56th Annual Meeting of the EAAP, June 5-8
2005, Uppsala Sweden,Session CG2.16
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LONGITUDINAL GENETIC ANALYSES OF FUNCTIONAL TRAITS IN DAIRY COWS USING DAILY RANDOM REGRESSION METHODOLOGY

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ABSTRACT

This study estimated heritabilities of daily observations on milk yield, milking speed, dry matter intake and live weight as well as genetic correlations among them over time using the random regression methodology. Data were from dairy cattle stationed in an experimental research farm over the past 10 years. All traits were recorded daily using automated machines. Estimated heritabilities were high, as expected from experimental farm datasets, and varied from 0.45 to 0.94 ($\bar{h}^2$=0.71) for MY, 0.29 to 0.80 ($\bar{h}^2$=0.55) for MS, 0.42 to 0.71 ($\bar{h}^2$=0.57) for LW and, 0.23 to 0.92 ($\bar{h}^2$=0.65) for DMI. Estimated genetic correlations varied from 0.16 to 0.64 between MY and MS, -0.47 to 0.29 between MY and DMI, -0.36 to 0.36 between MY and LW, -0.15 to 0.02 between MS and DMI, -0.42 to 0.03 between MS and LW and -0.89 to 0.29 between DMI and LW. Genetic correlations for MY, MS, DMI and LW at calving to middle of the lactation monotonly decreased to 0.40, 0.36, 0.14 and 0.36 and at the end of the lactation decreased to -0.06, 0.23, -0.07 and 0.09 respectively. Results could be useful when constructing selection indices for more than one trait, with an emphasis on time-dependent genetic selection.

INTRODUCTION

In order to construct the selection indices, for multitrait selection, genetic correlations are needed. The conventional selection indices use genetic correlations estimated by 305-day lactation-based models (e.g. Kadarmideen and Simm, 2002) but this may change in the future to include test-day specific genetic correlations. The current study estimates genetic correlation on a daily basis, between different functional traits. There are only very few studies investigating the traits we chose to analyze here. For some of these traits the obtained estimates will even be the first ones presented in the literature. The objective of this research was to estimate the functions of genetic parameters such as heritabilities and genetic correlations using daily test day experimental data for milk yield (MY), milking speed (MS), dry matter intake (DMI) and live weight (LW) using daily test day random regression methodology.

MATERIALS AND METHODS

Data

Data were obtained from first lactation records of dairy cows stationed at the Chamau research farm of the Swiss Federal Institute of Technology, Switzerland over the period of April 1994-2004. The experimental procedures of the farm followed the Swiss Law on Animal Protection and were approved by the Committee for the Permission of Animal Experiments of the Canton of Zug, Zug, Switzerland. Traits, MY, MS, roughage and concentrate intake and LW were recorded daily using automated units by METATRON (American Calan Inc., Northwood, NH, USA). The animals were housed in a free-stall barn. Milk production and other traits were measured two times (morning and evening) a day.

Data sets were created as follows. A minimum of 60 DIM and 5 kg of MY was required (Table 1). In order to estimate genetic correlations, data sets were created with the same times of measurement for all traits involved in bivariate analyses. The DMI was calculated by summing the concentrate and roughage intake. Sum of morning and evening measurements of milk production data per day was used for the analysis of MY and DMI while for MS and LW, the measurements were averaged.

Statistical Models and Analyses

Analyses. ASREML (Gilmour et al., 2001) software was used to estimate variance components. Results of the monthly phenotypic analyses were used as starting values in the genetic analyses to estimate variance components using an Average Information (AI-REML) algorithm as implemented in ASREML (Gilmour et al., 2001). A 5th order orthogonal polynomial was chosen for the fixed part of the model and quadratic random regressions fitted based on the preliminary analysis and work of Olori et al. (1999) and Coffey et al. (2001). The same fixed effects were fitted for all traits and are given in model (1).For each trait, individual deviations from the mean lactation curve were fitted for additive genetic effects using the random regression methodology. The animal model fitted was as follows;

$$y_{tij} = \sum_{l=1}^{5} \alpha_l v_{tl} + b_i + f + \sum_{l=1}^{3} \mu_{tl} a_{jl} + e_{tij}$$

where y_{tij} is MY (or MS, DMI, LW) produced by the j^{th} cow on day *t*. α_l are the fixed regression coefficients, *v* is the vector of the first five polynomials for the t^{th} day in milk; b_i is the fixed breed effect (b_1=Holstein-Friesian, b_2=Jersey, b_3=Brown Swiss, b_4=Simmental, b_5=Ayshire), f is other fixed effects including year at calving, season, age at calving (in months), year-season and DIM-breed interactions. a_{jl} is random regression coefficients for the genetic effects, respectively; μ_t is the vector of the two first orthogonal polynomial coefficients made on day t and e_{tij} is the random residual variance and it is assumed to vary by month. No permanent environmental effect was considered in the model because, due to the experimental conditions, most of the variability was observed in the genetic part and the environmental effects were found to be uncorrelated.

RESULTS AND DISCUSSION

The herd's mean MY, MS, DMI and LW were 17.16 kg/d, 1.94 kg/min, 17.42 kg/d, and 545.12 kg, respectively. Range of estimated heritabilities are provided in Table 1. Ranges were based on daily records from 1 to 305 days. Estimates varied from 0.45 to 0.94 ($\bar{h}^2$=0.71) for MY, 0.29 to 0.80 ($\bar{h}^2$=0.55) for MS, 0.42 to 0.71 ($\bar{h}^2$=0.57) for LW and, 0.23 to 0.92 ($\bar{h}^2$=0.65) for LW.

Heritability was found to be the highest in the middle of the lactation as was also observed by for example Jakobsen et al. (2002) or Druet et al. (2003) but in contrast to their findings estimates of heritabilities continue to increase throughtout the lactation.

Estimates of heritability for MS were found around 0.55 (ranging from 0.29 to 0.80). Although Zwald et al. (2005) found the heritability 0.17 using objectively and weekly measured field data using sire model with Bayesian methodology which is closer the results of subjectively measured studies; probably number of animals, and differences that could be observed under the some certain longitudinal settings when using sire and animal model (Jaffrezic et al., 2002) explains the differences in the estimated heritabilities between present and the refereed studies.

Estimated heritabilities over DIM for DMI shows an increase towards the end of the lactation and range from 0.23 to 0.92. Veerkamp and Thompson (1999), based on data from 628 heifers for the first 15 weeks of the lactation and using random regression model found the heritability equal to 0.30 whereas in present study it was estimated for that period to be 0.38. The differences concerning the number of animals, measurement stage of lactation, feeding regime and statistical methodology between various studies explain the differences obtained for the heritability estimates for dry matter intake (Van Arendonk et al., 1991).

We averaged morning and evening measurements to estimate the heritability for LW (ranging between 0.42 and 0.71, $\hat{h}^2$=0.57). Veerkamp (1998) noted that heritability estimates are generally high, especially when weight is based on average of more than one measurement. Veerkamp et al. (2000) found the heritability for the first 15 weeks equal to 0.61 using random regression model whereas we found for the specified period 0.52.

Longitudinal Genetic Correlations

Our results indicated that there is a moderate genetic correlation among MY and MS ($\bar{r}_g = 0.38$) that ranged from 0.16 to 0.64. Genetic correlations turned negative to positive around day 190 for MY and LW and ranged from -0.36 to 0.36. Veerkamp and Brotherstone (1997) explained that this phenomenon happens because body fat and live weight are closely related during some part of the lactation (genetic correlation from 0.27 to 0.67). Estimated genetic correlation among MY and DMI ranged from -0.47 to 0.29. Although we found day 76 for switched the correlations positive to negative; Veerkamp and Thompson (1999) found about days 42 for the specified point. Estimated genetic correlation between MS and DMI ranged from -0.15 to 0.02. Estimated genetic correlations between MS and LW ranged between -0.42 to 0.03 and MY versus LW ranged between -0.36 to 0.36 both followed a similar pattern. Genetic correlations between DMI and LW were found ranged between -0.89 to 0.29 and trend of genetic correlation is decreased and swithched negative towards the end of the lactation since feeding regime is adjusted according to production and since MY decreases towards the end of the lactation.

Table 1. Ranges of daily estimated heritabilities (on diagonal) and daily genetic correlations (below diagonal) between Milk Yield (MY), Milking Speed (MS), Dry Matter Intake (DMI), Live Weight (LW).

	MY	MS	DMI	LW
MY	0.45-0.94			
MS	0.16-0.64	0.29-0.80		
DMI	-0.47-0.29	-0.15-0.02	0.23-0.92	
LW	-0.36-0.36	-0.42-0.03	-0.89-0.29	0.42-0.71

CONCLUSIONS

Although, based on experimental data, these results show important patterns of genetic properties and relationships for many traits that are important for national dairy cattle breeding programs. These parameter estimates would be useful to construct selection indices for more than one functional trait, based on test-day specific genetic correlations, and to change trajectory of genetic profile/patterns. However correspondent statistics that capture the longitudinal nature of the measurements should be created for functional traits, as it is done for MY using persistency, in order to place the information into the selection indices. Since permanent environmental and residual effects had to be modeled together, probably this assumption increased estimates for heritabilities and genetic correlations. Since the sampling size was not large (as is typical for an experimental farm), results should still be interpreted carefully and confirmed in different cattle populations.

ACKNOWLEDGEMENTS

Authors thank all personnel in the research station of Swiss Federal Institute of Technology in Chamau, Zug, Switzerland for their help in data collection over number of years. Authors thank Dr. Kaspar Tschuemperlin, Dr. Christian Hagger, Dr Hans Leuenberger.

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