RELATIONSHIPS BETWEEN ADJUSTED LENGTH OF PRODUCTIVE LIFE AND OTHER TRAITS FOR SWEDISH DAIRY BULLS

U. Emanuelson[1], J. Carvalheira[2], P.A. Oltenacu[2] and V. Ducrocq[3]

[1]Swedish Association for Livestock Breeding and Production, S-631 84 Eskilstuna, Sweden
[2]Dept. Animal Science, Cornell University, 114 Morrison Hall, Ithaca, NY 14852-4801, USA
[3]Station de Génétique Quantitative et Appliquée, INRA, 78352 Jouy-en-Josas, France

SUMMARY

Product moment correlations between breeding values for length of productive life (LPL) adjusted for milk production and diseases, as predicted in a failure time analysis, and breeding values for other important traits were calculated for Swedish dairy bulls. The other traits were yield of protein, mastitis resistance, somatic cell counts, resistance to "other diseases", udder conformation, and stayability. Most correlations were low (<0.05) indicating that adjusted LPL may be a useful addition to the directly recorded functional traits. However, breed differences were found that need to be considered and investigated further.

Keywords: dairy cattle, survival analysis, functional traits, longevity, correlation.

INTRODUCTION

The length of productive life (LPL) of a dairy cow is important for her economic performance. Thus, productive life is a trait that has received an increasing attention in the animal breeding field (for reviews see Dekkers and Jairath 1994; Strandberg and Sölkner 1997). Actual life length is an impractical trait because of the long time before it is realized, and censoring of "incomplete" records is a problem. Stayability until a certain age or productive period could be used as an indicator of LPL, but, although not affected by censoring due to the definition of the trait, this measure leads to loss of information (Everett *et al.* 1976). However, methods to evaluate LPL are available, i.e. failure time analysis, that do account for censoring without any loss of information (Smith 1983; Smith and Quaas 1984; Ducrocq 1987).

The purpose of the present study was to estimate correlations between breeding values for LPL adjusted for milk production and diseases, as estimated with appropriate statistical methods, and breeding values for other important traits of Swedish dairy bulls.

MATERIALS AND METHODS

The data used for estimation of the correlations came from two sources. The first was official and unofficial BLUP proofs for yield of protein (PROT), mastitis resistance (M-RES), somatic cell counts (SCC), resistance to "other diseases" (O-RES), udder conformation (UDDER), and stayability (STAY) of progeny tested AI-bulls. The BLUP-procedure applied on yield is a single trait MGS model which has been described by Danell and Eriksson (1982). The BLUP-procedure for disease resistance and SCC, described by Eriksson and Wretler (1987), is a

single trait sire model with relationship matrix, and the model for udder conformation is a single trait animal model. Stayability reflects the proportion of daughters surviving the first lactation, and a single trait model without relationship matrix is applied.

The other source of data came from a random sample comprising 20% of all herds, with more than 15 cows, in the official Swedish milk-, AI- and disease-recording schemes. Complete lifetime information on pedigree, calvings, milk production, diseases, AI, and date of exit was available on all cows calving in these herds between Jan. 1 and Dec. 31 1991. The data included information on 35,407 cows in 1,647 herds, and 27,598 cows in 1,509 herds for the Swedish Red and White (SRB) and the Swedish Friesian (SLB) breeds, respectively. Survival, as a measure of length of productive life (LPL), was analyzed with a proportional hazards model, as applied in the "Survival Kit" (Ducrocq and Sölkner 1994), using a Weibull parametric curve:

$$\lambda(t,x(t),z(t))=\lambda\rho(\lambda t)^{\rho-1}\exp\{x(t)'b+z(t)'u\}$$

where:

$\lambda(t,x(t),z(t))$ is the hazard function of an individual depending on time t,

$\lambda\rho(\lambda t)^{\rho-1}$ is the Weibull baseline hazard function,

b is the parameter vector of fixed effects,

$x(t)$ is the vector of fixed covariates,

u is the parameter vector of random effects, and

$z(t)$ is the vector of the random covariates.

The fixed effects in the model were parity, stage of lactation, milk yield, risk factor diseases (by time of occurrence) and the interactions between stage of lactation and diseases, where stage of lactation, diseases and their interaction were treated as time-dependent. Milk yield was the mean of kg fat-corrected milk recorded at the second and third test months after calving, shown to be closely related to 305-d lactation yield (Danell 1982). Risk factor diseases considered were veterinary treated cases of dystocia, retained placenta, metritis, ketosis, milk fever, cystic ovaries, locomotor disorders, and mastitis. Random effects were herd-season (assumed to follow a log-gamma distribution and algebraically integrated out from the joint posterior density) and sire, where the additive genetic relationship matrix for all bulls based on their sire and maternal grand sire relationships was incorporated. The sire's breeding values for adjusted LPL were obtained as a by-product at convergence.

RESULTS AND DISCUSSION

In total, 1,904 SRB bulls and 1,514 SLB bulls had breeding values for adjusted LPL estimated in the survival analysis based on the random sample of herds. Breeding values for the other traits were not found for all bulls, because some bulls were imported and without Swedish evaluation and because of identity mismatch (mostly due to errors in the pedigree information of cows). Correlations between breeding values for adjusted LPL and the other traits were therefore based on only 1,460 and 941 bulls of the two breeds, respectively.

Most correlations between adjusted LPL and production and functional traits were very low, especially in the SRB breed (Table 1). The correlations between protein yield and adjusted LPL were much lower than estimates by Reinhardt and Pasman (1996), that also used failure time analysis, but their model did not include diseases. We did not impose any restrictions on the reliabilities of breeding values, and the correlations may therefore be underestimated. Breeding values for adjusted LPL are expressed on the scale of relative risk of culling, and a low value is consequently favorable. A negative sign on correlations therefore means that selection on production and functional traits would reduce the relative risk of culling. This was also found for the correlations that were significantly different from zero, and for most of the others as well.

Table 1. Product moment correlations between sire proofs for yield of protein (PROT), mastitis resistance (M-RES), somatic cell counts (SCC), resistance to "other diseases" (O-RES), udder conformation (UDDER), stayability (STAY), and adjusted length of productive life (LPL) for Swedish Red and White (SRB) and Swedish Friesian (SLB) bulls

	SRB		SLB	
Trait	STAY	LPL	STAY	LPL
PROT	0.076**	-0.018	0.129***	-0.047
M-RES	0.186***	-0.049	0.362***	-0.300***
SCC	0.161***	-0.044	0.260***	-0.268***
O-RES	0.158***	-0.002	0.091**	0.021
UDDER	-0.034	-0.046	-0.036	-0.086**
STAY	—	-0.193***	—	-0.250***
LPL	-0.193***	—	-0.250***	—

The statistical model for survival did not include the phenotypic effects of milk yield and diseases as herd-year deviations. Furthermore, only diseases (and stage of lactation) were treated as time-dependent variables. Hence, the model might not have reflected the true influence of these factors on culling adequately.

Correlations between stayability and the other traits were much higher than those between adjusted LPL and the other traits. They were, however, lower than other Swedish estimates

(Lindhé *et al.* 1996). The higher correlations were expected since the model for LPL included milk yield and diseases, while the model for STAY does not. There was, however, no difference in the correlations with the two mastitis traits (M-RES and SCC) in the SLB breed. The reason for this is not known, but the massive import of foreign Holstein genes into the Swedish population may play a role.

The low correlation between adjusted LPL and other traits already included in the selection process of Swedish dairy bulls means that ranking of sires for LPL provides new information, since there is also considerable genetic variation in adjusted LPL (Carvalheira *et al.* to be published). The estimated correlations should, however, be validated on a larger data set, which is quite possible since failure time analysis is feasible to perform on larger populations than used in this study (Reinhardt and Pasman 1996; Ducrocq and Sölkner 1998).

REFERENCES

Danell, B. (1982) *Acta Agric. Scand.* **32**:83-92.

Danell, B. and Eriksson, J.-Å. (1982) *Acta Agric. Scand.* **32**:47-64.

Dekkers, JC.M. and Jairath, L.K. (1994) *Proc. 5th World Congress on Genetics Applied to Livestock Production* **17**:61-68.

Ducrocq, V. (1987) PhD Thesis, Cornell University.

Ducrocq, V. and Sölkner, J. (1994) *Proc. 5th World Congress on Genetics Applied to Livestock Production* **22**:51-52.

Ducrocq, V. and Sölkner J. (1998) *Proc. 6th World Congress on Genetics Applied to Livestock Production.*

Eriksson, J.-Å. and Wretler, E. (1987) Sire evaluation for diseases in Sweden. 38th Annual Meeting of the European Association for Animal Production, Lisbon, Portugal.

Everett, R.W., Keown, J.F. and Clapp, E.E. (1976) *J. Dairy Sci.* **59**:1505-1510.

Lindhé, B., Philipsson, J., Eriksson, J.-Å., Gundel, M. and Danielsson, D.-A. (1996) *INTERBULL Bulletin* **14**:91-95.

Reinhardt, F. and Pasman, E. (1996) *INTERBULL Bulletin* **14**:167-171.

Smith, S.P. (1983) PhD Thesis, Cornell University.

Smith, S.P. and Quaas, R.L. (1984) *J. Dairy Sci.* **67**:2999-3007.

Strandberg. E. and Sölkner, J. (1996) *INTERBULL Bulletin* **12**:111-119.