

Genetic association between milk lactose, freezing point and somatic cell score in Italian Holstein cows

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Summary

Milk data (n = 59,811) from 4,355 Holstein cows were used to estimate genetic parameters for lactose percentage (LP) and yield (LY), and other milk traits. Lactation curve of LP was very similar to that of milk yield and opposite to the lactation curve of somatic cell score (SCS). Heritability and repeatability of the investigated traits were assessed through univariate animal models, and genetic correlations with milk SCS and freezing point (FRP) were estimated using bivariate analyses. Fixed effects were herd-test-date, lactation stage, parity, calving season and the interaction between parity and stage of lactation. Random effects were animal, permanent environment and residual. Lactose percentage showed the highest estimates of heritability (0.44 ± 0.03) and repeatability (0.59 ± 0.01), whereas SCS and FRP showed the lowest estimates of heritability (0.12 ± 0.02 and 0.11 ± 0.01 , respectively) and repeatability (0.26 ± 0.01 for both traits). Lactose percentage was moderately correlated with SCS both phenotypically (-0.34) and genetically (-0.25 ± 0.08), suggesting that there are opportunities for considering LP as a potential trait to indirectly select for resistance to mastitis along with SCS. Freezing point was negatively genetically correlated with LP (-0.46 ± 0.05). Further studies are required to evaluate correlated responses for all traits, before LP, LY and FRP can be considered to be part of the current selection index or breeding objective of Italian Holstein dairy cattle.

Keywords: lactose, somatic cell score, freezing point, milk, genetic parameter

Introduction

Lactose is the main carbohydrate of bovine milk and its concentration is around 4.80% (Fox *et al.*, 2015). This compound is important during cheese making because it represents the substrate for bacterial fermentations, and in milk powder production, since it is the major solid in whey and it works as a matrix for other compounds (Sneddon *et al.*, 2015). The concentration of lactose in individual milk samples has been evaluated as a potential tool for mastitis identification (Bansal *et al.*, 2005; Gillon *et al.*, 2010), given its negative phenotypic correlation with SCS. In literature, phenotypic relationship between these two traits is low (-0.19) to moderately strong (-0.55) (Garcia *et al.*, 2015; Sneddon *et al.*, 2015). Lactose yield is important for determination of milk volume, since it is the principal osmotic regulator in udder (Fox *et al.*, 2015).

Milk FRP (°C) is the temperature at which milk freezes; it is affected by solids concentration and its value moves progressively towards zero in case of water addition to milk (Fox *et al.*, 2015). In Europe, the maximum limit of FRP for raw bulk milk is -0.520°C (Council Directive 92/46/EEC) and above this threshold there are penalties in milk payment systems because of suspect illegal addition of water (adulteration). However, sometimes some unadulterated individual milk samples show FRP values above the threshold, even if milk composition is normal. Negative phenotypic correlation (-0.35) between LP and FRP has been reported in literature (Hanuš *et al.*, 2010), suggesting that high-LP milk usually shows more negative (i.e. desirable) FRP values (Fox *et al.*, 2015).

Overall, there is a paucity of information on estimates of genetic parameters for LP, LY and FRP on large datasets, especially with regard to genetic correlations with other traits. Therefore, the objectives of the present study were a) to compute heritability and repeatability of the included traits, and b) to assess genetic, residual and permanent environmental correlations of LP and LY with SCS and FRP in a large dataset of Italian Holstein cows.

Material and methods

Data

Data were a random subset of herds with information on test-day milk yield (kg/d), composition traits (%), somatic cell count (SCC, cells/mL) and FRP (°C) from Italian Holstein cows recorded in Bolzano province (Italy) between January 2011 and December 2014. Fat percentage (FP), protein percentage (PP), LP and FRP were determined using MilkoScan™ FT6000 (Foss, Hillerød, Denmark), and SCC through Fossomatic™ FC (Foss, Hillerød, Denmark) in the laboratory of the South Tyrol Dairy Association (Bolzano, Italy). Milk yield, SCC and FRP were edited according to their frequency distribution, while FP, PP, and LP were edited following the International Committee for Animal Recording (ICAR) recommendations. Lactose yield was calculated as the product of milk yield and LP. To normalize the distribution, SCC was converted to SCS as $\text{SCS} = 3 + \log_2(\text{SCC}/100,000)$. Cows were from the first 5 lactations and from 5 to 480 days in milk. Contemporary groups were defined as cows sampled in the same herd and test-date (HTD), and HTD with less than 3 cows were discarded from the dataset. Also, a minimum of 3 test-day records per cow within lactation were guaranteed. A further editing was performed on age at calving, according to its distribution within parity order. The final dataset included 59,811 records from 4,355 Holstein cows and 266 herds.

Genetic analysis

A preliminary analysis of variance was performed on LP, LY, FRP and SCS with a mixed model that considered the fixed effects of HTD (7,530 levels), parity (1 to 5), classes of stage of lactation (class 1: ≤ 30 d, class 2 to 11: monthly classes, class 12: 331 to 390 d, and class 13: ≥ 391 d), calving season (4 levels: June to August, September to November, December to February and March to May), and the interaction between parity and classes of stage of lactation. The random effects were cow and the residual.

Heritabilities and genetic correlations were assessed from univariate and bivariate repeatability animal models, respectively, through ASREML software (Gilmour *et al.*, 2015). The models included the fixed effects described above and random effects of permanent environmental cow, additive genetic animal and residual. The pedigree ($n = 17,092$) included

cows with phenotypic records and their ancestors up to 6 generations back.

Results and discussion

Analysis of variance and phenotypic correlations

The coefficients of variation (CV) of LP and LY were 3.65% and 28.54%, respectively (Table 1), consistently with Tiezzi *et al.* (2013). Milk FRP and SCS exhibited the lowest (1.35%) and greatest CV (60.77%), similarly to findings of Hanuš *et al.* (2010) and Penasa *et al.* (2015). Lactation curve of LP resembled that of milk yield, whereas lactation curve of SCS presented an opposite trend (Figure 1). Pearson's correlations between LP and SCS within classes of stage of lactation showed that the relationship between the traits was stronger in mid than early and late lactation. This result suggested that the phenotypic association between LP and SCS was not constant within lactation. Overall phenotypic correlation between LP and SCS was negative and moderate (-0.34), which agreed with previous investigations (Miglior *et al.*, 2007; Sneddon *et al.*, 2015). This result discloses the potential phenotypic role of LP in individual milk for the early identification of intra-mammary infections.

Table 1. Mean, coefficient of variation (CV), additive genetic standard deviation (σ_g), heritability and repeatability (SE within parentheses) for the studied traits.

Trait	Mean	CV, %	σ_g	Heritability	Repeatability
Milk yield, kg/d	27.33	27.75	1.810	0.14 (0.02)	0.46 (0.01)
Lactose, %	4.75	3.65	0.102	0.44 (0.03)	0.59 (0.01)
Lactose yield, kg/d	1.30	28.54	0.089	0.14 (0.02)	0.46 (0.01)
Protein, %	3.37	11.23	0.177	0.35 (0.03)	0.58 (0.01)
Fat, %	4.00	16.09	0.339	0.42 (0.02)	0.48 (0.01)
Freezing point, °C	-0.525	1.35	0.002	0.11 (0.01)	0.26 (0.01)
Somatic cell score	2.92	60.77	0.548	0.12 (0.02)	0.26 (0.01)

Genetic parameters

Estimates of heritability for the traits considered in the present study are reported in Table 1. Comparably with findings of Miglior *et al.* (2007) and Visentin *et al.* (2017), LP showed the greatest heritability (0.44), followed by FP (0.42) and PP (0.35). Somatic cell score heritability was low (0.12), confirming estimates reported in previous genetic studies (Sneddon *et al.*, 2015; Visentin *et al.*, 2017). Heritability of FRP was low (0.11) and difficult to compare with other reports, since to our knowledge only Jonkus & Paura (2011) have assessed heritability (0.062) of FRP, but on a small dataset (794 milk samples) of Latvian Brown cows.

Regarding repeatability, the greatest estimates were obtained for LP (0.59) and protein percentage (0.58; Table 1), suggesting that early performance of cows will be a good predictor of later performance. On the other hand, the lowest estimates were obtained for FRP and SCS (0.26), meaning that temporary effects are predominant for these two traits and that more test-day records are required to predict later performance based on early performance. Estimations of repeatability for other milk characteristics were in agreement with those reported by Sneddon *et al.* (2015) and Visentin *et al.* (2017).

Residual, genetic and permanent environment correlations between LP and LY with

FRP and SCS are presented in Table 2. The permanent environment correlation between LP and FRP was high and negative (-0.72), meaning that permanent environments affecting these two traits operate in opposite direction at the cow level. Residual and genetic correlations between these two traits were moderate and negative (-0.58 and -0.46, respectively). In addition, a weak negative genetic association between LY and FRP was obtained (-0.10; Table 2).

Table 2. Residual, genetic and permanent environmental correlations of lactose percentage and yield with somatic cell score (SCS) and milk freezing point (SE within parentheses).

Trait	Correlation		
	Residual	Genetic	Permanent environmental
Lactose percentage with			
-lactose yield	0.26 (0.004)	0.32 (0.073)	0.11 (0.064)
-SCS	-0.30 (0.004)	-0.25 (0.079)	-0.22 (0.059)
-freezing point	-0.58 (0.003)	-0.46 (0.052)	-0.72 (0.051)
Lactose yield with			
-SCS	-0.18 (0.004)	0.05 (0.114)	-0.16 (0.040)
-freezing point	-0.03 (0.005)	-0.10 (0.099)	0.12 (0.051)

The genetic correlation between LP and SCS (-0.25; Table 2) was in accordance with findings of Miglior *et al.* (2007), Haile-Mariam & Pryce (2017) and Visentin *et al.* (2017). Moreover, permanent environmental correlation between LP and SCS was comparable with results of Miglior *et al.* (2007) and Haile-Mariam & Pryce (2017), suggesting that these two traits had inverse trends not only from a genetic point of view, but also within permanent environmental level. Lactose yield generally showed weak correlations with SCS, as previously reported by Miglior *et al.* (2007).

Conclusion

Lactose percentage is highly heritable and favourably genetically correlated with some low heritable milk traits such as SCS and FRP in Italian Holstein cows. On the other hand, LY weakly correlated with these traits, suggesting that LP rather than LY should be considered in genetic improvement schemes aimed to reduce SCS and improve udder health. Indeed, considering the inverse genetic association between LP and SCS, the inclusion of LP in the selection index of the Italian Holstein breed could aid to improve cow resistance to mastitis. Future studies will evaluate economic scenarios and simulate genetic progress with selection indexes including LP with different economic weights.

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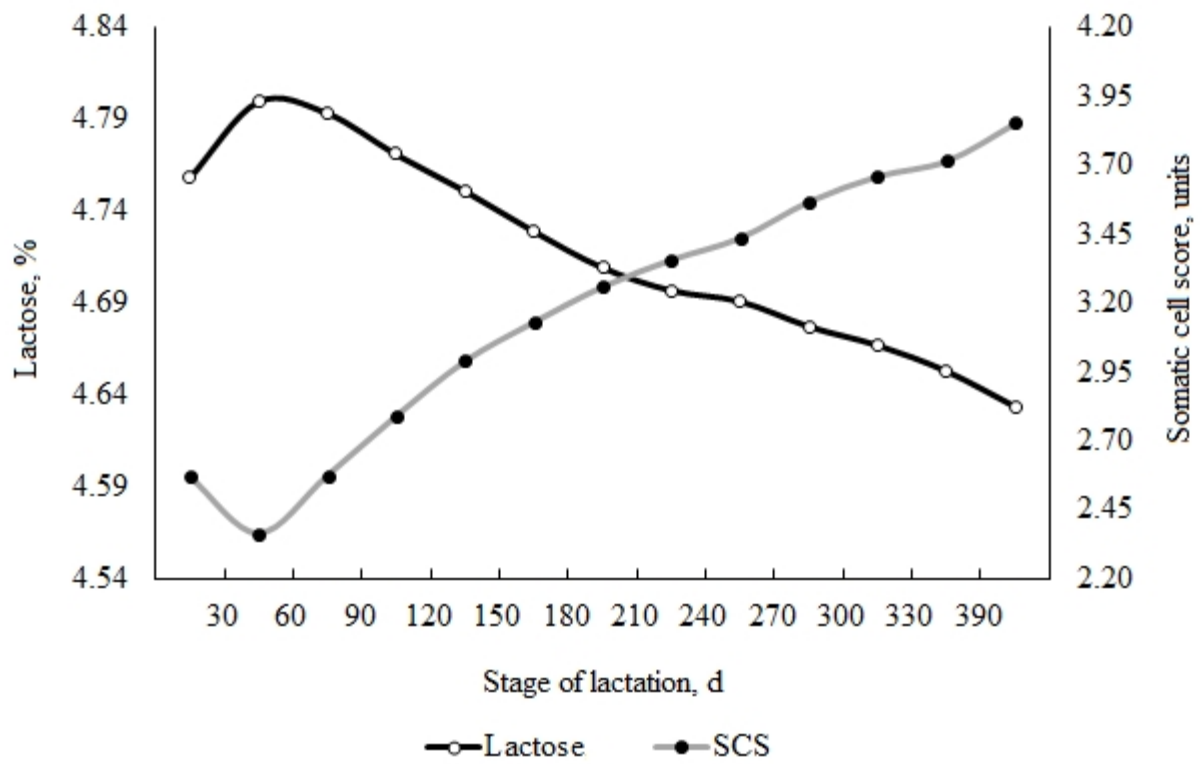


Figure 1. Least squares means of lactose percentage and SCS in different stages of lactation.