Estimates Of The Genetic Parameters For Local Turkey Of Azerbaijan For Body Weight With Random Regression Analysis

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Introduction

Random regression models (RRM), is a methodology that has been used for the genetic study of longitudinal data. It is recommended that application of RRM to growth traits will be a growing area of research (Schaeffer 2004). Recently, linear RRM have received major attention and Misztal (2006) has shown properties of linear spline functions used in RRM. For some traits, there may be many more data point at the younger ages, and there may be sequential selection. In general, estimating covariance matrices between certain ages of the trajectory can be useful as a reference for checking parameter estimates for covariance functions. Early researches reported that the heritability (h2) for BW of turkeys during the growing period in selected populations were 0.16 to 0.31 (Nestor *et al*. 2008). In this paper we used body weights which recorded at two weeks intervals as repeated measurements of the same trait in the random regression model.

Material and methods

Data consisted of 15562 individual body weights from 964 turkeys recorded at 1 and 2 to 32 by 2 weeks of age. Animals were bred in the breeding station of indigenous turkey located at Tatar (Elyasi *et al*. 2007). Body weight has been used as a common trait for both sexes as study of Kranis *et al*. (2006). To take into account the repeated measurements of weight for each animal, specific overall growth curve was modeled using a cubic smoothing spline with knots at 1, 2 to 32 by 2 weeks of age and the animal deviation to this curve was modeled using a random regression function. Following Verbyla *et al*. (1999), the model can be written as a random regression animal model:

$$\boldsymbol{y} = \boldsymbol{X}\boldsymbol{\beta} + \boldsymbol{Z}_s\boldsymbol{s} + \boldsymbol{Z}_u\boldsymbol{u} + \boldsymbol{W}\boldsymbol{p} + \boldsymbol{\varepsilon}$$

Where $\boldsymbol{y}$ is the vector of observations, $\boldsymbol{\beta}$ is the vector of fixed effects including fixed regression coefficients (the combination age.sex and the color) with incidence matrix $\boldsymbol{X}$. $\boldsymbol{s}$

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is the vector of female ($\boldsymbol{s_f}$) and male ($\boldsymbol{s_m}$) overall spline parameters with length 2*15 and covariance matrix $\begin{bmatrix}\sigma^2_{sm} & 0\\ 0 & \sigma^2_{sf}\end{bmatrix}$. $\boldsymbol{u}$ is a vector of genetic intercept ($\boldsymbol{u}_1$) and slope ($\boldsymbol{u}_2$) breeding value parameters for each animal in the pedigree with covariance matrix $\begin{bmatrix}\sigma^2_{u1} & \sigma_{u1u2}\\ \sigma_{u1u2} & \sigma^2_{u2}\end{bmatrix}\otimes \boldsymbol{A}$ where $\boldsymbol{A}$ is the relationship matrix and $\otimes$ represents the kronecker product, $\boldsymbol{p}$ is the vector of permanent environmental intercept ($\boldsymbol{p}_1$) and slope ($\boldsymbol{p}_2$)with covariance matrix $\begin{bmatrix}\sigma^2_{p1} & \sigma_{p1p2}\\ \sigma_{p1p2} & \sigma^2_{p2}\end{bmatrix}$. $\boldsymbol{\varepsilon}$ is the vector of random iid residuals. All data were analysed with the ASReml package (version 2.0 - Gilmour *et al*., 2006).

Results and discussion

Estimates of heritability increased over the trajectory and peaked at 0.60 around 20 to 32 weeks of age (Figure 1). The heritability for 16-week body weight was 0.56 ± 0.04 that is within reported estimates ranged 0.44 to 0.83 (Chapuis *et al*. (1996); Nestor *et al*. (2008)) . We found a general trend of increasing h2 for BW with age, concordant with the results of Wilson *et al*. (2005).

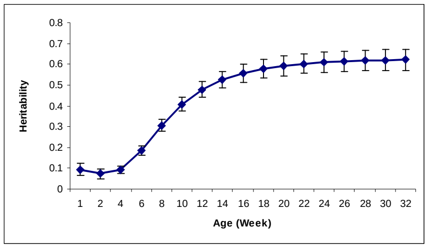

Figure 1: Estimation of genetic parameters (with SE) for body weight of local turkey.

Table 1 shows the phenotypic and genetic correlations between ages. In general, genetic correlation estimates were higher between adjacent ages, decreasing markedly with the increase of ages. Estimates ranged from -0.52 to 1.00. Negative genetic correlations were observed between ages at the beginning and at the end of recording period. As Figure 2 shows, the genetic correlation between subsequent ages approaches unity, however, the genetic correlation between week 2 and week 32 weights is moderate (-0.20) suggesting that early weights are not under exactly the same genetic control as weights taken at an older age. The genetic correlation between BW at first age week 1 and BW at ages after 6 week was negative. This pattern indicates the presence of negative additive genetic covariance between early-age and later BW traits, suggesting that some allelic variants cause individual growth trajectories to be below the average at early ages and above by age at 6 weeks. We examined polynomial quadratic for the estimation, but the convergence has not been obtained.

Convergence problems has been mentioned when estimating variance components with RRM (Anang *et al.* 2002). In this study to compare RRM to more spurious model, data were also analyzed with a simple repeatability model. For comparison of two models, we used the ratio of likelihood of chi-2 (19522) that was significant. Therefore it seems that RRM model is better than the simple model. The estimation of heritability with simple (univariate model) model was 0.4751 ± 0.0144.

Table 1: Estimates of heritability (diagonal), genetic (above diagonal) and permanent environmental (below diagonal) correlation of body weight.

	1	2	4	6	8	10	12	14	16	18	20	22	24	26	28	30	32
1	**0.10**	0,94	0,43	0,00	-0,20	-0,30	-0,37	-0,41	-0,43	-0,45	-0,47	-0,48	-0,49	-0,43	-0,51	-0,51	-0,52
2	0,99	**0.07**	0,70	0,33	0,13	0,03	-0,04	-0,08	-0,11	-0,13	-0,15	-0,16	-0,18	-0,18	-0,19	-0,20	-0,20
4	0,92	0,99	**0.09**	0,91	0,80	0,73	0,69	0,65	0,63	0,61	0,60	0,59	0,58	0,57	0,56	0,56	0,55
6	0,77	0,85	0,97	**0.19**	0,99	0,94	0,94	0,92	0,91	0,90	0,89	0,88	0,88	0,87	0,87	0,86	0,86
8	-0,03	0,70	0,86	0,97	**0.31**	1,00	0,99	0,98	0,97	0,97	0,96	0,96	0,95	0,95	0,95	0,95	0,94
10	0,45	0,56	0,77	0,91	0,98	**0.41**	1,00	1,00	0,99	0,99	0,99	0,98	0,98	0,98	0,98	0,97	0,97
12	0,33	0,45	0,68	0,86	0,95	0,99	**0.48**	1,00	1,00	1,00	1,00	0,99	0,99	0,99	0,99	0,99	0,99
14	0,23	0,35	0,61	0,79	0,91	0,97	1,00	**0.53**	1,00	1,00	1,00	1,00	1,00	1,00	0,99	0,99	0,99
16	0,15	0,28	0,53	0,74	0,88	0,95	0,99	1,00	**0.56**	1,00	1,00	1,00	1,00	1,00	1,00	1,00	1,00
18	0,22	0,22	0,49	0,72	0,85	0,93	0,97	0,99	1,00	**0.58**	1,00	1,00	1,00	1,00	1,00	1,00	1,00
20	0,04	0,17	0,45	0,67	0,82	0,91	0,96	0,97	1,00	1,00	**0.59**	1,00	1,00	1,00	1,00	0,57	1,00
22	0,00	0,13	0,40	0,64	0,80	0,89	0,95	0,97	0,99	1,00	1,00	**0.60**	1,00	1,00	1,00	0,62	1,00
24	-0,81	0,10	0,37	0,61	0,78	0,88	0,94	0,97	0,98	0,99	1,00	1,00	**0.61**	1,00	1,00	0,65	1,00
26	-0,06	0,07	0,35	0,59	0,76	0,87	0,93	0,96	0,98	0,99	1,00	1,00	1,00	**0.61**	0,99	0,68	1,00
28	-0,08	0,05	0,32	0,57	0,75	0,85	0,92	0,95	0,97	0,98	0,99	1,00	1,00	0,99	**0.62**	0,70	1,00
30	-0,10	0,03	0,31	0,56	0,73	0,84	0,91	0,95	0,97	0,98	0,99	0,99	1,00	1,00	0,99	**0.62**	1,00
32	-0,12	0,01	0,29	0,54	0,72	0,83	0,90	0,94	0,96	0,98	0,99	0,99	1,00	1,00	1,00	1,00	**0.62**

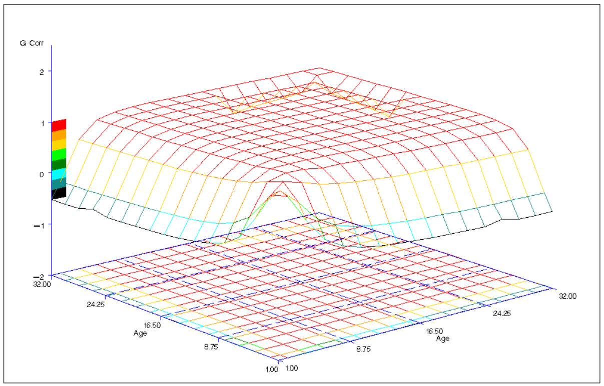

Figure 2: Graphical illustration of genetic correlation estimates for body weight along 1-32 week of ages.

Some studies reported overestimation of heritability or unexpected genetic correlations between test day milk yields at different stages of lactation using RRM (Brotherstone *et al.*, 2000; Kettunen *et al*., 2000). Generally an inflated variance estimate at the end age points has been noted as a problem in RR models (Hadjipavlou *et al.* 2009). Costa *et al*. (2008) reported negative correlation estimates for the extreme parts of the lactation in dairy cattle. In goose it has been showed that from the physiological perspective, body weight and its changes over time determined by various effects of genes depending on the age of individuals. Therefore, longitudinal models are the most favourable for analysing body weight data (Szwaczkowski *et al*. 2007). This study showed that genetic variation exists in the growth curves of local turkeys. As it is shown in sheep (Fischer *et al*. 2004) , body weight early in life is a different trait to weight later in life (Figure 2 and Table 1). The correlation between extreme ages may have been underestimated. Further investigation about selection potential for BW of local turkeys in early ages is needed.

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