Random Regression Model for Estimation the Genetic Parameters for Growth Traits in Charolais Breed

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Abstract

The aim of this study was the estimation the genetic parameters with random regression model for growth traits in Charolais cattle breed. The records were the body weight at birth, 200 and 365 days. The pedigree consisted in 2213 cattle: 159 sires, 1025 dams and 1029 cattle with records. The data were from Romanian Breeding Association for beef cattle. The mean for birth weight was 40.297±0.202 kg, for weaning weight was 220.287±1.296 kg, and the mean for weight at 365 days was 330.275±2.097 kg. The heritability for the birth weight and body weight at 200 and 365 days was 0.244, 0.519, 0.561. The genetic correlations between body weight at 1, 200 and 365 days were positive. The random regression model was adequate to estimate the genetic parameters for growth traits in Charolais beef cattle breed. For increase the profitability of farms it is necessary to improve the growth traits.

Keywords: cattle, body weight, selection, heritability

1. Introduction

The random regression model was used for growth traits for account the genetic correlation between measures of the same trait over time (Mc Gowan, 2023) [1]. Random regression model was used for analysis of longitudinal data or repeated records on animals over time (Schaeffer, 2004) [2].

The breeding objective for Charolais from Romania was a high body weight at weaning and at 365 days. The selection of beef has the aim at improving economic efficiency of beef production improving the feed efficiency of growing the beef cattle. In Romania, genetic evaluations for growth traits in beef cattle usually make use the multitrait animal model for prediction of breeding values of cattle and genetic parameters. In Romania the did not use of random regression model for growing traits, the random regression model being used for milk yield.

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Schaeffer (2004) [2] reported that the random regression model facilitates use of all weight recorded over time for each cattle. The growth traits are moderate to highly heritable (Venkataramanan, 2021) [3].

The estimation the genetic parameters with random regression model in beef cattle was realized by numerous authors: Arango et al. 2004 [4], Bohmanova et al., 2005 [5], Nesser et al. (2012) [6], Teixeira et al. (2018) [7], Khorshidi et al., 2020 [8], Vaz et al. (2024) [9].

Venkataramanan (2021) [3] reported that the random regression model has the advantage that the variance components could be estimated for any point in the trajectory of the growth curve and genetic parameters could be estimated for any age class. Genetic evaluation for growth traits with random regression model could be improved because this model was more adequate due to avoidance of age pre-adjustment and the possibility to take into account the specific environmental effect on the time of record (Meyer, 2004 [10]; Ghafouri-Kesbi et al., 2008 [11]).

The aim of this study was the estimation the genetic parameters for growth traits in beef with random regression model in Charolais cattle breed.

2. Materials and methods

The records were the body weight at 1, 200 and 365 days. The pedigree consisted in 2213 cattle: 159 sires, 1025 dams and 1029 cattle with records. From 1029 cattle with record 708 were females and 321 males. The data were from 2020 year. The data were from Romanian Breeding Association for beef cattle.
The growth traits were analysed using a random regression test-day model (Jamrozik & Schaeffer, 1997[12]):

$$y_{tijk} = TD_i + \sum_{m=0}^{3}(\beta_m \cdot z_{tm}) + \sum_{m=0}^{3}(\alpha_{jm} \cdot z_{tm}) + \sum_{m=0}^{3}(\gamma_{jm} \cdot z_{tm}) + e_{tijk}$$

Where:
y_{tijk} = test day (TD) body weight record "***k***" of cattle "***j***" at time "***t***";
TD_i = the data of body weight recording (the fixed effect)
β_m = fixed regression coefficient; α_{jm} = random regression coefficients for the breeding value;
γ_{jm} = random regression coefficients for the permanent environmental effect;
Z_{tm} = Legendre Polynomials at time ***t***;
e_{tijk}=residual error.

Legendre polynomials of order 3 were used as random regression functions for both the additive genetic and permanent environmental effects. The variance-covariance matrix was:

$$V=\begin{bmatrix} A \otimes G & 0 & 0 \\ 0 & I \otimes P & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

A = pedigree relationship matrix
Var (a) =$A \otimes G$; Var (a) = additive variance; Where $\otimes$ is Kronecker product function;
Var (p) = $I \otimes P$; Var (p) = environmental variance; G and P were the matrices of genetic and permanent environmental variances and covariances between random regression coefficients;
I = the identity matrix with the size equal with the number of cattle with records;
σ_e^2 = residual variance

The total heritability of body weight was estimated as:

$$h^2 = \frac{g_{tt}}{g_{tt} + p_{tt} + \sigma_e^2}$$

Where:
h^2= heritability for body weight during days in milk t;
g_{tt}= genetic variance
$g_{tt} = z_t' * G * z_t$
$p_{tt} = z_t' * P * z_t$
p_{tt}= permanent environmental variance
σ_e^2 = residual variance;
The genetic correlation was estimated as:
$r_{g\,t't} = \frac{g_{t't}}{\sqrt{g_{t't'} * g_{tt}}}$
$r_{g\,t't}$= genetic correlations between test-day t` and t yields;
$g_{t't}$= genetic covariances between two test days
z_t'= transpose of z

3. Results and discussion

In the table 1 were presented the descriptive statistics for body weight in Charolais beef cattle breed.

Table 1. The descriptives statistics for studied traits

Traits	Mean ± SEM	SD	Coeff. of variability (%)
Birth weight (kg)	40.297±0.202	6.5	16.137
Weight at 200 days (kg)	220.287±1.296	41.6	18.884
Weight at 365 days (kg)	330.275±2.097	67.297	20.376

The breed was the genetic factor which influenced the growth traits in beef cattle.
Tousova et al. (2014) [13] reported the higher means than in our study for birth weight, 49.6 kg, live weight at 210 days 310.7 kg and the live weight at 365 days of age was 496.5 kg in Charolais breed. Zhang et al. (2025) [14] reported lower means for birth weight 39.99 kg, weight at 6

months 203.5 kg and higher value for weight at 12 months 336.92 kg.
Johnston et al. (1992) [15] reported means for birth weight 42.77 kg, for weaning weight at 200 days age 250.98 kg, and weight at 365 days 476.05kg.
Phocas (2009) [16] reported higher mean for birth weight 45.2 kg than in our study and for weaning weight 267.1 kg.
In the table 2 were presented the heritability for the body weight estimated with random regression models.

Table 2. The heritability for the body traits

Traits	The heritability
Birth Weight	0.244
Weight at 200 days	0.519
Weight at 365 days	0.561

Korshidi et al. (2020) [8] reported the direct heritability estimated with random regression model for birth weight, weaning weight and weight at 365 days: 0.10, 0.13 and 0.22 and maternal heritability 0.01, 007 and 0.03.
Texeira et al. (2018) [7] reported the direct heritability estimated with random regression model for weight at 200 days 0.16 and for weight at 365 days 0.31 and maternal heritability 0.11 and 0.09.
Meyer (2009) [10] reported the heritability for birth weight 0.399 and for 200 days weight 0.145.
Vaz et al. (2024) [9] reported high values for direct heritability for weight at 205 days 0.60 and for weight at 365 days 0.60 and low maternal heritability 0.08 and 0.06.
Johnston et al. (1992) [15] reported the heritability for birth weight 0.25, 200-days adjusted weaning weight, 0.09, 365-days adjusted yearling weight 0.16 in Charolais breed.
Menendez-Buxadera et al. (2008) reported the heritability for weaning in Asturiana de los Valles beef cattle with random regression for early weaning 0.60, standard weaning 0.63 and late weaning 0.53.[17]
Nesser et al. (2012) [6] reported direct heritability for the birth weight 0.10, weaning weight 0.13, yearling weight 0.13 in Brangus cattle using random regression model.
Feng et al. (2025) [18] reported the heritability for birth weight was 0.215, for weight at 6 months 0.239 and 0.362 for weight at 12 months.
In the table 3 were presented the genetic correlations between body weight at studied ages.
Schenkel et al. (2002) [19] reported the heritability for birth weight 0.325, the weight at 28 days 0.332, at 56 days 0.351, at 84 days 0.370, 112 days 0.387 and 140 day 0.402.
Iwaisaki et al. (2005) [20] obtained direct heritability for yearling weight obtained with a random regression model with a linear spline function 0.48. Estimates obtained with this model may be superior to multitrait model due to better modeling of age in both fixed and random effect [20].

Table 3. The genetic correlations between studied traits

	Birth weight	Weight at 200 days	Weight at 365 days
Birth weight	1	0.086	0.391
Weight at 200 days	0.086	1	0.034
Weight at 365 days	0.391	0.034	1

The genetic correlation between the birth weight and weight at 200 days was low and positive. The genetic correlation between birth weight and weight at 365 days was medium and positive. The genetic correlation between weight at 200 days and weight at 365 days was low and positive.
Paneru et al. (2024) [21] reported that the benefits of the random regression model were: was a more flexible method for genetic evaluation for early and late growth and no need for age correction. Schaeffer (2004) [2] reported that the pattern of animal growth over time could be modeled by random regression and that body weights were cumulative over time.
Because the growth traits had moderate to high heritability, making the selection of specialized breeds withing breeding programs an important strategy for improving these traits [14].
The heritability estimates obtained through random regression model was higher than those obtained by univariate analysis, due the additional information obtained through the growth curve [3].
Random regression model appeared a preferable alternative for genetic evaluation of growth trait in beef [10]. Random regression model allowed to study changes in genetic variability with time and allowed selection of individuals to alter the general pattern of response over time [2].
Becker Scalez et al. (2018) [22] reported that random regression models are often more appropriate for genetic evaluation of body weight because describe phenotypic and genetic change over time.

The random regression model could be used for estimate the breeding value for dry mater intake (Schrauf, 2024) [23]. The selection on feed efficiency traits can help to reduce costs and improve sustainability in cattle industry (Schrauf, 2024) [23].

Ramos et al. (2024) [24] reported that feed efficiency plays a major role in the overall profitability and sustainability of the beef cattle industry, and it is directly related to the reduction of the animal input and methane emissions. To calculate feed efficiency traits were necessary the average daily feed intake and weight gains [24]. Ramos et al. (2024) [24] considered that the random regression models allowed fitting random genetic and environmental effects over time by considering the covariance between daily records.

4. Conclusions

The heritability for weight at 200 days and weight at 365 days were high in Charolais breed. The correlations between birth weight and weight at 365 days was medium and positive. The random regression model was adequate to estimate the genetic parameters for growth traits in Charolais beef cattle breed.

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