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Genetic association between somatic cell score and milk lactose in early- to mid-lactation of first calving Fleckvieh cows

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Abstract

The present study aimed to assess genetic correlations of milk lactose (percentage and yield), lactose to fat ratio and lactose to protein ratio with somatic cell score (SCS) in the first half of lactation, the period with the highest risk of mastitis in cows. More than 35,000 first lactation records from Austrian Fleckvieh breed were available for this purpose. A linear animal model was adopted for the genetic analysis, with inclusion of age at calving and year-month of calving as fixed effects, and additive genetic animal, herd-year of calving and residual as random effects. The average SCS in the first 150 days in milk was low (1.53 ±1.29) compared with values reported in literature for other breeds in first lactation. Heritabilities of lactose percentage, lactose to fat ratio and lactose to protein ratio were high, ranging between 0.65 and 0.71. According to lactose yield and SCS, their heritabilities were equal to 0.3 and 0.2, respectively. Since the focus was on the first lactation, where the heritability of lactose is reported to be the highest, these results agreed with expectations. The strongest genetic correlation was found between SCS and lactose percentage, and the weakest between SCS and lactose yield, suggesting that lactose percentage and yield have different variability at animal level and different potential roles at genetic level. Both lactose to fat ratio and lactose to protein ratio showed weak and negative genetic correlation with SCS. Further research is required to assess relations between lactose and recorded mastitis data, with the final goal of validating lactose level as udder inflammation indicator and explore its potential role in breeding programs to reduce cow's susceptibility to mastitis.

Keywords: Austrian Fleckvieh, bovine milk, genetic correlation, lactose, SCS

Introduction

In most routine genetic evaluations for mastitis resistance, somatic cell score (SCS) is used as an indirect indicator, due to the scarce availability of direct measures on the target trait. However, in some cases, the typical peak of SCS could be not present during udder inflammation; in addition, SCS is reported to vary even without inflammation. Therefore, the correlation with actual mastitis diagnosis has been reported to range from 0.3 to 0.8 (Heringstad et al., 2000; Koeck et al., 2010a). Individual information on SCS is recorded monthly and thus it is generally adopted as indicator of subclinical and chronic cases (Heringstad et al., 2000). Any additional indicator traits for mastitis resistance would be useful. Lactose, the milk sugar synthetized in mammary cells starting from blood glucose (Fox et al., 2015), may be a be valid candidate to be included in udder health indexes, together with milk electrical conductivity and minerals (Løvendahl and Weisbjerg, 2017). In cosmopolitan dairy breeds, lactose percentage has been reported to be negatively correlated with SCS. Indeed, when udder inflammation occurs, the permeability of basal membrane of mammary cells increases and lactose from milk passes to blood and then to urine (Fox et al., 2015). This strong link between lactose and udder environment makes this component a potential informative, low-cost and available trait for monitoring mammary health status. In addition, lactose ratios, namely lactose to fat (L:F) and lactose to protein (L:P), have not been phenotypically or genetically investigated yet, neither considered as potential informative phenotypes for udder health or cows' energy balance. Therefore, the present paper aims to investigate genetic relationships of SCS with milk lactose and its derived ratios in the first 150 days in milk (DIM) of Austrian Fleckvieh cows.

Materials and methods

Milk data of first parity Fleckvieh cows from 1 to 150 DIM were extracted from the Austrian national cattle database. Available traits were: milk yield, SCC, lactose, fat and protein percentages, lactose to fat (L:F) and lactose to protein (L:P) ratios and milk yield. Lactose yield was computed by multiplying milk yield and lactose percentage. The Test Interval Method suggested by International Committee for Animal Recording, ICAR (2014) was adopted to calculate lactation (5 to 150 DIM) traits. In order to get an approximate Gaussian distribution (Figure 1) for statistical analyses, SCC was converted into SCS [$SCS = 3 + \log_2(SCC/100\ 000)$].

After restrictions on age at calving (20.4 to 42 months) and conventional editing on milk traits, data from 37,428 first lactation cows calving between January 1, 2010 and October 21, 2017 in 1,357 herds were available. The pedigree (n=130,961) included cows with lactation data and their ancestors up to 4 generations back. The average inbreeding coefficient was 1.5%. (Co)variance components were estimated on VCE6 software (Groeneveld et al., 2008), adapting the Austrian-German-Czech routine genetic evaluation model:

$$y = Xb + Za + Wh + e,$$

where y was the vector of phenotypic records of the trait; b was the vector of fixed effects of calving age (6 classes) and year-month of calving (94 levels); a was the vector of random animal genetic effect; h was the vector of random effect of herd-

year of calving (6,534 levels) and *e* was the vector of random residuals. *X*, *Z*, and *W* were incidence matrices relating the corresponding effects to the dependent variable.

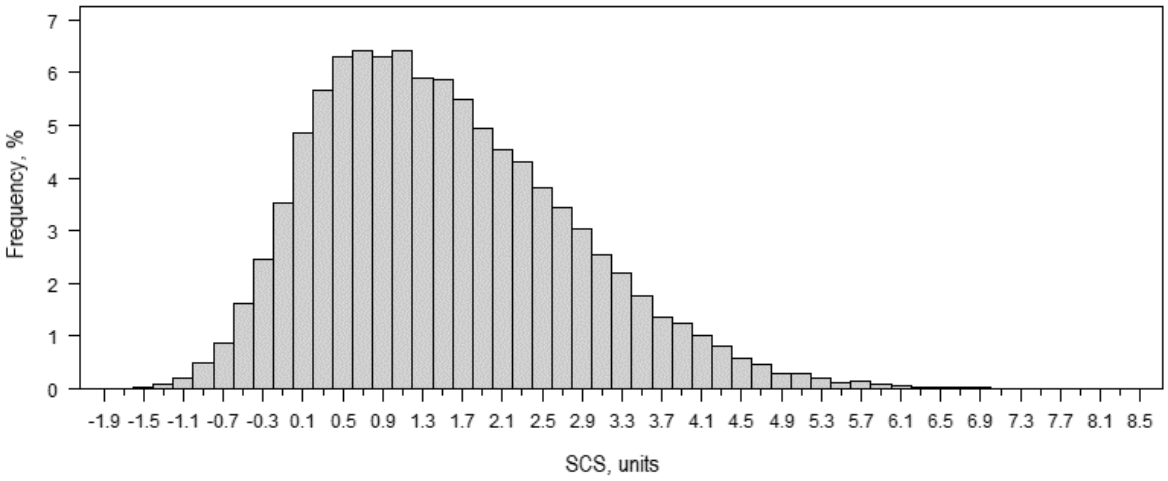

Figure 1. Frequency distribution of 150 d SCS.

Results

In the present study, SCS ranged from -2.26 to 10.22, with an average value of 1.53 ±1.29. Lactose percentage and yield averaged 4.89 ±0.12% and 180.35 ±37.69 kg, respectively. Since lactose is the main milk solid, L:F and L:P were found greater than unity, being 1.25 ±0.15 and 1.52 ±0.13, respectively. Estimates of heritability for the investigated traits are depicted in Table 1, together with the proportion of phenotypic variance explained by random effect of herd-year of calving.

The most and the least heritable traits were L:P (0.71 ±0.01) and SCS (0.2 ±0.02). The proportion of phenotypic variance explained by herd-year of calving effect was larger for milk and lactose yields, two very dependent traits at biological level, usually exhibiting similar variance components.

Correlations between SCS and target traits are presented in Table 2. Lactose percentage in the first 150 DIM negatively associated to SCS both at phenotypic and genetic level; lactose yield, on the other hand, showed weaker associations with SCS. Similarly to lactose percentage, L:F and L:P were negatively associated with SCS, even if with a weaker magnitude.

Table 1. Heritabilities with standard errors (SE) and proportion of phenotypic variance (%) explained by the random herd-year of calving effect for SCS, milk yield, fat, protein and lactose percentages, lactose yield, lactose to fat ratio and lactose to protein ratio

Variable	Heritability	SE	Herd-year of calving (%)
SCS (units)	0.2	0.02	10.95
Milk yield (kg)	0.29	0.01	43.6
Fat percentage	0.58	0.01	11.77
Protein percentage	0.57	0.02	20.97
Lactose percentage	0.69	0.01	8.5
Lactose yield (kg)	0.3	0.01	43.84
L:F	0.65	0.02	8.74
L:P	0.71	0.01	14.67

Table 2. Genetic (standard errors between parenthesis) and phenotypic correlations of SCS with lactose percentage and yield, lactose to fat ratio and lactose to protein ratio

	SCS	
	Genetic	Phenotypic
Lactose percentage	-0.24 (0.031)	-0.23
Lactose yield (kg)	0.06 (0.04)	-0.07
L:F	-0.12 (0.034)	-0.13
L:P	-0.09 (0.005)	-0.13

Discussion

The average milk composition (results not shown) was comparable to that reported in previous studies on Fleckvieh cows. Even if productive performances are nowadays comparable to those of specialized dairy breeds, Austrian dual-purpose Fleckvieh cows are known to be more robust and less susceptible to mastitis, with the lowest SCS among all dairy breeds in Austria (Koeck et al., 2010b; ZuchtData, 2015). In addition, in the present study only first calving cows were included, and therefore, as expected, the average SCS was lower than that reported in other studies considering

multiparous cows of different breeds. Average lactose percentage was similar to mean lactose percentage (4.9%) reported by Penasa et al. (2016) for the whole lactation of first calving Holstein cows. Overall, the average lactose percentage in the present study was greater than that reported in studies including multiple parities. This outcome agreed with findings of Miglior et al. (2007) and Haile-Mariam and Pryce (2017). The negative trend of lactose percentage across parities could be attributed to the negative role of both lower amount of available blood glucose (i.e. great metabolic stress) and higher incidence of mastitis that characterize pluriparous cows (Wathes et al., 2006). The coefficient of variation of lactose yield (20.39%) was much greater than that of lactose percentage (2.47%), confirming that biological regulations that determine the concentration of lactose in milk (ionic equilibrium) are more conservative than those that determine the amount of synthetized lactose from blood glucose. Penasa et al. (2016) reported a slightly higher coefficient of variation for lactose percentage (3.4%) compared to the present study. Heritabilities for 150-d milk yield, fat and protein percentage were greater than estimates reported for the entire lactation of Fleckvieh cattle by Ederer et al. (2014). Somatic cell score exhibited a comparatively high heritability in first parity, in agreement with estimates of Koeck et al. (2010a) for multiparous cows of the same breed (0.13) and Miglior et al. (2007) in first parity Canadian Holstein (0.19). Lactose percentage and its ratios were highly heritable, confirming the greater additive genetic variance that characterizes this trait, especially in early lactation and in first parity cows, similarly to Gillon et al. (2010) and Satoła et al. (2017). Since strictly related to milk yield, lactose yield was less heritable than lactose percentage, as reported by Sneddon et al. (2015) and Haile-Mariam and Pryce (2017). The associations between SCS and lactose percentage were in the same direction of estimates reported by Miglior et al. (2007), Gillon et al. (2010) and Visentin et al. (2017). On the other hand, phenotypic and genetic relations between lactose yield and SCS were close to 0.05, but in opposite direction. The differences in the correlations estimated for lactose percentage and yield suggested that these two traits should be considered individually, since the physiological and biological mechanisms affecting them are different and they do not report same information. Heritabilities for L:F and L:P were higher than those for fat and protein percentages; however, comparison with the literature is difficult, since this is the first investigation reporting genetic parameters for these ratios. Their correlations with SCS were negative, yet weaker than that of lactose percentage. The presence of both fat and protein components, usually only marginally associated with SCS (Loker et al., 2012), could unfavorably affect the magnitude of these relationships. However, the additional value of considering ratios instead of lactose percentage only, is the possibility to drive the genetic selection also of other milk solids.

Conclusions

This is the first genetic study specifically focusing on associations between SCS and milk lactose traits in Austrian Fleckvieh dual-purpose cows. Heritabilities and genetic correlations with SCS can be exploited for genetic purposes. However, in order to make lactose a new indicator of mastitis and a potential candidate for mastitis resistance breeding schemes, further genetic investigations with inclusion of real diagnosis and multiparous cows are needed. The correlations of SCS with L:F and

L:P were too weak to make these ratios promising phenotypes as indicators for udder health; however there is room for investigating their association with metabolic traits.

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