Genetic Parameters of Cow Functional Survival and Correlations with Predictor Conformation and Farmer-Opinion Traits with Recommendations for Genetic Evaluation

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Abstract

Functional survival is defined as a dairy cow's ability to be retained in the herd for functional reasons (e.g. good health) independent of milk production and fertility. In this study, we defined two sets of functional survival traits between each of the first four lactations, in which the effects of culling for production and fertility were removed, based on: (1) farmer-recorded culling reasons, and (2) a set of rules based on commonly recorded data fields for production and reproductive traits. We estimated genetic parameters of cow functional survival traits, along with predictor cow conformation and farmer's opinion traits, and assessed predictors for their utility in genetic evaluation of functional survival. All functional survival traits had low heritability (0.002 to 0.013), with slightly lower heritabilities for rules-based functional survival traits. Body condition score (BCS) had the strongest genetic correlations with early functional survival (0.46, 0.38 with survival in the first and second parities) and weaker correlations with later functional survival (0.15, 0.19 with survival in the third and fourth parities). In contrast, udder traits had the strongest genetic correlations with later functional survival traits (0.29 to 0.40). Milking Speed was correlated with functional survival in all parities (0.28 to 0.33) as was Legs straightness (-0.14 to -0.30). The genetic correlations of rules-based functional survival traits with conformation and farmer-opinion traits were similar to those based upon farmer-recorded culling reasons. We estimated the accuracies of sire genetic evaluations of functional survival using selection index modelling for scenarios where daughter records for conformation, farmer-opinion traits, and survival became available at increasing ages. The best predictors of overall functional survival included BCS and Milking Speed (early survival) and Udder Overall and Legs (late survival). For a bull with 50 daughters recorded for all traits, conformation and farmer-opinion traits produced an accuracy of 0.48 for the prediction of overall functional survival prior to any available survival scores on a bull's daughters, a substantial improvement over the accuracy of functional survival from first to second lactation (0.30). The prediction accuracy of overall functional survival improved to approximately 0.53 when these four predictor traits and functional survival to second lactation observations were combined. Therefore, we recommend including four predictor traits in the genetic evaluation of functional survival.

Key words: dairy, survival, conformation, genetic parameters, accuracy

Introduction

Functional survival is defined as a cow's ability to be retained in the herd over time for functional reasons (e.g. good overall health) independent of milk production and fertility (Imbayarwo-Chikosi *et al.,* 2015; van Pelt *et al.,* 2016). In practice, genetic evaluation of functional survival is challenging because exact culling reasons are seldom well recorded in commercial dairy herds. The current New Zealand genetic evaluation system calculates Residual Survival to estimate cows' health-related retention, independent of production and fertility (DairyNZ, 2011). However, the Residual Survival approach is complex and has some limitations, particularly if genetic relationships among traits change over time, and differ between breeds. A simpler evaluation for dairy cow functional survival using currently-recorded dairy conformation and farmer-opinion traits as indicators would be preferable.

The objectives of this study were: 1) define functional survival phenotypes for cows with known recorded reasons for removal from the herd and use industry data and a rules-based

approach to identify phenotypes for cows with unknown removal reasons: 2) estimate genetic parameters of functional survival traits and their genetic correlations with conformation and farmer-opinion traits; 3) predict the accuracy of sire estimated breeding value (EBV) for the functional survival trait using daughter cow functional survival, conformation, and farmer-opinion records to define a set of traits to incorporate into genetic evaluation.

Materials and Methods

Data

We defined functional survival phenotypes as the ability to be retained in the herd across the first five parities: Surv12 = survival from lactation 1 to 2, Surv23 = survival from lactation 2 to 3, Surv34 = survival from lactation 3 to 4, and Surv45 = survival from lactation 4 to 5. For each of these, we assigned binomial phenotypes: 1 = survived, and 0 = died or culled.

We also defined two additional sets of functional survival traits. For farmer-recorded functional survival (Survf), phenotypes were filtered so that cows with recorded non-functional reasons for removal of low production (LP), empty (MT; non-pregnant), low fertility (LF), late calver (LC), infertility or poor fertility (IF), calving trouble (CT), or abortion (AB) had survival phenotypes set to missing. Rules-based functional survival (Survrf) identified additional non-functional removals. Rules were: 1) removal reason recorded as code LP, MT, LF, LC, IF, CT or AB; 2) if no reason was recorded, then predict as non-functional cull if identified by at least one of the following criteria: pregnancy scan diagnosis of empty (indicates probable low fertility), culled after 200 DIM (indicates probable low fertility and/or production), culled in groups of ≥5 cows on the same day at >200 days past pregnancy scan (group culling at end of lactation indicates probable low fertility and/or production), or cow in herd's bottom 10% for milk production. All cows identified as fertility or production culls according to these rules had survival phenotypes set to missing.

In addition, industry data were obtained for 18 conformation and farmer-opinion traits that are scored in New Zealand sire proving herd cows at approximately the peak of their first lactation (DairyNZ, 2014): Milking Adaptability, Temperament, Milking Speed, Owner Opinion, Stature, Weight, Capacity, Rump Angle, Rump Width, straightness of rear Legs, Udder Support, Fore Udder, Rear Udder, Front Teat Placement, Rear Teat Placement, Udder Overall, Dairy Conformation, and Body Condition Score (BCS).

The total dataset consisted of 1 671 304 records from New Zealand Holstein-Friesian (NZHF), overseas Holstein-Friesian (HF), Jersey (JE) and crossbred cows that first calved in seasons 2000 to 2009 (11 579 herds, 52 103 contemporary groups). For the purposes of developing and testing the rules-based approach, records were restricted to cows from herd-years where 80% of cows had a meaningful fate cause recorded.

Genetic Analysis

We estimated genetic parameters for survival, conformation, and farmer-opinion traits using ASReml 4.1 (Gilmour *et al.,* 2015) via a series of linear animal models. The model for each survival trait contained a fixed effect of herd-season contemporary group, fixed covariate of age at calving at the beginning of the time period (i.e. for Surv12 = parity 1 age at calving; for Surv23 = parity 2 age at calving; etc.), fixed covariates of proportions of HF and NZHF ancestry, fixed covariates of breed-specific heterosis and recombination effects in crosses of JE, HF and NZHF, a random animal effect, and a random residual. For conformation and farmer-opinion traits, the model was the same except the covariate of age at first calving was fixed.

We fitted four-trait models to each set of functional survival traits. Phenotypic correlations among survival traits are not straightforward because an individual must have a survival phenotype of "1" to have any subsequent survival record; therefore, these are not presented. We fitted bivariate models to each pairwise combination of functional

survival traits with conformation and farmer-opinion traits.

Due to the large dataset and the large size of the pedigree, genetic analyses were run on replicate sub-samples of the data. Sampling was constrained to yield subsets of the population with a minimum herd-season group size of ten individuals. Each replicate subset contained an average 44 595 cow records, of which 25 433 had Surv12f recorded and 18 700 had conformation and farmer-opinion traits recorded (Table 1).

Accuracy of Evaluation

We used the estimated genetic parameters to identify sets of functional survival, conformation, and farmer-opinion records most useful for genetic evaluation of functional survival. Selection index methods to predict the accuracies of sire genetic evaluation of overall farmer-recorded functional survival in scenarios where daughter records for conformation and farmer-opinion traits and survival became available at increasing ages.

Overall functional survival T was defined as a weighted sum of genetic values for each farmer-recorded functional survival trait:

$$T = g_{Surv12f} + 0.730g_{Surv23f} + 0.472g_{Surv34f} + 0.28g_{Surv45f}$$

where 1, 0.730, 0.472 and 0.284 are relative trait weights and g_i are genetic values of each farmer-recorded functional survival trait i. We based relative trait weights on approximate changes in the proportions of herd replacements required when cow survival rates for successive parities in the herd were modified. Survival in later parities is less important than early survival, because fewer cows are still alive to express the later survival traits, and the costs of replacing older cows are lower because their expected future life is less than that of younger cows.

For these calculations, we assumed the sire evaluation was derived from 50 daughter records for each trait, and used our estimates of phenotypic variances, heritabilities, and genetic correlations between functional survival,

conformation, and farmer-opinion traits. We assumed that the phenotypic correlations between survival traits were 0. Genetic correlations among conformation and farmer-opinion traits were from Cue *et al.* (1996), except for those with BCS which we estimated using Pearson correlations of EBVs from high-accuracy sires in the data. Phenotypic correlations among all conformation and farmer-opinion traits were from Pearson correlations of observations in the data used in this study.

Results & Discussion

Genetic parameter results presented here are means of individual results obtained from subsample analyses along with standard errors of the means (SEM).

Genetic Parameters

All functional survival traits had low heritabilities (0.002 to 0.013), with slightly lower heritabilities for rules-based functional survival traits (Table 2), which agrees with previous research (Imbayarwo-Chikosi *et al.,* 2015; van Pelt *et al.,* 2016). Furthermore, both milk production and fertility are probably more heritable than survival, so removing production and fertility culling from the survival trait definition is expected to remove genetic variance. Component survival traits, such as survival from parity 2 to 3, also tend to have lower heritability than corresponding part-whole (cumulative) survival definitions, such as survival from parity 1 to 3 (e.g. Harris and Montgomerie, 2007). This is due to the shorter time intervals that increase the survival incidence towards one, which for a binomial trait reduces genetic variance to a greater extent than it reduces environmental variance (Dempster and Lerner, 1950).

Genetic correlations among component survival traits were positive and moderate-high in magnitude (mean rG = 0.5 to 0.9; Table 3). This suggests that similar genes are involved in functional survival over the first five parities, and genetics for early survival can be indicative of genetics for later survival.

Mean conformation and farmer-opinion trait genetic parameters are presented in Table 2 and Table 4. Heritabilities were generally in the expected range for structural traits (e.g. Cue *et al.,* 1996). Body condition score had the strongest genetic correlations with survival in first and second parities (0.46 and 0.38) and weaker correlations with later functional survival in the third and fourth parities (0.15 and 0.19). Udder Support, Fore Udder and Udder Overall had the strongest genetic correlations with later functional survival traits (0.29 to 0.40). Milking Speed was correlated with functional survival in all parities (0.28 to 0.33) as was Legs (-0.14 to -0.30). Genetic correlations of rules-based functional survival with conformation and farmer-opinion traits were similar to those based upon farmer-recorded culling reasons (results not presented). These results are generally similar to those of Cue *et al.* (1996) who reported that early survival traits had significant correlations with producer-scored Milking Adaptability, Milking Speed and Farmer Opinion, but no significant correlations with inspector-scored conformation traits.

Accuracy of Evaluation

Selection index calculations indicated that early functional survival from first to second lactation (Surv12f) can be used as an indicator of the overall functional survival index, with predicted accuracy of sire evaluation of 0.30 (Table 5). However, evaluations must wait until the beginning of the daughters' second lactation to record phenotypes for this trait.

Several conformation traits recorded at peak of first lactation can be used for earlier evaluation. Predicted accuracies of sire evaluation indicated that for the combined functional survival index, the most important indicator conformation trait was BCS, followed by Milking Speed, then udder traits (Fore Udder, Udder Overall and Udder Support; accuracy=0.20 to 0.25) and Legs (Table 5). Body Condition Score is the best predictor because it had the strongest genetic correlations with the most economically important early survival traits. Milking Speed also had strong predictive ability because it had moderate genetic correlations with all survival traits. Udder traits were of secondary importance due to good correlations with Surv23f, Surv34f and Sur45f. Legs was less important due to correlations with only later survival traits that had lower economic value. Combining information from multiple conformation and farmer-opinion traits substantially improved accuracy, with BCS plus Udder Overall providing an accuracy of 0.42, and a scenario using the four predictor traits of BCS, Milking Speed, Udder Overall and Legs providing an accuracy of 0.48. Therefore, these conformation and farmer-opinion traits are predicted to provide more accurate survival evaluations prior to any survival records being available on a bull's daughters. The prediction accuracy of overall functional survival further improved to approximately 0.53 when functional survival to second lactation was added to these four conformation and farmer-opinion traits.

Conclusions

Estimates of genetic parameters indicate that cow functional survival traits, as defined in this study, could be used for genetic evaluation in New Zealand. To improve accuracy of early evaluation prior to survival records being available, it is recommended to incorporate conformation and farmer-opinion traits (BCS, Milking Speed, Udder Overall and Legs) that are recorded during cows' first lactation in sire proving herds as predictors of cow functional survival.

Acknowledgements

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Table 1. Mean descriptive statistics for functional (f) and rules-based functional (rf) survival (Surv), conformation and farmer-opinion traits, and genetic model effects for 10 replicate data subsets used in bivariate analyses

	n	mean	sd	min	max
Surv12f	25 433	0.91	0.29	0	1
Surv23f	21 039	0.92	0.26	0	1
Surv34f	17 872	0.92	0.27	0	1
Surv45f	14 389	0.89	0.31	0	1
Surv12rf	24 547	0.93	0.26	0	1
Surv23rf	20 351	0.95	0.22	0	1
Surv34rf	17 177	0.95	0.22	0	1
Surv45rf	13 597	0.94	0.24	0	1
Milk Adapt.	17 263	6.02	1.48	1	9
Temperament	17 298	6.17	1.44	1	9
Milking Speed	17 288	6.21	1.33	1	9
Opinion	17 259	6.42	1.40	1	9
Weight	19 107	4.72	1.31	1	9
Stature	19 124	5.78	1.35	1.6	9
Capacity	19 124	6.24	0.99	2	9
Rump Angle	19 124	4.80	0.69	1.4	8.9
Rump Width	19 124	6.08	0.83	2	9
Legs	19 124	6.19	0.62	2.1	9
Udder Support	19 124	5.90	1.04	1	9
Fore Udder	19 124	5.65	1.09	1	9
Rear Udder	19 124	5.63	1.07	1	9
Front Teat Place.	19 124	4.45	0.70	1	8.3
Rear Teat Place.	19 123	5.83	0.97	1.2	9
Udder Overall	19 122	5.63	1.07	1	9
Dairy Conform.	19 121	6.37	0.96	1.4	9
Body Cond. Score	18 959	4.02	0.48	1.3	8.61

Table 2. Genetic (VarG) and residual (VarR) variances and heritability (h^2) estimates for functional (f) and rules-based functional (rf) survival (Surv) and conformation and farmer-opinion traits.[a]

Trait	VarG	VarR	h^2
Surv12f	0.00076	0.07571	0.010
Surv23f	0.00036	0.06489	0.006
Surv34f	0.00089	0.07349	0.012
Surv45f	0.00115	0.08808	0.013
Surv12rf	0.00050	0.06077	0.008
Surv23rf	0.00011	0.04689	0.002
Surv34rf	0.00028	0.04611	0.006
Surv45rf	0.00042	0.05628	0.007
Milk Adapt.	0.1177	1.3340	0.081
Temperament	0.1202	1.2468	0.087
Milking Speed	0.1093	0.8900	0.109
Opinion	0.1049	1.1628	0.082
Weight	0.1539	0.3851	0.286
Stature	0.1882	0.3707	0.336
Capacity	0.1260	0.5665	0.182
Rump Angle	0.0949	0.3037	0.238
Rump Width	0.0697	0.4210	0.142
Legs	0.0270	0.3032	0.082
Udder Support	0.1528	0.7124	0.176
Fore Udder	0.1651	0.7945	0.171
Rear Udder	0.1622	0.7196	0.184
Front Teat Place.	0.0810	0.3374	0.193
Rear Teat Place.	0.1904	0.5187	0.268
Udder Overall	0.1668	0.7475	0.182
Dairy Conform.	0.0797	0.6362	0.111
Body Cond. Score	0.0281	0.1288	0.179

[a]Values are mean estimates from replicate analyses Survival traits: 4 replicates, VarG SEM = 0.0000 to 0.00018, VarR SEM = 0.00067 to 0.00139, h^2 SEM = 0.0001 to 0.0022. Conformation/farmer-opinion traits: 36 to 40 replicates, VarG SEM = 0.0007 to 0.0072, VarR SEM = 0.0011 to 0.0097, h^2 SEM = 0.003 to 0.006.

Table 3. Genetic correlations[a] among functional (above diagonal) and rules-based functional (below diagonal) survival (Surv) traits.

	Surv12	Surv23	Surv34	Surv45
Surv12	-	0.678	0.771	0.725
Surv23	0.525	-	0.649	0.807
Surv34	0.512	0.650	-	0.790
Surv45	0.539	0.936	0.803	-

[a]Values are mean estimates from 8 replicate analyses, SEM = 0.001 to 0.039

Table 4. Genetic correlations[a] between functional survival and conformation traits.

	Surv12f	Surv23f	Surv34f	Surv45f
Milk Adapt.	0.17	0.03	0.18	0.05
Temperament	0.04	-0.03	0.08	0.02
Milking Speed	0.33	0.29	0.33	0.28
Opinion	0.23	-0.02	0.37	0.06
Weight	-0.09	-0.26	-0.08	-0.27
Stature	-0.09	-0.20	-0.05	-0.28
Capacity	0.06	-0.07	-0.07	-0.19
Rump Angle	0.00	-0.13	-0.29	-0.08
Rump Width	0.04	0.02	0.06	-0.07
Legs	-0.19	-0.14	-0.20	-0.30
Udder Support	0.06	0.32	0.35	0.29
Fore Udder	0.16	0.30	0.40	0.36
Rear Udder	0.00	0.18	0.16	0.08
Front Teat Place.	-0.09	0.07	0.03	0.01
Rear Teat Place.	-0.11	-0.05	-0.10	-0.08
Udder Overall	0.08	0.32	0.38	0.29
Dairy Conform.	0.14	0.11	0.16	-0.07
Body Cond. Score	0.46	0.38	0.15	0.19

[a]Values are mean estimates from 8 to 10 replicate analyses, SEM = 0.04 to 0.15

Table 5. Predicted sire accuracy of evaluation for an overall functional survival (Surv) index assuming 50 daughter indicator trait records

Indicator traits	Accuracy
Surv12	0.30
Body Condition Score	0.31
Milking Speed	0.27
Udder Overall	0.21
Legs	0.16
Body Cond. Score + Udder Overall	0.42
Body Cond. Score + Milking Speed + Udder Overall + Legs	0.48
Body Cond. Score + Milking Speed + Udder Overall + Legs + Surv12	0.53