

Genetic and Phenotypic Parameters of Longevity in Australian Dairy Cattle

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ABSTRACT

A new method of evaluating cows for longevity based on survival scores (S_i) is presented. Survival is defined as $S_i = 1$ if the cow survives from i to $i + 1$ yr after first calving, or $S_i = 0$ if the cow does not.

Herd Improvement records on 253,000 AI-bred cows were used to calculate survival scores, and the genetic and phenotypic parameters of these scores were examined. Survival was constant at .85 to .86 until S_4 after which it declined. Average productive life was 5.8 to 6.6 yr, which is consistent with other Australian estimates. Heritability of survival was low (.004 to .088), especially for S_1 and S_2 . Genetic correlations among survival scores was highest in early years (up to S_4), and first lactation milk and fat yields were more highly correlated with early than with late survival. Survival scores were also genetically correlated with temperament, particularly for S_0 and S_1 . For routine sire evaluation, survival scores could be used in a multitrait or a repeatability model. However, given the high longevity of Australian cows and the low heritability, improvement in longevity might be more easily achieved by nongenetic means.

INTRODUCTION

Longevity, or length of productive life, is an important trait affecting dairy farm profitability. Increasing longevity reduces replacement costs, changes herd age structures with a higher proportion of older (higher producing) cows in the

herd, and can increase culling for milk production. The economic value of longevity in Australian dairy herds has been estimated to be between .4 to .5 the value of milk production (3, 10, 15). Because some culling is for low production, the economic value of longevity overlaps that of lifetime milk production. The value of adding genetic evaluation for longevity to existing evaluations for production depends on their ability to identify sires whose daughters fail for reasons other than low production.

Various authors have presented alternatives for measuring longevity. Gaalaas and Plowman (7), Hogue and Hodges (13), and Parker et al. (19) used a measurement of total productive life, e.g., age at culling, length of productive life, or number of lactations. This approach, however, can only be used once the cows are actually dead or culled and is therefore unsatisfactory, since farmers and AI organizations must make their decision on bull selection before such a trait can be evaluated.

In 1976, Everett et al. (5) defined "stayability" as the measurement of survival of cows in the herd to a predetermined age, e.g., 36, 48, 60, 72, or 84 mo. They found the genetic correlation between stayability to 48 mo and stayability to other ages to be .86 or greater and concluded that genetic evaluation of bulls could be based on stayability to 48 mo (6).

However, this approach ignores the information contained in other stayability scores. For instance, stayability evaluated at 48 mo disregards stayability to other ages. If all the information were included, the accuracy of evaluating bulls could be improved. A multitrait analysis would do this but with a huge increase in computing requirements. If genetic correlations between all stayabilities were assumed to be 1.0 and all sire variances assumed equal, a repeatability model could be used. However, neither of these assumptions is correct.

As an alternative, we propose measuring longevity in terms of a series of survival scores

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(S_i) defined as $S_i = 1$ if the cow survives from i years to $i + 1$ yr after first calving and $S_i = 0$ if the cow does not survive; S_i is undefined or missing if the cow was culled or died before i yr post first calving.

The advantages of analysis based on these survival scores are: 1) In a sire model, residuals are uncorrelated, which simplifies a repeatability or multitrait analysis. In a repeatability model, no cow effect or variance is needed. 2) Because the mean of the survival codes changes little with age, the assumption that sire variances are equal may be more correct than for stayabilities. 3) Animals that enter the recording system late in life can still be included in data on subsequent survivals, whereas inclusion of such animals leads to bias in the analysis of stayabilities. 4) Length of time in the herd after first calving is more relevant than total life and is unaffected by age at first calving (17).

Smith and Quaas (22) proposed a nonparametric analysis of length of herd life that utilizes all information but assumes that the genetic correlations between all survival scores is 1.0. With an appropriate transformation [e.g., complementary log-log i.e., $\log(-\log S)$], the repeatability model applied to survival scores is equivalent to a discrete time version of their model.

The objective of this study was to provide estimates of the genetic and phenotypic parameters affecting survival scores in Australian dairy cattle and of the relationship of survival to other traits.

MATERIALS AND METHODS

Data

Data of 253,000 daughters of AI bulls were extracted from the Victorian State file of the Australian Dairy Herd Improvement Scheme (ADHIS) (11). This file stores milk production information as whole lactation yields prior to 1979 and as individual test day yields after 1979. Test day data allow more accurate comparison of cows for milk yield than whole lactation data. Therefore, we decided to separate the data into two data sets, i.e., cows first calving prior to 1979 and cows first calving after 1979. First lactation test day yields were adjusted for age at test day and stage of lacta-

tion and combined across test days to predict deviation from herd average over a completed (300 d) lactation by the production index methodology of Beard (1). Whole lactation data were adjusted for age and month of calving, again according to the correction factors found in Beard (1). The pedigree of each cow was traced, and from this her breed composition for the five major breeds was calculated, i.e., percentage Holstein-Friesian (HF), Jersey, Ayrshire, Guernsey, and Australian Illawarra Shorthorn. The proportion of maximum heterosis expected was calculated for each cow. For example, heterosis was 0% for purebreds, 100% for first crosses, and 50% for back crosses. Cows with unknown breeding, with an age at first calving less than 20 or greater than 36 mo, or with lactation yields outside a valid range were discarded from the data file.

Calculation of Survival Scores

For each survival score, S_i , where S_i represents the probability of survival in the herd from i to $i + 1$ yr post first calving, cows were assigned as having a known or an unknown survival. Although farmers are provided with a series of lactation termination codes (e.g., dried off, sold-mastitis) very few use these codes (17). Therefore, it is only by a cow's failure to calve again after the previous lactation that we can tell if she has been culled or is dead. This assumption may sometimes be invalid, so to allow adequate time for cows to calve again, a survival score was classified as unknown or missing where the herd was withdrawn from herd recording within 2 yr of her last calving or the close of data (April 1986) fell within 2 yr of her last calving.

Statistical Analysis

An initial analysis of the data by least squares was based on the model:

$$Y = \mu + h_i + m_j + \sum_k b_{lk} P_k + b_2 H + e_{ijk}$$

where:

Y = dependent variable,
 h_i = herd year effect i , which was absorbed,

- m_j = month j of first calving effect,
 $\sum_k b_{1k} P_k$ = linear regression of Y on the proportion of genes (P) from the breed k ,
 $b_2 H$ = linear regression of Y on the proportion of heterosis expected (H), and
 e_{ijk} = random error.

Dependent variables included: 1) Survival scores for both data sets. For test day data these scores were calculated to S_5 . For whole lactation data, scores up to S_8 were calculated. However, there were limited data available for S_5 test days, so only the mean is reported in this case. 2) First lactation milk and fat yields, age at first calving, and length of first lactation.

Estimation of heritabilities and genetic correlations used data on HF and only included sires with a minimum of 14 daughters in each data set. Variance components and sire proofs were estimated by REML according to the model:

$$Y = h_i + m_j + s_k + e_{ijkl}$$

where:

- Y = survival values,
 h_i = effect of the herd year i ,
 m_j = effect of the month j of first calving,
 s_k = random effect of the sire k , and
 e_{ijkl} = random error.

Computation was based on the REML methodology developed by Smith and Grasser (21), which allows many rounds of iteration to be performed cheaply. Variance components were estimated using all sires, but an additional analysis was carried out for milk and fat yield, and survival score S_0 in which sires with second crop daughters were treated as fixed effects. This was to determine whether REML estimates were biased due to some selected older or imported sires having larger daughter numbers than other sires in the sample.

In addition, although linear models are often used to analyze binomial data, nonlinear models such as those of Gianola and Foulley (9) are more theoretically sound. Therefore, survival

S_0 was also analyzed using the nonlinear model of Gianola and Foulley (9), and the correlation of sire proofs produced by this analysis and the linear model was calculated. Because of the large number of traits involved it was too computationally demanding to calculate genetic correlations from a multivariate REML. Instead, a method similar to that of Calo et al. (4) was used. Approximate genetic correlations were estimated as:

$$r_{g(x,y)} = \frac{\text{COV}(X, Y)}{(\sigma_{sx}^2 \sigma_{sy}^2)^{1/2}}$$

where $\text{COV}(X, Y)$

$$= \frac{\sum b_x b_y - [(\sum b_x \sum b_y)/n]}{\sum R_x R_y}$$

$$\sigma_{sx}^2 = \frac{\sum b_x^2 - [(\sum b_x)^2]/n}{n-1} \times 1/\bar{R}_x$$

and b_x = sire estimated breeding value for trait x , R_x = reliability of that breeding value estimate, and \bar{R}_x = average reliability across all sires.

In addition to the sire proofs for survival scores calculated from the univariate REML analyses, estimated breeding values for milk, fat, protein, and overall type, published by the ADHIS, and sire proofs for temperament and milking speed, calculated from Victorian Artificial Breeders progeny test data were used. Estimates of genetic correlations calculated between sire proofs are unbiased, provided there are no error correlations between data on different traits. This is true of the survival scores and of other traits where sire proofs were based on independent sets of daughters. For instance, temperament and milking speed proofs are based on daughters born since 1979 and therefore are independent of survival proofs based on the whole lactation data set. Where there is some error correlation, the estimated genetic correlations will be biased in the direction of the phenotypic correlations.

RESULTS

Overall means for survival are presented in Figure 1. There is good agreement between the

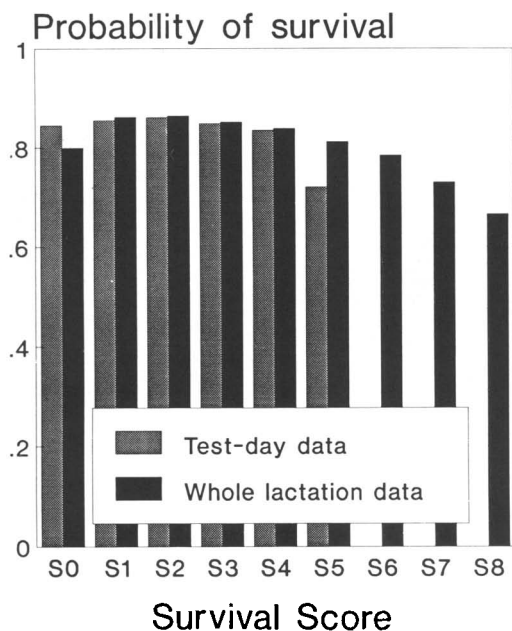


Figure 1. Overall means for survival scores S₀ to S₈.

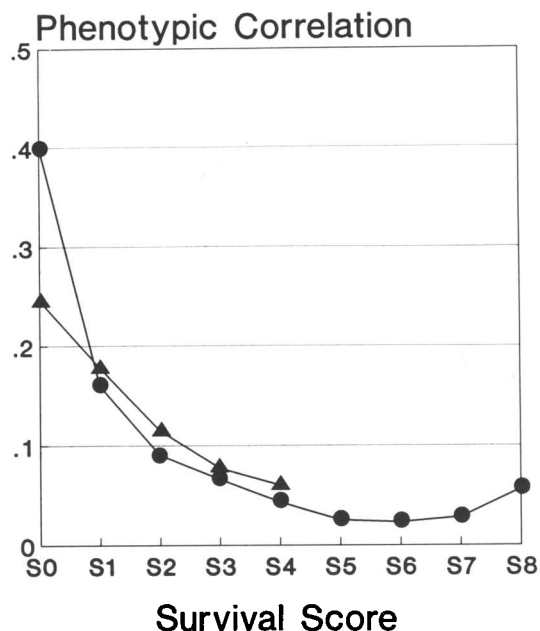


Figure 2. Phenotypic correlation of survival with first lactation fat yield for test day data (▲) and whole lactation data (●).

survival proportions from the test day data set and the whole lactation data set. Survival is approximately constant at .85 to .86 until S₄, after which it declines. The overall survival values are .85 for test day data and .83 for whole lactation data, which corresponds to an overall replacement rate of .15 to .17 and an average productive life of 5.8 to 6.6 yr per cow.

The phenotypic correlations of survival scores with first lactation fat yield are shown in Figure 2. First lactation fat yield was moderately correlated with survival early in life; however, the correlation decreased to less than .1 after S₂. The correlation of survival score with first lactation milk yield showed a similar trend, although the correlations were slightly lower (S₀ r_p = .38 and .24 for whole lactations and test day data, respectively). Age at first calving was not correlated with survival at any stage. First lactation length was moderately correlated with survival S₀ but not with subsequent survival. Month of first calving had a highly significant effect on survival up to and

TABLE 1. Effect of breed and heterosis on the proportion of cows surviving.

Survival score	Jersey - HF ¹	Heterosis
Test day data		
S ₀	-.04***	.04***
S ₁	-.08***	.04***
S ₂	-.09***	.03***
S ₃	-.11***	.03*
S ₄	-.12***	.06**
Whole lactation data		
S ₀	-.04*	.04***
S ₁	-.03	.04***
S ₂	-.02	.03*
S ₃	-.06*	.03*
S ₄	-.04	.03*
S ₅	-.08*	.05**
S ₆	-.04	.06**
S ₇	.08	.10**
S ₈	-.06	.04

*P<.05.

**P<.01.

***P<.001.

¹Holstein-Friesian.

including S₂. The effect was consistent between data sets and between survival scores. The effect is illustrated in Figure 3, which shows the month of first calving effects on survival (S₀) for the test day data. Cows calving from March to September were more likely to survive than cows calving from October to February.

The effect of breed on survival is presented in Table 1. There were insufficient numbers in breed groups other than HF and Jersey to include them for analysis. Survival of Jerseys was generally less than that of HF. Heterosis for survival was consistently near .03 to .04 and was significant for all but one survival score.

Heritabilities and genetic correlations based on weighted sire proofs for survival scores are presented in Table 2. The average number of effective daughters used to calculate the sire proofs was 101. The heritability of all survival scores was low, ranging from .4 to 8.8% (although this upper value was based on few sires), and the coefficients of variation were very high. Survival from 0 to 1 yr post first calving (S₀) had a higher heritability than subsequent survival scores (2.8% for test day data). The heritabilities of first lactation yields in the

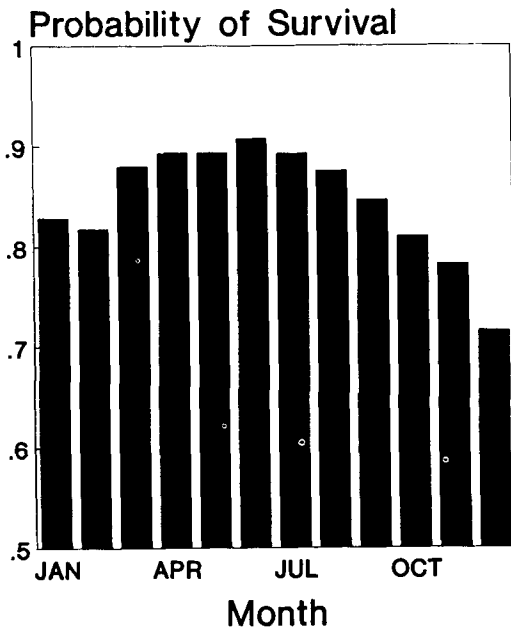


Figure 3. Least squares means for the effect of month of first calving on survival (S₀) for test-day data.

TABLE 2. Heritabilities and genetic correlations for survival scores.¹

	Test day data								Whole lactation data							
	S ₀	S ₁	S ₂	S ₃	S ₄	S ₀	S ₁	S ₂	S ₃	S ₄	S ₅	S ₆	S ₇	S ₈		
No. of sires	283	229	161	97	51	199	156	131	108	84	71	59	36	23		
Test day data	2.8 ± .7	.5 ± .2	.5 ± .4	1.2 ± 1.1	.7 ± .9	5.3 ± 1.5	4. ± .2	1.2 ± .8	2.2 ± 1.3	3.7 ± 1.9	1.8 ± 1.4	3.3 ± 2.2	8.8 ± 5.6	8.8 ± 1.1		
	102	75	95	-9	-28	87	77	38	90	111	23	35	9			
	99	97	95	-9	-28	87	77	38	90	111	23	35	9			
	24	97	95	-9	-28	87	77	38	90	111	23	35	9			
	-21	-16	-9	-28	-28	87	77	38	90	111	23	35	9			
Whole lactation	59	59	71	63	-43	53 ± 1.5	4. ± .2	1.2 ± .8	2.2 ± 1.3	3.7 ± 1.9	1.8 ± 1.4	3.3 ± 2.2	8.8 ± 5.6	8.8 ± 1.1		
S ₀	59	51	77	69	-10	87	77	38	90	111	23	35	9			
S ₁	52	123	55	58	-6	44	100	43	100	111	23	35	9			
S ₂	83	130	109	78	-9	100	100	43	100	111	23	35	9			
S ₃	83	130	109	78	-9	100	100	43	100	111	23	35	9			
S ₄	41	60	6	67	-31	85	112	79	100	111	23	35	9			
S ₅	94	125	51	123	-33	79	112	79	100	111	23	35	9			
S ₆	-12	-23	-18	-27	-11	1	-3	-52	1	31	71	80	0			
S ₇	39	67	55	31	-6	51	69	51	80	42	6	-17				
S ₈	13	4	10	-1	5	25	36	58	0	6	6	-17				

¹Heritabilities (h² ± SE) are on the diagonal. Genetic correlations (r_g%) are below diagonal.

TABLE 3. Genetic correlations between survival and associated traits.¹

	Milking speed	Temperament	Overall type	First lactation		
				Milk (L)	Fat (kg)	Protein (kg)
Test day data						
S ₀	.44	.51 (118)	.45 (87)	.35	.37	.24 (283)
S ₁	.49	.67 (83)	.35 (68)	.52	.88	.45 (229)
S ₂	.68	.01 (53)	-.16 (54)	.26	.72	.30 (161)
S ₃	-.16	.17 (23)	-.06 (30)	-.04	.70	.14 (97)
S ₄				-.04	-.19	-.46 (51)
Whole lactation						
S ₀	.19	.28 (24)	-.03 (26)	.51	.66	.36 (199)
S ₁				.47	.49	.33 (156)
S ₂				.38	.56	.26 (131)
S ₃				.33	.86	.50 (108)
S ₄				.05	.48	.02 (84)
S ₅				-.27	.66	.04 (71)
S ₆				.18	-.05	.03 (59)
S ₇				.42	.13	.00 (36)
S ₈				.44	.36	-.88 (23)
Temperament	.42 (119)					
Overall type	-.19	.33 (40)				
First lactation						
Milk	.14	.27 (119)	.16 (87)			
Fat	.21	.24 (119)	-.06 (87)	.76		
Protein	.12	.25 (119)	.04 (87)	.92	.66 (422)	

¹Correlations based on less than 20 sires have been excluded. Numbers of sires for preceding correlations are in parentheses.

test day data were estimated to be 24% for fat yield and 26% for milk yield. A separate calculated based only on young sires found heritability of first lactation fat yield to be 27% and survival (S₀) to be 3.6%. Because heritabilities are low (relative to their standard errors), the estimated genetic correlations between survival scores will have large standard errors. Genetic correlations greater than 1 or less than -1 are the result of this, especially where the number of sires used in calculating the correlations is small. As a guide, the numbers of sires used for each correlation is approximately equal to the number of sires in the smaller data set. The genetic correlations appear to fall into two groups. Correlations between S₀ to S₃ are high, average r_g (weighted by sire numbers) being .85 for test-day data and .73 for whole lactation data; correlations among the remaining survival scores are lower.

Table 3 contains the genetic correlations between survival and some of its associated traits, namely milking speed, temperament, overall type, and first lactation milk and fat yields. The number of sires used in each comparison is also

presented. Correlations based on less than 20 sires are excluded from this table.

To reduce the effects of sampling errors in the estimation of genetic correlations, average correlations among groups of survival scores were calculated. Average genetic correlations for survival scores based on the groupings S₀ to S₃ and S₄ to S₈, and the average correlations for the associated traits, weighted by number of sires, can be found in Table 4. These correlations are averaged over both data sets. Among the workability traits, temperament has the highest correlation with survival. On average, milking speed and overall type were lowly correlated with survival. First lactation yield is more highly correlated with early than late survival. Agreement is good between the average correlations based on test day yields and those based on whole lactation yields.

We analyzed the S₀ data with a log-log transformation [$\log(-\log S_0)$] in the nonlinear model of Gianola and Foulley (9). However, the estimates of sire and fixed effects failed to converge and, in fact, diverged. Experimentation showed that this can occur even with very

TABLE 4. Average genetic correlations (weighted by sire number) for survival and associated traits.

	Average		
	S ₀ -S ₃	S ₄ -S ₈	Overall
S ₀ -S ₃	.79		
S ₄ -S ₈	.35	.06	
First lactation			
Milk yield	.38	.06	.32
Fat yield	.63	.27	.56
Protein yield	.26	-.12	.25
Temperament	.58	.75	.61
Milking speed	.23	.07	.19
Overall type	.26	-.13	.19

simple fixed effect models when a complementary log-log transformation is combined with binomial errors. It occurs if an individual survives when the model predicts a very low probability of survival. In this case, in the next round of iteration, the weight times the working y -value for this animal becomes very large, which causes a failure to converge. To overcome this problem, we changed to a logit transformation, $\log [S/(1 - S)]$. In this case, the weight times the working y -value never becomes very large and sire solutions converged very quickly. The correlation between the 283 sire solutions obtained after five rounds of iteration and those obtained from the linear analysis was .99.

DISCUSSION

Survival Characteristics

The proportions of cows culled (Figure 1) are generally below those presented in the literature, especially for older age groups. The average number of lactations from herds in Canada and the United States ranged from 3.2 to 4.8 lactations (7, 8, 12, 19), whereas our culling rates correspond to 5.8 to 6.6 lactations per cow. However, our results agree with our own earlier findings of an average replacement rate of 18%, corresponding to a productive life of 5.6 yr (17), and with a subsequent analysis for 600,000 AI bred cows across all Australian states, which found average productive life to be 6.25 yr (L. P. Jones, personal communication). Jackson (15) also studied replacement rates sporadically for 1938 to 1977 in New

Zealand where conditions are similar to those in Australia, and although culling rates ranged between 10.7 and 21.2%, the mode and the most recent values was around 17 to 18% (or a productive life of 5.9 yr).

Several factors could be contributing to the relatively long productive life of Australian dairy cattle. Between 1974 and 1987, the average herd size of Victorian herd testing farms increased from 97.3 to 114.7 cows (11). To facilitate this increase, farmers may have decreased their culling rates. Also, by basing the analysis only on AI-bred cows, the replacement rates observed might be biased if AI bred cows are retained in the herd preferentially over non-AI bred cows. This is likely since the average production of AI bred cows is 500 kg more milk and 12 kg more fat per lactation than that of non-AI bred cows (11). Although only 54% of cows in Victoria are AI bred, only 21% of herds have less than 10% AI bred cows, and only 9% of herds have greater than 90% AI bred (11). Thus, the 70% of herds with intermediate numbers of AI and non-AI bred cows are probably contributing heavily to this effect.

Despite these biases, real differences in management and production conditions obviously exist between the extensive, pasture-based Australian dairy industry and the intensive industry in other countries, which could cause differences in productive life. For instance, most herds use AI for only a short period each year and do not use AI on virgin heifers. Therefore, they generate barely enough AI-bred heifers to replace the small number of cows culled each year. Many of the economic evaluations of longevity that have been presented in Australia and overseas have relied on starting values for productive life below that reported here. Therefore, they may have overestimated the value of increasing longevity in Australia.

The genetic correlations of survival with first lactation yield indicates that low production is an important reason for culling at all ages although it is highest in the early years of life. The decline in the phenotypic correlation between first lactation yield and survival scores (Figure 2) is more marked than the decline in genetic correlations because of the imperfect repeatability of milk yields. Although reproduction culling was not analyzed directly in this paper, some measure of its importance can be

judged by the highly significant month of calving effects observed. In Victoria, where calving is seasonal, the majority of cows calve in July and August to optimize the benefits of spring feed. Because farmers generally attempt to synchronize calving, cows calving in the nonoptimal period reflect reproductive problems. That those cows are not retained in the herd is shown by the lower survival of cows calving from October to February. Cows calving from March to June have a greater value in the herd and are kept longer than cows calving at other times of the year because of the incentive paid to farmers to milk cows during this normally nonproductive period.

The analysis of breeds indicated that HF survive significantly longer than Jerseys in the same herds. The differential survival of HF and Jerseys, however, is biased by the changing breed structure in the Victorian dairy population, which has been gradually changing from predominantly Jerseys to predominantly HF. It is difficult to separate the effect of culling on the basis of a breed replacement policy from other effects that could cause higher culling of Jerseys. Parker et al. (19) found no difference in age at death or culling between HF and Jerseys in a herd that was not culled for type or production. Burnside et al. (2) showed that fewer Canadian Jerseys were culled for reproductive and breakdown conditions than for HF, although Jerseys had proportionally more deaths and a greater degree of culling for production. It is likely then that much of the effect experienced in the Australian breeds is due to breed replacement policy. Because of the heterosis found, crossbreds survive better than purebred HF.

Considerations of Methodology

The genetic correlations between sire proofs for production traits are in good agreement with those found by Meyer et al. (18), who analyzed first lactation yields. The small increase obtained in the heritability estimates for milk, fat, and survival indicate that there is no need to treat older sires as fixed effects. Because these sires have a larger number of daughters, they improve the precision of parameter estimates for lowly heritable traits such as survival. Similarly there is no advantage in analyzing survival using a nonlinear model because the correlation between sire proofs for survival was nearly 1.

Implications for Genetic Improvement

The low heritability of survival found in this analysis is consistent with heritabilities reported elsewhere, although it is at the lower end of the range. Heritabilities for longevity based on length of productive life ranged from 3 to 10% (12, 23). Based on stayabilities, heritabilities were calculated to be between 2 and 8% (14, 20). In agreement with our results, Everett et al. (6) found genetic correlations between stayabilities to be less than 1. Because stayability to 48 mo is a part of stayability to older ages, it is not surprising that genetic correlations among stayabilities are higher than among survival scores.

Basing a genetic improvement on a trait of such low heritability leads to two problems. First, response to selection will be very slow. Assuming a heritability of 2.8%, under a realistic genetic improvement program with 100 young bulls tested per year, each with 100 effective daughters and where 20% of bulls are selected as proven bulls the maximum genetic progress in these selected bulls will be 3.6%. That is a survival increase of their daughters from .85 to .868. Second, if genetic improvement is based on estimated breeding values for some measure of longevity such as survival, large daughter numbers would be needed to attain reasonable reliability. For example, again based on a heritability of 2.8%, the following daughter numbers would be required: 40% reliability = 95 effective daughters, 70% reliability = 334 effective daughters, and 99% reliability = 14,157 effective daughters.

Many bulls do not have high daughter numbers, and it is unlikely that farmers would be willing to base their selection of bulls on sire proofs of such low reliability. These problems would be overcome to some extent by an analysis based on all survival scores. This would improve the accuracy of bull evaluation by allowing all available information to be used. Because the genetic correlations between survival scores are less than 1.0, use of a repeatability model would not be strictly correct. A multitrait model could be used and would have the advantage of providing separate estimates of breeding value for survival at different ages. For instance, breeding value for S_0 might reflect mainly culling for low production and poor temperament while breeding value for S_4 might reflect breeding value for "udder break-

down". However, it is possible that when computing costs are considered a repeatability model, although not theoretically correct, may be economically optimum.

Alternatively selection for longevity could be achieved through selection for one or more of the associated traits. Given the moderate genetic correlation of fat production with survival (average $r_g = .63$ for survival S_0 to S_3), we would expect that selection for production would indirectly improve longevity. However, to realize this improvement, culling for production must be decreased, which decreases the gain in production in second and later lactations achieved by selection of bulls with high breeding values. If culling percentages are held constant, the increase in longevity will not be realized. Indirect selection on the basis of other associated traits could be used. However, of those traits analyzed in this study, only temperament with $r_g = .61$ explained a significant proportion of the genetic variability in survival (37%). A selection index incorporating production, survival, and temperament may be the best way to achieve improvement in both production and longevity. However, given the existing long productive life of Australian dairy cattle, the relatively low economic value of survival, and the difficulties involved in direct selection for survival, improvement in longevity may be more easily achieved by nongenetic means.

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