Genetic Evaluation Of Growth In The Dual-Purpose Bulls

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Introduction

Growth traits, such as bodyweight and particularly average daily gains, are important performance indicators for dual-purpose cattle breeds (Cantet *et al.* (2003)). For such growth traits, there is an increased availability of repeated records per animal gathered over a certain test period. Legarra *et al.* (2004) developed a methodology for the conversion of parameters of multi-trait and random regression models. The objective of this paper is to adjust random regression models suited for the analysis of average daily gains. Due to special data preparations, it became possible to use a multi-trait model as reference model. The time-dependent heritability values estimated with various random regression models, which differed in their polynomial degree, were compared to the results from the reference model. The further focus of this study lies on the estimation of breeding value (BV) for average daily gains during the test period for both model variants and on the comparison of the estimated breeding value using rank correlations and top-lists.

Material and methods

The data analyzed in this study were gathered from more than 6000 bulls of Czech Pied breed, performed tested from 1971 to 2007 at 7 test stations. The bulls were progeny of a total of 253 sires, thus every bull had 26 half-sibs on average. The time period from 12 to 420 days of age was observed. In order to be able to evaluate the performance data with a multi-trait model (MTM), 8 age periods were defined. As average daily gain (DG1 to DG8) of a certain animal within these 50-day age periods, the performance with the smallest temporal distance to the middle of the age period (i.e. d = 37, 88, 139, 190, 241, 292, 343 and 394) was selected. The effects of station, year and season were taken into account through the creation of Herd*Year*Season classes (HYS) with 3-month intervals chosen for the season. Per HYS class, at least 40 records were required to be available. Let y_{ijk} be the record of animal j in HYS-class i for trait k gathered at age d_{ijk}. For the MTM, we then obtain the following shape:

$$y_{ijk} = \beta_{0,ik} + \beta_{1,ik} d_{ijk} + \beta_{2,ik} d_{ijk}^{2} + a_{ijk} + p_{ijk} + e_{ijk}$$

Here, $\beta_{m,ik}$ denotes fixed regression coefficients (with m= 0,1,2), a_{ijk} is the additive genetic effect of animal j in HYS-class i for trait k, p_{ijk} represents the permanent environmental effect of animal j, and e_{ijk} is the random residual effect.

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The following random regression model (RRn) was used for the analysis of average daily gains:

$$y_{ijk} = \sum_{m=0}^{n} \delta_{im}\phi_m(t_{ijk}) + \sum_{m=0}^{n} \alpha_{jm}\phi_m(t_{ijk}) + \sum_{m=0}^{n} \gamma_{jm}\phi_m(t_{ijk}) + e_{ijk} \quad n = 2,\dots,4$$

With: $y_{ij\,k}$ = gain at age k of animal j in Herd*Year*Season i, t_{ijk} = the standardized age in interval (-1,1), $\varphi_m(.)$ = the orthogonal Legendre polynomial of degree m, δ_{im} = fixed regression coefficients within Herd*Year*Season i, α_{jm} = the additive-genetic random regression coefficient of animal j, γ_{jm} = the permanent environmental regression coefficient of animal j, and e_{ijk} = random residual effect.

The estimation of variance components made use of the REML method of the program VCE5 (Kovac *et al*., 2002).

Results and discussion

The estimates of the heritability based on MTM and on the RRM at the 8 points of measurement are listed in Table 1. With values of 0.261, 0.164 and 0.069, the comparison of the h^2-values estimated with the MTM and those estimated with models RR2, RR3 and RR4 showed significant lower values for trait DG1. For the models with polynomials of the 3rd and 4th degree, the strongest underestimations were found at the beginning of the test period. The MTM and RRM differed only slightly in their h^2-values for traits DG2 to DG8.

Table 1: Comparison of h^2 coefficients for varying age estimated with different models

Model	DG1	DG2	DG3	DG4	DG5	DG6	DG7	DG8
MTM	0.290	0.100	0.132	0.168	0.203	0.167	0.130	0.045
RR2	0.261	0.115	0.104	0.147	0.164	0.134	0.094	0.129
RR3	0.164	0.071	0.115	0.148	0.162	0.156	0.120	0.073
RR4	0.069	0.083	0.112	0.180	0.190	0.148	0.129	0.076

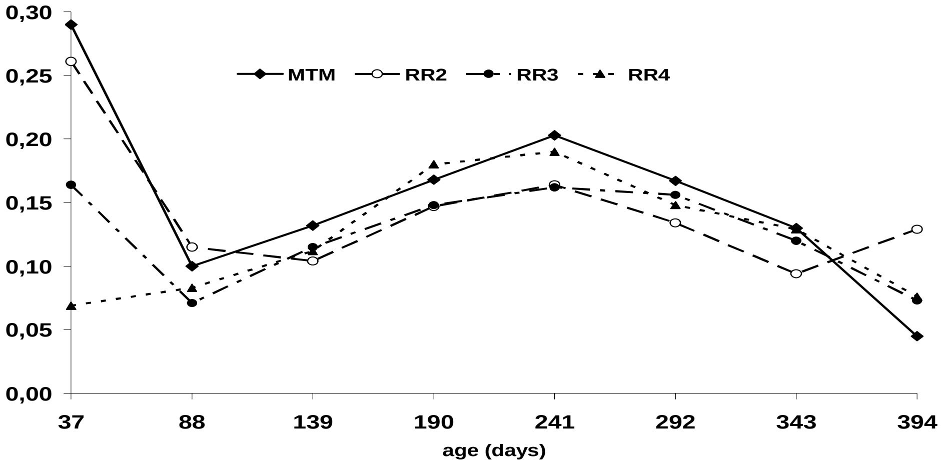

Figure 1: Estimated heritability function of RRM compared to the MTM estimates

The trends in the heritability estimates over the age for the comparison of RRM with the MTM are shown in Figure 1. For lower age values, the heritability estimates based on models RR3 and RR4 do not match with those from the MTM. However, the trait DG1 involved significant lower number of observation in comparison with the other traits. For intermediate and high age periods, the estimates of models RR3, RR4 and the MTM are very similar. The trend in the heritability estimates for the MTM can quite easily be modeled with the help of the estimated h2-curves of models RR2 and RR3.

In the Table 2 are given the means and standard deviations of the BV for all animals (with base value 0) as well as for the percentage rates of animals with highest BV due to MTM. With a decreasing proportion of the selected animals, the means increase, whereas the standard deviation of the BV is reduced. A comparison of the means shows that the closest match for all percentage rates is achieved for MTM and RR4.

Table 2: Means ($\overline{x}$) and standard deviations (in g) of breeding values for the top animals and for all animals estimated with the MTM and RRM

top %	**1**		**10**		**20**		**50**		**100**	
	$\overline{x}$	std	$\overline{x}$	std	$\overline{x}$	std	$\overline{x}$	std	$\overline{x}$	std
MTM	80.6	9.4	52.3	12.5	41.6	14.2	23.7	18.0	0	30.1
RR2	66.3	12.9	42.3	13.9	34.0	14.5	19.6	16.8	0	26.4
RR3	75.8	12.8	48.2	14.1	38.5	15.0	22.0	17.9	0	28.8
RR4	80.0	12.2	52.3	14.3	41.7	15.8	24.1	19.0	0	31.3

The rank correlations between the BV estimated with MTM and those from the RRM are listed in Table 3. For percentage rates of 10, 20, 50 and 100% model RR4 provided the highest value of correlations with MTM. Only for rate of 1% model RR3 achieved slightly higher value (0.790) when compared with model RR4. The rank correlations between RR2 and RR4 turned out to be lower then the correlations between RR models with adjacent polynomial degrees.

Table 3: Rank correlations between the breeding values estimated using the MTM and those estimated using RRM for the top animals and for all animals

top (%)		**1**	**10**	**20**	**50**	**100**
MTM	**RR2**	0.625	0.677	0.733	0.826	0.938
	RR3	0.790	0.781	0.834	0.903	0.969
	RR4	0.757	0.806	0.859	0.919	0.975
RR2	**RR3**	0.868	0.875	0.893	0.926	0.972
	RR4	0.561	0.672	0.745	0.831	0.937
RR3	**RR4**	0.741	0.789	0.852	0.914	0.972

Using the BV from the analyzed models, top-lists for the best 1 and 10% of all animals were compiled with consideration first given to all animals (including pedigree) and then given to only bulls with at least one record (see Table 4). The top-lists based on the BV estimated using MTM were compared to those estimated using the RRM. In addition, the number of animals appearing both in the top-list of MTM and in the top-list of one of the RRM was determined. Model RR2 showed the smallest number of common animals in both top-lists. In contrast, the relative proportions of common animals in the top-lists of MTM and the models RR3 and RR4 are higher. There is no significant difference between RR3 and RR4.

Table 4: Number (N) and proportion (in %) of common animals in the selected top lists of the MTM and RRM for all animals and for those with at least one record

Model	**all of animals**				**animals with records**			
	top 1% list (=71)		**top 10% list(=713)**		**top 1% list (=64)**		**top 10% list(=642)**	
	N	**%**	**N**	**%**	**N**	**%**	**N**	**%**
RR2	46	65	557	78	42	66	500	78
RR3	53	75	588	83	48	75	532	83
RR4	52	73	605	85	48	75	548	85

Conclusion

From the estimated rank correlations between the models as well as from the calculated numbers of common animals in different top-lists, it follows that models RR3 and RR4 bring breeding values with significantly higher degree of similarity to the values from MTM then those yielded by model RR2. If the approved multi-trait model is chosen as reference model, the RRM of 3rd and 4th polynomial degree are to be recommended for the estimation of breeding values for the average daily gain. The use of RRM models becomes a necessity when all available records per animal are to be considered instead of only those with the smallest temporal distance to the middle of the established time periods.

Some proceedings based on the presented methodology have been used for routine evaluation of young bulls since 2007 (Krejčová *et al.* (2008); Přibyl *et al.* (2008)). Future research activity should be focused on the validation of methodology by evaluation of independent data sets which prolonging the observed period to a higher age of the animals, and which test other types of functions.

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