Genetic Evaluation of Growth for Beef Bulls at a Performance-test Station

L. Vostrý[*†], J. Přibyl[†*], K. Mach[*], Z. Veselá[*], B. Hofmanová[*]and I. Majzlík[*]

Introduction

Growth is a very complicated trait. The growth ability of cattle is generally evaluated for genetic or feeding experiments by means of body weight at different ages or by means of average daily gains in a definite time period.

For accurate evaluation of the growth ability of bulls, it is necessary to determine the significant effects influencing the growth of bulls under test. Growth is a cumulative characteristic where weight gain at a given moment is influenced by the preceding history of the animal. It was demonstrated in several studies that the herd of origin effect was closely related to the growth ability of bulls in a subsequent test (Schenkel et al. (2003); Přibylová et al. (2004)). This is so because environmental conditions and herd management influence weight variability at the beginning of the test, and consequently, average daily weight gains during the test are influenced. Liu and Makarachian (1993), e.g., studied the influence of bull age and weight at the beginning of the test on the growth ability of bulls under test. However, this influence of pre-weaning environmental conditions may persist until the termination of the test. Different herd conditions lead to growth compensation in animals which should be distinguished from the effect of genetic constitution. The cited authors stated that the evaluation of growth on the basis of weight gains in consecutive growth segments was more suitable than evaluation according to body weights because it is possible to determine more exactly the effects of fixed and random environment which influence the animal growth during particular periods.

Material and methods

Data from a field test and from performance test stations on both body weight and average daily gains were provided by the Czech Beef Breeders Association (www.cschms.cz). The evaluation was performed by multi-breed AM with genetic groups according to breeds incorporated into the relationship matrix. Ten breeds of beef cattle were included in the analysis. Each breed was represented by animals with an 88 – 100% gene share of the given breed born in 1990 – 2005.

Data: Data from the field test were data on 24 017 average daily gains from birth to 120 days of age (ADG120) and 16 427 records on average daily gains from 120 to 210 days of age (ADG210) for young bulls and heifers. Data from the performance test station comprised 3 429 records on the average daily gains of tested bulls (ADGT).

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[*] Czech University of Life Sciences Prague, 165 00 Prague, Czech Republic

[†] Institute of Animal Science, 104 01 Prague, Czech Republic,

Statistical model: Variance components and genetic parameters were estimated using the multi-trait animal model. Different models were tested that were based on animal models used for the standard estimation of breeding value of a field test (Přibyl et al. (2003)) and bulls at performance test stations (Přibylová et al. (2004)).

Table 1: Models

Model		*AgeD*	*SEX*	*HYS*	*HLCO*	*bAB + b^{2}AB*	*a*	*m*	*tp*	*pe*
1	*PWW*	F=fixed	F	F			R=random	R	R	
	ADGT	F		F	F	F	R			
2	*PWW*	F	F	F			R	R	R	R
	ADGT	F		F		F	R			R

PWW - pre-weaning weight (ADG120, ADG210), ADGT - average daily gain in performance test stations, AgeD - effect of dam's age, SEX - effect of sex, HYS – preweaning: effect of herd×year×season; test station: test station×year×season, HLCO - effect of herd level of calf's origin according reaction norm, bAB+b^{2}AB - linear and quadratic regression on age at the beginning of test, a - effect of animals, m - maternal genetics effect, tp - maternal permanent environment effect, pe - permanent environmental effect of animal.

We assume that effects a and m are correlated with each other and that the remaining effects (tp, pe and e) are independent of each other within the particular traits. We also assume that the effects show normal random distribution with zero average and variance (σ^2).

$$V\begin{bmatrix} a \\ m \\ tp \\ pe \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 & 0 & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 & 0 & 0 \\ 0 & 0 & I\sigma_{tp}^2 & 0 & 0 \\ 0 & 0 & 0 & I\sigma_{pe}^2 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

where:

σ^2_a – additive genetic variance of direct effect, σ^2_m – additive genetic variance of maternal effect, σ_{am} – genetic covariance of direct and maternal effect [Cov(a,m)], σ^2_{tp} – variance of the effect of permanent maternal environment, σ^2_{pe} – variance of the effect of permanent environment of animal, σ^2_e – variance of the effect of residual error, A – relationship matrix, I – identity matrix

Results and discussion

Table 2 shows the estimated values of the coefficient of direct and maternal heritability (h^2_a, h^2_m), genetic correlations of direct and maternal effect (r_a, r_m), and correlations between direct and maternal effect (r_{am}).

Negligible differences were determined in the values of direct heritability coefficients (h^2_a) for the daily gains studied. The values of h^2_a for average daily gains were in the following ranges: 0.16 – 0.17 for ADG120, about 0.13 for ADG210, and about 0.27 for ADGT. The omission of the fixed effect of HLCO decreased the value of h^2_a in ADG120. However, the value of h^2_a in ADGT increased. This increase in the value of h^2_a in ADGT was caused by the higher value of σ^2_a. Schenkel et al. (2004) reported markedly higher values of h^2_a for average daily gains (pre-weaning gains – 0.36, gain during test 0.34 to 0.41). The same values of h^2_a

for gains during test as those of Schenkel et al. (2004) were also published by Eriksson et al. (2002).

Genetic correlations of direct effect (r_a) for the particular traits ranged from 0.079 to 0.480. The highest value of r_a was estimated between ADG120 and ADG210. A moderate correlation between the models was determined for ADGT and the other average daily gains. The highest values of r_a were calculated in Model 1. In the Model 2, the values of r_a were influenced by the inclusion of the random effect of the animal permanent environment. The high value of r_a estimated by all tested models between ADG120 and ADG210 can be explained by the fact that ADG120 and ADG210 are under the influence of very similar environmental conditions (grazing system).

Coefficients of maternal heritability (h^2_m) for average gains showed, similar to those in h^2_a, only negligible changes for the estimation by the tested models. The values of h^2_m for ADG120 ranged above 0.12 – 0.13 and for ADG210 above 0.04. The markedly lower value of h^2_m was estimated for ADG210 in all the models tested. The results document that ADG210 was influenced to a large extent by a direct effect, while maternal effect does not influence ADG210 very much. Similar to that of h^2_a, Schenkel et al. (2004) calculated a higher value of h^2_m for pre-weaning growth (h^2_m = 0.36) than was estimated in this paper. In their paper, Schenkel et al. (2004) confirmed our assumption that maternal traits did not substantially influence growth during the test.

Table 2: Estimates of direct and maternal heritability (diagonal) and genetic correlations

	Model 1	ADG120*a*	ADG210*a*	ADGT*a*	ADG120*m*	ADG210*m*
Model 1	ADG120*a*	**0.172**	0.480	0.252	-0.595	-0.092
	ADG210*a*		**0.132**	0.111	-0.242	-0.231
	ADGT*a*			**0.274**	0.070	0.336
	ADG120*m*				**0.128**	0.791
	ADG210*m*					**0.037**
Model 2	ADG120*a*	**0.158**	0.477	0.239	-0.597	-0.089
	ADG210*a*		**0.130**	0.082	-0.250	-0.248
	ADGT*a*			**0.277**	0.078	0.362
	ADG120*m*				**0.117**	0.797
	ADG210*m*					**0.038**

Animal permanent environment

The random effect of the animal permanent environment (*pe*) showed lower values for average daily gains (Table 3). The values of c^2 accounted for ca. 3 to 36% of the total variability of the traits studied. The highest value of c^2 was estimated in ADG120 and the lowest in ADGT. This low value of c^2, as mentioned above, was caused by a marked change in environmental conditions, i.e., rearing vs. test conditions.

Table 3 shows the correlations of the animal permanent environment (r_{pe}) among average daily gains. Comparison of the values of r_{pe} within the particular models showed that the highest value was estimated between ADG120 and ADGT (0.419). On the contrary, the lowest value of r_{pe} was calculated between ADG210 and ADGT. The negative value of r_{pe}

between ADG210 and ADGT can be explained in the following way: the animals which had lower gains in the pre-weaning period due to effects connected with the management and environmental conditions of the herds compensated their growth during the test. On the other hand, the animals which had good growth in the pre-weaning period of demonstrated slower their growth under standardized test conditions as a result of the effect management and environmental conditions on the herds. This negative value of r_{pe} between ADG210 and ADGT becomes more important, since c^2 assumes a low value in ADGT. Several authors (e.g. Tong et al., (1986)) also estimated a mean negative environmental correlation (-0.41 to -0.09) between pre-weaning growth and growth in a station test. Schenkel et al. (2002) reported that due to the influence of the above-mentioned growth compensation, a problem of correct evaluation and subsequent selection of bulls for breeding might arise. These problems could be minimized by the multi-trait model comprising pre-weaning growth.

Table 3: Correlations between the permanent environments of an individual

	Model 2		
Vlastnosti	ADG120	ADG210	ADGT
ADG120	**0.301**	0.211	0.419
ADG210		**0.175**	-0.366
ADGT			**0.027**

Conclusion

Bulls for performance test stations undergo pre-selection. The results showed that model 2 was the most suitable for genetic evaluation of the growth of beef bulls, in which the random effect of the animal permanent environment was included and from which the fixed effect of HLCO was omitted.

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