Variance Components Of Growth In Polish Sheep Described By Random Regression Models

A. Wolc[*†], E. Barczak [*], J. Wójtowski [‡], P. Ślósarz [‡] and T. Szwaczkowski[*]

Introduction

In Poland over last decades the economic importance of wool production has been gradually decreasing therefore the major income of sheep breeders is nowadays generated through lamb production. This led to an interest in developing selection strategy to achieve weights and body composition on the level of consumers' demands. The papers by Dobek et al. (2004) and Szwaczkowski et al. (2006) described genetic variation in body weight at birth and at 28 days in the Polish sheep population. These studies however, were based on only two measurements per animal so did not consider the longitudinal nature of body weight. Two main approaches were recommended recently for genetic evaluation of growth in sheep: fitting nonlinear regression (eg. logistic, exponential, Gompertz or Richards models) to the data and estimating genetic parameters for growth curves (Lambe et al. 2006) or using random regression methodology (Lewis and Brotherstone (2002); Fisher et al. (2004); Molina et al. (2007)). Despite many advantages and increasing popularity of the second approach random regression models sometimes lead to overestimation of variance components at the ends of age trajectory (López-Romero and Carabaño (2003)). Therefore it is worthy to check the behavior of covariance curves by more standard approaches like multi-trait analysis. Therefore, the objective of this study was to estimate genetic parameters of body weight in sheep using random regression and multi-trait models.

Material and methods

The records on sheep from Wielkopolska region were made available from three experimental farms of the Department of Small Mammal Breeding and Animal Materials of Poznan University of Life Sciences. Body weight was measured at birth and at 28, 56,100 and 150 days (+/- 5 days) and standardized for these ages. Numbers of records and means for different age classes are given in Table 1.

Table 1. Mean and standard deviation for body weight (kg) in different age classes

	N	mean	SD
BW0	31694	4.38	0.87
BW28	29489	12.34	2.56
BW58	7856	23.00	5.21
BW100	25455	29.36	5.80
BW150	19245	38.99	6.72

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[*] Department of Genetics and Animal Breeding, University of Life Sciences in Poznan, Wołyńska st. 33, 60-637 Poznan, Poland

[†] Department of Animal Science, Iowa State University, 239C Kildee Hall, Ames, IA, 50011-3150, USA

[‡] Department of Small Mammal Breeding and of Animal Materials, University of Life Sciences in Poznan, Zlotniki, Sloneczna st. 1, 62-002 Suchy Las, Poland

The pedigree included 37790 animals with 736 sires and 9318 dams with recorded progeny. A more detailed description of the population was given by Dobek et al. (2004).

Statistical analyses. The data were analyzed according to the following model using linear regression on age

$$y_{ijk\ln} = F_i + \sum_{m=1}^{m_1} b_m z_{mn} + \sum_{m=0}^{m_2} a_{jm} z_{mn} + \sum_{m=0}^{m_3} m_{lm} z_{mn} + \sum_{m=0}^{m_4} pe_{jm} z_{mn} + e_{ijk\ln}$$

where:

y_{ijkn} is a body weight at the n-th month on animal j in the fixed effect i,

F_i represents the fixed effects pertaining to y and includes herd (3 levels), sex (2 levels), birth type (3 levels), age of mother at birth (10 levels), year of birth (17 levels), line (8 levels)

b_m is the m-th fixed regression coefficient,

a_{jm} is the m-th random regression coefficients for the additive genetic effect of animal j,

m_{lm} is the m-th random regression coefficients for the maternal environmental effect of dam l,

pe_{jm} is the m-th random regression coefficient for the permanent environmental effect of animal j,

z_{mn} is the value of m-th degree Legendre polynomial at month n,

e_{ijkln} is a random residual effect,

m_1 to m_4 are degrees of covariates fitted to fixed, genetic, and permanent environment effects, with m_1=2 and m_2 to m_4 equal to 1.

Heterogeneous residual variance was assumed across ages.

For comparison a multitrait model was used assuming measurements at different ages were separate but correlated traits. The analysis was performed using ASREML (Gilmour et al. (2006)).

Results and discussion

In the analysed period body weight was increasing with age and so was the standard deviation so that the coefficient of variation reminded at the relatively constant level of 17-22% across ages. Almost linear growth in the first 5 months of life was also registered in other sheep breeds like Poll Dorset, Somalis Brasileira and Santa Inês (Oliveira (2008)). The average growth and growth rate in our population was higher than in Santa Ines sheep (Sarmento at al. (2006)). The limitation of this study comparing to for example experimental flock described by Lewis and Brotherstone (2002) was that weights corrected for five ages were available, with much fewer records at age 56 days, so only a few observations were available per animal. Therefore, we decided to use only mean and slope for genetic, maternal and permanent environmental effects. We estimated separate residual variance for each age class as according to several studies an assumption of homogenous residuals does not hold for growth traits in small ruminants (Lewis and Brotherstone (2002), Fisher at al. (2004), Sousa et al. (2008)). However, as there was a good agreement between random regression and multi-trait models, except weight at first month were the estimates for residual plus permanent environmental components were higher under RRM than MT we think that the model was sufficient to describe the data. The variance of all components taken into account (additive genetic, maternal, residual) was increasing with age (Figure1).

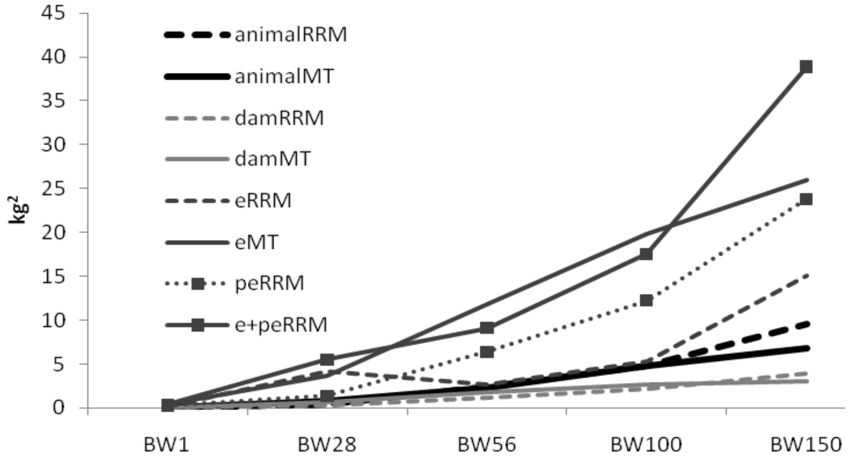

Figure 1. Variance components of body weight in sheep under random regression and multi-trait models

An increase of direct additive genetic variance with age was observed by Sarmento et al (2006) in Santa Ines sheep and by Molina et al. (2007) in Spanish Merino. The proportion of maternal effect was decreasing with age, whereas direct heritability tended to increase over time (Figure 2).

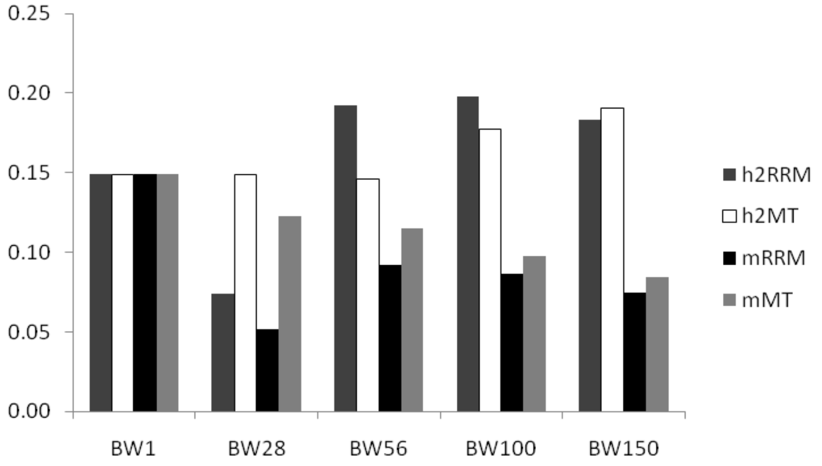

Figure 2. Genetic parameters of body weight in sheep under random regression and multi-trait models. h2RRM – heritability under random regression model, h2MT – heritability under multi-trait model, mRRM – proportion of maternal environmental component under random regression model, mMT – proportion of maternal environmental component under multi-trait model

The tendency for increasing direct heritability, decreasing maternal effect and relatively constant proportion of individual permanent environmental component was also estimated by Sarmento et al. (2007). A very similar pattern was also observed in Poll Dorset sheep by Fisher et al. (2004) and Lewis and Brotherstone (2002). In the analysed population the estimates of repeatability under random regression model were between 0.64 and 0.70 except the first month where it dropped to 0.29. Different shapes of variance component curves were estimated for Brazilian populations by Oliveira (2008), these however for Poll Dorset, Somalis Brasileira were based on small numbers of records. For Chokla sheep (Kushwaha et al. (2009)) under comparable model direct heritability was 0.23 at birth, 0.22 at 3 months, and 0.16 at 6 months whereas maternal environmental effect was high at birth $c^2 = 0.19$, and low for older ages 0.07 and 0.08 for 3 and 6 months, respectively. An alternative approach to modeling growth by fitting nonlinear growth curves and estimating heritability for curve parameters was presented by Lambe et al. (2006) with moderate to high estimates. The changes in genetic determination of body weight with age were confirmed by molecular study of Hadjipavlou and Bishop (2008), who found age-dependent quantitative trait loci in Scottish Blackface lambs.

Conclusion

The results confirm that there is a scope for genetic improvement in growth pattern in Polish sheep.

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