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Genetic analysis of live weight of Sardi sheep using random regression and multi-trait animal models

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ABSTRACT

Genetic parameters and breeding values for live weight from birth to weaning (85 days) of Sardi sheep were estimated using random regression (RR) and multi-trait (MT) animal models. A longitudinal data set for live weight of 44,509 lamb progeny of 605 sires and 18,569 dams were used to describe variance components along growth curve trajectory using RR model. This data set was collected in 89 flocks between 2001 and 2012, with a total of 45,941 animals in the pedigree. Eleven RR models were compared based on the log likelihood and Akaike information criterion. The model with the best fit was found to include quadratic Legendre polynomials for direct and maternal genetic effects and direct permanent environment effects and a linear polynomial for maternal permanent environment effects, including covariance between direct and maternal genetic effects and a heterogeneous residual variance. Direct and maternal heritabilities were 0.11 and 0.03, respectively, at the first day of age, and 0.37 and 0.10, respectively, at 85 days of age. The increase of heritability and genetic variance indicated that there was a large potential for selection of Sardi sheep and suggested that selection during the study period would be more effective if it was done on weaning weight. The low genetic correlation between early weight and weaning weight suggests that these traits are controlled by different genes. Genetic parameters obtained at the selected ages (i.e. 10, 30, 70 days) using MT and RR models were generally similar, but the two methods produced different ranking of genetic merit. This study has demonstrated the possibility of applying RR model for routine genetic evaluation of Sardi sheep.

1. Introduction

Sheep production is an important source of animal protein and red meat in Morocco. Sheep population is mainly composed of indigenous breeds adapted to climatic and poor range conditions of the country (Boulanouar and Benlekhal, 2006). The Sardi breed is one of the main sheep breeds used for meat production in Morocco. Its breeding area is located in the Center-West of the country. Due to its large population (about two million head) and its socio-economic role, there is an increasing interest for improving this breed through a selection scheme (Chikhi and Boujenane, 2003).

Currently, a breeding program is carried out by professional breeders of the National Association of Sheep and Goats (ANOC) to improve Sardi breed's growth performance. This program is mainly based on recording body weight and genetic evaluation of growth performance at constant ages using multi-trait (MT) approach.

One alternative to the MT model is the random regression (RR) model, which was proposed to facilitate the estimation of genetic parameters for traits that change continuously along the time (Fischer et al., 2004). Meyer (2004) reported that the accuracy of genetic evaluation for growth in beef cattle could be improved by using the RR model without the need of correcting towards certain landmark ages. RR model also makes the use of data for individual animals more efficient, resulting in an increase of the accuracy of genetic evaluation. Furthermore, in RR model fewer parameters are needed to describe longitudinal data compared with the MT model. Moreover, in comparison to a multivariate model, RR model allows the estimation of less biased variances and covariances (Kirkpatrick et al., 1990).

Application of RR methodology in routine genetic evaluation of the Sardi breed requires conducting a genetic study applied to the growth performance of this breed to study the feasibility of this approach in comparison with the MT model.

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This study aims: (1) to analyze the genetic (co) variance components, (2) to estimate breeding values for Sardi sheep's live weight at different ages (i.e. between birth and 85 days) using RR model, and (3) to numerically compare the resulting estimates with those obtained using MT model.

2. Material and methods

2.1. Data collection

The data analyzed were obtained from the breeding program of Sardi sheep managed by the ANOC in Morocco. Data were collected over a period of 12 years, from 2001 to 2012, in 89 flocks in the breeding program of ANOC.

Data collection was carried out by certified monitors that conducted regular weighing of lambs every 21 days (±3 days) from birth to weaning during two lambing seasons (autumn and winter). Thus, a maximum of four weights were recorded for each lamb. The original database contains records of weight and genealogy of 47,233 lambs.

2.2. Data editing

The original database was edited to create a longitudinal data set with age and corresponding live weight (LW) of lambs to perform the random regression analysis. Lambs without birth date or with missing weight were discarded. Flocks with less than 50 observations and LW out of the range, defined as the average ± 3.5 standard deviations were deleted. At the end of the process, a new dataset was created and used for the RR model with 173,883 observations from 44,509 lambs with at least two records for LW from birth to 85 days old. These lambs were progeny of 605 sires and 18,569 dams. The pedigree file contained a total of 56,909 animals (lambs, sires and dams) from eight generations. The number of records in each age and the corresponding mean LW are given in Fig. 1.

The birth weight was not included in this study, since inconsistent correlations with other weights were found, probably due to the influence of the pregnancy stage and the maternal effects. For this reason, Fischer et al. (2004) excluded the birth weight from their studies since it was found to be accompanied by inexplicable noise, probably caused by the proximity of the weighing to the time of birth, as well as other maternal factors. Thus, they can often be inaccurate and hence misleading. Meyer (2001) showed a significant effect of the inclusion of birth weight in Australian beef calves on increasing the order of the polynomial fit in the RR model. Thus, the study focused on the period between the first day of age (one day after birth day) and the age of 85 days.

In a second step, the data were adjusted linearly by the interpolation method to the fixed age of 10, 30 and 70 days for MT analyzes. These adjusted LW were also edited, validated and those data outside the range of average ± 3.5 standard deviations were deleted. The number of animals and the pedigree structure are similar to those of the RR model. This database was analyzed by a MT model and merged with that of the RR model in order to compare the results for the same animal. A general descriptive information about this database is presented in Table 1.

2.3. Statistical analyses

Preliminary analyses were carried out to determine the fixed effects affecting weight using Proc Mixed (SAS, 2002) and find the best order of fit for fixed regression on age to model the population trajectory. Orders of fit beyond quadratic were not significant, and therefore, quadratic regression was used in the fixed part of the models for all RR model analyses.

Table 1
Statistical description of data.[a]

Item	W10d (kg)	W30d (kg)	W70d (kg)
No. of records	43486	44103	43521
Mean	5.55	8.96	16.16
Minimum	1.90	4.18	8.20
Maximum	10.30	22.36	28.93
Standard deviation	1.28	1.82	2.77

[a] W10d = weight at 10 days of age; W30d = weight at 30 days of age; W70d = weight at 70 days of age.

2.3.1. RR model

Different linear models were applied to the RR model data set to provide a general description of the growth curve of Sardi sheep. For the genetic analysis, the following basic RR model was applied:

$$y = Xb + \sum_{k=0}^{ka-1} Z_a a_k + \sum_{k=0}^{km-1} Z_m m_k + \sum_{k=0}^{kp-1} Z_p p_k + \sum_{k=0}^{kw-1} Z_w w_k + \epsilon_r$$

Where:y is the vector of live weight of animal i at age j.b is a group of fixed effects represented by contemporary group with 1093 levels (combination of flock, lambing year (12 levels: from 2001 to 2012)) and season (2 levels: autumn and winter), age at lambing of the dam (8 levels: 2, 3, . . ., 9 years old) and a combination of lamb sex (2 levels: male and female) and litter size (2 levels: 1 and 2), and X is the incidence matrix.a_k and m_k are the direct and maternal genetic effects, respectively (with dimension n = number of animals) and k coefficients of the random regression (k_a and k_m are the order of fit).p_k and w_k are the random environmental individual permanent and maternal permanent effect with dimensions I_n and I_w (w = number of dams), respectively. The orders of Legendre polynomial were k_p and k_w, respectively.Z_a, Z_m, Z_p and Z_w are incidence matrices connecting the effects to the data vector with a dimension of n x k_a for $Z_{a,}$ n x k_m for $Z_{m,}$ n x k_p for Z_p and w x k_w for $Z_{w.}$ The elements of these matrices are $Z_i = \Phi_i = \forall_i(t^*_{ij})$ where $\forall_i$ are the coefficients of the selected polynomial and t^*_{ij} is the jth age of ith animal expressed in standardized form to use the Legendre polynomial (Φ_x) of order $\mathbf{k_x}$ (with x = a, m, p, w). The term $\sum$ means that the total effects are obtained by the sum of corresponding Φ_x.

$\in_r$ is residual variance vector modeled considering either homogeneity of variances across all ages or the heterogeneous non correlated residual variance with 12 classes of one week each.

The genetic parameters were estimated using a linear function of the corresponding components, following ASReml manual (Gilmour et al., 2009) and applying classical formulas. Nevertheless, the results from RR model must receive an additional treatment as proposed by Jamrozik and Schaeffer (1997). The variances of direct (σ^2_{aj}) and maternal (σ^2_{mj}) genetic effects for LW at any point of the scale of jth age can be estimated by:

$$\sigma^2_{aj} = \Phi'_{aj} K_a \Phi_{aj}$$

$\sigma^2_{mj} = \Phi'_{mj} K_m \Phi_{mj}$The variance of maternal environmental effects (σ^2_{wj})

$$\sigma^2_{wj} = \Phi'_{wj} K_w \Phi_{wj}$$

The genetic covariance between ages j and k for direct genetic effects (σ_{ajk}) and maternal genetic effects (σ_{mjk}) will be:

$$\sigma_{ajk} = \Phi'_{aj} K_a \Phi_{ak}$$

$$\sigma_{mjk} = \Phi'_{mj} K_m \Phi_{mk}$$