Joint Evaluation of Survival and Fertility in Dairy Cattle with a Linear Model

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Introduction

There is an intricate relationship between milk production, fertility and survival of cows, which is further confounded by management decisions on the farm. Holsteinization and selection for high milk production can be associated with reduction in cow fertility (Pryce et al., 1998; Silvia, 1998; Harris and Winkelman, 2000) because of its impact on physiological factors affecting reproduction such as energy balance, ovarian function, heat detection and conception in dairy cows (Buckley et al., 2000; Snijders et al., 2001; Westwood et al., 2002).

In the evaluation of longevity, productive lifespan is taken at the time from birth to death. Culling for poor production is regarded as voluntary culling and often accounted. Currently culling due to poor fertility is classified along with health as reasons for involuntary culling and are not adjusted for. This suggests that selection for productive life is expected to result in improvement in health and fertility of cows. It has been shown however that a higher response in fertility and mastitis incidence would be obtained from selection for fertility related or mastitis related productive life than from selection on length of productive live (Roxström and Strandberg, 2002). A joint evaluation of fertility and longevity is therefore desirable especially where these two are important index traits in the breeding goal. A joint analysis of both traits further allow information from one to augment the other. This is particularly important where longevity is based on reappearance in the next lactation (a binary trait) and calving interval (a censored trait) is the only available measure of fertility.

Routine evaluation of fertility, based on direct measures, is often limited by the availability of artificial insemination data in many countries. Also length of productive life is a trait which manifest only late in the animal's life. One option in these circumstances is to use predictor traits. Calving interval (CIV) can be regarded as a suitable predictor of fertility because of the genetic correlation between it and various direct measures of fertility (Pryce et al., 1997; 1998). Many linear type traits are predictors of herd survival because of their association with the health and productivity of dairy cows. In a seasonal calving production system, CIV is also an important index trait (Veerkamp et al., 2002).

Analysing calving interval alone as a measure of fertility presents a problem because only animals that survive to the next lactation have a calving interval. Evaluation based on this trait alone will be biased because of pre-selection as culled animals with the worst fertility problems, will not be included in the analysis (See Olori et al., 2002a). A combined analysis of CIV and survival is expected to account for most of the genetic variation in fertility that is possible from calving dates. Combining milk yield and correlated linear traits in a joint analysis further ensures that information from these traits are utilised in predicting breeding values for fertility and survival and makes it possible for early evaluation of young bulls.

This study describes a linear model for the joint evaluation of calving interval (a censored trait) and survival (a binary trait and censored trait) as measures of fertility and longevity. It also describes the impact of model on the international longevity evaluation from the recent multiple across country evaluation (MACE) for longevity pilot study (van der Linde and de Jong, 2003).

Materials and Method

Data

Data was obtained from milk recording and type classification records. Calving interval (CIV) was derived from calving dates and considered as a

different trait in each lactation. Left censored records, occasioned by cows entering milk recording in later lactations, were included in the analysis. Survival was defined in terms of reappearance in the subsequent lactation. A cow is considered to have survived the previous lactation (SUV=1) and censored in the current lactation (SUV=99), if her latest test date is within 140 days of the latest herd test date. The cow is assumed culled (SUV=0) otherwise. Four linear type traits namely, Angularity (ANG), Body Condition Score (BCS), Foot angle (FA) and Udder depth (UD) were chosen as predictors based on their genetic relationship with the objective traits and predictive value. In making this decision, the genetic correlation between the type and survival traits were estimated, whereby survival and calving interval data was used from herds without type classification data available while SUV and CIV data was deleted from the records of herds with type data. This allowed us to eliminated possible bias that may be due to type preferences in pedigree herds.

Genetic parameters

Variance components were estimated with a sire model using ASREML (Gilmour et al., 1998). Relationships between sires (through their sires and dams) were included for two generations. Because of the structure of the data the environmental covariance between SUV and CIV is undefined and inestimable hence it was fixed at 3 times the sire covariance (see Olori et al., 2002a; Pool et al., 2002).

Breeding value estimation

Breeding values were estimated for all 13 traits in a single multivariate analysis. The pedigree file included bull with daughters and up to 2 generations of their pedigree (maternal and paternal). Genetic groups were not defined or included in the pedigree. Genetic adjustment of survival for production was on the genetic scale, i.e. done post breeding value estimation Breeding values for each trait (CIV and SUV) in lactations 1 to 3 were subsequently averaged (with equal weight on each) to obtain a single breeding value for the respective trait. Reliabilities were calculated for SUV and CIV in each lactation as well as the 4 type traits simultaneously using the effective number of daughters approach.

Converted proofs were calculated for foreign bulls if data and conversion equations were available for the country of first test (Olori et al., 2002b). The domestic proofs for bulls progeny tested in Ireland were subsequently included in the Interbull Pilot longevity MACE evaluation (van der Linde and de Jong, 2003).

Results and Discussion

Table 1 shows the heritability and genetic correlation between calving interval, production adjusted survival (adj_SUV) and milk yield. Table 2 shows the heritability of four type traits and their genetic correlation with milk yield, calving interval and adj_SUV. Heritability of CIV and adj_SUV were slightly higher in lactation one and ranged between 2% and 5%. CIV in the second lactation was more highly correlated with adj_SUV in all lactations. Both traits were positively correlated with milk yield, which supports the reported undesirable genetic association between production and fertility. Correlation between CIV, adj_SUV and the four type traits ranged from low (0.01) to moderate (0.46). Correlation between BCS and adj_SUV changed from positive in lactation one to negative in lactation three which may be due to possible change in selection objective in terms of culling for fertility and production reasons in first versus later lactations. BCS in this study was a point measure taken only in the first lactation. Adj_SUV was positively correlated with FA and UD but negatively correlated with Angularity.

Breeding values for progeny test bulls ranged from –9 to 12 days for calving interval and from –4 to 4% for survival. Inter-quartile range was about 4 days and 2% for CIV and adj_SUV respectively. The distribution indicates that the top 25% of bulls had a minimum TA of 0.91% for survival and a maximum TA of –1.27 days for CIV. Variance of the breeding values was slightly higher for bulls with daughters compared to converted proof for both traits. The standard deviation of calving interval and survival breeding values obtained with the multiple lactation model were higher than those obtained from a joint analysis of milk yield, calving interval and survival in the first lactation only. In that analysis, the range was about 11 days for CIV and 8% for survival from the three trait model (Olori et al., 2002a). A wider variation in fertility and survival breeding values was obtained with

information from later lactations and the linear traits as expected in the current analysis. Figure 1 shows the distribution of CIV sire PTAs for domestic and foreign bulls. A summary domestic, converted and MACE TAs for survival as well as domestic and converted TAs for CIV for bulls in Ireland is presented in Table 3.

MACE Results

There was no difference between combined and direct longevity proofs for Irish bulls (Correlation=0.99). The MACE proofs were also highly correlated with the domestic proofs (r=0.94) for domestic bulls with daughters (Figure 1b). The correlation between MACE and converted proofs for foreign bulls was however, relatively low (0.57 and 0.58). This may be due to the fact that converted proofs were predicted from a combination of traits while the MACE proofs were based on a single trait. Because of the low heritability of longevity, a more accurate prediction, in the absence of direct measures, may be obtained from several related traits than from a single trait. Figure 1 shows the relative frequency distribution of calving interval and survival transmitting abilities from various sources for domestic and foreign bulls in Ireland.

Conclusions

A joint evaluation of fertility and survival traits was implemented with a linear model. All traits were derived from standard milk recording and linear classification data. This 13 trait model allowed more variation in genetic merit for fertility (based on calving interval) and survival to be expressed compared to evaluation based on first lactation records only. In the recent International test evaluation of longevity across countries, this model stands up among the rest and gave similarly accurate bull proofs with an average correlation of 0.55 across participating countries. This low correlation may be improved with a multiple trait MACE for longevity which will allow information from correlated traits to be utilised.

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Table 1. Heritability (on the diagonal) and genetic correlations for calving interval, survival and milk yield in lactations 1, 2 and 3.

	CIV1	CIV2	CIV3	Surv1	Surv2	Surv3	Milk1	Milk2	Milk3
CIV1	**0.05**								
CIV2	0.94	**0.03**							
CIV3	0.85	0.90	**0.03**						
Surv1	-0.33	-0.45	-0.26	**0.03**					
Surv2	-0.32	-0.49	-0.36	0.87	**0.02**				
Surv3	-0.20	-0.39	-0.28	0.75	0.93	**0.02**			
Milk1*	0.50	0.51	0.64	0 (0.24)	0 (0.56)	0 (0.47)	**0.39**		
Milk2*	0.52	0.49	0.61	0 (0.14)	0 (0.48)	0 (0.40)	0.96	**0.36**	
Milk3*	0.45	0.47	0.66	0 (0.33)	0 (0.42)	0 (0.48)	0.89	0.90	**0.31**

Surv=Survival adjusted for milk yield

* values in parenthesis are correlation before adjustment for milk yield).

Table 2. Genetic correlation between calving interval, survival and milk yield in lactations 1, 2 and 3 with linear type traits.

	h^2	CIV1	CIV2	CIV3	Surv1	Surv2	Surv3	Mlk1	Mlk2	Mlk3
Angularity	0.30	0.38	0.46	0.35	-0.37	-0.19	-0.08	0.59	0.50	0.53
Foot Angle	0.14	0.14	-0.08	0.01	0.28	0.21	0.20	-0.01	0.05	0.04
Udder Depth	0.33	-0.01	-0.11	-0.38	0.13	0.26	0.15	-0.27	-0.22	-0.32
BCS	0.22	-0.18	-0.18	-0.19	0.33	-0.04	-0.21	-0.36	-0.26	-0.32

Note : h^2 =Heritability, BCS=Body Condition Score

Table 3. Summary of national, MACE and converted calving interval and survival proofs (TA) for domestic and foreign bulls in Ireland.

Trait	Bull & Type of proof	Mean	SD	Minimum	Q1	Q3	Maximum
Calving Interval	Domestic-National	0.84	3.24	-9.17	1.27	3.06	12.12
	Foreign -Converted	0.84	2.49	-9.44	0.85	2.58	10.88
Survival	Domestic- National	-0.03	1.35	-4.01	-0.97	0.91	4.01
	Domestic -MACE	-0.05	1.35	-3.93	-0.96	0.87	4.01
	Foreign - MACE	-0.19	1.02	-4.14	-0.85	0.51	3.45
	Foreign - Converted	-0.53	0.95	-4.07	-1.14	0.07	3.39

Figure 1. Relative frequency distribution of calving interval sire PTAs for domestic and foreign bulls.
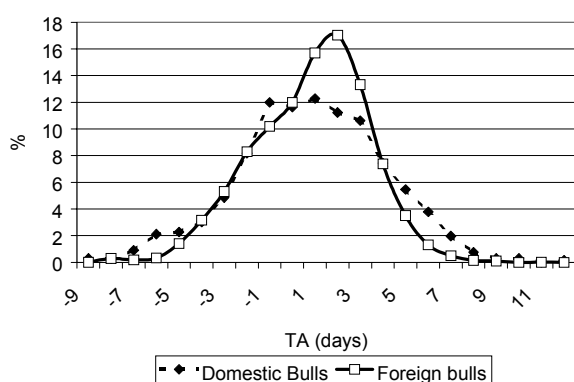

Figure2. Relative frequency distribution of functional survival sire PTAs for domestic and foreign bulls