Genetic description of growth traits in Markhoz goat using random regression models

Khabat Kheirabadi [a,*], Amir Rashidi [b]

[a] Young Researchers and Elite Club, Sanandaj Branch, Islamic Azad University, Sanandaj, Iran
[b] Department of Animal Science, Faculty of Agriculture, University of Kurdistan, Kurdistan, Iran

ABSTRACT

The objective of the present study was to estimate genetic parameters and genetic trends for body weight traits in Markhoz goat using random regression (RR) models. In this study, 12,116 test-day body weight records of 3078 Markhoz goats, from birth to 365 days of age, were used to compare RR models in which fixed and random effects were modeled using Legendre polynomials. The best model for direct genetic and maternal temporary environmental effects (common litter) included cubic, for direct permanent environmental effect included quadratic and for maternal permanent environmental effect included linear Legendre polynomials with a heterogeneous error structure. Direct heritability increased from 0.17 at birth to 0.32 at 120 days of age then decreased suddenly to 0.27 at 240 days of age and increased thereafter. Some estimates for the highest ages with the least records tended to be overestimated, in particular heritability beyond 340 days. Variances due to direct permanent and maternal permanent environmental effects, respectively, were the highest and the lowest compared with the other sources of variation. This study has demonstrated the possibility of application of RR models for routine genetic evaluation of Markhoz goat in Iran. Although the results confirm that there is a scope for genetic improvement in growth pattern in Markhoz goat, but the genetic changes of body weight for selected ages (120-d and 200-d) have not shown a substantial tendency among the years.

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1. Introduction

Markhoz goat is a fleece and meat breed, found in the regions of Kurdistan and west Azerbaijan provinces in Iran (Rashidi et al., 2008). Historically, these animals had an important cultural role in Kurdistan since the mohair obtained from these animals is used as a raw material for making national clothes. In fact, the name is derived from these local clothes (Maraz). However, due to the increased market demand for goat meat in recent years, most of income from goat husbandry is now from meat (Rashidi et al., 2011). To design an efficient improvement program and genetic evaluation system for these economically traits, accurate estimates of the genetic parameters and also the genetic relationships between the traits are inevitable (Safari et al., 2005). Accuracy of genetic evaluations depends on how well the assumptions of the model match the data (Wiggans and VanRaden, 1991). Traditionally, the longitudinal data (measurements obtained sequentially from the same animal over time; Meyer, 1998) has

been described by univariate 'repeatability' or multivariate models. The former does not explain the genetic variation along the trajectory (continuous age scale), and the latter usually results in over parameterization (Meyer, 1998). Random regression (RR) models and the resulting covariance functions have recently been recognized as ideally suited to the analysis of longitudinal data in animal breeding and the description of the resulting covariance structure (Kirkpatrick et al., 1990; Fischer et al., 2004; Meyer, 2004). In contrast to traditional models, this approach allow appropriate modeling of the genetic parameters by avoiding age pre-adjustment, feasibility of taking into account of specific environmental effects on the time of recording, decreasing of the generation interval, increasing of accuracy of breeding values, feasibility of calculating variance of every age and covariance among any pair of ages (Schaeffer, 2004; Meyer, 2004, 2005). Studies investigating the use of RR models for genetic evaluation of body weight in Markhoz goat are scarce. Therefore, the objective of the present study was to model variations in growth trajectory of Markhoz goats by RR models.

Table 1
Description of the data set.

Observations (n)	12,116
Mean (kg)	14.53
SD (kg)	8.37
Animals with records (n)	3078
With 3 records (n)	998
With 4 records (n)	1278
With 5 records (n)	802
Animals in the analysis (n)	3502
Sires (n)	202
Dams (n)	1206
Sires with records and progeny (n)	131
Dams with records and progeny (n)	778

2. Materials and methods

2.1. Data and herd management

The data set and pedigree information included 12116 live weight records from birth to 365 days of age of 3078 Markhoz goats. Animals with records were progeny of 202 sires and 1206 dams. A general description of the dataset is given in Table 1.

Number of records and average weights for different ages are shown in Fig. 1. Body weights increased from 2.5 kg at birth to 25.6 kg at about 365 days of age. These records were collected from 1992 to 2012 at Markhoz Goat Performance Testing Station in Sanandaj (1373 m above mean sea level and $35°20'$ N latitude and $47°.00$ E longitude), Kurdistan, Iran. In the station, does expose to selected bucks at about 18 months of age for first time. Annually 20–30 bucks were randomly allocated to mate with about 10 or 15 does each, with sire identification recorded. The mating season commences in October and ends in November. The bucks were used for 1–3 mating season. Kidding season starts in early February and ends in late March. After kidding, kids were weighed, ear-tagged and their parents identified. In addition, kidding date, sex of kid and type of birth were recorded. The suckling stages lasts for 100 days on average. All kids were weaned at the same day, without necessarily at the same age. More details on the environment and flock management were described by Rashidi et al. (2008, 2011).

2.2. Statistical analysis

Changes in the mean with age were modelled through a fixed quartic regression using Legendre polynomials of age (in days). Preliminary least-squares analyses ignoring animals (with the help of the GLM procedure of SAS Institute Inc., 2003) were carried out to determine the order of polynomial fit required to model the population trajectory and orders of fit beyond quartic were nonsignificant. This fixed regression describes the 'overall' or 'average' growth curve of all animals with records (Lewis and Brotherstone, 2002). The fixed effects of sex (male and female), type of birth (single and twin), year of birth (1992–2012) and age of dam (2–6 and ≥ 7) significantly affected growth ($P < 0.001$) and thus constituted the fixed part of the animal model.

Four sets of random regression coefficients were fitted to the data. These included direct genetic effects, direct permanent and maternal permanent environmental effects and maternal temporary environmental effects (common litter). All RR models fitted Legendre polynomials of age at weighing (in days) as independent variables. The second to fourth order of polynomial were fitted for all random effects to identify the minimum order of fit required for each random effect, and therefore identifying the most parsimonious model that describe the data. The general model can be represented as follows:

$$y_{ij} = F_{ij} + \sum_{m=0}^{k_A-1} \alpha_{im}\phi_m(t_{ij}) + \sum_{m=0}^{k_B-1} \gamma_{im}\phi_m(t_{ij})$$
$$+ \sum_{m=0}^{k_C-1} \delta_{im}\phi_m(t_{ij}) + \sum_{m=0}^{k_D-1} \rho_{im}\phi_m(t_{ij}) + \varepsilon_{ij}$$

where y_{ij} denote the j-th record for animal i taken at time t_{ij}, t_{ij} is the age of recording for y_{ij}, standardized to $(-1 < t < 1)$ for which Legendre polynomials are defined and $\phi_m(t_{ij})$ is the corresponding m-th Legendre polynomial. F_{ij} represents the fixed effects pertaining to y_{ij} (i.e., age of dam, sex of kid, type of birth and year of birth). α_{im}, γ_{im}, δ_{im}, ρ_{im} are the m-th random regression coefficients for direct additive genetic effects, direct permanent environmental effects, maternal permanent environmental effects (half-sibs across years) and common litter effects (full-sibs within year), respectively; and k_A-1, k_B-1, k_C-1 and k_D-1 are the corresponding order of (polynomial) fit for each effect. Finally, ε_{ij} denotes the residual error.

Residual variance was assumed to be (a) constant (homogeneous) over time or (b) heterogeneous, considering 7 classes- (1–20, 21–60, 61–160, 161–260, 261–320, 321–340 and 341–365 days), 10 classes- (1–20, 21–60, 61–100, 101–160, 161–240, 241–260, 261–300, 301–320, 321–340 and 341–365 days) or 17 classes-depending on age (1–20, 21–60, 61–80, . . ., 321–340 and 341–365 days). When 10 or 7 classes were used, the variances were divided according to similarity based on the residual variance estimated with the model containing 17 classes. To define the best structure to model the residual variances, the order of fit for the other random effects (i.e. animal, direct permanent and maternal permanent environmental and common litter effects) were kept constant and equal to two.

2.3. Covariance functions (CF) and breeding value (BV) calculations

Random regression analyses yield **K** matrices involving (co)variance between RR coefficients. The CF can be written in matrix notation as: $\hat{G} = \phi k_A \phi'$ where $\hat{G}$ is the genetic covariance matrix of order t for direct genetic effects at t given ages, and ϕ is a t by k matrix with Legendre polynomials (Meyer and Hill, 1997). The same operation was applied for all other random factors. Covariances between RR coefficients pertaining to different random factors were assumed to be zero. All analyses were performed using the WOMBAT software package with AI-REML methodology on a Linux operating system (Meyer, 2007).

Over the course of growth, daily BV computed for each animal from the random regression coefficients. Let v be a vector containing daily BV for days of age 1 to 365, then v can be calculated as:

$v_{ij} = t_j \times \alpha'_i$, where α_i represents solution for animal i, and t_j is the vector of coefficients of the Legendre polynomial corresponding to standard j-th days of age. Genetic trends were obtained by regression means of predicted breeding values on year of birth for each trait. Genetic trends analyses were performed with the regression procedure of the SAS software package (SAS Institute Inc., 2003).

2.4. Model choice

Models with different orders of fitting and random effects were compared by maximum likelihood ratio test (LRT). The log-likelihood ratio test only allows comparisons between nested models and tends to favor models with higher number of parameters (Meyer, 2000; Albuquerque and Meyer, 2001). Restricted maximum likelihood forms of information criteria such as AIC (Akaike's Information Criterion) and BIC (Schwarz's Bayesian Infor-