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## Multiple trait national genetic evaluation for cow longevity

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### ABSTRACT

In New Zealand genetic evaluation for cow longevity was based on a single trait model where the phenotypic record was actual or predicted days survived in the milking herd. Cows which were yet to express their actual longevity received a predicted phenotypic record based on the milk production and liveweight production values, traits other than production (TOP), and fertility breeding values. The prediction equation was a proxy for a multiple trait model. At the time of implementation a full multiple trait model was not computationally feasible. A study was undertaken to investigate the feasibility of developing a full multiple trait model. The multiple trait model has the advantage of incorporating the appropriate genetic relationships among the predictor traits and the longevity traits, as well as allowing different genetic correlations among the individual longevity traits. The first stage of the study was to estimate the genetic correlations among all traits under genetic evaluation and two longevity traits; survival from first to second lactation and first to fifth lactation. Data used for genetic correlation estimation was from first lactation records from the Sire Proving Scheme herds for seasons 1987 to 2005. The two fertility traits, 42 day calving rate and percent mated in the first 21 days, had the highest genetic correlations with the longevity traits, ranging from 0.84 to 0.27. Body condition score, management TOP and the milk production traits had moderate genetic correlations with the longevity traits, ranging from 0.42 to 0.24. Somatic cell score, udder support, udder overall, legs, capacity and dairy conformation had low genetic correlations with the longevity traits but were significantly greater than zero. Four longevity traits, and 9 predictor traits were included in a national genetic evaluation for cow longevity. The 9 predictor traits were chosen from the traits that had significant genetic correlations with cow longevity and contained genetic information that was not already included in other predictor traits. Comparisons between sire breeding values from the single trait model and the multiple trait model show good agreement with a correlation of 0.95 for Animal Evaluation enrolled sires. Investigation of the sire breeding values shows that the multiple trait model puts a greater emphasis on cow fertility than the single trait model.

**Keywords:** longevity; genetic evaluation; multi-trait model; dairy cows.

### INTRODUCTION

Ensuring profitable cows continue to be profitable beyond just a small number of lactations should have a positive economic impact on dairy farming. The rationale is that rearing costs are spread over a greater number lactations with a reduction in the number of replacements required annually. Longevity has been defined as the ability for a cow to delay culling. Increased longevity will allow the farmer to focus on voluntary culling for poor performance and to reduce the number of replacements needed every year.

Longevity has low heritability ranging between 0.02 and 0.10 (Veerkamp *et al.*, 2001; Boldman *et al.*, 1992). There are a number of statistical models for national genetic evaluation of longevity. Three major classes of model are used: productive life, life span models and survival analysis models. Multiple trait models are used to divide the lifetime into a number of traits usually based around

individual lactations. Some models extend the multiple trait to a random regression model to model survival across lactations (Veerkamp *et al.*, 2001). Models utilising the frailty model in survival analysis are preferred for longevity data where the records are time to event data and subject to censoring. However, animal model survival analyses are not computationally feasible and incorporating non-unity genetic correlations among survival to different ages is not possible.

Breeding for longevity presents a problem with the time required to obtain reliable estimates of longevity on sires. For a sire to get a highly reliable breeding value the first crop daughters have to have had the opportunity to survive beyond the fifth lactation. However, the sire has been used extensively in the population by this time. To overcome this problem a number of genetic evaluations use predictor traits to provide an early indication of the longevity breeding value (BV) with reasonable accuracy (Boldman *et al.*, 1992).

Usually the longevity BV from longevity data and longevity BV from predictor traits are combined in to a single longevity BV using selection index theory as a two-step procedure. In a multiple trait model it would be possible to do a joint analysis of the longevity data and the predictor trait data jointly, thereby avoiding the two-step process.

The previous longevity national genetic evaluation model in New Zealand was a single trait model where the data was actual or predicted longevity. For cows with actual longevity data the actual data was used. For cows with censored records, a predicted longevity record was used. The prediction was based on an expected life regression from a survival analysis which included a number of predictor traits including milk production, traits other than production (TOP) and fertility traits. At the time of implementation it was recognised that full multiple trait approach including the predictor traits and longevity data jointly would be better, however this type of analysis was not computationally feasible for national data sets at that time.

The objectives of this study were to: find a subset of traits that would be useful predictors of longevity; explore the use of predictor traits in a multiple-trait model for estimating the longevity BV; and develop a new national longevity evaluation system that was computationally feasible.

## MATERIALS AND METHODS

### Data

Survival, milk production, body condition score (BCS), TOP scores, mating and calving records were extracted from the NZ Dairy Core Database. The extract was done in July 2006 and included all 270 day milk, fat and protein yields and TOP records from 1987 onwards. All mating and calving records from 1990 were included in the extract, records prior to 1990 were excluded due to data quality issues. Two fertility traits were used in the analysis, percent mated in the first 21 days of the herd's mating period in parity 1 (PM21) and 42-day calving rate (CR42) from the parity 1 matings (Harris *et al.*, 2005). Four survival traits were defined; survival from lactation 1 to lactation 2 (SV12), through to, survival from lactation 1 to lactation 5 (SV15). The survival traits were coded as binary variables with 0 indicating failure to survive. Recording of culling and deaths is not complete on the New Zealand Dairy Core Database. If a cow's most recent record indicating that it was still alive was dated more than 365 days prior to the extract date, then the cow was

considered to have not survived beyond its age at the last known record date. A cow with no record indicating either death or successful survival during the period 365 days prior to the extract date was coded as missing for the appropriate survival trait. Monitoring a cow's survival across multiple herds across dairy seasons was possible because nearly all herds are recorded on the New Zealand Dairy Core Database. Four milk production traits were used in the analysis, namely, first lactation 270-day milk, fat, protein yields and average first lactation somatic cell count on the log 2 scale. Contemporary groups were defined on a parity-herd-season-year basis. Season was defined as spring or autumn calving. Pedigree and breed data were extracted from the Animal Evaluation routine genetic evaluations for production. Ancestors were traced back to 1939. Animals born before 1960 were considered to be the base population.

### Genetic Parameter Estimation

The data for the variance component analyses was a subset of the dataset described above containing Livestock Improvement's Sire Proving Scheme (SPS) herds in the years 1990 to 2004. A total of 221,224 cows were used for this study. The breed composition of the cows was 1% Ayrshires, 52% Friesians, 22% Jerseys, and 25% crosses of these breeds. A sire-maternal-grandsire model that included all eight traits simultaneously allowing for missing data was used. The estimation of (co)variance components used restricted maximum likelihood with a multivariate linear sire model using the average information algorithm of Johnson & Thompson (1995). There were 4270 sires in the pedigree.

An initial data analysis was undertaken to calculate the genetic correlations between each of the milk production, TOP, fertility and BCS traits and SV12 or SV15. Nine of the 23 traits were selected as predictor traits for survival. The criteria for selection was that the traits had to have a genetic correlation with SV12 or SV15 that was significantly different from zero (standard error multiplied by 1.96 for  $Pr < 0.05$ ) and contributed independent sources of information because they had low or moderate genetic correlations with each other. A second data analysis was undertaken where all the (co)variance components were estimated for all nine traits and the four survival traits.

### Statistical Model for National Genetic Evaluation

A multiple-trait (MT) animal model was used for the national genetic evaluation of survival on the dataset containing the 9 predictor traits and the

four survival traits. The model could cope with missing data on any combination of traits. Each individual trait record was modelled as:

$$y_{ijkl} = hys_{ij} + \sum_{s=1}^6 ht_{is} w_{ns}^h + a_{ik} + e_{ijkl}$$

where:

- $y_{ijkl}$  is the record for  $i$ th trait,
- $hys_{ij}$  is the  $j$ th herd-year-season fixed effect for a cow's a first lactation for trait  $i$ , with season referring to spring or autumn calving period,
- $ht_{is}$  is the linear regression coefficient for the  $s$ th heterosis effect for trait  $i$ ,
- $w_{ns}^h$  is the  $s$ th heterosis covariate for animal  $n$ ,
- $a_{ik}$  is the random additive genetic effect of animal  $k$  for trait  $i$ ,
- $e_{ijkl}$  is the random residual associated with record  $y_{ijkl}$ .

Heterosis factors were fitted to account for the effects of crossbreeding, different factors were fitted by breed combination to account for the effect of different genetic distances among the major breeds in the estimated heterosis effects. Genetic groups were assigned by breed, gender of missing parent, birth year and country of origin. Four breed classes were assigned genetic grouping, namely, Holstein-Friesian, Jersey, Ayrshire-Red, and other breeds. Genetic groups were assigned in 5-year intervals from 1960 to 1980 then yearly, with the first birth year group being prior to 1960. Country of origin was defined as NZ, North American and other. Gender of missing parent was defined as female or male. If a genetic group had less than 200 animals per group birth years were clustered. No clustering occurred across breed, origin or gender genetic groups. The mixed model equations were solved using a preconditioned conjugate gradient solver (Stranden & Lidauer, 1999) and iteration on data with code reordering (Tsurata *et al.*, 2001).

## RESULTS

Simple statistics for the 4 survival traits from the 12,757,633 survival records are given in Table 1. The increasing number of missing records from

trait SV12 to SV15 reflects number of current cows who have not had an opportunity to survive to later lactations. The average survival rates in Table 1 are consistent with industry statistics published by Anon (2005).

Table 2 provides genetic correlations between the 23 predictor traits and SV12 and SV15 from the SPS data. The genetic correlations among the TOP traits and SV12 in Table 2 are consistent with Cue *et al.* 1996. The genetic correlations among the fertility traits and SV12 and SV15 are consistent with previous estimates published in Harris & Winkelman (2000). The following 9 traits were selected from the 23 predictor traits; 270-day protein yield, SCC, BCS, CR42, milking speed, overall opinion, legs, udder overall and dairy conformation. All nine traits had genetic correlations with SV12 or SV15 that was significantly different from zero. One milk production trait was selected because all three milk production traits are highly genetically correlated, thus, adding two extra milk production traits will have little effect on the longevity breeding value accuracies. The same was true for the fertility traits PM21 and CR42, the 3 management TOP traits, adaptability to milking, temperament and overall opinion and the TOP udder traits, udder support, front udder and udder overall.

The heritabilities, genetic and phenotypic correlations among the four survival traits are given in Table 3. They are consistent with those reported by Harris & Winkelman (2000). The magnitudes of the heritabilities are consistent with values reported in other countries (Veerkamp *et al.*, 2001; Boldman *et al.*, 1992).

The estimates for breed heterosis from the national evaluation analysis show that the first cross Holstein-Friesian x Jersey cow has an advantage of 4.5% greater probability of surviving from lactation 1 to 2 compared to the average of the parental breeds for first parity. The magnitude of the heterosis increases from SV12 through to SV15 with values of 6.9%, 8.2% and 9.0% for SV13, SV14 and SV15, respectively. The heterosis values for SV12 and SV15 are of similar magnitudes to those reported by Harris & Kolver (2001).

**Table 1:** Statistics from the national data for four survival traits.

Trait <sup>1</sup>	Number	Number of missing records	Proportion Surviving	Phenotypic Standard Deviation
SV12	12,276,210	481,423	0.873	0.337
SV13	11,549,948	1,207,685	0.777	0.416
SV14	10,744,822	2,012,811	0.691	0.453
SV15	9,879,010	2,878,623	0.604	0.469

<sup>1</sup>SV1j = Survival from lactation 1 to lactation j

**Table 2:** Genetic correlations between the two survival traits and the twenty three predictor traits.

	SV12	SV15
Milk yield	0.249	0.247
Fat yield	0.423	0.414
Protein yield	0.424	0.418
SCC	-0.156	-0.040
PM21	0.578	0.266
CR42	0.841	0.478
BCS	0.370	0.240
Adaptability	0.219	0.243
Temperament	0.157	0.158
Milking Speed	0.072	0.220
Overall Opinion	0.330	0.379
Stature	-0.042†	0.040†
Capacity	0.186	0.114
Rump Width	0.038†	-0.006†
Rump Angle	0.037†	0.018†
Legs	-0.119	-0.074
Udder Support	0.114	0.083
Front Udder	0.117	0.117
Rear Udder	0.042†	0.042†
Front Teat Placement	0.036†	0.036†
Rear Teat Placement	-0.083	-0.083
Udder Overall	0.113	0.113
Dairy Conformation	0.235	0.183

† genetic correlation not significantly from zero

**Table 3:** Heritabilities (diagonal), genetic (below diagonal) and phenotypic (above diagonal) correlations between the four survival traits.

	SV12	SV13	SV14	SV15
SV12	0.028	0.696	0.562	0.483
SV13	0.937	0.043	0.804	0.687
SV14	0.908	0.983	0.048	0.849
SV15	0.886	0.968	0.990	0.055

All the standard errors were less than 0.07 and 0.01 for correlations and heritabilities, respectively.

Within and across breed summary statistics for sires and a comparison with the previous total longevity BVs and the new longevity BVs expressed in days survived, are given in Table 4.

**Table 4:** Summary statistics for total longevity in days and SV15 converted to days survived.

	Total longevity (days)				
	Number	Mean	Standard Deviation	Minimum	Maximum
All Breeds	19345	26	242	-1065	961
Holstein-Friesian	9621	44	226	-866	961
Jersey	7187	18	241	-917	762
Ayrshire	1452	-29	222	-827	592
Other Breeds	495	-313	294	-1065	340
	New longevity (days)				
	Number	Mean	Standard Deviation	Minimum	Maximum
All Breeds	19345	9	231	-1055	809
Holstein-Friesian	9621	29	222	-857	809
Jersey	7187	1	218	-947	657
Ayrshire	1452	-57	216	-727	564
Other Breeds	1188	-332	292	-1055	358

The total longevity and the new longevity BVs have similar means and ranges both with and across breed. The correlation among total longevity and the new longevity BVs for sires with at least 30 herd tested daughters is 0.95 across breed and ranges from 0.94 to 0.96 within breed.

## DISCUSSION

The genetic association between all the first lactation traits currently used in routine animal evaluation with two survival traits SV12 and SV15 were calculated. The production traits, TOP management traits and the fertility traits all show moderate to high genetic correlations with SV12 and SV15 even though these traits were measured in lactation 1. The characteristics displayed in lactation 1 that contribute to a cow's ability to survive have a degree of repeatability across lactations. Milking speed is more strongly associated with SV15 than with SV12. It is likely that a cow with slow milking speed will display this characteristic throughout her lifetime, with this factor becoming a bigger hazard for culling as volume yields and milking times increase with age. The TOP udder traits display the weakest genetic association with survival which indicates that sire selection for udder traits does not have a marked impact on cow survival.

The 13 trait multiple trait longevity model was computationally feasible. The model allows information on 9 predictor traits to be incorporated in the analysis. Information on the 9 predictors is available during or at the end of the sire's first crop daughters first lactation which is much sooner than the daughters survival data becomes available. The multiple trait model optimally combines the survival data and predictor trait data based on the genetic correlations and amount of data on each trait. This is in contrast to the previous method where the predictor traits were used to extend

censored survival records using a phenotypic regression that took no account of accuracy of the individual predictor traits. The multiple trait longevity model accounts for the genetic correlations among the survival traits, given that SV12 is not a perfect predictor of SV15.

Predictor traits have different impacts on a cow's likelihood of surviving at different time intervals throughout her life. For example, poor fertility is likely to be a major factor in the early lactations, but is less of a factor in later lactations as most genetically sub-fertile cows have already been culled. The multiple trait longevity model simultaneously accounts for the genetic correlations among the four survival traits and for the specific correlation that each of these traits has with the predictor traits. SV12 is highly correlated with SV15, and SV12 is highly correlated with CR42. So CR42 has a large impact on SV15 when the SV15 records are missing in the case of a bull with younger daughters. For bulls with daughters with actual SV15 records, the impact of CR42 records on SV15 breeding value estimates is much reduced.

### CONCLUSION

A new method for estimating longevity breeding values has been developed that includes information on four direct survival traits and on predictor traits: protein yield, SCC, CR42, BCS, milking speed, overall opinion, legs, udder overall and dairy conformation.. The model improved the accuracy of the estimated longevity breeding values by using all information in a multiple trait model and should improve the response to selection for longevity under the nationally adopted selection index known as Breeding Worth.

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