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Estimation of genetic parameters for growth-related traits and evaluating the results of a 27-year selection program in Baluchi sheep

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ABSTRACT

The aim of the present study was to estimate (co) variance components and genetic parameters for growth traits of Baluchi sheep as well as to study the response of Baluchi sheep to selection for yearling live weight. Data and pedigree information used in this study were collected at the Abbasabad Sheep Breeding Station from 1983 to 2011. Studied traits were birth weight (BW), 3-month weight (W3), 6-month weight (W6), 9-month weight (W9) and yearling weight (W12). Six different animal models were fitted, including or ignoring maternal effects. Estimates of breeding values were obtained by the best linear unbiased prediction (BLUP) method. Genetic trends of studied traits were estimated by regressing mean of breeding values on birth year. On the four gametic pathways, generation intervals were estimated as the average age of parents at the birth of their progeny. The estimates of direct heritability (h^2) for traits studied were low and ranged between 0.03 (W6) and 0.15 (W12). Maternal genetic and environmental effects were significant on traits studied. Maternal heritability m^2) was 0.09 at birth but decreased gradually and reached 0.02 at yearling age. Likewise, maternal permanent environment variance as a proportion of phenotypic variance (c^2) decreased from 0.13 at birth to 0.05 at yearling age. Phenotypic correlations between various traits were positive and increased with older pairs of ages. The corresponding direct genetic correlations were all positive, with a tendency for higher estimates between pairs of older ages. Genetic changes over the experiment were −0.13 kg, 0.192 kg, 0.082 kg, 0.147 kg and 0.459 kg for BW, WW, W6, W9 and W12, respectively. Annual genetic gain for BW, WW, W6, W9 and W12 were, respectively, ≈0.00 g, 7g, 4g, 7 g and 14 g per year. The average generation interval was 3.50 years. The lower generation interval was observed on the ram side compared with the dam side (3.35 year vs. 3.81 year), indicating faster generation turnover for sires than for dams. Overall, results showed a moderate genetic improvement in growth traits of Baluchi sheep. In addition, because of significant maternal effects on growth-related traits of Baluchi sheep, to have an accurate genetic evaluation, these effects need to be considered in any breeding program aimed at improving growth traits of this breed.

1. Introduction

Body weight is economically an important trait in sheep. The improving growth performance using selection schemes is a key method to increase meat production in lamb breeding systems. However, selection for growth is intricate by the fact that in mammal species growth related traits are determined not only by the additive genetic value but also by maternal effects (Ghafouri-Kesbi and Baneh 2012). Several studies show that animal models which disregard maternal effects might result in overestimation of direct heritability (Ghafouri-Kesbi and Eskandarinasab, 2008; Utrera 2008; Barazandeh et al., 2012) and, as a consequence, a corresponding upward bias in predicted responses to selection occurs. So, accounting for both direct and maternal effects would result in a more accurate estimation of variance components and increase accuracy of selection (Robinson, 1996).

Success of a breeding program can be measured by actual change in breeding value expressed as a proportion of theoretical change of the breeding value mean for the trait under selection (Jurado et al., 1994). Moreover, estimating genetic and environmental trends in populations allows assessment of the effectiveness of selection procedure and gives the opportunity for monitoring management conditions such as nutrition and health status (Kovac and Groenveld, 1990).

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One of the important Iranian sheep breeds is Baluchi that accounts for slightly more than 12% of the total sheep population (Kamalzadeh and Shabani, 2007). It is a small sized, fat-tailed breed well adapted to a wide range of harsh environmental conditions in the eastern parts of Iran. Coat color is white with pigmented head and legs and the wool is coarse with medullation. Although lots of genetic data for growth traits has been reported in the literature (see for example Safari et al. (2005) and references therein), they are not extendable to Baluchi sheep because estimation of genetic parameters is influenced by several factors such as breed differences, data structure, etc. The present study, therefore, was conducted to (1) estimate (co) variance components and genetic parameters due to direct and maternal effects for growth related traits of Baluchi sheep and (2) evaluating the results of a 27 years selection program in Baluchi sheep.

2. Material and methods

2.1. Data and management

The data used in the present study were collected from Abbasabad Sheep Breeding Station (flock 1), Mashhad, Khorasan Razavi, Iran. This experimental population of Baluchi sheep was founded in early 1960s with the aim of improving other flock in the region. Selection of rams was based on body weight, body conformation score at the 1 years and pedigree information on type of birth. In general, the flock is reared by following conventional industrial procedures. The mating period commenced in August and September and lasted for 51 days. Lambing took place from beginning of February to the end of March. At birth, the relevant information about newborn such as sex, birth type, birth date, birth weight, sir ID and dam ID were recorded. In addition, body weights were recorded at monthly intervals starting from birth until 4 months of age. Records of body weights for 6, 9 and 12 months of age were also documented. Lambs were weaned on average age of 90 days. After weaning, ewes and young animals were kept on natural pasture during spring and summer and indoors during winter and received a ration consisted of wheat and barley straw, alfalfa hay, sugar beet pulp and concentrate. To protect animals from various diseases vaccinations were performed twice a year. The sheep were dewormed with drugs and dipped in anti-parasite bath twice a year. The sick animals were kept in separate boxes until they had recovered.

The traits studied were: birth weight (BW), weaning weight (WW), 6-month weight (W6), 9-month weight (W9) and yearling weight (W12). Weaning weight was adjusted to 90 days of age by adding 90 times the pre-weaning average daily gain to birth weight. Adjusted 6-month weight (180 days) was obtained by adding t times the post-weaning daily gain to weaning weight, where t is the number of days between weaning and 6-month age. Adjusted 9-month weight (270 days) and yearling weight (365 days) was also calculated in a similar fashion.

2.2. Statistical analysis

The general linear model (GLM) procedure of the SAS Institute Inc. (2004) was used for determining which fixed effects have significant influences on traits. The analysis showed that fixed effects of year of birth (1994–2011), sex (male and female), type of birth (single, twin and triplet) and age of dam at lambing (2–8 years old) were significant ($p < 0.05$). These fixed effects were fitted in the subsequent models for estimating genetic parameters. Variance and covariance components and genetic parameters were estimated using the Wombat (Meyer, 2007) by fitting six single-trait animal models. The models were as follows:

$$\text{Model1}: Y = X\beta + Z_1 a + e$$

$$\text{Model2}: Y = X\beta + Z_1 a + Z_3 c + e$$

$$\text{Model3}: Y = X\beta + Z_1 a + Z_2 m + e\text{with}\mathrm{Cov}(a,m) = 0$$

$$\text{Model4}: Y = X\beta + Z_1 a + Z_2 m + e\text{with}\mathrm{Cov}(a,m) = A\sigma_{am}$$

$$\text{Model5}: Y = X\beta + Z_1 a + Z_2 m + Z_3 c + e\text{with}\mathrm{Cov}(a,m) = 0$$

$$\text{Model6}: Y = X\beta + Z_1 a + Z_2 m + Z_3 c + e\text{with}\mathrm{Cov}(a,m) = A\sigma_{am}$$

where, y is the vector of observations, b is the vector of fixed effects, a and m are the vectors of random direct and maternal additive genetic effects, respectively, c is the vector of random permanent maternal environmental effects and e is the vector of residuals. X, Z_1, Z_2 and $Z_3$are incidence matrices for β, a, m and c respectively. A is the relationship matrix, the expected value for y is $X\beta$; $V[a]$, $V[m]$, $V[c]$ and $V[e]$ are $\sigma^2{}_a$, $\sigma^2{}_m$, IND $\sigma^2{}_c$ and IN $\sigma^2{}_e$, respectively, where I is an identity matrix with orders of ND (number of dams) or N (number of records). Direct and maternal heritabilities (h^2 and m^2) were estimated as $\sigma^2 a/\sigma^2 p$ and $\sigma^2 m/\sigma^2 p$, respectively, where $\sigma^2 a$, $\sigma^2 m$ and $\sigma^2 p$ are estimates of direct genetic, maternal genetic and phenotypic variances. Models were compared using the Akaike Information Criterion (AIC) to find the best model for each trait. AIC is defiened as AICi = −2 log Li + 2 pi, where log Liis the log likelihood, and piis the number of parameters obtained for each model. The model that has the lowest AIC, is the appropriate model for that trait (Akaike, 1974).

Genetic and phenotypic correlations were estimated using a multi-variate analysis applying the best model determined in univariate analyses. The fixed effects included in the multi-trait animal models were those in single-trait analyses.

Genetic change for traits over the experiment was calculated by subtracting the mean of the estimated breeding values at the beginning of the experiment from the mean of the estimated breeding values at the end of the experiment. Genetic trends were obtained by regressing the means of predicted breeding values obtained from multi-variate analysis on year of birth for each trait. Genetic trend analyses were performed with the regression procedure (Proc Reg) of the SAS (SAS Institute Inc., 2004SAS, 2004; SAS Institute Inc., Cary, NC). The generation interval was estimated as the average age of the parents (rams and dams) at the birth of their progeny.

The generation interval of four gametic pathways, sire to son (L_{mm}), sire to daughter (L_{mf}), dam to son (L_{fm}), and dam to daughter (L_{ff}), was obtained from records of birth dates of registered animals in each year and the birth dates of their sires and dams. The average generation interval (L) was computed from:

$$L = \frac{L_{mm} + L_{mf} + L_{fm} + L_{ff}}{4}$$

3. Results

Characteristics of the pedigree and data structure are summarized in Tables 1 and 2, respectively. As shown, the pedigree is deep, number of record per each trait is high and the average number of progeny per dam is high enough to obtain accurate estimates of direct and maternal genetic parameters. Among traits studied, W9 had the minimum coefficient of variation (CV). The reason of less CV for W9 may be due to less variation and effect of outside environment on this trait. According to Salako (2006), larger variation