Effect of breed fraction on dairy traits in cattle

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SUMMARY

The objective of the study was to asses the influence of breed fraction on milk yield traits and to evaluate the impact of breed fraction on the prediction of breeding values for Simmental breed. As breed fraction the percent of Holstein (HOL) was taken. More than half a million lactation records (201 to 305-day) of cows with known percent of Simmental and Holstein breeds included in milk recording scheme in the period 1990-2006 were selected from the national milk recording database. Pure breed was defined as having more than 86 % of genes of the same breed. For the evaluation of breed fraction the linear regression approach was applied. In a study of purebred Simmental (SIM), purebred HOL and records of upgraded Simmental (upSIM) with fixed linear model the yields have increased for 24.8 kg milk, 0.9 kg fat and 0.7 kg protein with every percent of HOL. Using single-trait repeatability animal model, records of SIM and records of SIM jointed together with upSIM with max 50 % HOL (SIMpop) were evaluated with and without adjustment for the effect of breed fraction. Estimates of genetic variances were higher for SIMpop than for SIM, which resulted in the estimates of heritability from 0.15 to 0.20 for SIMpop and 0.14 to 0.17 for SIM. Breeding values for SIMpop predicted without adjustment for the effect of breed fraction in the model highly increase with the percent of HOL.

INTRODUCTION

Crossbreeding is a suitable method to increase the production in dairy cattle, particularly because of its effect on traits secondary to milk yield (McAllister, 2002). In order to improve milk traits and some dairy functional traits, upgraded Simmental and Holstein (red) dairy bulls have been mated to Simmental dual purpose cows in Slovenia since the seventies. During this process, a great variety of crossbred combinations has been formed. After the repeated matings, the percentage of Holstein genes in Simmental breed increased and the upgraded animals represent 12 % of milk-recorded cows (Sadar et al., 2006). Due to the skin color inheritance, the upgraded animals were still red spotted and in many cases treated as Simmental animals without taking breed fraction into account. These animals were treated as purebred Simmental in the genetic evaluations as well. No breed fraction or other crossbreeding effects were taken into account, although it had an effect on the genetic evaluation (Harbers, 1997). Crossbreeding effects are included in the models for genetic evaluations of dairy traits in several countries (Interbull, 2000). The effect of breed fraction may have an impact on the prediction of breeding values for dairy traits in Slovenian Simmental population as well.

The objective of this study was to asses the influence of breed fraction on milk yield traits in standard lactation and to evaluate the impact of breed fraction on the prediction of breeding values for Simmental breed.

MATERIAL AND METHODS

For the investigation of the effect of the breed fraction on dairy traits, the milk production records of Simmental and Holstein cows and their crossbreds were studied. First to fifth lactations starting with calvings in the period from 1990 to 2005 were included. The traits studied were: milk (kg), protein (kg), and fat (kg) yield in standard lactations (201 to 305-day). Milk production data and pedigree information were collected from the database of Slovenian cattle recording scheme (Logar et al., 2005). Criteria for data inclusion were at least 60 kg protein and at least 60 kg fat yield, age at first calving within 17-48 months and age at calving within 17-110 months. Only data on animals with known birth date and breed fraction of Simmental and red or black Holstein were used. Breed fraction or proportion of different breeds was calculated from the original pedigree information for all animals included and for their ancestors as well, and ranged from 0 to 100 percents.

Three related sets of data were analyzed. The first set comprised records of the two pure breeds (Simmental and Holstein) and their crossbreds. An animal was taken as purebred if 87 % or more of genes came from the same breed. Crossbred cows with 14 - 86 % of Holstein breed were generally a result of upgrading with red Holstein. In the first data set (Table 1) a total of 504644 lactation records were included, 257562 of Simmental breed, 34423 of upgraded Simmental (14-86 % Holstein) and 212659 of Holstein. The number of records as well as the phenotypic mean and standard deviations for all traits and age at calving by breeds are given in Table 1 and by breeds and lactations in Table 2, all for the first set of data.

Table 1. Means and standard deviations for milk yield, fat and protein yield and age at calving by breed

Breed *	HOL breed (%)	No. of records	Milk yield (kg)	Fat yield (kg)	Protein yield (kg)	Age at calving (month)
SIM	0 - 13	257562	4203 ± 1158	173.8 ± 53.1	139.8 ± 41.0	49.1 ± 18.7
SIM x HOL	14 - 86	34423	5120 ± 1492	210.8 ± 63.5	167.7 ± 50.0	45.7 ± 17.6
HOL	87 - 100	212659	6513 ± 1629	262.9 ± 71.1	210.3 ± 54.6	47.0 ± 17.6
Total		504644	5239 ± 1785	213.9 ± 75.4	171.4 ± 58.6	48.0 ± 18.2

* SIM-Simmental, HOL-Holstein;

Table 2: Means and standard deviations for milk yield, fat and protein yield and age at calving by breed and lactation

Breed *	Lactation	No. of records	Milk yield (kg)	Fat yield (kg)	Protein yield (kg)	Age at calving (month)
SIM	1	74707	3855 ± 991	160.0 ± 46.1	127.6 ± 35.6	28.3 ± 3.6
	2	63053	4190 ± 1150	174.3 ± 53.3	140.8 ± 41.3	41.7 ± 4.5
	3	51103	4426 ± 1206	183.1 ± 55.8	147.3 ± 42.7	55.0 ± 5.4
	4	39373	4451± 1210	182.7 ± 55.4	147.4 ± 42.5	68.2 ± 6.2
	5	29326	4401 ± 1187	179.2 ± 53.9	145.0 ± 41.5	81.5 ± 7.1
SIM	1	11989	4748 ± 1283	196.4 ± 54.9	155.0 ± 43.7	28.3 ± 3.7
x	2	9238	5190 ± 1506	215.1 ± 64.0	172.1 ± 50.7	41.6 ± 4.5
HOL	3	6247	5471 ± 1591	225.1 ± 68.4	179.2 ± 53.1	54.8 ± 5.3
	4	4160	5418 ± 1582	220.9 ± 67.8	176.2 ± 52.3	68.0 ± 6.1
	5	2789	5259 ± 1562	262.9 ± 71.1	170.1 ± 51.0	82.0 ± 6.9
HOL	1	71647	5993 ± 1368	241.3 ± 59.1	192.6 ± 47.1	29.0 ± 3.9
	2	56009	6571 ± 1652	266.8 ± 72.1	215.3 ± 55.3	42.6 ± 4.7
	3	40757	6937 ± 1686	280.9 ± 74.8	223.7 ± 56.5	55.8 ± 5.5
	4	27317	6927 ± 1700	278.8 ± 75.3	222.1 ± 56.2	68.8 ± 6.3
	5	16929	6837 ± 1703	272.6 ± 74.9	217.9 ± 56.1	81.6 ± 6.9

* SIM-Simmental, HOL-Holstein; all with the same % of HOL breed as in Table 1;

Only purebred Simmental (SIM) records presented in Table 1 and Table 2 were included in the second data set. Jointly 257562 lactation records of SIM were obtained from 94302 cows in 8589 herds. Records included in the second data set and 27229 lactation records of upgraded Simmental cows with mostly 50 % of Holstein breed were included in the third data set. The highest percentage of Holstein breed in the third data set was thus 50 %, as in the national genetic evaluation for the Simmental breed. The third data set which included animals currently as Simmental breed was therefore named Simmental breed population (SIMpop). The SIMpop records were obtained from 104893 cows in 8865 herds. Descriptive statistic for all traits studied and the age at calving in the first to fifth lactation for SIMpop are given in table Table 3.

Table 3. Means and standard deviations for milk yield, fat and protein yield and age at calving for Simmental breed population (SIMpop) by parities

Breed *	Lac-tation	No. of records	Milk yield (kg)	Fat yield (kg)	Protein yield (kg)	Age at calving (month)
SIMpop	1	83955	3928.8 ± 1037.1	163.1 ± 47.6	129.9 ± 36.8	28.3 ± 3.6
	2	70281	4268.9 ± 1202.8	177.6 ± 55.0	143.3 ± 42.7	41.7 ± 4.5
	3	56101	4498.6 ± 1255.7	186.0 ± 57.4	149.5 ± 44.0	55.0 ± 5.4
	4	42793	4511.5 ± 1252.3	185.1 ± 56.7	149.2 ± 43.5	68.2 ± 6.2
	5	31661	4450.3 ± 1222.5	181.0 ± 55.0	146.5 ± 42.3	81.5 ± 7.1
Total	1-5	284791	4270.5 ± 1201.4	176.5 ± 54.5	141.8 ± 42.2	48.8 ± 18.6

* SIMpop-Simmental and Simmental x Holstein; % HOL breed from 0 to 50 %

The effect of breed fraction on dairy traits was initially studied on the first data set with records from Simmental and Holstein breeds and their crossbreds (Table 1). The percentage of Holstein breed in each cow was taken as an effect of breed fraction. Therefore, breed fraction represented an individual breed effect of Holstein breed. For the evaluation of effect of breed fraction linear regression approach was applied. Solutions in fixed linear model were obtained by PROC GLM of SAS (SAS Institute Inc. 2004). The following linear model was used:

$$y_{ijkl} = \mu + G_i + C_j + S_k + M_l + b_1 A_{ijkl} + b_2 A_{ijkl}^2 + b_3 L_{ijkl} + b_4 B_{ijkl} + e_{ijkl} \qquad [1]$$

where

y_{ijkl} = observed value of the milk performance trait (milk, fat, protein yield in 201-305 days) of genotype i in lactation j that started with calving in the year k and month l;
μ = overall mean;
G_i = fixed effect genotype i (i = 1, 2, 3);
C_j = fixed effect of lactation j (j = 1, 2, 3, 4, 5);
S_k = fixed effect of calving season k (in years, k = 1, 2, …, 16);
M_l = fixed effect of month of calving l (l = 1, 2, …, 12);
b_1, b_2 = linear and quadratic regression coefficients of dependent variable y on age at calving;
A = continuous variable representing age at calving (in months);
b_3 = linear regression coefficient of dependent variable y on length of lactation;
L = continuous variable representing length of lactation;
b_4 = linear regression coefficient of dependent variable y on breed fraction (% of Holstein);
B = continuous variable representing breed fraction;
e_{ijkl} = random residual.

For further studies the second and the third data set were used. Univarate analyses were performed in the studies of effect of breed fraction on genetic and environmental parameters in SIM and in SIMpop. Genetic and other parameters were estimated using single-trait repeatability animal model with restricted maximum likelihood (REML) as applied in VCE-5, Version 5.1.2 (Kovač et al., 2002). Two statistical models were used: model 2, where effect of breed fraction was included as linear regression and model 3 without the breed fraction effect.

$$y_{jklmn} = \mu + C_j + S_k + M_l + b_1 A_{jkl} + b_2 A_{jkl}^2 + b_3 L_{jkl} + b_4 B_{jkl} + h_m + p_n + a_n + e_{jklmn} \qquad [2]$$

$$y_{jklmn} = \mu + C_j + S_k + M_l + b_1 A_{jkl} + b_2 A_{jkl}^2 + b_3 L_{jkl} + h_m + p_n + a_n + e_{jklmn} \qquad [3]$$

where the effects are as before in model 1 and:

y_{jklmn} = observed value of the milk performance trait (milk, fat, protein yield in 201-305 days) on animal n in lactation j that started with calving in year k and month l in herd m;
h_m= random effect of herd m;
p_n = random permanent environmental effect of cow n;
a_n = random additive genetic effect of animal n;
e_{jklmn} = random residual.

The direct additive genetic effect (a_n) was assumed to be normally distributed with mean zero and variance $\mathrm{var}[\mathbf{a}] = [\sigma_a^2] \otimes \mathbf{A}$, where σ_a^2 is the direct additive genetic variance for the trait, and **A** is the additive relationship matrix. Other random effects were assumed to be normally distributed with mean zero as well. The variances are $\mathrm{var}[\mathbf{h}] = [\sigma_h^2] \otimes \mathbf{I}_h$ and $\mathrm{var}[\mathbf{p}] = [\sigma_p^2] \otimes \mathbf{I}_p$, where σ_h^2 is herd and σ_p^2 is permanent environmental variance of the cow. Matrices I_h and I_p are the corresponding identity matrices. The residuals were assumed to be normally independent and identically distributed with mean zero and variances $\mathrm{var}[\mathbf{e}] = [\sigma_e^2] \otimes \mathbf{I}_e$. Heritability ($h^2$) and repeatability ($r$) for each trait were calculated by the equations:

$$h^2 = \sigma_a^2 / \sigma_{total}^2 \text{ and } r = \frac{\sigma_a^2 + \sigma_p^2}{\sigma_{total}^2} \text{ where } \sigma_{total}^2 = \sigma_a^2 + \sigma_h^2 + \sigma_p^2 + \sigma_e^2 .$$

RESULTS AND DISCUSSION

Data from purebred and crossbred animals (Table 1, Table 2) was studied initially. All the effects included in the statistical model 1 for milk, fat and protein yield were found to be highly significant ($P<0.001$). The average phenotypic distances between pure breeds were 2310 kg milk, 89.1 kg fat and 70.5 kg protein in 201-305 days of lactation (Table 1), while the crossbreds were placed between purebreds. By the model adjustment the yield was increasing for 24.8 (± 0.29) kg milk, 0.9 (±0.01) kg fat and 0.7 (±0.01) kg protein with every percent of Holstein breed. The phenotypic difference between pure breeds for milk yield was slightly lower than that estimated with the model (model 1). The differences in fat and protein yield are negligible. The results obtained indicated a significant difference in the production of Simmental and upgraded Simmental cows.

The study was continued in the field of genetic evaluation. Purebred Simmental records (SIM, second data set) and purebred Simmental records joined together with records of upgraded Simmental cows (SIMpop, third data set) were evaluated using models 2 and 3. Estimates of variance components for SIM did not differ much between the statistical models (Table 4). The differences in estimates between the models were higher for SIMpop. Generally the estimated variance components were higher for SIMpop than for SIM. For all traits studied the genetic variances were higher in SIMpop than in SIM and increased for SIMpop in the model where breed fraction effect was excluded (model 3). Consequently, the estimates of heritability were higher for SIMpop than for SIM and higher for SIMpop if breed fraction effect was not included in the model. An increase of genetic variation in SIMpop was expected because of favorable effect of crossbreeding on increased genetic variation (Swan and Kinghorn, 1992; VanRaden, 1992). For all traits studied and both data sets a large amount of total variability of the traits studied was explained by herd effect. Numerous herds with small number of observations per herd resulted in high variances of the herd effect. Estimates of repeatability range from 0.28 to 0.33. The estimated variance components presented in table Table 4 are in agreement with those used in the national genetic evaluation.

Table 4. Estimates of additive genetic (σ_a^2), herd (σ_h^2), permanent environmental (σ_p^2), residual variance (σ_e^2), heritability (h^2) with standard errors (*se*), and repeatability (*r*) for milk, protein, and fat yield by statistical models for Simmental breed (SIM) and Simmental breed population (SIMpop)

	Model 2						Model 3					
Estimates/ Yield trait	σ_a^2	σ_h^2	σ_p^2	σ_e^2	$h^2 \pm se$	r	σ_a^2	σ_h^2	σ_p^2	σ_e^2	$h^2 \pm se$	r
Breed						SIM						
Milk	156218	333444	130212	290818	0.17 ± 0.0034	0.31	157070	333674	129875	290808	0.17 ± 0.0034	0.31
Fat	260.8	637.7	258.2	650.4	0.14 ± 0.0033	0.29	262.0	638.3	257.8	650.4	0.14 ± 0.0033	0.29
Protein	148.2	461.5	155.7	331.2	0.14 ± 0.0030	0.28	148.6	461.8	155.6	331.2	0.14 ± 0.0030	0.28
						SIMpop						
Milk	176779	350373	130864	300198	0.18 ± 0.0032	0.32	199423	355236	120032	300127	0.20 ± 0.0030	0.33
Fat	291.8	660.5	259.2	665.7	0.16 ± 0.0030	0.29	333.7	668.3	238.5	665.6	0.18 ± 0.0029	0.30
Protein	167.1	481.4	156.5	339.1	0.15 ± 0.0030	0.28	186.9	486.8	146.7	339.1	0.16 ± 0.0029	0.29

On the base of estimated genetic and other parameters breeding values were predicted for SIMpop by statistical models 2 and 3. Differences in breeding values predicted with models 3 (no effect of breed fraction) and breeding values predicted with model 2 (effect of breed fraction included) for every particular animal were calculated. Additionally, linear regression of difference in breeding values on breed fraction was estimated. Difference in breeding values increased for 11.07 (±0.0111) kg milk, 0.45 (±0.0006) kg fat and 0.30 (±0.0003) kg protein with the percentage of breed fraction. That confirms expectations that purebred Simmental animals are in subordinate position if breed fraction effect is not taken into account. The contribution of breed fraction to the predicted breeding values is more clearly evident from averages of differences in breeding values by breed fraction (% of Holstein breed) presented in Figure 1. Animals with higher percentage of Holstein breed received higher breeding values when breed fraction effect was not included in the evaluation model. Likewise, in the study of Harbers (1997) the breeding values changed after the inclusion of correction for effect of crossbreeding in the statistical model for milk production. Similar as in this study, with animals where correction had no effect, no differences in breeding values were found.

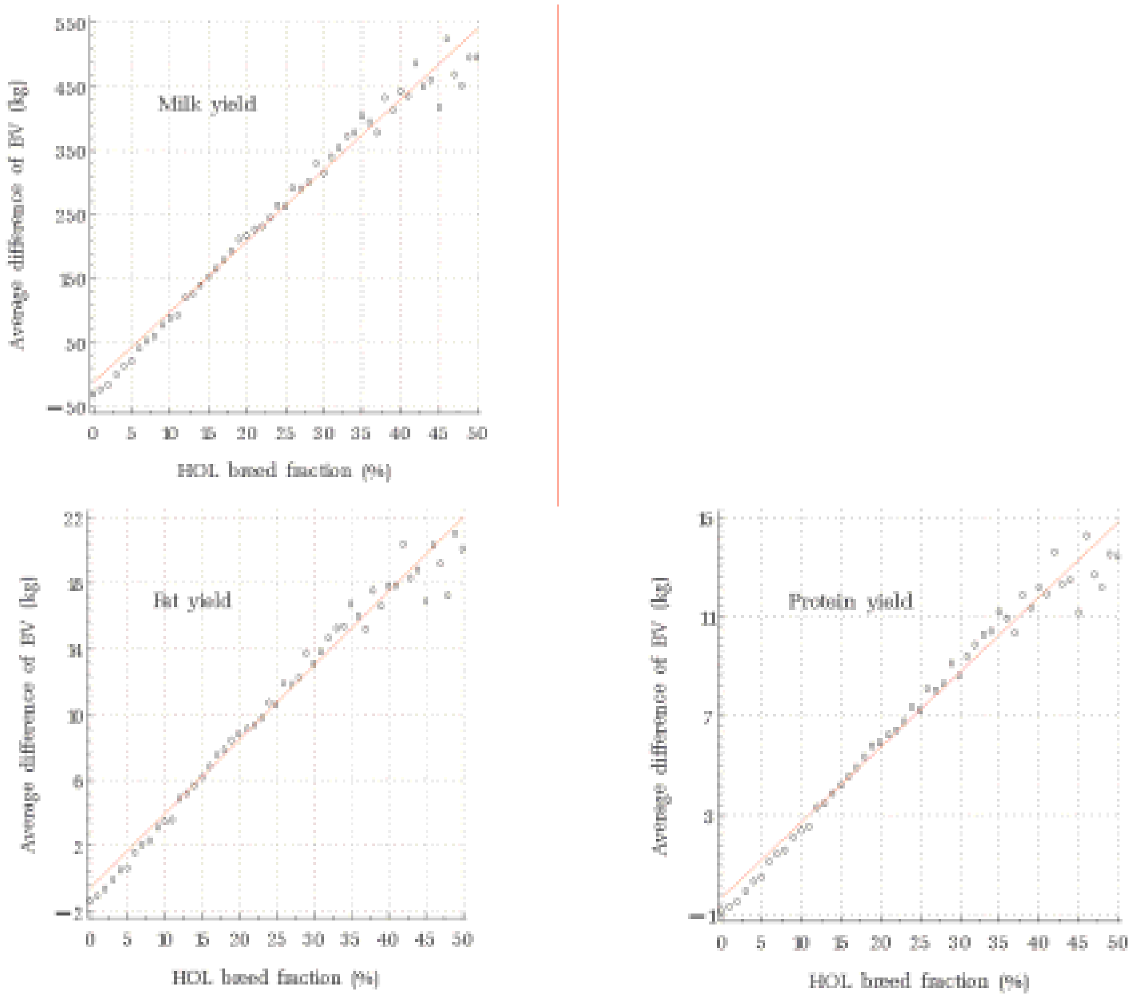

Figure 1. **Average difference of breeding values (BV) predicted with two models (without and with the effect of breed fraction) regarding to Holstein (HOL) breed fraction for milk, fat and protein yield**

The results obtained indicated that breed fraction has an effect on predicted breeding values for SIMpop and, consequently, that in the evaluation of upgraded Simmental population at least breed fraction has to be taken into account. Treating of upgraded animals as purebred has negative influence on the selection in Simmental breed. Upgraded animals are therefore receiving higher genetic value and thus have higher chance to be selected than the purebred ones. There are many benefits of crossbreeding and upgrading. But it has to be realized that in crossbreeding scheme genetic improvement is based on the performance of purebred animals and we then utilize improved animals in crossbreeding schemes (Roughsedge and Simm, 2002). Therefore, reliable evaluation is needed that would provide useful information and aid the breeders with the selection of proper animals. Possible solution is to find specific model for a joint evaluation of purebred and crossbreed records as in VanRaden et al. (2007).

The records of crossbred dairy cattle need to be adjusted for crossbreeding effects (Harbers, 1997; VanRaden and Sanders, 2003). An important and extensive part of this study was finding and calculation of breed fractions, which enabled further research. The unique identification of animals including breed fraction permits the use of production data in order to estimate additive and non-additive genetic parameters (McAllister, 2002). With less systematic crossbreeding, estimation of crossbreeding effect is difficult to determine (Van Vleck , 1997). Simplification of estimation of crossbreeding effects was made in the study. Only the breed fraction effect of Holstein as an individual breed effect on dairy traits was studied. In this way further investigation for the estimation of a specific crossbreeding effect will be needed. Other traits of importance should also be investigated. Therefore, the study needs to be continued to find suitable solution for accurate prediction of genetic value for SIMpop.

CONCLUSIONS

Summarizing the results and the discussion, the significant effect of breed fraction on milk, fat and protein yield was observed. The breed fraction effect should be taken into account in the genetic evaluation for Simmental breed where population consists of pure bred and upgrade animals. Further investigation to find a suitable solution for accurate prediction of genetic value for SIMpop is therefore necessary.

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