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Genetic correlations between the cumulative pseudo-survival rate, milk yield, and somatic cell score during lactation in Holstein cattle in Japan using a random regression model

O. Sasaki,*[1] M. Aihara,† A. Nishiura,* and H. Takeda*
*Institute of Livestock and Grassland Science, National Agriculture and Food Research Organization, Tsukuba 305-0901, Japan
†Livestock Improvement Association of Japan Inc., Tokyo 135-0041, Japan

ABSTRACT

Trends in genetic correlations between longevity, milk yield, and somatic cell score (SCS) during lactation in cows are difficult to trace. In this study, changes in the genetic correlations between milk yield, SCS, and cumulative pseudo-survival rate (PSR) during lactation were examined, and the effect of milk yield and SCS information on the reliability of estimated breeding value (EBV) of PSR were determined. Test day milk yield, SCS, and PSR records were obtained for Holstein cows in Japan from 2004 to 2013. A random subset of the data was used for the analysis (825 herds, 205,383 cows). This data set was randomly divided into 5 subsets (162–168 herds, 83,389–95,854 cows), and genetic parameters were estimated in each subset independently. Data were analyzed using multiple-trait random regression animal models including either the residual effect for the whole lactation period (H0), the residual effects for 5 lactation stages (H5), or both of these residual effects (HD). Milk yield heritability increased until 310 to 351 d in milk (DIM) and SCS heritability increased until 330 to 344 DIM. Heritability estimates for PSR increased with DIM from 0.00 to 0.05. The genetic correlation between milk yield and SCS increased negatively to under −0.60 at 455 DIM. The genetic correlation between milk yield and PSR increased until 342 to 355 DIM (0.53–0.57). The genetic correlation between the SCS and PSR was −0.82 to −0.83 at around 180 DIM, and decreased to −0.65 to −0.71 at 455 DIM. The reliability of EBV of PSR for sires with 30 or more recorded daughters was 0.17 to 0.45 when the effects of correlated traits were ignored. The maximum reliability of EBV was observed at 257 (H0) or 322 (HD) DIM. When the correlations of PSR with milk yield and SCS were considered, the reliabilities of PSR estimates increased to 0.31–0.76. The genetic parameter estimates of H5 were the same as those for HD. The rank correlation coefficients of the EBV of PSR between H0 and H5 or HD were greater than 0.9. Additionally, the reliabilities of EBV of PSR of H0 were similar to those for H5 and HD. Therefore, the genetic parameter estimates in H0 were not substantially different from those in H5 and HD. When milk yield and SCS, which were genetically correlated with PSR, were used, the reliability of PSR increased. Estimates of the genetic correlations between PSR and milk yield and between PSR and SCS are useful for management and breeding decisions to extend the herd life of cows.

Key words: dairy cattle, genetic evaluation, survivability, reliability

INTRODUCTION

Estimates of genetic correlations between longevity and milk yield in cows vary among studies (e.g., Tsuruta et al., 2005; Pritchard et al., 2013; Tokuhisa et al., 2014), suggesting variation in environmental factors. Genetic correlations between the length of herd life and milk yield decrease yearly, from high positive values to low negative values (Tsuruta et al., 2004; Hagiya et al., 2012a; Haile-Mariam and Pryce, 2015), indicating that correlations need to be assessed periodically. Negative genetic correlations have been reported between longevity and SCS and between longevity and mastitis (Hagiya et al., 2012b; Pritchard et al., 2013; Weller and Ezra, 2015). In these studies, longevity traits have been estimated for the whole productive life or at each parity. Therefore, trends in genetic correlations between longevity and both milk yield and SCS during lactation could not be traced. The risk of becoming ill for high-producing dairy cows increases as the energy deficit increases in the early stage of lactation (Heuer et al., 1999; Čejna and Chládek, 2005; Toni et al., 2011). Accordingly, the genetic correlation between longevity and milk production may differ among lactation stages; specifically, genetic correlations may be higher during early stages than later lactation stages. Using a random

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[1] Corresponding author: sasa1@affrc.go.jp

regression model, Sasaki et al. (2015) reported that the cumulative pseudo-survival rate (**PSR**) could reflect changes in genetic parameters during lactation. Therefore, it is possible to assess changes in genetic correlations during lactation between PSR and milk production traits and SCS using random regression models. If these genetic correlations are high, milk production traits and SCS are expected to increase the reliability of the EBV of PSR (Tsuruta et al., 2005; Hagiya et al., 2012b).

In this study, our aim was to investigate changes in genetic correlations among PSR, milk yield, and SCS during lactation and to determine the effect of milk yield and SCS information on the reliability of EBV of PSR. These findings may inform management and breeding decisions aimed at extending the herd life of cows.

MATERIALS AND METHODS

Data

Data sets containing test day information from 2004 to 2013 were obtained from the Livestock Improvement Association of Japan (http://liaj.lin.gr.jp/) and from the National Livestock Breeding Center (http://www.nlbc.go.jp/index.asp). The first calving ages of cows in this data set were between 18 and 35 mo. Data from 3,306 herds, containing 110 or more test days from 2008 to 2013 and 25 or more cows per test day, were extracted from this data set and included in the analysis. All data for the first 5 lactation test-day records between 6 and 455 DIM were collected from these herds. The entire data set was randomly divided into 2 subsets based on herds owing to computational limitations, and 1 was used for the analysis. This subset was randomly divided into 5 subsets, using the same criteria as before, and the genetic parameters were estimated in each subset independently (**Data1–5**; Table 1). The data consisted of test day milk yield, SCS, and PSR records. Test-day SCS was calculated as follows: SCS = $\log_2[(\text{SCC})/100] + 3$ (Ali and Shook, 1980). The PSR value was estimated according to the methods of Sasaki et al. (2015). The day of cow removal from her herd was considered the last test day of the cow when the interval between the last test day of the cow and the last test day of her herd was longer than 120 d. When the interval between the last test day of the cow and the last test day of her herd was less than 120 d, the last test day of the cow was considered the day of censoring. When a cow was alive until September 2013, or when her herd was withdrawn from the herd test, the cow had a censored record. The calving records of a cow that was removed before the first test day of lactation were not included in the data set. The removal day of this cow was the dry-off day of prior parity. The PSR value was determined according to whether the cow was alive (1) or absent (0) in her herd on the test day within the lactation period. The PSR record for the last test day before the removal day of a cow was coded 0, and the subsequent test-day records in the same parity for the cow were coded 0 until 455 DIM. The PSR record of a cow in the parities before the parity at removal was coded 1, and the last test day before the dry-off day of a cow was considered the day of censoring. The PSR record for the day of censoring of a cow was coded as 1, and the subsequent test-day records in the same parity of the cow were considered missing. When a cow was dried off after 455 DIM, the last test day of the cow before 456 DIM was considered the day of censoring and it was coded 1. When a cow was removed after 455 DIM, the last test day of the cow before 456 DIM was considered the removal day, and it was coded 0. The PSR records in the parities subsequent to the removal parity were considered missing. Related animals in the pedigree record were defined as cows for which PSR records were available and the ancestors traced back 3 generations from the cows with test-day records (Table 1).

Models

Data were analyzed using the multiple-trait random regression animal model, with slightly different models

Table 1. Summary of raw data used to estimate genetic parameters for each data set (Data1–5)

					Milk yield			SCS		
Data set	No. of herds	No. of cows	No. of related animals	No. of cows removed	No. of records	Mean	SD	No. of records	Mean	SD
Data1	166	39,388	83,486	23,663	1,005,547	29.1	8.8	1,002,073	2.63	1.82
Data2	168	42,025	93,805	25,633	1,042,383	29.8	9.0	1,037,861	2.62	1.82
Data3	162	40,888	83,389	24,386	1,044,649	29.5	9.0	1,038,200	2.67	1.86
Data4	164	40,361	85,252	24,517	1,007,869	28.8	8.9	1,006,702	2.65	1.84
Data5	165	42,894	95,854	26,301	1,071,692	29.7	9.0	1,071,689	2.62	1.78