

Sire evaluations at different levels of milk production

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ABSTRACT

Data were 49,693 first 305-d lactation milk kg, fat kg and fat percentage from the Gdańsk region. Black and White cows were daughters of 523 Black and White and 27 Holstein-Friesian bulls. Herds were stratified into three levels, based on the mean milk yield.

Genetic and residual variances were estimated by the restricted maximum likelihood method (REML). The model included effects of herd-year-season of calving, and of genetic groups. The same model was used for BLUP evaluation of sires. All calculations were done on linear and logarithmic scales, within the three production levels.

Heritabilities of milk yield, fat yield and fat content increased with increasing mean production. Similar estimates were obtained on the linear and log scales. Genetic variance increased on both scales, the same way heritabilities did. Error variances of milk and fat yield followed the same pattern on the linear scale. On the log scale for those two traits, the highest error variance was obtained at the medium production level. Correlations between sire breeding values estimated at different production levels were close to expected correlations. Genetic correlations between levels were low for fat yield, especially between the high and the other levels. This seems to suggest a certain amount of genotype-environment interaction. Evaluation and selection of sires at low production might adversely affect genetic progress.

KEY WORDS: milk production, genetic correlation, heritability

INTRODUCTION

Sire evaluation for production traits in Poland is based on first 305-d lactations of daughters from large state farms. The cow population is characterized by low average overall yields and relatively large variation among herds. In several studies it was shown that the standard deviation increases with the increase in mean milk and fat yield. Also genetic components of variance were often higher at higher production levels (Danell, 1982; Hill et al., 1983; Lofgren et al., 1985; Mirande and Van Vleck, 1985; De Veer and Van Vleck, 1987). Majority of studies concerning expression of a genotype in different environments and heterogeneity of variances were carried out on much higher production than that studied in this paper.

The purpose of this study was to determine the effects of different production levels on genetic and residual variance components and BLUP sire evaluation results in a population with low overall milk yield.

DATA AND METHODS

Data were 49,693 first 305-d lactation milk kg, fat kg and fat percentage from the Gdańsk region. Black and White cows were daughters of 523 Black and White and 27 Holstein-Friesian bulls. Genetic groups were defined according to the strain and bulls' year of birth. Herds were stratified into three levels, based on the mean milk yield: below 3,000 kg (488 bulls with 16,464 daughters; 3,001 to 4,000 kg (544 bulls with 24,137 daughters) and above 4,001 kg (331 bulls with 9,092 daughters).

Genetic and residual variances were estimated by the restricted maximum likelihood method (REML). The model included effects of herd-year-season of calving, and of genetic groups. The same model was used for BLUP evaluation of sires. All calculations were carried out on linear and logarithmic scales, within the three production levels.

Genetic correlations between production levels were approximated by the adjustment procedure given by Calo et al. (1973). Expected correlations were calculated as a function of the accuracy of sire transmitting abilities (Hickman et al., 1969).

RESULTS AND DISCUSSION

Average milk production at three levels (low, medium and high) and numbers of bulls and daughters are given in Table 1. This data was used to evaluate the genetic parameters.

TABLE 1
Characteristics of data by average herd production level

Level	Milk kg	No. of bulls	No. of daughters
L	< = 3000	488	16,464
M	3001 - 4000	544	24,137
H	> 4000	331	9,092
	Milk yield (kg)	Fat yield (kg)	Fat %
L mean	2714	105.61	3.89
sd	461	19.53	0.32
M mean	3426	135.74	3.96
sd	643	27.42	0.33
H mean	4630	187.60	4.05
sd	849	36.61	0.34

TABLE 2
Estimates of variance components and heritabilities (h^2) with standard errors (h^2_{SE}) at different production levels

	Error variance	Sire variance	h^2	h^2_{SE}
Milk yield (kg) linear				
L	176,635	8,288	0.18	0.04
M	325,768	27,132	0.31	0.04
H	484,455	50,641	0.38	0.08
Milk yield (kg) log				
L	0.0222	0.0010	0.16	0.04
M	0.0288	0.0024	0.30	0.04
H	0.0252	0.0027	0.38	0.08
Fat yield (kg) linear				
L	300	7.05	0.09	0.03
M	556	31.97	0.22	0.03
H	844	50.56	0.23	0.07
Fat yield (kg) log				
L	0.0254	0.0005	0.08	0.03
M	0.0315	0.0018	0.22	0.03
H	0.0272	0.0018	0.24	0.07
Fat % linear				
L	0.073	0.002	0.11	0.03
M	0.071	0.003	0.15	0.03
H	0.074	0.008	0.41	0.08
Fat % log				
L	0.0048	0.0001	0.11	0.03
M	0.0045	0.0002	0.15	0.03
H	0.0045	0.0005	0.41	0.08

Table 2 shows the estimates of sire and error variances and heritabilities by production level. Heritability of milk yield increased with the production level, from 0.18 to 0.38. Both components of variance also increased, with the genetic component growing faster. A similar pattern was found for fat yield but heritabilities were lower (from 0.09 to 0.23). Heritabilities of fat content for two lower production levels were small (0.11 and 0.15). Only in the highest production level heritability reached the magnitude usually reported in the literature (0.41).

Logarithmic transformation does not change heritabilities of studied traits. The changes occurred in the relative magnitude of variance components. In milk

and fat yield the error variance on the log scale was highest at the medium level, lowest at the low level and intermediate at the high level. Fat content had the highest error variance at the low level and slightly lower and of the same magnitude at the medium and high levels. Sire variance showed the same increasing pattern on the log scale and on the linear scale for all traits.

The increase of heritabilities with increasing production level found in our study is in agreement with other research (see e.g. Danel, 1982; Mirande and Van Vlec, 1985; De Veer and Van Vleck, 1987). In these papers it was also shown that sire variance was related to the mean. However, for records transformed to logarithms, the error variance usually decreased as production level increased (Mirande and Van Vleck, 1985) or remained on the same level (De Veer and Van Vleck, 1987). In our study the error variance for milk and fat yield was smaller for the high than for the medium level. The low level had the smallest error variance. This seems to show that the multiplicative model is not quite adequate to describe the records.

Genetic and phenotypic correlations among three traits within each production level showed similar magnitude.

Table 3 presents the correlations between BLUP predicted differences of the same bulls evaluated on records of daughters split according to the production level. The values of all correlations were close to their expected values, on both scales. The genetic correlations between levels of production were near unity for milk yield. However, for fat yield correlations were much lower. The highest genetic correlation on the untransformed records was found between the low and medium levels (0.73), correlations between high and medium and high and low were much less than unity (0.68 and 0.66 respectively). In other studies the correlations among sire values at different production levels were usually above 0.8 (Danell, 1982), and their authors concluded that genotype-environment interaction does not have to be considered in the selection programs. In our data

TABLE 3
Correlations between bull BLUP breeding values (r_s), genetic correlations (r_g) and expected correlations (r_{exp}) estimated at different production levels (on linear and log scale) with minimum 10 daughters/bull

		Milk kg		Fat kg		Fat %		r_{exp}
		r_s	r_g	r_s	r_g	r_s	r_g	
L-M	linear	0.64	0.94	0.50	0.74	0.53	0.78	0.68
	log	0.63	0.93	0.50	0.74	0.52	0.76	
L-H	linear	0.59	0.95	0.41	0.66	0.65	1.05	0.62
	log	0.57	0.92	0.38	0.61	0.65	1.06	
M-H	linear	0.57	0.93	0.42	0.69	0.61	1.00	0.612
	log	0.55	0.90	0.43	0.70	0.61	1.00	

this is the case for milk yield, but much lower genetic correlation coefficients for fat yield showed that ranking of bulls at the high level was substantially different from that at the low and medium level. This seems to suggest that a certain amount of interaction in fat yield is present in our data and is connected with the lower production levels. Evaluation and selection of sires at low production might adversely affect genetic progress.

CONCLUSIONS

Heritabilities of milk yield, fat yield and fat content increased with increasing mean production. Similar estimates were obtained on the linear and log scales.

Genetic variance increased on both scales in the same manner as heritabilities did. Error variances of milk and fat yield followed the same pattern on the linear scale. On the log scale for those two traits, the highest error variance was obtained at medium production.

Correlations between sire breeding values estimated at different production levels were close to expected correlations.

Genetic correlations between levels were relatively low for fat yield, especially between the high and the other levels. This seems to suggest a certain amount of genotype-environment interaction.

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STRESZCZENIE

Ocena wartości hodowlanej buhajów z uwzględnieniem różnych poziomów produkcji mleka

Badaniami objęto wydajność mleka i tłuszczu oraz procentową zawartość tłuszczu w mleku w pierwszych 305-dniowych laktacjach 49693 krów rasy czarno-białej, pochodzących z okręgu gdańskiego. Krowy były córkami 523 czarno-białych buhajów i 27 buhajów odmiany hol-sztyno-fryzyskiej. Obory podzielono na trzy grupy, w zależności od średniej wydajności mleka.

Genetyczne i resztowe wariancje oszacowano przy pomocy metody największej wiarygodności

z ograniczaniem (REML). Model analizy zawierał efekty stada-roku-sezonu ocielenia i grupy genetycznej. Taki sam model został użyty do oceny wartości hodowlanej buhajów przy pomocy metody BLUP. Wszystkie obliczenia w obrębie trzech poziomów wydajności stad wykonano na danych oryginalnych oraz po ich zlogarytmowaniu.

Odziedziczalność wydajności mleka, tłuszczu i procentu tłuszczu w mleku wzrastała wraz ze wzrostem średniego poziomu produkcji. Oszacowania okazały się podobne dla danych oryginalnych i, podobnie jak odziedziczalność, zachowały się wariancje genetyczne. Wariancje błędu dla wydajności mleka i tłuszczu dla danych oryginalnych również wzrastały wraz ze wzrostem poziomu produkcji. Po zlogarytmowaniu najwyższą wariancję błędu stwierdzono w stadach o średnim poziomie wydajności. Korelacje między oszacowaniami wartości hodowlanej tych samych buhajów na różnych poziomach wydajności okazały się zbliżone do wartości oczekiwanych. Korelacje genetyczne między poziomami wydajności były niskie dla kg tłuszczu, szczególnie między wysokim a pozostałymi dwoma poziomami produkcji. Sugeruje to możliwość występowania interakcji genotyp-środowisko. Wynika stąd, że oszacowanie wartości hodowlanej w oborach o niskim poziomie wydajności i oparta o to selekcja może ujemnie wpływać na wielkość osiąganego postępu genetycznego.