Genetic Relationships under Different Management Systems and their Consequences for Dairy Cattle Breeding

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Summary

Advances in breeding and management resulted in a considerable increase of production traits in Austrian dairy cattle. Besides, low input systems were also established. Possible genotype by environment interactions (G x E) and genetic antagonisms dependent on production level might indicate the need for separate breeding programmes for dairy farms differing in management intensity. Thus, G x E and genetic correlations (r_a) between milk yield and selected fitness traits were estimated for Upper Austrian Fleckvieh cattle under high and low production levels. Data of the current herdbook cow population and their dams were extracted. Two data sets were selected based on the herd average of milk; extensive (≤6,000 kg herd average) and intensive (≥9,000 kg herd average) farms. Yield deviations were used for the analysis of yield traits, functional longevity, reproduction traits and milking speed; raw data were used for somatic cell count (SCC). For yield deviations, a model including the effects year of birth (fixed) and animal (genetic, random) was applied, while a model close to the routine evaluation was run for SCC. The lowest r_a between extensive and intensive farms was found for protein yield ($r_a = 0.89$) while r_a values close to unity were found for all functional traits. Genetic antagonisms between milk yield and functional traits were stronger in intensive systems, however, standard errors were large. Currently, separate breeding programmes for different management intensities do not seem to be necessary.

Key words

dairy cattle, genotype environment interaction, genetic correlation, breeding programmes

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Aim

Both, advances in breeding and management resulted in a considerable increase of production traits in Austrian dairy cattle. Besides a marked intensification in dairy farming, low input systems were also established at the same time. For example, 95,000 dairy cows were kept under organic farming regulations in Austria in 2011 (BMLFUW, 2012), which at least partly implies restrictions with regard to feeding of concentrates. Besides, other low-input strategies like pasture-based systems also gain importance (e.g., Steinwidder et al. 2010). In this context it is questioned whether selected dairy breeding animals are actually the best for all kinds of environments. Possible genotype by environment interactions might indicate the need for different breeding goals and breeding programmes for dairy farms differing in management intensity. Besides, genetic antagonisms between traits may be affected by different environments or selection. Thus, the aims of the study were to estimate (1) genotype by environment interaction (G x E) for different production levels and (2) genetic correlations between milk yield and selected fitness traits (functional longevity, days from calving to first insemination, days between first to last insemination, somatic cell count) under different production levels in Austrian Fleckvieh (dual purpose Simmental) cattle. Based on the results, a suggestion whether different breeding programmes are currently needed for intensive and extensive systems should be given.

Material and methods

Data of Fleckvieh herdbook farms in the Austrian federal country Upper Austria were extracted from the data base. Data were restricted to the current cow population and their dams. To account for different management intensity, two separate data sets were selected based on the average milk yield; extensive (≤6,000 kg herd average) and intensive (≥9,000 kg herd average) farms. For the estimation of genetic parameters, yield deviations (i.e., performance deviations corrected for environmental effects) were used for all traits except for somatic cell count. In total, 3,515 and 3,933 (functional longevity) to 24,376 and 35,947 (somatic cell count) records were available for extensive and intensive farms, respectively (Table 1). In order to receive yield deviations, the same environmental effects as in the routine Austrian/German genetic evaluation were considered. Interbull (2013) provides a description of these routine joint genetic evaluations. Further details may be found in Fürst et al. (2013). As environmental effects are already accounted for in yield deviations, only the effect of year of birth and the random genetic effect of the animal were fitted in the model for the estimation of genetic parameters. However, no yield deviations were available for somatic cell count (SCC). Thus, SCC values of the first three lactations were transformed to somatic cell score (SCS = $\log_2(SCC/100,000)+3$)) and a model including the fixed effects parity*age and year*month, the covariate days in milk and the random effects herd*year and permanent environment as well as the random genetic effect of the animal was applied. By means of REML and the software package VCE6 (Groeneveld et al., 2010), bivariate models, treating the respective traits as separate traits in both environments, were used to estimate heritabilities and genetic correlations. For all analyses based on yield deviations, heritabilities were calculated as

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2};$$

while for somatic cell score, heritability was calculated as

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{hy}^2 + \sigma_e^2}$$

with σ_a^2 = additve genetic variance of animal, σ_{hy}^2 = variance of the random effect herd*year and σ_e^2 = residual variance.

In such analyses, when observations of an animal may only be found in either of the two environments, the residual covariance is omitted by VCE6 (Groeneveld et al., 2010).

Results and discussion

The term G x E describes possible interactions between genotypes and environments. For a breeding population that means in the worst case – i.e. strong G x E - that re-rankings of breeding animals in different environments could happen. Best animals under intensive conditions do not necessarily need to be the best for extensive conditions and *vice versa*. Reasons for G x E may be that the same genes act differently under different environmental conditions or that different genes may act under different environmental conditions (Falconer and Mackay, 1996). One possibility to assess G x E is to estimate genetic correlations (r_a) for the trait as expressed in different environments. Robertson (1959) suggested a limit of r_a = 0.8; in case of lower correlations G x E may be pronounced. In the Austrian Fleckvieh population, milk and protein yield produced rather high and similar heritabilities (h^2 = 0.45 to 0.55) considering different management intensities (Table 1). As expected, heritabilities for functional traits and milking speed were low and moderate, respectively. Among all traits, the lowest genetic correlation between extensive and intensive farms was found for protein yield (r_a = 0.893). However, it can be assumed that protein yield is more or less the same under both environmental conditions and that mostly the same genes are affecting its expression. Even greater genetic correlations were estimated for the group of functional traits, ranging from 0.999 to 1.000 (Table 1). Results thus indicate that the bulls' rankings are the same for those functional traits under extensive and intensive conditions. Similar results were also found when defining the environment by organic or non-organic farming rather than extensive or intensive management. Genetic correlations ranged from 0.899 (protein yield) to 1.000 (all reproduction traits and somatic cell count). Analysing potential G x E in the Bavarian Fleckvieh for different management intensities and organic farming, all genetic correlations found were higher than 0.90, and thus in accordance to the results for the Austrian population (Gerber et al., 2006). In a review, König et al. (2005) reported genetic correlations between countries to be mostly larger than 0.8. Only in cases of large differences between climate and production systems lower correlations may be found. An indication of G x E gives the low across country correlation of 0.75 between the German-Austrian and New Zealand Brown Swiss population, the latter predominantly kept in pasture based systems (Interbull, 2012). However, different trait definitions and methods in the genetic evaluation also need to be taken into account when discussing across country correlations.

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Table 1. Number of observations (N) and genetic parameters (h^2 = heritability, r_a = genetic correlation) and their standard errors in brackets for selected traits within extensive (≤6,000 kg herd average) and intensive (≥9,000 kg herd average) Fleckvieh herdbook farms in Upper Austria

Trait[1]	Extensive		Intensive		r_a
	N	h^2	N	h^2	
Milk yield	5,400	0.55 (0.03)	5,770	0.54 (0.03)	0.953 (0.037)
Protein yield	5,393	0.45 (0.04)	5,762	0.50 (0.04)	0.893 (0.053)
Functional longevity	3,515	0.15 (0.03)	3,933	0.11 (0.02)	1.000 (0.001)
Non Return Rate 56	4,198	<0.01 (<0.01)	4,808	0.01 (0.01)	0.999 (0.010)
CFI[2]	4,213	0.07 (0.02)	4,833	0.08 (0.02)	1.000 (<0.001)
FLI[3]	4,140	0.06 (0.02)	4,796	0.03 (0.02)	0.999 (0.004)
Somatic Cell Count	24,376	0.12 (0.04)	35,947	0.17 (0.04)	0.999 (0.008)
Milking speed	4,901	0.26 (0.03)	5,395	0.32 (0.04)	1.000 (0.001)

[1] For all traits except somatic cell count yield deviations (performance deviations corrected for environmental effects) were used, [2] CFI = days from calving to first insemination, [3] FLI = days between first to last insemination. For all reproduction traits, only cows were considered.

Genetic correlations between milk yield and functional longevity, days from calving to first service, days from first to last service and somatic cell count, respectively, were also estimated to assess possible different genetic correlations under different management intensities (Table 2). Due to the restricted data set, standard errors of the genetic correlations were rather high. Thus, results need to be interpreted with caution. However, in tendency antagonistic relationships were found to be stronger under intensive rather than extensive management systems. Linkage (genes that have a tendency of being inherited together as located on the same chromosome) and pleiotropy (genes affecting more than one trait) were reported to be the reasons for antagonistic relationships (Falconer and Mackay, 1996). Genetic parameters

number of +/- combinations the longer selection takes place (e.g. Fürst and Sölkner, 2002). Aside from linkage and pleiotropy, the so-called "Resource Allocation Theory" (Beilharz et al., 1993) and the "Energy metabolism hierarchy" (Wade and Jones, 2004) may also reveal approaches to explain differently strong antagonistic relationships under extensive and intensive environments. In case of limited energy resources, ways need to be found how to distribute them. Wade and Jones (2004) stated that energy is first used for essential functions including heart and circulation but also milk production, followed by reducible functions like thermo-regulation or motion and finally for expandable functions including reproduction. If resources become limited, the competition for resources increases and thus the antagonism increases as well (Sölkner and James, 1994). However, it could also be argued that the increasing genetic antagonism between milk yield and fertility under high intensities it is only partly caused by genetics. According to Wade and Jones (2004) infertility due to negative energy balance is reversible as soon as the energy balance becomes positive again.

Conclusions

Only a slight genotype by environment interaction could be detected for yield traits in Austrian dairy cattle. For functional traits, no G x E was found. A tendency for stronger genetic antagonistic relationships between milk yield and functional traits under intensive management could however be observed. Nevertheless, standard errors of the estimated genetic correlations were rather high and thus results should be interpreted with caution. From the results of this study it may be followed that different breeding programmes for different management intensities are currently not necessary. Re-ranking of bulls depending on environment will be marginal. Besides, individual breeding goals of breeders are very similar (Steininger et al., 2013, unpublished results). Apart from that, the splitting of a population means that each becomes smaller resulting in lower selection possibility. At the same time, costs will increase when bulls are tested within different breeding programs. As bulls are generally tested under different production levels and a large number of breeding values is available for dairy and functional traits, the current Fleckvieh breeding program offers appropriate bulls for a wide range of management systems.

Table 2. Genetic correlations (r_a) and their standard errors in brackets between milk yield and selected traits within extensive (≤6,000 kg herd average) and intensive (≥9,000 kg herd average) Fleckvieh herdbook farms in Upper Austria

Traits[1]	Extensive	Intensive
	r_a	r_a
Milk yield - Functional longevity	-0.159 (0.051)	-0.192 (0.115)
Milk yield - CFI[2]	0.115 (0.154)	0.314 (0.132)
Milk yield – FLI[3]	0.214 (0.181)	0.442 (0.225)
Milk yield – Somatic cell count	0.106 (0.274)	0.564 (0.153)

[1] For all traits but somatic cell count yield deviations (performance deviations corrected for environmental effects) were used, [2] CFI = days from calving to first insemination, [3] FLI = days between first to last insemination

are measures that may vary e.g. depending on population, data quality or methodology applied in the estimation procedure. Selection may also affect genetic parameters. While unwanted genes are partly eliminated, desirable genes are fixed. Thus, genetic variance is reduced. In case of two traits, genes also only contribute to genetic correlation as long as they are not fixed or eliminated. When selecting on two traits, -/- combinations are however eliminated, +/+ are fixed resulting in an increasing

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