Short communication
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Long-term effect of minor genetic changes of milk components on somatic cell count

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Abstract

Selection pressure on protein content (PC), and thus milk composition changes have manifested as an increasingly narrow fat - protein ratio (FPR). In addition, higher somatic cell count (SCC) in milk has been observed in recent years, and that is why it is hypothesized that milk composition changes affect cow's immune response resulting in higher SCC. 2,459,250 test day (TD) records of 127,499 Slovenian Simmental (SIM) cows from years 2004 to 2017 were used for this study. For the estimation of (co)variance components two multiple trait animal TD models were used (M1, M2). M1 included SCC and FPR while M2 included SCC, fat content (FC) and PC. For comparisson of results parameters from the routine single-trait national genetic evaluation were used. Heritability estimates (h^2) for SCC, FC and PC from M2 (0.34, 0.29, 0.38 respectively) were very similar to those form national evaluation; h^2 for FPR was lower than for the other traits (0.22). Both, estimated genetic correlation (r_g=-0.1) and estimated phenotypic correlation (r_p=-0.007) among SCC and FPR in M1 were negative and low. r_p in M2 were positive, but low for all three trait pairs (0.062-0.076) and r_g for SCC-PC was similar (0.069). Conversely, FC-PC r_g (0.502) was positive and moderate whereas SCC-FC r_g (-0.046) was negative and low. Results confirm the hypothesis by suggesting the possibillity of unpredicted and unwanted long-term cumulative effect of seemingly irrelevantly small genetic changes of individual trait.

Keywords: fat – protein ratio, genetic parameters, selection pressure, somatic cell count

Introduction

Scientific discoveries confirming connections between human health and nutrition, and following human diet changes towards low fat intake have had an impact on dairy sector (e.g. Krauss et al., 2000). Demand for low fat dairy products has increased, and milk fat's economic value has dropped. Milk market changes resulted in selection pressure on protein content (Welper, 1991). To asses resulting genetic changes, economically important heritable traits – fat content (FC), protein content (PC), fat - protein ratio (FPR), and somatic cell count (SCC) have been studied. Between FC and PC moderate positive correlation has already been estimated (r=0.53), and weaker, but also positive correlation was also estimated for SCC to PC and FC (r=0.24-0.29 and r=0.103-0.13, respectively) (Rajčević et al., 2003; Cinar et al., 2015). FPR has also been found to be correlated to both SCC and clinical mastitis (Negussie et al., 2013). FPR and SCC are used to assess cow's health status; SCC gives an information on udder health (mastitis), mainly through its leucocyte component, which is closely associated with udder's immune response while it also represents an indicator of milk quality and hygiene (Concha, 1986; Burvenich et al., 1994). It is believed that although minor, genetic intervention in form of selection emphasis on single production trait also affects other correlated biological traits (Oltenacu and Broom, 2010). Thus, the selection pressure made on PC and it's increase that expresses as narrowed FPR, may have a negative impact on animal's health, reflecting in form of immune response – elevated SCC.

The study aims to present an effect of genetic change of a single economically important production trait (PC) on correlated trait that reflects animal's health (SCC) over time in Slovenian Simmental (SIM) cattle.

Materials and methods

Research was performed by estimating the (co)variance components for SCC, FPR, FC and PC in two- and three-trait models, and comparing the results to the routine national single-trait (co)variance component evaluation. Data records of Slovenian SIM cattle population included in national milk recording scheme were used. The data set consisted of 2,459,250 test day records stemmed from 127,499 cows, gathered in years 2004 to 2017. The data were obtained from the National dairy milk recording database of Agricultural Institute of Slovenia. Traits considered in the analysis were FC (%), PC (%), SCC (x10^3 cells/ml), and FPR. Distribution of raw SCC values was right skewed hence the data were transformed using binary logarithm ($\log_2$). Distribution of resulting SCC values was close to normal. To estimate (co)variance components by software package VCE-6 (Groeneveld et al., 2010) animal test day models were used. Model 1 (M1) included SCC and FPR while model 2 (M2) included SCC, FC and PC. Statistical models were the same as for the routine national genetic evaluation:

$$y_{ijklm}=\mu+ C_i + b_{Ij}(t/305)+ b_{IIj}(t/305)^2+ b_{IIIj}\ln(t/305)+ b_{IVj}\ln^2(t/305)+ P_j+ hy_k + pe_{jl} + a_{ijkl} + e_{ijklm}$$

and included population mean (μ); calving season (C_i; calving year x month interaction); state of lactation with lactation curve shaped by Ali-Schaeffer, nested within parity ($b_{Ij}(t/305) + b_{IIj}(t/305)^2 + b_{IIIj}(t/305) + b_{IVj}\ln^2(t/305)$ (Ali and Schaeffer, 1987); parity ($P_{j;}$ j = 1, 2, 3, 4, 5); herd-year (hy_k); permanent environmental effect (pe_{jl}); additive genetic effect (a_{ijkl}), and random residual (e_{ijklm}).

Results and discussion

The h^2 for SCC, FC and PC from M2 do not differentiate substantially from the estimates from national evaluation. h^2 for SCC are very similar for all evaluations (0.34-0.35). h^2 for FC from national evaluation (0.28) is lower, but similar to h^2 from M2 (0.29). h^2 for PC from national evaluation and M2 are the same (0.38). From all the traits, h^2 is the lowest for FPR (0.22; Table 1). SCC h^2 in this study are higher than the reported 0.21 by Ivkić et al. (2012) for the same breed. The h^2 for FPR is in agreement with the h^2 of Negussie et al. (2013) which was between 0.13 and 0.25.

Table 1. Estimates of (co)variance components and genetic parameters from routine single-trait evaluation, M1 and M2

	Trait	h^2	δ_a^2	δ_e^2	r_g ± SE	r_p ± SE
Routine evaluation	SCC	0.34	1.39	1.63		
	FC	0.28	0.15	0.35		
	PC	0.38	0.04	0.05		
M1	SCC	0.35	1.4	1.63		
	FPR	0.22	0.01	0.03		
	SCC-FPR				-0.1±0.003	-0.007±(-0.02)
M2	SCC	0.34	1.39	1.63		
	FC	0.29	0.15	0.35		
	PC	0.38	0.04	0.05		
	SCC-FC				-0.046±0.0008	0.065±0.04
	SCC-PC				0.069±0.001	0.076±0.12
	FC-PC				0.502±0.002	0.062±0.27

h^2: heritability; δ_a^2: genetic (animal) variance; δ_e^2: error variance; r_g: genetic correlation; r_p: phenotypic correlation; SE: standard error

Comparing the h^2 with Missanjo et al. (2013), who reported 0.08, 0.44 and 0.42 h^2 for SCC, PC and FC, respectively. In Jersey breed, h^2 for SCC in this study are significantly higher although h^2 for PC are similar, and h^2 for FC is lower. Compared to Holstein population (0.17; Jamrozik and Schaeffer, 2012) h^2 for SCC in Slovenian SIM population seems also to be higher while h^2 for FPR is lower than their (0.71). r_g between SCC-FPR (-0.1), SCC-PC (0.069), FC-PC (0.502), and between SCC-FC (-0.046) are low to moderate (Table 1). The latter is negative which agrees with results of Negussie et al. (2013) that ranged from -0.01 to 0.2. Negative r_g for SCC-FPR indicates that selection on PC affects SCC oppositely and as such negatively affects animal's health. Since the estimate is low, it's impact can be observed gradually over time. This is confirmed by low, negative r_p between SCC-FPR (-0.007) whereas r_p for SCC-FC and FC-PC (0.065 and 0.062, respectively), and r_p for SCC-PC (0.076) are similar and somewhat higher. Missanjo et al. (2013) estimated low r_g and r_p (both -0.01) between SCC-PC for Jersey breed, and besides being negative, they were almost 7 times lower than the ones in this study. r_g for SCC-FPR from Jamrozik and Schaeffer (2012) for Holstein cows was low and positive (0.04) and thereby did not agree with results in this study. Positive r_g between SCC-PC indicates that the increase of PC also increases SCC. FPR is calculated by dividing the FC with PC, which means that FPR is closely connected to both FC and PC. FC and PC have moderate positive r_g, but their genetic connection to the SCC is opposite. Since the PC is the one that has been increased, it can be concluded on the r_p that PC has greater effect on SCC than FC. That is also why selection on PC affects SCC in a negative way (increasing the SCC). There are not enough studies that estimate (co)variance components made on FPR to effectively compare the results. No matter how small, genetic changes of one trait impact other traits on the long term, which calls for even more careful consideration when making selection decisions.

Conclusions

SCC and FPR are economically important, heritable traits used in cattle selection to determine milk quality and health status, especially udder health of cows. Changing guidelines in human nutrition have led to high selection pressure on PC, followed by milk composition change. The study confirms positive r_g between PC and FC as milk components of interest, but also estimates negative r_g and r_p between SCC and FPR. The results show negative, weak connection between milk composition change and udder health that can be phenotypically seen over longer period of time. Detailed analysis of future selection decisions aiming to change milk component ratios is suggested.

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