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Short communication: Genetic relationships between functional longevity and direct health traits in Austrian Fleckvieh cattle

C. Pfeiffer,*[1] C. Fuerst,† V. Ducrocq,‡ and B. Fuerst-Waltl*
*University of Natural Resources and Life Sciences (BOKU), Department of Sustainable Agricultural Systems, Division of Livestock Sciences, Vienna, Gregor-Mendel-Straße 33, A-1180 Vienna, Austria
†ZuchtData EDV-Dienstleistungen GmbH, Dresdner Straße 89/19, A-1200 Vienna, Austria
‡INRA, UMR 1313, Génétique Animale et Biologie Intégrative (GABI), 78350 Jouy-en-Josas, France

ABSTRACT

The aim of this study was to conduct a multitrait 2-step approach applied to yield deviations and deregressed breeding values to get genetic parameters of functional longevity, clinical mastitis, early fertility disorders, cystic ovaries, and milk fever of Austrian Fleckvieh cattle. An approximate multitrait approach allows the combination of information from pseudophenotypes derived from different statistical models in routine genetic evaluation, which cannot be estimated easily in a full multitrait model. A total of 66,890 Fleckvieh cows were included in this study. For estimating genetic parameters, a simple linear animal model with year of birth as a fixed effect and animal as a random genetic effect was fitted. The joint analysis of yield deviations and deregressed breeding values was feasible. As expected, heritabilities were low, ranging from 0.03 (early fertility disorders) to 0.15 (functional longevity). Genetic correlations between functional longevity and clinical mastitis, early fertility disorders, cystic ovaries, and milk fever were 0.63, 0.29, 0.20, and 0.20, respectively. Within direct health traits genetic correlations were between 0.14 and 0.45. Results suggest that selecting for more robust disease-resistant cows would imply an improvement of functional longevity.

Key words: approximate multiple trait, health trait, functional longevity, genetic parameter, cattle

Short Communication

The importance of functional traits in modern dairy breeding programs is increasing worldwide. Besides a broad range of functional traits such as fertility, longevity, and calving traits, direct health traits gained more importance due to their effects on farm economy, animal welfare, and customers' concerns about food safety recently (Egger-Danner et al., 2012). Since 2010, clinical mastitis (**CM**), early fertility disorders (**EFD**), cystic ovaries (**CO**), and milk fever (**MF**) are an integral part of the routine genetic evaluation of Austrian Fleckvieh cattle (dual-purpose Simmental; Fuerst et al., 2011). Currently, these traits are evaluated separately. As reported for other populations (Ducrocq et al., 2001), true genetic and residual correlations or heterogeneous reliabilities are neglected when these traits are subsequently combined into a total merit index or other subindices. Functional traits usually have a low additive genetic variance and are antagonistically correlated with production traits. However, lowly heritable traits benefit from being analyzed together with highly heritable correlated traits in a multivariate approach. Accuracy can be increased compared with univariate analysis due to simultaneous genetic evaluation of correlated traits and better data connectedness because genetic and residual covariances between traits are included. A full multivariate estimation of all traits based on phenotypic data could be considered as the optimum methodology, but is usually not feasible (Mrode, 2014) due to the large numbers of traits involved in a breeding program. Therefore, an approximate multitrait approach was proposed by Ducrocq et al. (2001) and validated on simulated data by Lassen et al. (2007) and Pfeiffer et al. (2015). Apart from an increase of accuracy, Lassen et al. (2007) could show that using an approximate multitrait model for predicting breeding values led to a higher genetic trend compared with univariate analysis. Estimated breeding values were not significantly different when computed in an approximate multitrait approach compared with a full multitrait model based on phenotypic data (Lassen et al., 2007; Pfeiffer et al., 2015). This genetic trend is unbiased by selection on one or several correlated traits. Finally, these EBV can be easily combined in a total merit index (**TMI**) because the optimum weights in the TMI are simply the trait economic values when a multiple trait evaluation is performed. In Austrian Fleckvieh cattle, the main reasons for culling are fer-

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[1] Corresponding author: christina.pfeiffer@boku.ac.at

tility disorders (22.9%) and udder diseases (13.5%; ZuchtData, 2015). Disease-related losses are high in dairy cattle production (Beaudeau et al., 1999). Health disorders lead to early culling and decrease longevity. Several estimates of heritabilities of health traits and a few estimates of genetic correlations between them are reported in literature (e.g., Heringstad et al., 2005; Koeck et al., 2010; Fuerst et al., 2011). However, genetic correlations between health traits and functional longevity are not available due to no or limited access to direct health data in most countries (Egger-Danner et al., 2012) and due to methodology constraints. Hence, the objectives of this study were to conduct an approximate multitrait 2-step approach applied to yield deviations (**YD**) and deregressed breeding values (**drEBV**) deducted from different statistical models and to estimate heritabilities, genetic and residual correlations between functional longevity (**LONG**), CM, EFD, CO, and MF in Austrian Fleckvieh cattle. In total, 66,890 Fleckvieh cows of 2 Austrian regions, with a maximum of 12.5% non-Fleckvieh-gene proportion, recorded for all 5 traits and born between 2004 and 2009, were selected for estimating genetic parameters. Data were further restricted to sires, which were progeny tested and had at least 20 daughters, whereas only the first 1,000 daughters were considered for highly used sires. Their pedigree was traced back as far as possible, yielding 202,430 animals. All health traits were recorded as binary traits (0 = healthy, 1 = diseased within a certain time period) in all lactations. As described in Fuerst et al. (2011), CM consists of acute and chronic mastitis 10 d ante-partum (**a.p.**) to 150 d postpartum (**p.p.**). Diagnosis of retained placenta, puerperal diseases, or metritis from day of calving until 30 d p.p. was recorded as EFD. The observation period for CO was 30 d p.p. to 150 d p.p. The MF was recorded 10 d a.p. to 10 d p.p. If cows were involuntarily culled within the described time spans and because of udder health problems, fertility disorders, or metabolic diseases, their respective diagnosis was also recorded. These animals were considered as diagnosed in the health monitoring system and were also included in the analysis. In the first step, longevity was analyzed using the Survival Kit v6 software (Mészáros et al., 2013). The following statistical model is currently used in the joint routine genetic evaluation of Austria and Germany:

$$\mathrm{h(t)} = \mathrm{h}_{0,\mathrm{ls}}\,(\tau) \times \exp\{\Sigma \mathrm{m}[\mathrm{f_m(t)} + \mathrm{hy_k(t)} + \mathrm{s_i} + 0.5\mathrm{mgs_j}]\},$$

where h(t) is the hazard of a cow t days after her first calving; $\mathrm{h}_{0,\mathrm{ls}}\,(\tau)$ is the Weibull baseline hazard function per lactation l and stage of lactation s with scale parameter λ and shape parameter ρ; $\mathrm{hy_k(t)}$ is the random time dependent effect of herd-year following a log-gamma distribution; $\mathrm{f_m(t)}$ represent the fixed effects of region-year-season, age at first calving, relative performance within herd (fat + protein yield; time dependent), change of herd size (time dependent), an indicator of alpine pasturing (time dependent), and heterosis and recombination loss; $\mathrm{s_i}$ is the random sire genetic effect; and $\mathrm{mgs_j}$ is the random maternal grandsire genetic effect. The random effects $\mathrm{s_i}$ and $\mathrm{mgs_j}$ were assumed to follow a multivariate normal distribution with mean zero and variance $\mathbf{A}\sigma_s^2$, where σ_s^2 is the variance among sires and **A** is the relationship matrix. The YD equivalents and their corresponding weights were computed as a function of the cumulative hazard of each particular individual [for a more detailed description, see Ducrocq (2001) and Ducrocq et al. (2001)].

Breeding values for health traits were estimated univariately using following linear animal model:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z_h h} + \mathbf{Z_a a} + \mathbf{Wp} + \mathbf{e},$$

where **y** is the vector of observations of CM, EFD, CO, and MF; **b** is the vector of systematic effects, including fixed effects of parity × age at calving, calving year and month, and type of recording (electronically by the veterinarians or by the performance recording organization during routine milk recording) by year; **h** is the vector of random herd-year effects with $\mathrm{N}(0,\ \mathbf{I}\sigma_\mathrm{h}^2)$, where **I** is the identity matrix and σ_h^2 represents the herd-year variance; **a** is the vector of random additive genetic effects with $N\left(0, \mathbf{A}\sigma_\mathrm{a}^2\right)$, where **A** represents the numerator relationship matrix and σ_a^2 represents the animal variance; **p** is the vector of the permanent environmental effects of the cow; **e** is the vector of the random residual effects, with $N\left(0, \mathbf{I}\sigma_\mathrm{e}^2\right)$, where **I** is the identity matrix and σ_e^2 is the residual variance. The **X**, $\mathbf{Z_h}$, $\mathbf{Z_a}$, and **W** represent the corresponding incidence matrices (Fuerst et al., 2011). Health traits were then deregressed using a univariate de-regression based on the approach of Jairath et al. (1998) and Schaeffer (2001), which is implemented in the program package MiX99 (Lidauer et al., 2013). The de-regression procedure uses the estimated breeding values and their respective effective daughter contributions as weights only considering the general mean as fixed effect. Based on approximate Interbull reliabilities (Strandén et al., 2000), effective own performances (Edel et al., 2009) were calculated and used as weighting factors for drEBV in the multivariate estimation of genetic parameters. In the second step, after computing YD equivalent