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Approximate multivariate genetic evaluation of functional longevity and type traits in Austrian Fleckvieh cattle

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ABSTRACT: To optimize the subindex for functional longevity in Austrian Fleckvieh, an approximate multivariate approach was analyzed. Genetic parameters for functional longevity and five type traits were estimated multivariately based on yield deviations. Genetic parameters differed slightly from the ones used in the routine evaluation. Indices and reliabilities computed in a full multivariate approach were defined as reference and compared with three other approaches: (1) is based on approximate genetic correlations and selection index theory; (2) is an approach using multivariate estimates of genetic correlations; (3) is a univariate approach ignoring auxiliary traits. Rank correlations of indices based on different approaches were above 0.90, except for those based on univariate EBVs. Variances of indices were lower for the multivariate approach when reliabilities were low. Results indicate that reliabilities and variances of indices are overestimated for the approaches that are based on selection index theory.
Keywords: functional longevity approximate multivariate approach total merit index

Introduction

Improvement of the total merit index (TMI) is currently a major topic in the joint genetic evaluation of Austrian and German Fleckvieh (dual purpose Simmental) and Brown Swiss. In 2002, the TMI based on selection index theory was introduced in the transnational genetic evaluation. The use of selection index theory is however faced with some challenges: Traits or group of traits are usually evaluated separately based on different statistical models, and hence true genetic and phenotypic correlations or heterogeneous reliabilities are neglected (Ducrocq et al. 2001). A full multivariate estimation of all traits based on raw data is usually not feasible, but could be considered as the optimum methodology (Mrode, 2005). Thus, an approximate approach was proposed by Ducrocq et al. (2001), which is characterized by multivariate estimation based on yield deviations. This approximate approach was validated on simulated data. Genetic gain was increased and the estimation of genetic parameters was improved (Lassen et al. 2007). As a first step, this approach was tested for the functional longevity subindex in this study. Breeding values (EBV) for longevity were estimated using survival analysis techniques based on a Weibull sire maternal-grandsire model (Fuerst et al., 2013). For inclusion in the TMI, EBVs for longevity were combined with EBVs of auxiliary type traits using selection index theory. Genetic correlations between longevity and type traits were derived applying the

approximate method of Calo et al. (1973), ignoring residual correlations. This might lead to biased index values and reliabilities (r^2). The first aim of this study was to estimate genetic parameters for longevity and selected type traits based on yield deviations (YD). The second aim was the comparison of indices and their variances using four different approaches.

Materials and Methods

Data. For estimating variance components, YDs of longevity and type traits of 74,292 Austrian Fleckvieh cows born between 2002 and 2011 were used. The pedigree included 240,268 animals. Afterwards, EBVs were computed for 409,206 animals. In accordance with routine genetic evaluation, the type traits hip width, body depth, muscularity, feet and legs and udder score were used as auxiliary traits.

Statistical analyses. For all six traits, YDs and weights were computed univariately using Survival Kit v6 (Ducrocq et al. 2010) for longevity and MiX99 (Lidauer et al. 2011) for type traits, respectively. YDs for longevity were computed as a function of the cumulative hazard of a particular individual (Ducrocq, 2001). YDs were used for all further approaches, including variance component estimation based on an animal model using ASReml 3.0 (Gilmour et al. 2009).

The first approach (A1) was a full multivariate animal model based on YDs of all six traits. For the second approach (A2), EBVs were calculated separately for each trait. By means of genetic correlations which were computed in the full multivariate variance component estimation, these EBVs were then combined into a longevity index. For the third approach (A3), approximate genetic correlations from the routine evaluation were used instead of the ones estimated with the full multivariate model (Table 1). Longevity indices A2 and A3 were calculated by the method described by Miesenberger (1997), which is based on selection index theory. Residual covariances are assumed to be zero in this approach. In both cases A2 and A3, the economic weight for longevity was set to 100%; i.e. no weight was put on the type traits. In the fourth approach (A4), EBVs for functional longevity were used ignoring auxiliary type traits. Reliabilities were calculated by means of the program ApaX (Stranden et al. 2001). Based on the r^2 of approach A4, EBVs were grouped into eight classes (1 to 10%, 11 to 20%, 21 to 30%, 31 to 40%, 41 to 50%, 51 to 60%, 61 to 70% and >70%). Comparisons of the four dif-

ferent approaches were carried out by Tukey´s multiple comparison and Spearman rank correlations (SAS, 2008).

Table 1. Approximate genetic correlations used for longevity and the type traits hip width (hw), body depth (bd), muscularity (mu), feet and legs (fl) and udder (ud) of A3.

Type trait	Genetic correlation
hw	-0.13
bd	-0.28
mu	0.15
fl	0.36
ud	0.39

[&]For calculation, breeding values were standardized to a mean of 100 and standard deviation of 12 units, higher values being favorable

Results and Discussion

Genetic parameters. Heritabilities (h^2), genetic and phenotypic correlations of the 6-trait estimation are given in Table 2. Standard errors for all parameters are small (below 0.05). Heritabilities for longevity, muscularity and udder are slightly differing from the values used in the routine evaluation (12%, 28% and 24%, respectively, Fuerst et al. 2013). Compared to the approximate correlations (Table 1), genetic correlations with longevity are slightly lower for all traits, except for feet and legs and udder score. The results confirm the negative genetic correlation of size to longevity and the positive correlation of functional conformation traits. The correlation of the muscling of the cows to longevity turns out to be close to zero in this dataset. Although the differences to the approximate Calo-correlations are rather small, the use of genetic parameters estimated multivariately is preferable.

Table 2. Estimates of genetic parameters[&] for longevity (long), hip width (hw), body depth (bd), muscularity (mu), feet and legs (fl) and udder (ud).

trait	long[§]	hw	bd	mu	fl	ud
long	**0.08 ±0.006**	-0.08[a]	-0.14	-0.08[a]	0.39	0.40
hw	-0.01	**0.23 ±0.011**	0.64	0.39	-0.04[a]	0.03[a]
bd	-0.02	0.45	**0.22 ±0,011**	0.17	-0.06[a]	0.02[a]
mu	0.006[a]	0.42	0.29	**0.36 ±0.012**	-0.08	-0.27
fl	0.08	0.06	0.08	0.10	**0.11 ±0.007**	0.40
ud	0.10	0.04	0.05	0.007[a]	0.24	**0.30 ±0.011**

[&]Heritabilities and standard errors (±SE) on diagonal, genetic correlations above diagonal and phenotypic correlations below diagonal
[§]Higher YD values are favorable
[a]Not significantly different from zero (P>0.05)

Breeding values and reliabilities. Spearman rank correlations between longevity indices estimated with approaches A2 and A3 and the reference approach A1 are above 0.90 over all reliability groups (Table 3). As expected, correlations increase with increasing reliabilities. Approach A2 shows increasing advantages over A3 with higher reliabilities; only with very low reliabilities does A3 show slightly higher correlations. Rank correlations between A4 and A1 are markedly lower as no auxiliary traits are included in this case. Figure 1 shows the standard deviation of indices for methods A1 and A2 grouped by the reliabilities of A4. A2 leads to higher variances of indices, particularly when reliabilities are low. This is probably due to neglecting residual covariances in the approach of Miesenberger (1997) used in the routine evaluation. This is also related to overestimated reliabilities for A2 and A3 compared to the reference approach A1. Higher reliabilities are expected when using multivariate estimation because of better connectedness in the data, as genetic and residual covariances between traits are taken into account. Reliabilities increase when the absolute differences between genetic and residual correlations are large (Thompson and Meyer, 1986). This suggests that reliabilities and variances of indices are overestimated in the routine evaluation.

Table 3. Spearman rank correlations of EBVs with EBVs from approach A1 grouped by their reliabilities.

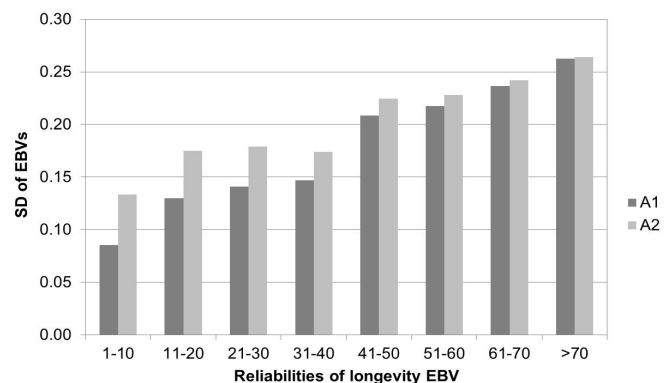| Reliability	A2	A3	A4
1-10%	0.900	0.914	0.814
11-20%	0.917	0.922	0.837
21-30%	0.937	0.932	0.888
31-40%	0.938	0.922	0.873
41-50%	0.976	0.949	0.897
51-60%	0.983	0.959	0.911
61-70%	0.989	0.965	0.942
>70%	0.991	0.987	0.981

Figure 1. Standard deviation (SD) of EBVs grouped by reliabilities.

Conclusions

Estimation of genetic parameters based on YDs in a multivariate animal model is feasible and could easily

replace the use of the approximation by Calo et al. (1973). The current method based on selection index theory leads to slightly overestimated variances and reliabilities, particularly in case of low reliabilities. A multivariate approach utilizing YDs seems to be feasible for routine evaluation but has to be investigated in more detail. An alternative approach based on de-regressed proofs instead of YDs should also be tested. Furthermore the inclusion of genomic information has to be solved.

Acknowledgments

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