Genetic Parameters of Austrian Fleckvieh Cattle in Organic and Conventional Production Systems with Different Levels of Management Intensity

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Summary

Improvement of breeding and management has resulted in a considerable improvement of production and many fitness traits in Austrian dairy cattle. Apart from that, a variety of different dairy production systems, comprising organic, extensive to intensive systems can be observed in Austria. It can be assumed that different breeding goals exist in different production systems which would cause differences in genetic parameters and would imply the necessity of adapted breeding objectives. Therefore, the aim of the study was to estimate genetic parameters of three different production systems (organic, conventional low and high level of farm intensity) for three productions (milk kg, fat kg, protein kg) and six fitness traits (persistency, somatic cell score, functional longevity, milking speed, udder health index and fertility index) using an approximate multivariate two-step approach. In general, heritabilities and genetic correlations were similar in all three production systems. Heritabilities ranged from 0.04 for fertility index for the farms with a low level of farm intensity to 0.65 for milk kg for farms with a high level of farm intensity. Almost no deviations were found between the genetic correlations across the defined production systems. Due to the similar results it can be concluded that breeding objectives are similar in different production systems and currently breeding objectives do not need to be adjusted.

Key words

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Introduction

During the last decades, milk yield increased tremendously in Austrian dairy cattle populations. On average a genetic trend of +91 kg milk per year can be observed for the largest Austrian cattle breed Fleckvieh (dual purpose Simmental). At the same time an improvement of functional traits could hardly be noticed (ZuchtData, 2016). In the same time period the number of extensive and organic production systems increased. Organic production systems (PS) are affected by stricter legal regulations (e.g. feeding regime, medical treatments, access to pasture, space allowance, etc.). Currently, about 18% of all Austrian dairy cows are milked on organic farms (BMLFUW, 2015). Besides an amplified organic dairy sector, also the number of low input PS increased (Horn et al., 2014). Low input farms are characterized by reducing production costs via reducing concentrate, increasing forage based diets and breeding for robust and fertile cows (Steinwidder, 2013). According to Yin et al. (2012) low input farms are not necessarily following organic regulations. Due to consciously chosen extensive farming strategies on the one hand and legal regulations for organic farms on the other hand, it can be assumed that organic and extensive dairy farmers follow different breeding goals. Results of a survey showed that organic dairy farmers put significantly more weight on fitness traits than on production traits when they were asked for their individual breeding goals (Steininger, 2015, unpublished results). Also, representatives of organic agriculture may postulate different breeding objectives (Steinwidder and Krogmeier, 2014) for different PS. Due to the variety of dairy PS in Austria it has to be questioned whether selected dairy breeding animals are actually the best for different PS applied in Austria. So far, Austria has no separate breeding program for organic or extensive dairy cattle. Therefore, the aim of the study was to estimate genetic parameters for three different PS (organic, conventional low intensity farm management; conventional high intensity farm management) to verify if the populations were already selected for different purposes. Genetic parameters were estimated for milk yield (MILK), fat kg (FAT), protein kg (PROT), persistency (PERS), somatic cell score (SCS), functional longevity (LONG), milking speed (MISP), udder health index (UHI) and fertility index (FI) of Austrian Fleckvieh using an approximate multivariate two-step approach applied to yield deviations (YD) and de-regressed breeding values (drEBV). This procedure is carried out in two steps: first, univariate pseudo-phenotypes (drEBV, YD) and their corresponding weights are computed. Second, a multivariate animal model is applied to pseudo-phenotypes (Lassen et al., 2007; Pfeiffer et al., 2015) to estimate variance components and breeding values. The applied methodology allows the combination of information from pseudo-phenotypes derived from different statistical models. For further details regarding the approximate multivariate two-step approach see Pfeiffer et al. 2015 and 2016.

Production systems, animals and statistical analysis

Production systems

The whole Austrian Fleckvieh cow population born between 1999 and 2011, with a maximum of 12.5% non Fleckvieh-gene

proportion was used as data basis. Furthermore, known parents were required, all phenotypes for the traits of interest had to be recorded and each farm had to have at least a herd size of five lactating cows. The population was split into cows which were milked at least for one lactation in organic (European Commission, 2008; EC no. 889/2008) or conventional PS, respectively. Additionally, cows of the conventional PS were further dived into groups according to the intensity of farm management. The intensity of farm management was defined according to farm's routine genetic evaluation's herd-year-effect for milk yield. The herd-year-effect can be considered as an indicator for farm management, due to the correction of systematic environmental effects and half of the dams merit while breeding values are estimated (Gerber et al., 2006). Cows were then ranked according to the average herd-year effects expressed on 1st lactation milk yield over the last twelve years. All cows with a herd-year-effect which deviated at least two standard deviations from the mean where selected to define the groups with a high intensity farm management (ConH) or a low intensity farm management (ConL). The average of milk kg in the two conventional PS had a difference of 2.000 kg milk. Due to a limited number of cows on organic farms, no further selection of data was conducted. Hence, data from 46,015 cows were used for the organic PS (Organic). A summary of all three production systems is given in Table 1. Pedigrees for all three populations were traced back

Table 1. Summary and classification of production systems for different levels of farm intensity according to the average herd-year-effect of the farms

Level of farm intensity	Organic	Conventional low	Conventional high
Number of animals	46,015	30,840	53,882
Number of farms	2,657	1,911	1,486
Range of herd-year-effect*	3,274 – 7,287	1,948 – 4,800	6,220 – 8,350
Mean*	5,076	4,452	6,558
SD*	574	305	312

*kg milk (expressed as 1st lactation milk yield)

as far as possible yielding in 162,560 cows for Organic, 118,010 for ConL and 159,943 for ConH, respectively.

Model

After computing YD equivalent for LONG and drEBV for all other traits (procedure described in Pfeiffer et al. 2015 and 2016), either a univariate or a bivariate model was fitted for estimating heritabilities and genetic correlations, respectively. This was done using the program package ASReml 3.0 (Gilmour et al., 2010). The following model was applied:

$$y^* = Xb + Za + e$$

where y^* indicates the YD for LONG or drEBV for MILK, PERS, SCS, MISP, UHI and FI for a given animal, respectively; b is the vector of the fixed year of birth effects; a is the vector of the random additive genetic effects and e is the vector of the random residual effects. X and Z represent the incidence matrices for fixed and random effects, respectively.

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Results und discussion

The heritabilities (Table 2) of all traits of the defined productions systems were in general similar, ranging from 0.04 for FI (ConL) and LONG (ConH), respectively to 0.65 for MILK (ConH). Values have to be interpreted with caution. They are not directly comparable with usual estimates obtained from phenotypic data. Due to the different number of records of each animal, residual (co)variances are (co)variances between averages of residuals. Due to the average residual (co)variance it can be assumed that heritabilities are slightly overestimated. The effect of the genotype depends on the environment and h^2 can just be compared when it is evident that no genotype by environment interaction exists (Visscher et al., 2008). Pfeiffer et al. (2016) found out that no genotype by environment interaction exists in this data set. However, the highest heritabilities were observed in ConH for almost all traits, except for LONG and FI. These results are in accordance with former studies (e.g. Ahlmann et al., 2011; Sundberg et al., 2010). With a more specialized and intense production system heritabilities increased. The lowest h^2 was estimated for ConL, except for LONG and UHI. Although the differences between h^2 are small, dairy farms with an intensive management usually perform a stricter breeding goal and the threshold for selection is higher. According to the results it might be similar in organic production systems and less strict in production systems with an extensive management. Unfortunately, no information about farms' individual breeding goals, housing conditions, feeding or access to pasture was available. This would support the interpretation of results. Regarding the selection of sires of dams, the largest overlap was observed between Organic and ConL (2.334), followed by Organic and ConH (2.246) and finally ConL and ConH (2.206).

The genetic correlations (r_a) were similar across all production systems. Table 3 shows the r_a between MILK and FAT, PROT, PERS, SCS, LONG, MISP, UHI and FI for all the production systems ranging from -0.32 between MILK and FI (ConL) to 0.86 between MILK and PROT (ConH), respectively. However, the most unfavourable r_a between MILK and fitness traits were found in ConL.

These results are in accordance with Castillo-Juarez et al. (2002) and Kolmodin et al. (2002), who also estimated the most unfavourable r_a in extensive production systems. Nauta et al. (2006) and Pfeiffer et al. (2016) estimated G x E for organic, intensive and extensive production systems. All authors found

Table 3. Genetic correlations and standard errors in brackets between milk kg and fat (FAT), protein kg (PROT), persistency (PERS), somatic cell score (SCS), functional longevity (LONG), milking speed (MISP), udder health index (UHI) and fertility index (FI) of the three different production systems

	Milk kg		
	Organic	Conventional low	Conventional high
Fat kg	0.66 (0.011)	0.70 (0.011)	0.66 (0.009)
Protein kg	0.84 (0.005)	0.85 (0.006)	0.86 (0.004)
Persistency	-0.04 (0.020)*	-0.12 (0.050)	0.01 (0.016)*
SCS	-0.003 (0.029)*	0.09 (0.034)	0.01 (0.024)*
Functional longevity	-0.23 (0.046)	-0.29 (0.050)	-0.23 (0.052)
Milking speed	0.36 (0.026)	0.45 (0.030)	0.34 (0.021)
Udder health index	-0.01 (0.034)*	0.05 (0.040)*	0.01 (0.027)*
Fertility index	-0.15 (0.052)*	-0.32 (0.062)	-0.14 (0.050)

*not significantly different from zero

no severe G x E between several traits. Authors assumed that particularly the feeding regime is a crucial point. Especially in organic and extensive production systems a restriction of concentrate can affect milk performance. It can be assumed that the genetic potential of MILK is not fully used in extensive production systems. Genetic correlations among MILK, FAT and PROT were between 0.66 and 0.84 for Organic, 0.70 and 0.85 for ConL, 0.66 and 0.86 for ConH, respectively. Genetic correlations between fitness traits were in general in the same range across all PS ranging from -0.42 between SCS and MISP to 0.93 between SCS and UHI for Organic, -0.33 between SCS and MISP to 0.95 between SCS and UHI for ConL and -0.44 between SCS and MISP to 0.94 between SCS and UHI for ConH, respectively. Pfeiffer et al. (2016) investigated G x E interactions for almost the same traits, the same populations and defined production systems but with less data. Authors found no severe evidence for the occurrence of G x E in all traits of interest and could not show a re-ranking of bulls. Results of the current study show that there is no big difference in genetic parameters and farmers selected cows for almost the same breeding goal. Results of this study augment the conclusion of Pfeiffer et al. (2016) that no autonomous breeding program for organic or extensive dairy farms is required, due to a marginal genetic difference in dairy populations.

Table 2. Heritabilities (h^2) and standard errors (SE) for all traits of the three different production systems

	Organic		Conventional low		Conventional high	
	h^2	SE	h^2	SE	h^2	SE
Milk kg	0.63	0.014	0.59	0.016	0.65	0.011
Fat kg	0.50	0.014	0.45	0.016	0.55	0.012
Protein kg	0.57	0.014	0.51	0.016	0.57	0.012
Persistency	0.56	0.014	0.52	0.016	0.62	0.011
SCS	0.23	0.013	0.22	0.015	0.29	0.013
Functional longevity	0.07	0.009	0.09	0.011	0.04	0.006
Milking speed	0.27	0.014	0.21	0.014	0.33	0.013
Udder health index	0.12	0.012	0.15	0.013	0.21	0.012
Fertility index	0.06	0.007	0.04	0.007	0.05	0.007

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Conclusion

Heritabilities and genetic correlations of the defined PS are similar. Although a huge variety of dairy production systems is presented in Austria, farmers are likely to determine the same breeding goals. A separate breeding program is not necessary at the moment.

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