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Genetic parameter estimates in South Africa Holstein cattle

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Abstract

A total of 79687 (after editing) first lactation records for milk (MY), butterfat (BFY) and protein (PRY) yield, as well as butterfat (BFP) and protein (PRP) percentages were obtained from the South African Holstein Society for animals that were registered and participating in the South African National Dairy Animal Improvement Scheme. The records cover a period of 21 years (1980 to 2000). Variance components, heritability, the genetic and phenotypic correlation estimates were obtained by REML procedures using an animal model. Heritability estimates for MY, BFY, PRY, BFP and PRP were 0.37, 0.29, 0.33, 0.47 and 0.60 respectively. The genetic correlation estimates of MY with BFY, PRY, BFP and PRP were 0.72, 0.89, -0.49 and -0.45, respectively, while those of BFY with PRY, BFP and PRP were 0.85, 0.24 and -0.02. The genetic correlations of PRY with BFP and PRP were -0.25 and -0.04, while the correlation estimate between BFP and PRP was 0.62.

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Introduction

Milk yield and milk composition are the most important economic traits used for selection in dairy cattle (Hallowell *et al*., 1998), accounting for between 80 and 90% of gross income (Everett & Pearson, 1992). Improvement of these traits should therefore receive the first priority in any selection programme. Progress is largely dependent on the effective utilization of the additive genetic variance and the genetic relationship among the traits. This necessitates accurate estimations of the genetic parameters for the traits concerned. The objective of the study was to obtain estimates of variance components, variance ratios as well as genetic and phenotypic correlations for first lactation milk (MY), butterfat (BFY) and protein (PRY) yields as well as butterfat (BFP) and protein (PRP) percentages.

Materials and Methods

The original database of first lactation records consisted of progeny of 113056 dams and 1429 sires of the South African Holstein breed, distributed over 1205 herds. These data were edited to comply with the following minimum standards: 10 animals and two sires per herd-year-season (HYS) contemporary group; data of at least three years per herd; at least five progeny per sire. After editing, the revised data set comprised of 79687 records. Only registered animals, participating in the South African National Dairy Animal Improvement Scheme from 1980 to 2000, were included. The traits studied were milk (MY), butterfat (BFY) and protein (PRY) yields, as well as butterfat (BFP) and protein (PRP) percentages.

Variance components for milk traits were estimated by Restricted Maximum Likelihood procedures of Gilmour *et al.* (2000). All analyses included the full pedigree consisting of 117294 records. Subsequently, two-trait animal models were fitted, which allowed the calculation of relevant correlations between traits, together with their appropriate standard errors.

The basic single-trait animal model fitted was:

$$y = Xb + Zu + e$$

Where:
- y = a vector of observations for MY, BFY, PRY, BFP and PRP,
- b = a vector of fixed effects of HYS (6877 levels), age at calving (18 to 41 months) and milking frequency (2 or 3 times a day),
- u = a random vector associated with the additive genetic effect of the animal,
- X and Z = incidence matrices for fixed and random effects respectively and
- e = a vector of unknown residual effects.

The expected means and the variance structure for the effects in the general statistical model for the single-trait analyses were assumed to be:

$$E(y) = Xb \qquad E(u) = 0 \qquad E(e) = 0$$
$$Var(u) = A\sigma_a^2 \qquad Var(e) = I\sigma_e^2 \qquad Var(y) = ZAZ'\sigma_a^2 + I\sigma_e^2$$

where: A is the numerator relationship matrix, I an identity matrix, σ_a^2 the direct additive genetic variance and σ_e^2 the residual variance. All the remaining (co)variances due to dominance and epistatic deviations were assumed to be zero.

The effect of the sire x herd interaction was tested as an additional random factor. It was, however, not significant and was thus excluded from the model.

Results and Discussion

The general statistics for the milk traits are presented in Table 1.

Table 1 Overall means, standard deviation (s.d.) coefficients of variation (c.v.), maximum (Max) and minimum (Min) values, for milk yield (MY), butterfat yield (BFY), protein yield (PRY), butterfat percentage (BFP) and protein percentage (PRP)

Parameter	MY (kg)	BFY (kg)	PRY (kg)	BFP (%)	PRP (%)
Overall mean	6792	239	215	3.53	3.17
s.d.	1799	65	56	0.39	0.20
c.v. (%)	26.49	27.30	25.98	11.05	6.31
Max	12296	438	429	5.00	4.24
Min	2024	87	64	1.83	2.35

Estimates of variance ratios are presented in Table 2.

Table 2 Estimates of the heritability (bold print on the diagonal), genetic correlations (below the diagonal) and phenotypic correlations (above the diagonal) for milk yield (MY), butterfat yield (BFY), protein yield (PRY), butterfat percentage (BFP) and protein percentage (PRP)

Trait	MY	BFY	PRY	BFP	PRP
MY	**0.37 ± 0.010**	0.78 ± 0.002	0.94 ± 0.001	-0.33 ± 0.004	-0.32 ± 0.004
BFY	0.72 ± 0.011	**0.29 ± 0.011**	0.85 ± 0.001	0.31± 0.004	-0.04 ± 0.005
PRY	0.89 ± 0.004	0.85 ± 0.006	**0.33 ± 0.010**	-0.18 ± 0.004	0.02± 0.005
BFP	-0.49 ± 0.017	0.24 ± 0.021	-0.25 ± 0.020	**0.47 ± 0.010**	0.46 ± 0.004
PRP	-0.45 ± 0.015	-0.02 ± 0.020	-0.04 ± 0.019	0.62 ± 0.011	**0.60 ± 0.009**

The heritability estimates of milk yield are in accordance with the results obtained by Pander *et al.* (1992, for Jersey cattle), Guo *et al*. (2002) and Ojango & Pollot (2002). At 0.35, the international heritability estimate for milk yield in Holsteins is in close accordance with the present value (Interbull, 2004). The present estimate of the heritability of butterfat corresponds to that obtained by Van Tassell *et al.* (1999). The heritability of protein yield was consistent with estimates reported by Pander *et al*. (1992) and Interbull (2004). Estimates for percentage traits were in agreement with the parameters reported for second lactation Ayrshire cows by Hallowell *et al.* (1998). Heritability estimates in this study varied from medium (butterfat and protein yields) to high (milk yield and percentage traits).

The genetic correlations among yield traits in the present study are highly positive and are in agreement with the results obtained by Pander *et al.* (1992) and Roman & Wilcox (2000). This high relationship among yields indicates that selection for milk yield will result in positive correlated responses in butterfat and protein yields. The genetic correlation between butterfat yield and butterfat percentage is in agreement with results obtained by Pander *et al.* (1992), while those for protein yield and butterfat percentage correspond with an estimate obtained by De Jager & Kennedy (1987). The genetic correlation between butterfat yield and protein percentage, and that between protein yield and protein percentage are, however, negative and low and not in agreement with any of the literature values reviewed.

Both the genetic and phenotypic correlations obtained for milk yield with the percentage traits are in agreement with results obtained by Rege (1991) and Rosati & Van Vleck (2002).

Conclusions

Heritability and correlation estimates obtained in the present study are in agreement with the values used in the international evaluation of Holstein cattle (Interbull, 2004) as well as results reviewed in the literature. The estimates varied from medium (butterfat and protein yields) to high (milk yield, and butterfat and protein percentages).

The highly positive genetic relationships between yield traits indicated that a favourable correlated response to selection for butterfat and protein yields can be expected when selection for milk yield is carried out. The presence of a negative genetic correlation between milk yield and percentage traits is, however, unfavourable. In planning breeding goals for South African Holstein cattle, it is important to consider percentage traits in breeding goals by including them in the index – either to improve them, or at least to maintain them at the present levels.

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