Scientific Papers. Series D. Animal Science. Vol. LXVIII, No. 1, 2025
ISSN 2285-5750; ISSN CD-ROM 2285-5769; ISSN Online 2393-2260; ISSN-L 2285-5750

ESTIMATION THE GENETIC PARAMETERS FOR BIRTH WEIGHT AND WEANING WEIGHT IN LIMOUSINE BREED

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Abstract

The objective of this study was to estimate the breeding values and genetic parameters for birth weight and weaning weight in Limousine cattle breed with multivariate maternal animal model for selection. Data consisted of records of 1207 cattle from Romanian Breeding Association for Beef cattle. The direct breeding values for birth weight were between -7.890 and 7.049 and for weaning weight -55.381 and 60.818 kg. The maternal breeding values for birth weight ranged between -1.701 and 1.810 and for weaning weight -22.453 and 20.747. The direct and maternal heritability for birth weight were 0.105, respectively 0.035, for weaning weight 0.662, respectively 0.246. The total heritability for birth weight was 0.92 and 0.655 for weaning weight.

***Key words**: birth and weaning weight, breeding values, genetic parameters, multivariate maternal animal model.*

INTRODUCTION

Beef farming has an important role in agriculture in many countries. The factors which influence the meat production are genetic factors: breed, individual, physiological factors as age, sex and environmental factors. In beef cattle the phenotype of calves is influenced by the ability of dam to assure favourable nutritional environmental for progeny (Grosu & Oltenacu, 2005). The birth weight and weaning weight are the traits influenced by maternal genetic effects. The maternal animal model is a good model for genetic evaluation of growth traits because it presents both the genetic and maternal effects. The animals are selected in function of the direct breeding values and maternal breeding values. In the breeding program of Limousine breed are included the meat production traits and reproduction traits. The multi-trait animal model is the optimal model for genetic evaluation of cows because it uses the performance of cows and its relatives, the genotypic and environmental correlation between the traits and the relative economic values of the traits including in breeding objective (Grosu et al., 2019). The use of this model leads to an increase in the accuracy of the selection. The simultaneous genetic evaluation for multiple traits can be noticed worldwide, because this makes it possible the use the information supplied by the genetic correlations between the traits. Determines a higher accuracy of the estimated breeding values for the traits with low heritability (Grosu et al., 2013). The multiple trait model was described by Henderson & Quass (1976), Pollak & Quass (1981), Polak et al. (1984). Multi-trait animal model can be used for calving and reproduction, for disease traits, for production traits and conformation traits in evaluation of cattle, in beef breeds for the meat and reproduction performance, calf survival and growth traits. Weik et al. (2022) reported that in the breeding programs can incorporate both maternal and finishing traits as selection criteria. The objective of this study was to estimate the breeding values and genetic parameters for birth weight and weaning weight in Limousine cattle breed with multivariate maternal animal model for selection.

MATERIALS AND METHODS

The data used in this study provide from Romanian Breeding Association for Beef cattle. For Limousine breed, the pedigree contents 2562 animals: 1207 cattle with records, 149 sire and 1206 dams. The cattle with records from Limousine were born in 2022. The values for calves' birth weight and weaning weight were checking with Grubs test if the values were in acceptable limits.

$$\hat{v} = \frac{X_{MIN,MAX}-\bar{X}}{\sigma}, \text{ where:}$$

$\hat{v} = the\ tested\ value$;
X= the value tested;
σ = standard deviation;
$\bar{X}$ = the mean.

The fixed part of the model included the sex of calves with two levels, male and female. The random effects were the direct genetic effects, the maternal genetic effects and the permanent environmental effects. For estimate the genetic parameters was used the restricted maximum likelihood method with a multivariate maternal animal model. Statistical analysis was performed using R 3.5.1. statistical software (https://www.r-project.org/).

The multivariate maternal model was (Mrode & Thompson, 2005):

$$y = Xb+Zu+Wm+Spe+e$$

y = the vector of observations,

$$y = \begin{bmatrix} y1 \\ y2 \end{bmatrix}$$

$$X = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix}, \hat{b}=\begin{bmatrix} \hat{b}_1 \\ \hat{b}_2 \end{bmatrix}, Z = \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix},$$

$$\hat{u} = \begin{bmatrix} \hat{u}_1 \\ \hat{u}_2 \end{bmatrix} \quad W = \begin{bmatrix} W1 & 0 \\ 0 & W2 \end{bmatrix}$$

$$S = \begin{bmatrix} S1 & 0 \\ 0 & S2 \end{bmatrix} \; p = \begin{bmatrix} pe1 \\ pe2 \end{bmatrix} e = \begin{bmatrix} e1 \\ e2 \end{bmatrix}$$

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix}\begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix}\begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix}\begin{bmatrix} m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} S_1 & 0 \\ 0 & S_2 \end{bmatrix}\begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

y1 = vector of observations for the trait 1;
y2 = vector of observation for the trait 2;
b = the vector of the fixed effect represented by sex;
b1 = the vector of observation of the fixed effect represented by sex for trait 1;
b2 = the vector of observation of the fixed effect represented by sex for trait 2;
u = the vector of the random animal effects;
u_1= the vector of the random animal effects for trait 1; u_2 =the vector of the random animal effects for trait 1;
m= the vector of the random maternal genetic effects;
m_1= the vector of the random maternal genetic effects for trait 1; m_2= the vector of the random maternal genetic effects for trait 2;
p_e = the vector of the permanent environmental effects;
p_{e1}= the vector of the permanent environmental effects for trait 1; p_{e2}= the vector of the permanent environmental effects for trait 2;
e = the vector of the random residual effects;
e_1= the vector of the random residual effects for trait 1; e_2= the vector of the random residual effects for trait 2;
X, Z, W and S are the incidence matrices referring to animal performance, to the fixed effects, to the direct effects, the maternal effects and to the permanent environmental effects.

$$var\begin{bmatrix} u_1 \\ u_2 \\ m_1 \\ m_2 \\ pe_1 \\ pe_2 \\ e_1 \\ e_2 \end{bmatrix}\begin{bmatrix} g_{11}A & g_{12}A & g_{13}A & g_{14}A & 0 & 0 & 0 & 0 \\ g_{21}A & g_{22}A & g_{23}A & g_{24}A & 0 & 0 & 0 & 0 \\ g_{31}A & g_{32}A & g_{33}A & g_{34}A & 0 & 0 & 0 & 0 \\ g_{41}A & g_{42}A & g_{43}A & g_{44}A & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & q_{11} & q_{12} & 0 & 0 \\ 0 & 0 & 0 & 0 & q_{21} & q_{22} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & r_{11} & r_{12} \\ 0 & 0 & 0 & 0 & 0 & 0 & r_{21} & r_{22} \end{bmatrix}$$

A = the kinship matrix between animals;
I = the identity matrix;
σ_a^2= the additive genetic variance for the direct effects;
σ_m^2 = the additive genetic variance for the maternal effects;
σ_{am} = the additive genetic covariance between the direct and maternal effects;
σ_{pe}^2 = the variance due the permanent environmental effects;
σ_e^2 = the variance of the residual error.

- the direct heritability $h_{a=}^2\sigma_a^2/\sigma_p^2$

where σ_p^2 is the phenotypic variance

- the maternal heritability = $h_{m=}^2\sigma_m^2/\sigma_p^2$
- the covariance between direct and maternal effects as proportion of the phenotypic variance ($\sigma_{am}/\ \sigma_p^2$)
- the total heritability (Wilham et al., 1972):

$$h_T^2 = \frac{\sigma_a^2 + 0.5\sigma_m^2 + 1.5\sigma_{am}}{\sigma_p^2}$$

h_T^2 is the total heritability, and σ_p^2 is the phenotypic variance

The standard error of heritability was:

$$s.e.(\boldsymbol{h^2} = \sqrt{\left[\left(\frac{\partial h^2}{\partial \sigma_g^2}\right)^2 (se_g)^2 + \left(\frac{\partial h^2}{\partial \sigma_e^2}\right)^2 (se_e)^2 + 2\left(\frac{\partial h^2}{\partial \sigma_g^2}\right)^2 \left(\frac{\partial h^2}{\partial \sigma_e^2}\right)^2 \rho_{g,e} se_g se_e\right]}$$

where:

$$\frac{\partial h^2}{\partial \sigma_g^2} = \frac{\sigma_e^2}{(\sigma_g^2+\sigma_e^2)^2}$$

$$\frac{\partial h^2}{\partial \sigma_e^2} = \frac{-\sigma_g^2}{(\sigma_g^2+\sigma_e^2)^2}$$

(Hoj Edwards, 2017).

- the ratio of the maternal permanent environment to phenotypic variance (c^2);
- r_{am} the genetic correlation between the direct and maternal effects:

$$r_{am} = \frac{\sigma_{am}}{\sqrt{\sigma_a^2 \cdot \sigma_m^2}}$$

$$G_1 = \begin{bmatrix} g_{11} & g_{12} \\ g_{21} & g_{22} \end{bmatrix}$$

$$G_2 = \begin{bmatrix} g_{13} & g_{14} \\ g_{23} & g_{24} \end{bmatrix}$$

$$G_3 = \begin{bmatrix} g_{33} & g_{34} \\ g_{43} & g_{44} \end{bmatrix}$$

G = the matrix for direct and maternal effects

$$k1 = G_1 * A^{-1}$$

$$k2 = G_2 * A^{-1}$$

$$k3 = G_3 * A^{-1}$$

g_{11}, g_{22} = the additive genetic variance for the direct effects for traits 1, 2;

g_{13}, g_{14}= the additive genetic covariance between the direct and maternal effects;

g_{33}, g_{44}= the maternal genetic variance:

$$\mathrm{Q} = \begin{bmatrix} q_{11} & q_{12} \\ q_{21} & q_{22} \end{bmatrix} \; \mathrm{R} = \begin{bmatrix} r_{11} & r_{12} \\ r_{21} & r_{22} \end{bmatrix}$$

Q = matrix for permanent environmental effects ;

q_{11}, q_{22} = the variance for permanent environmental effects for traits 1, respectively 2;

q_{12}, q_{21} = the covariance for permanent environmental effects;

R = the matrix for residual effects;

r_{11}, r_{22}=the variance for residual effects

r_{12}, r_{21}=the covariance for residual effects.

RESULTS AND DISCUSSIONS

The growth traits are important economic traits in Limousine breed. In the Table 1 were presented the statistics for birth weight and weaning weight in Limousine breed.

The means for birth weight and weaning weight obtained in our study were influenced by the sex of animal. The weight at birth and weaning were greater for males than the females. In our study the number of females was greater than the number of males. The weight can be influenced by the different environmental conditions in the farms.

The coefficient of variability was smaller for birth weight showing the population present homogeneity for this trait, for weaning weight the coefficient of variability was higher showing the heterogeneity for this trait. Putra et al. (2020) reported the mean for Limousine males for birth weight was 38 kg and for weaning weight was 155.17 kg. The vales from our study for birth weight were higher than the values reported by Pilarczyk & Wojcik (2007) for females 31.2 and for males 33.5 kg but for the weight at 210 days the means were lower in our study than 237.9 for heifers and 256.2 kg for bulls. Jakubec et al. (2003) reported a mean for birth weight 29.19 kg and for the weight at 210 days of 216 kg in Limousine breed from Czech Republic, the values from our study were higher. Cundiff et al. (1986) reported the mean for birth weight 38.9 kg and for weight at 200 days 198 kg in Limousine breed. Rezende et al. (2022) reported a mean of 247.73 kg the weight at 210 days.

Table 1. The descriptive statistics for birth weight and weaning weight

Specification	Birth weight	Weaning weight
Mean±Standard error (kg)	38.111±0.130	222.502±1.037
Standard deviation	4.55	36.059
Coefficient of variability)%)	11.93	16.206
Number of cattle (head)	1207	1207
Mean±Standard error for males	39.463±0.288	231.202±2.179
Number of males (head)	302	302
Standard deviation	5.017	37.879
Coefficient of variability (%)	12.713	16.383
Mean±Standard error (kg) for females	37.66±0.144	219.6±1.604
Standard deviation	4.335	48.280
Coefficient of variability (%)	11.511	21.985
Number of females (head)	905	905

In the Table 2 were presented the means for birth weight and weaning weight for males and females obtained from BLUP solutions. The means from BLUP were realized a reciprocal correction of presented effects in model. The standard errors associated with the results were computed from the square root of the diagonal of the generalized inverse (Mrode & Thompson, 2005). The standard errors of means were lower from means estimated with BLUP methodology than the standard errors of arithmetic means. By Student test observed that were very significant difference between means for males and females for birth weight t calc>$t_{\infty;0.001}$, 5.22>3.29 and for weaning weight t calc>t∞;0.001, 3.83>3.290.

Table 2. The means for birth weight and weaning weight from BLUP solutions

Specification	Birth weight	Weaning weight
Mean±Standard error for males	39.433±0.171	230.444±1.256
Mean±Standard error (kg) for females	37.751±0.123	220.078±0.927

The direct and maternal breeding values for the birth weight and weaning weight for the best cattle in Limousine breed were presented in the Table 3.

Table 3. The direct and maternal breeding values for birth weight and weaning weight for the best cattle

Birth weight	Birth weight	Weaning weight	Weaning weight
Direct breeding values	Maternal breeding values	Direct breeding values	Maternal breeding values
7.049	1.810	60.818	20.747
7.007	1.789	60.020	20.605
6.844	1.684	60.013	20.175
6.819	1.683	59.863	19.855
6.819	1.673	58.218	19.218
6.736	1.645	57.939	19.157
6.715	1.607	57.767	18.762
6.709	1.603	56.974	18.717
6.684	1.580	56.877	18.696
6.677	1.563	56.541	18.497

The direct breeding values for the best cattle for birth weight ranged between 6.677 and 7.049 and the maternal breeding values were from 1.563 and 1.810. For weaning weight, the direct breeding values ranged between 56.541 and 60.818 and maternal breeding values were from 18. 497 and 20.747.

In the Table 4 were presented the relative direct breeding values for cattle for birth weight and weaning weight.

Table 4. The relative breeding values for birth weight and weaning weight

Birth weight	Weaning weight
Direct relative breeding values	Direct relative breeding values
134.420	134.855
134.212	134.398
133.419	134.394
133.299	134.308
133.299	133.366
132.897	133.207
132.792	133.109
132.763	132.654
132.644	132.599
132.608	132.407

In the Table 5 were presented the genetic parameters for birth weight and weaning weight estimated with multivariate maternal animal model.

Table 5. The genetic parameters for birth weight and weaning weight estimated with multivariate maternal animal model

Item	Birth weight	Weaning weight
σ_a^2	5.969	559.270
σ_m^2	2.012	207.960
σ_{am}	-1.122	-73.583
σ_{pe}^2	46.73	1.598
σ_e^2	1.103	1.651
σ_p^2	56.944	844.064
c^2	0.820	0.002
σ_{am}/σ_p^2	-0.019	-0.087
r_{am}	-0.323	-0.215
h_a^2	0.105±0.082	0.662±0.019
h_m^2	0.035±0.105	0.246±0.024
h_T^2	0.092±0.067	0.655±0.008

Rezende et al. (2022) reported the direct heritability for the weight at 210 days 0.22 and the maternal heritability 0.08 in Limousine breed. Keeton et al. (1996) reported the direct heritability 0.25 and maternal heritability 0.19 in Limousine breed. The heritability observed in our study was higher than the value reported by Van Niekerk and Neser (2006) in Limousine breed (0.19) for weaning weight.

CONCLUSIONS

The heritability for birth weight was low and for weaning weight was high when was estimated with multivariate maternal animal model. In the selection of cattle, it is necessary the choose the best method for the genetic evaluation of the animals.

ACKNOWLEDGEMENTS

This work was supported by funds from the National Research Projects 8.1.2 and 8.1.3 granted by the Romanian Ministry of Agriculture and Rural Development and from Romanian Breeding Association for Beef Cattle.

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