



## Random regression models to explore genetic variation and genetic variability in the growth curve of Baluchi lambs

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### ABSTRACT

The aim was to apply Random Regression Model (RRM) to describe growth curve of Baluchi lambs. Data was retrieved from an experimental population of Baluchi sheep and consisted of body weight records from 50 to 400 days of age. Regressions for the direct and maternal random effects in the RRM were modeled using different combinations of legendre polynomials with orders from one (i.e., simple repeatability model, SRM) to four. Mean trends were also modeled through a quadratic regression on orthogonal polynomials of age. Homogeneity and heterogeneity of error variance were considered along growth trajectory. The Akaike's Information Criterion (AIC) and Bayesian Information Criterion (BIC) were computed to compare different models. According to AIC and BIC values, simple repeatability model was the worse model and resulted in greater estimates of error variance. A RRM with legendre polynomials of orders 4, 4, 4, and 4 for direct additive genetic, direct permanent environment, maternal additive genetic and maternal permanent environmental effects was selected as the parsimonious model. The AIC and BIC values significantly increased when maternal effects excluded from the parsimonious model. Direct heritability ( $h^2$ ) decreased from 0.32 at 50 days of age to 0.09 at 90 days of age and increased thereafter to a peak at 400 days of age (0.42). Direct permanent environmental effect ( $p^2$ ) was minimum at 50 days of age (0.20), increased gradually and reached the maximized value around 150 days of age (0.54) and decreased thereafter. Maternal heritability ( $m^2$ ) was close to zero at 50 days of age, but increased thereafter to a peak at 400 days of age (0.08). Maternal permanent environmental effect ( $c^2$ ) was 0.22 at 50 days of age, decreased sharply to 0.01 at 100 days of age when it fixed below 0.05 until end of trajectory. Measures of genetic and environmental variability (coefficient of variations:  $CV_A$ ,  $CV_B$ ,  $CV_M$  and  $CV_C$ ) had the almost similar patterns with corresponding genetic and environmental parameters. Direct and maternal correlations were positively high between adjacent weighs but decreased with increasing number of days between records. In general, estimates of genetic parameters and coefficient of variations showed opportunity for genetic improvement in growth curve of Baluchi lambs.

### 1. Introduction

Henderson Jr (1982) suggested Random Regression Models (RRM) to model traits that are recorded repeatedly during an organism's life (i.e., longitudinal data). The RRM was originally suggested to analysis human biological data and it took 10 years to apply RRM to performance records of livestock (Schaeffer and Dekkers, 1994). Regarding analyzing growth data, RRM can be considered as an intermediate between the more traditional approaches of either treating size as a single trait with repeated measures, under the simplifying and likely erroneous assumption that variance components are constant with age (i.e., simple repeatability model, SRM), or treating size as a series of age-specific traits linked by a covariance structure (Meyer, 1998). The

advantages of RRM in analyzing growth data have illustrated by Meyer (2004) who showed that by replacing traditional Multi Trait Animal Models (MTM) with RRM, the accuracy of genetic evaluation of body weight increased by at least 4%. It is because RRM allows for presence of missing data, doesn't need to pre-adjustment of records, ease model parameterization via reducing the number of parameters to be estimated, and can partition animal permanent environmental component from phenotypic variance. For these reasons, in recent years we have evidenced an increasing use of RRM for the analysis of repeated records of livestock (Meyer, 2004; Ghafouri-Kesbi et al., 2008; Rafat et al., 2011; Samadi et al., 2013).

The Baluchi breed is a small sized breed of sheep and belongs to the fat-tailed breeds category. Historically, it is originated from southwest

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Pakistan, eastern Iran and southern Afghanistan. With a large population, it accounts approximately for 12% of the total sheep population in Iran (Kamalzadeh and Shabani, 2007). In this breed, coat colour is white with pigmented head and legs and the wool is coarse with medullation. Today, nearly all of the Baluchi population are reared in the Khorasan province and mainly farmed for meat production. This breed is known with appropriate growth characteristics which together with their large population make them to be an appropriate breed for selection programs aimed at increasing the meat production.

The accuracy of genetic evaluation affects the success of selection programs and as discussed above applying RRM increases the accuracy of genetic evaluation. In spite of this, so far, body weight records of Baluchi sheep has not been analysed with RRM, though genetic parameters obtained by traditional single trait animal models have been reported for this breed (Gholizadeh and Ghafouri-Kesbi, 2015). Compared with a single trait animal model, RRM models genetic parameters more appropriately owing to avoidance of age pre-adjustment and possibility of taking into account of specific environmental effects on the time of recording (Ghafouri-Kesbi et al. (2008). Therefore, in this study, weight records of Baluchi sheep from 50 to 400 days of age were analysed using RRM to estimate age-specific phenotypic variance and its genetic and non-genetic components. Results can be used by Baluchi sheep breeders for future selection programs.

## 2. Material and methods

### 2.1. Data

Body weight records and pedigree information on Baluchi lambs were obtained from Abbasabad Sheep Breeding Station (flock 1), Mashhad, Khorasan Razavi, Iran. In the early 1960s an experimental population of Baluchi sheep comprised of two flocks was founded in the Khorasan Razavi province close to Mashhad. The aim was to establish a nucleus population as a genetic source to improve the whole population of Baluchi sheep. Selection of rams carried-out based on body weight, body conformation score at the 1 year of age and pedigree information on type of birth. In the flock, natural service was applied during August and September and lasted for 51 days. Lambing commenced in February and continued to March. At birth, lambs were weighed, tagged, sexed, and identified to their parents. Lambs were weaned from their mothers at an average age of 90 days. After weaning, ewes and young animals were kept on natural pasture as separate flocks. The animals were kept indoors during late autumn and winter months and received a ration consisted of wheat and barley straw, alfalfa hay, sugar beet pulp and concentrate. Vaccinations were performed twice a year to protect animals from various diseases. The sheep were dewormed with drugs and dipped in antiparasite bath twice a year. Rams and ewes were kept in the flock for maximum three and six breeding years, respectively; however, barren ewes that do not lamb as well as extra rams were cooled sooner.

Data was monitored several times and records with uncertain dates or weights were removed from data file. No birth weight records were available from birth to 50 days of age, thus only 50–400 day BW records were included in data set. According to Fischer et al. (2004)'s recommendation, we excluded birth weight from the analyses. It is necessary to avoid the problem of “end effect of polynomials” or Runge's phenomenon (Kirkpatrick et al., 1994; Meyer, 1998). Meyer (2001) showed that inclusion of birth weight significantly increased the order of polynomial fit required. Also, Lewis and Brotherston (2002) and Ghafouri-Kesbi et al. (2008) reported that because birth weight has low genetic correlation with body weights measured later in life, it should be treated as a different trait. Animals with 1 and 2 records were also removed from the data. Editing for records with uncertain dates or weights, removing birth weights and eliminating animals with lower than 3 records yielded in a total of 22,179 records on 7149 animals.

### 2.2. Statistical analysis

To determine significant fixed effects, least square analyses using the GLM procedure of (SAS, 2004) were done. The effect of year of birth, sex, type of birth and age of dam at lambing were analysed. All of these effects were found to be significant and therefore included in the final model of analysis. Two modeling approaches were applied to the data as follow:

#### 2.2.1. Simple repeatability model (SRM)

This model considers different measurements at different ages as a realization of the same genetic trait. It assumes genetic and phenotypic correlations of unity, i.e. that all genetic and phenotypic variances and co-variances are of the same magnitude. Similarly, all phenotypic variances are considered identical and phenotypic correlations and co-variances among all measurements are assumed to be the same. For more details refer to Meyer and Hill (1997) and Meyer (1999). The SRM was as follows:

$$y = Xb + Z_1a + Z_2p + Z_3m + Z_4c + e$$

where  $y$  is the vector of observations;  $Z_1$ ,  $Z_2$ ,  $Z_3$  and  $Z_4$  are incidence matrices corresponding to the fixed effect ( $b$ ), random direct additive genetic effect ( $a$ ), random direct permanent environmental effect ( $p$ ), random maternal additive genetic effect ( $m$ ), and random maternal permanent environmental effect ( $c$ ); and  $e$  is the random residual errors. The variance and covariance structures are based on the following assumptions:

$$\begin{aligned} a &\sim N(0, I\delta_a^2), \\ p &\sim N(0, I\delta_p^2), \\ m &\sim N(0, I\delta_m^2), \\ c &\sim N(0, I\delta_c^2), \\ e &\sim N(0, I\delta_e^2), \end{aligned}$$

where  $I$  is identity matrix,  $\delta_a^2$ ,  $\delta_p^2$ ,  $\delta_m^2$ ,  $\delta_c^2$  and  $\delta_e^2$  are direct additive genetic variance, direct permanent environmental variance, maternal additive genetic variance, maternal permanent environmental variance and residual (temporary environment) variance, respectively.

#### 2.2.2. Random regression model (RRM)

In contrast to SRM in which all variance components are assumed to be constant, in RRM variance components can vary across ontogeny. According to Kirkpatrick et al. (1990), the RRM for body weight recorded at different times (including direct and maternal additive genetic and direct and maternal permanent environmental random effects) could be represented as follows:

$$\begin{aligned} y_{ij} = & F_{ij} + \sum_{m=0}^3 \beta_m \varphi_m(t_{ij}^*) + \sum_{m=0}^{k_A-1} \alpha_{im} \varphi_m(t_{ij}^*) + \sum_{m=0}^{k_M-1} \gamma_{im} \varphi_m(t_{ij}^*) \\ & + \sum_{m=0}^{k_P-1} \delta_{im} \varphi_m(t_{ij}^*) + \sum_{m=0}^{k_C-1} \rho_{im} \varphi_m(t_{ij}^*) + \varepsilon_{ij} \end{aligned}$$

where  $y_{ij}$  is the  $j^{th}$  record from  $i^{th}$  animal;  $t_{ij}^*$  is the standardized ( $-1 < t < 1$ ) age at recording;  $\varphi_m(t_{ij}^*)$  is the  $m^{th}$  Legendre polynomials of age;  $F_{ij}$  is a set of fixed effects;  $\beta_m$  are the fixed regression coefficients for modeling the population mean;  $\alpha_{im}$ ,  $\gamma_{im}$ ,  $\delta_{im}$  and  $\rho_{im}$  are the random regression coefficients for direct genetic, maternal genetic, and direct and maternal permanent environmental effects, respectively;  $k_{A-1}$ ,  $k_{M-1}$ ,  $k_{P-1}$  and  $k_{C-1}$  are the corresponding order of (polynomial) fit for each effect and  $\varepsilon_{ij}$  denotes the residual effect. RRM analyses considering different orders of fit for the four random effects were carried out. The aim was to determine the most parsimonious model describing the data. After determining the most parsimonious model, maternal effects were dropped from the model of analysis and change in Log Likelihood was measured. The aim of doing so was to determine

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