	LS^{ut}	TLW^{ul}	LS^{bl}	LS^{btl}	TLW^{bl}	TLW^{btl}
σ^2a	0.021±0.008	0.092±0.037	0.066±0.052	0.024±0.008	0.029±0.012	0.099±0.048	0.120±0.052
σ^2pe	0.006±0.004	0.020±0.016	0.096±0.044	0.007±0.004	0.010±0.007	0.102±0.039	0.093±0.039
σ^2e	0.178±0.008	0.317±0.043	1.476±0.063	0.177±0.008	0.149±0.014	1.461±0.062	1.457±0.061
σ^2p	0.205±0.008	0.429±0.056	1.639±0.065	0.208±0.009	0.187±0.016	1.661±0.066	1.670±0.068
h^2	0.10±0.04	0.21±0.07	0.04±0.03	0.11±0.04	0.15±0.06	0.06±0.03	0.07±0.03
R	0.13±0.04	0.26±0.07	0.10±0.03	0.15±0.03	0.21±0.05	0.12±0.03	0.13±0.03

ul = univariate linear model, ut = univariate threshold model, bl = bivariate linear model, btl = bivariate threshold linear model, h^2 = heritability estimate and r = repeatability estimate.

Regarding the TLW trait, using a univariate linear model, the estimates of additive genetic variance, permanent environmental variance, and residual variance were 0.066±0.052, 0.096±0.044, and 1.476±0.063, respectively. However, when TLW was analyzed jointly with a categorical trait, treatingit as continuous using a bivariate linear model, the corresponding estimates were0.099±0.048, 0.102±0.039, and 1.461±0.062, respectively. Further improvements were achieved when we modeled the categorical trait appropriately using a bivariate threshold linear model, yielding estimates of 0.120±0.052 for additive genetic variance, 0.093±0.039 for permanent environmental variance, and 1.457±0.061 for residual variance. These results indicate that modeling the categorical trait using the threshold linear approach enhances the estimation of genetic parameters for TLW. In particular, the increase in additive genetic variance suggests a more effective partitioning of the genetic contribution, while the decrease in residual variance implies a more accurate fit of the model to the data.

Safari *et al.* (2005) reported that threshold models are more suited for traits with discrete distributions and can benefit from multivariate frameworks by borrowing strength across different traits. Similarly, Habtegiorgis *et al.* (2022) found that incorporating multiple traits into a multivariate model improved the accuracy of genetic evaluations for reproductive traits in Doyogena sheep. These findings underscore the importance of using multivariate models in genetic evaluations, particularly for traits with low heritability estimates like litter size and total litter weight at birth. By accounting for the genetic correlations among traits, multivariate approaches can provide more accurate and reliable estimates, facilitating more effective selection strategies in sheep breeding programs.

Table 3 showed that heritability and repeatability estimates for litter size and total litter weight at birth in Sohagi sheep varied significantly across the four statistical models used. For litter size, heritability estimates ranged from 0.10 ± 0.04 (univariate linear model) to 0.21 ± 0.07 (univariate threshold model). Repeatability estimates followed a similar trend, ranging from 0.13 ± 0.04 to 0.26 ± 0.07, respectively. The higher estimates for both heritability and repeatability obtained from the univariate threshold model for litter size are expected, as threshold models typically provide larger estimates on the underlying scale for categorical traits by accounting for their non-normal distribution (Ziadi *et al.*, 2024). Also, Mohammadi (2012) found that univariate threshold models are superior to univariate linear models for genetic parameters estimation.

Conversely, the bivariate threshold linear model and the bivariate linear model generally produced lower heritability and repeatability estimates for LS compared to the univariate threshold model, however, these bivariate models often offered improved precision indicated by smaller standard errors. For instance, the heritability estimate of litter size was 0.11 ± 0.04 (bivariate linear model) and 0.15 ± 0.06 (bivariate threshold linear model). The corresponding repeatability estimates were 0.15 ± 0.03 and 0.21 ± 0.05, respectively. These results are consistent with the results of Osinowo *et al.* (1993), who used a bivariate linear model to analyze LSin Yankasa sheep**,** reporting h^2 estimates of 0.11.This trend of lower estimates accompanied by higher precision from bivariate threshold linear models aligns with findings by Ziadi *et al.* (2024), who, studied Tunisian Barbarine sheep, noted that multivariate models analyzing litter size along with growth traits like birth weight, 90day weight, and average daily gain, effectively partition genetic variance between correlated traits, leading to more reliable estimates.

Mohammadi *et al.* (2012) and Mekkawy *et al.* (2010) concluded that threshold models are the preferred method for estimating genetic parameters and genetic evaluation, especially when combined with linear modeling approaches. Therefore, considering the genetic interplay between litter size and total litter weight at birth, the estimates derived from bivariate threshold models are considered more appropriate for genetic evaluation and breeding program design.

In this study, heritability estimates of LS obtained from the bivariate threshold linear model (0.15) and the univariate linear model (0.10) were consistent with values of 0.15 and 0.09**,** respectively, reported by Ziadi *et al.* (2024) for Barbarine sheep**.**

The heritability estimates for TLW were relatively low, ranging from 0.04 ± 0.031 using the univariate linear model to 0.07 ± 0.030 with the bivariate threshold linear model. Similarly, the repeatability estimates followed an increasing trend, rising from 0.10 ± 0.028 to 0.13 ± 0.029, respectively. This upward trend in both heritability and repeatability estimates for TLW when using the bivariate threshold linear model suggests that incorporating a biologically related trait, such as litter size, allows for better partitioning of the genetic and permanent environmental variances shared between traits. By accounting for the covariance structure across traits, the bivariate model reduces residual variance and improves the precision of genetic parameter estimates. Comparable findings were reported by Ziadi *et al.* (2024), who emphasized the effectiveness of bivariate models in enhancing the estimation of genetic parameters for weight-related reproductive traits in sheep.

The genetic and phenotypic correlations between LS and TLW were estimated using two methods: the bivariate threshold linear model and the bivariate linear model (Table 4). The bivariate threshold linear model showed a high genetic correlation of 0.98 ± 0.006 and a phenotypic correlation of 0.94 ± 0.007. Similarly, the bivariate linear model indicated a strong positive genetic correlation of 0.99 ± 0.021 and a phenotypic correlation of 0.87 ± 0.006. The consistently high and positive genetic correlations in both models suggest a significant level of shared genetic control affecting both LS and TLW. This means that genes increasing litter size tend to also increase total litter weight, and vice versa. The slightly lower genetic correlation estimate from threshold model may reflect its more refined approach to modeling the discrete nature of litter size.

The phenotypic correlations are notably high and positive, indicating a strong observable relationship between the two traits. This means that larger litters tend to be heavier. The higher phenotypic correlation observed in the threshold model compared to the linear model may be attributed to the different way each model addresses the underlying distribution of litter size. Overall, these strong genetic and phenotypic correlations highlight the interconnectedness of these reproductive traits and suggesting that selection for one trait is likely to result in a correlated change in the other. These results are consistent with those of Ziadi *et al.* (2018) and Boujenane *et al.* (2021), who reported similarly high genetic and phenotypic correlations between litter size and total litter weight at birth in different sheep breeds.

Table 4. Estimated Genetic (above diagonal) and phenotypic (below diagonal) correlations and their posterior standard deviation between litter size at birth (LS) and total litter weight at birth (TLW) using bivariate linear model and bivariate threshold linear model

Type of Model		LS	TLW
Bivariate linear model	**LS**		0.99±0.021
	TLW	0.87±0.006	
Bivariate threshold linear model	**LS**		0.98±0.006
	TLW	0.94±0.007	

The current study investigated the consistency of estimated breeding values (EBVs) for litter size (LS) and total litter weight at birth (TLW) using Spearman rank correlations across different genetic evaluation models (Table 5). The very high correlation for LS between the univariate linear model and univariate threshold model (0.99), along with the strong correlations observed in bivariate models (approximately 0.93), indicates that the ranking of animals for LS remains highly consistent. This consistency holds true whether the trait is analyzed individually or jointly, and whether it is modeled using linear or threshold approaches. These findings reflect the robustness of the EBVs for LS across different statistical frameworks.

Lower rank correlations (0.44 and 0.59) were observed for TLW between the univariate and bivariate models. This suggests that the inclusion of LS in the multivariate analyses influenced the ranking of animals for TLW. This implies a genetic association between these two traits including that information from LS contributes to a more accurate estimation of EBVs for TLW.

Furthermore, the higher correlation (0.86) between the two bivariate models (linear model vs. Threshold linear model) demonstrates that while the modeling approach for LS (continuous vs. categorical) has some impact, the main improvement in consistency comes from incorporating LS into the genetic evaluation. This underscores the advantage of multivariate models, particularly when traits are genetically correlated, as they improve the stability and accuracy of genetic evaluations. These results align with findings with those Matos *et al.* (1997) and Ziadi (2024), who reported a high correlation between breeding value estimates obtained from linear and threshold models.

Table 5. Spearman rank correlation coefficients for ewes' breeding values derived from univariate linear model, univariate threshold model, bivariate linear model and bivariate threshold linear model for litter size at birth (LS) and total litter weight at birth in Sohagi sheep

Trait	Univariate linear model + Univariate threshold model	Univariate linear model + Bivariate linear model	Univariate linear model + Bivariate threshold linear model	Univariate threshold model + Bivariate linear model	Univariate threshold model + Bivariate threshold linear model	bivariate linear model + Bivariate threshold linear model
LS	0.99	0.93	0.93	0.93	0.93	0.85
TLW	-	0.44	0.59	-	-	0.86

CONCLUSION

This study compared four statistical models for analyzing two traits: litter size (discrete) and total litter weight at birth (continuous). The models assessed were univariate linear, univariate threshold, bivariate linear, and bivariate threshold models. The threshold model may be the most appropriate for analyzing LS. Among the models tested, the bivariate threshold linear model was found to be the most accurate and suitable for the estimation of genetic parameters. Both genetic and phenotypic correlations between litter size and total litter weight at birth were found to be very high, reflecting a strong association between these traits.

A Spearman rank correlation analysis of breeding values derived from all four models showed consistently high level of concordance, particularly for litter size. Notably, the bivariate threshold linear model accounts for both the correlation between the two traits and the categorical nature of litter size, which enhances its precision and effectiveness. This makes the threshold linear model especially valuable for selection programs, as it more accurately captures the genetic architecture behind mixed continuous and discrete traits. As a result it improves the efficiency of genetic improvement for litter traits in sheep. In practice, breeding programs could apply this model (bivariate threshold linear) by ranking and selecting ewes based on the estimated breeding values for both litter size and total litter weight at birth. Furthermore, a selection index incorporating both LS and TLW traits is proposed to enhance genetic evaluation strategies in Sohagi sheep.

REFERENCES

Al-Dahl, D.M. E., S.L. Shihab and H.M.S. Hadi, 2022. Seasonal Influence on Productive and Growth Performance in Awassi Sheep. Asian Journal of Dairy and Food Research, 41*(2):192-195.*https://doi.org/10.18805/ajdfr.DRF-249ARCC Journals.

Balogun, R.O., M.E. Olayemi and O.A. Osinowo, 2021. Environmental Factors Affecting Birth Weight And Litter Size In Yankasa Sheep. Nigerian Journal of Animal Production, 20:14-19. https://doi.org/10.51791/njap.v20i.2096

Boujenane, I., A. Chikhi, M. Sylla and M. Ibnelbachyr, 2013. Estimation of genetic parameters and genetic gains for reproductive traits and body weight of D'man ewes.Small Rumin. Res. 113: 40-46.

Boujenane, I., M. Ibnelbachyr, and A. Chikhi, 2021. *Genetic correlations between ewe reproductive and lamb weight traits in D'man sheep*. Journal of Livestock Science and Technology, 9(2):4-49.

Casellas, J., G. Caja, A. Ferret and J. Piedrafita, 2007. Analysis of litter size and days to lambing in the Ripollesa ewe. I. Comparison of models with linear and threshold approaches. Livestock Science, 106(1-2):71-79.

de Villemereuil, P., H. Schielzeth, S. Nakagawa and M. Morrissey, 2016. General methods for evolutionary quantitative genetic inference from generalised mixed models. Genetics, 204(3):1281-1294.https://doi.org/10.1534/genetics.115.186536

Doloksaribu, M., R.M. Gatenby, Subandriyo and G.E. Bradford, 2000. Comparison of Sumatra sheep and hair sheep crossbreds. III. Reproductive performance of F2 ewes and weights of lambs. Small Rumin. Res. 38:115-121.

Elnahas, A., and R. Elsaid, 2022. Effect of Inbreeding on Birth, Weaning and Yearling Weights in Sohagi Sheep. Journal of Animal and Poultry Production, 13(12):179-183.

Fathallah, S., I. Bodin and I. David, 2016. *Genetic heteroscedastic models for ordinal traits: application to sheep litter size*. Genetics Selection Evolution, 48, 30. https://doi.org/10.1186/s12711-016-0202-4.

Gbangboche, A.B., M. Adamou-Ndiaye, A.K.I. Youssao, F. Farnir, J. Detilleux, F.A. Abiola and P.L. Leroy, 2006. Non-genetic factors affecting the reproduction performance, lamb growth and productivity indices of Djallonké sheep. *Small Ruminant Research*, 64(1–2):133–142.

Geweke, J., 1992. Evaluating the Accuracy of Sampling-Based Approaches to the Calculation of Posterior Moments. In: J. M. Bernardo, J. O. Berger, A. P. Dawid & A. F. M. Smith (eds.), Bayesian Statistics 4 (pp. 169–193). Oxford University Press.

Habtegiorgis, K., A. Haile, T. Getachew, A. Jimma and D. Gemiyo, 2022. Litter size, litter weight and lamb survivability of Doyogena sheep under community-based breeding programs in Ethiopia. *Heliyon*, 8:1-7.

Mandal, A., G. Dass and P.K. Rout, 2012. Genetic analysis of growth and feed conversion efficiency of Muzaffarnagari lambs under intensive feeding system. International Journal of Livestock Production, 3(4):47-52.

Matos, C.A.P., D. Thomas, D. Gianola, M. Perez-Enciso and I. Young, 1997. Genetic Analysis of Discrete Reproductive Traits in Sheep Using Linear and Nonlinear Models: II. Goodness of Fit and Predictive Ability. J. Anim. Sci., 75:88–94.

Mekkawy, W., R. Roehe, R.M. Lewis, M.H. Davies, L. Bünger, G. Simm and W. Haresign, 2010. Comparison of repeatability and multiple trait threshold models for litter size in sheep using observed and simulated data in Bayesian analyses. J Anim Breed Genet., 127(4):261-71. https://DOI: 10.1111/j.1439-0388.2010.00852.x

Misztal, I., D. Lourenco and S. Tsuruta, 2024. GIBBSF90+: Software for Bayesian Inference in Linear and Threshold Animal-Breeding Models Using Gibbs Sampling. University of Georgia, Athens, GA, USA.

Mohammadi, H., M.M. Shahrebabak1, H.M. Sharebabak1 and M. Vatankhah, 2012. Estimation of genetic parameters of reproductive traits in Zandi sheep using linear and threshold models. Czech J. Anim. Sci., 57,2012(7):382–388.

Moreno, C., 1993. Estudio de los Componentes Genéticos del Modelo Umbral. Ph.D. Thesis, Universidad de Zaragoza, Zaragoza, Spain.

Mrode, R.A., 2014. Linear models for the prediction of animal breeding values (3rd ed.). Boston, MA:CABI.

Ødegard, J., T. Meuwissen, B. Heringstad and P. Madsen, 2010. A simple algorithm to estimate genetic variance in an animal threshold model using Bayesian inference. Genet. Sel. Evol. 42(29):1-7. https://doi.org/10.1186/1297-9686-42-29.

Osinowo, O.A., B.Y. Abubakar and A.R. Trimnell, 1993. Genetic and phenotypic relationships between gestation length, litter size and litter birth weight in Yankasa sheep. Animal Reproduction Science, 34:111-118.

Ptáček, M., J. Ducháček, L. Stádník, J. Hakl and M. Fantová, 2017. Analysis of multivariate relations among birth weight, survivability traits, growth performance, and some important factors in Suffolk lambs, Arch. Anim. Breed., 60:43-50.https://doi.org/10.5194/aab-60-43-2017.

Roshanfekr, H., P. Berg, K. Mohammadi and Mirza E. Mohamadi, 2015. Genetic parameters and genetic gains for reproductive traits of Arabi sheep. Biotechnology in Animal Husbandry, 31(1):23-36.

Safari, E., N.M. Fogarty and A.R. Gilmour, 2005. A review of genetic parameter estimates for wool, growth, meat and reproduction traits in sheep. *Livestock Production Science*, 92(3):271–289.

dos Santos, J.D.C., E.P. Saraiva, E.C. Pimenta Filho, G.C.X. Neta, L.K.C. Morais, H.S. Teti and S.S. Fidelis, 2023. Neonatal mortality of lambs in production systems in a semi-arid environment: main risk factors. The Journal of Agricultural Science. 161(3):438-449. https://doi:10.1017/S0021859623000291.

SAS., 2003. SAS User's Guide: Version 9.1. SAS Institute Inc., Cary, NC.

Taye, M., A. Abebe, S. Lemma, S. Gizaw, A. Mekoya and M. Tibbo, 2010. Reproductive performances and survival of Washera sheep under traditional management systems at yilmanadensa and quarit districts of the Amhara national regional state, Ethiopia.J. Animal Sci. Vet. Adv. 10(9):1158-1165.

Yavarifard, R., N. Ghavi Hossein-Zadeh and A.A. Shadparvar, 2015. Estimation of genetic parameters for reproductive traits in Mehraban sheep. Czech Journal of Animal Science, 60(6):281-288.

Ziadi, C., S. Bedhiaf-Romdhani and A. Molina, 2024. Estimation of Genetic Parameters for Litter Size and Growth Traits in a Prolific Line of Tunisian Barbarine Sheep. Ruminants, 4(2):256–266. https://doi.org/10.3390/ruminants4020018.

Ziadi, C., and S. Bedhiaf-Romdhani, 2018. Genetic parameters of reproductive traits in a prolific "W" line. In Proceedings of the Barbarine Sheep. 69th Annual Meeting of the European Federation of Animal Science, Dubrovnik, Croatia, 27–31.

تقدير مكونات التباين باستخدام الطرق البايزية لحجم البطن والوزن الكلي للمواليد عند الولادة في الأغنام السوهاجي

أحمد النحاس[1]، رضا السعيد[2]

١- قسم الإنتاج الحيوانى، كلية الزراعة، جامعة سوهاج
٢- قسم التنمية المتواصلة، معهد الدراسات والبحوث البيئية، جامعة مدينة السادات، المنوفية، مصر

تهدف الدراسة إلى تقدير مكونات التباين لصفة حجم البطن والوزن الكلي للمواليد عند الولادة في الأغنام السوهاجي باستخدام الطرق البايزية. جُمعت البيانات من عام ٢٠٠٣ إلى عام ٢٠٢٢ في المزرعة التجريبية لجامعة سوهاج، وشملت سجلات ١,٤٦٤ نعجة، وهي نتاج ٥١ كبش و٣٢٥ أم، لتقييم تأثير العوامل البيئية المختلفة على هذه الصفات. بلغ متوسط حجم البطن ١,٢٥ ± ٠,٠١ حمل، بينما كان متوسط الوزن الكلي للمواليد عند الولادة ٣,٧٤ ± ٠,٠٣ كجم لكل نعجة. لتقدير المتوسطات البعدية والإنحرافات المعيارية للمعالم الوراثية لكل من حجم البطن والوزن الكلي للمواليد عند الولادة، أُستخدم النموذج الخطي أحادي المتغير، والنموذج العَتَبِي أحادي المتغير، والنموذج الخطي ثنائي المتغير، والنموذج الخطي العَتَبِي ثنائي المتغير، وذلك باستخدام برنامج +GIBBSF90. بالنسبة لحجم البطن، تراوحت تقديرات المكافئ الوراثي من ٠,١٠ (النموذج الخطي أحادي المتغير) إلى ٠,٢١ (النموذج العَتَبِي أحادي المتغير)، بينما تراوحت تقديرات المعامل التكرارى من ٠,١٣ إلى ٠,٢٦، متبعةً نفس الاتجاه. أما بالنسبة للوزن الكلي للمواليد عند الولادة، فقد تباينت تقديرات المكافىءالوراثى من ٠,٠٤ (النموذج الخطي أحادي المتغير) إلى ٠,٠٧ (النموذج الخطي العَتَبِي ثنائي المتغير)، مع قيم للمعامل التكرارى تراوحت بين ٠,١٠ و٠,١٣، متبعةً هي الأخرى إتجاهًا مشابهًا. أظهر النموذج الخطي العَتَبِي ثنائي المتغير إرتباطًا وراثيًا مرتفعًا بلغ ٠,٩٨ وارتباطًا مظهريًا بلغ ٠,٩٤. في حين أشار النموذج الخطي ثنائي المتغير أيضًا إلى إرتباطات إيجابية قوية، حيث بلغت قيم الإرتباط الوراثي والمظهري ٠,٩٩ و٠,٨٧ على التوالي. بالنسبة لحجم البطن، تُظهر إرتباطات سبيرمان للرتب بين القيم التربوية المقدرة من الأربعة نماذج ثباتًا في ترتيب الحيوانات عبر النماذج المختلفة، بغض النظر عن النموذج الإحصائي المستخدم. بناءً على هذه النتائج، يمكن إقتراح دليل إنتخاب يضم صفتي حجم البطن والوزن الكلي للمواليد عند الولادة لتحسين إستراتيجيات التقييم الوراثي في الأغنام السوهاجي.