

Genetic evaluation of herd life in Canada: Current status and future outlook

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Abstract

Official genetic evaluations for dairy sires have been published in Canada since the winter of 1996. Evaluations are available for five major breeds (Ayrshire, Brown Swiss, Guernsey, Holstein, and Jersey). The most recent evaluation for Holsteins included records from 1,652,884 daughters of 80,197 sires, of which 5900 were eligible for official publication. Published evaluations combine information from daughter survival (direct herd life) and conformation traits (indirect herd life). Direct genetic evaluations of herd life are based on a multiple-trait linear animal model, in which survival in each of the first three lactations are considered correlated traits. Factors related to fat and protein yield are included in the model, so functional herd life is the trait evaluated. Heritability of herd life is assumed to be 0.04 for each lactation. Evaluations for the three lactations are then combined into an overall evaluation for direct herd life based on their relative economic values. Evaluations for indirect herd life are based on an index of evaluations for composite traits for mammary system, feet and legs, rump, and body capacity. Sire evaluations for the direct and indirect measures of herd life are combined into an overall evaluation for herd life using the methodology employed by Interbull to combine genetic evaluations across countries. Published sire evaluations are expressed as predicted transmitting abilities for the number of lactations of functional survival of daughters, centered at a base of 3 lactations, and range from approximately 2.3 to 3.5. Herd life is included in Canada's Total Economic Value (TEV) Index with a weight of 4 relative to 10 for production and 1.5 for udder health. Future changes in the genetic evaluation for herd life may include the adoption of a survival analysis. A survival analysis would be more appropriate statistically than is the current linear model and would account properly for censored records. Also, adoption of a survival analysis may increase the consistency of international evaluation, because several European countries have recently adopted survival analyses for their domestic evaluations. However, the survival analysis would be more computationally demanding and would likely be limited to a sire model. In addition, the survival analysis model would require the assumption that survival is the same genetic trait across an animal's lifetime. The feasibility of a survival analysis of herd life in Canada is being studied.

1. Introduction

“Balanced Breeding” has long been the motto of the Canadian dairy cattle breeding industry. Simply, balanced breeding refers to the consideration of type or conformation traits in the breeding goal, in addition to yield of milk or milk solids. Some breeders were primarily interested in the direct or superficial aspects of type as it related to the showing or simple aesthetics, but most considered type traits important for its indirect effects on the longevity of cows. Clearly, these breeders realized the economic importance of longevity, scientific studies (Allaire and Gibson 1992, Jairath and Dekkers 1994) indicate the value of longevity is about 50% that of yield traits, but lacked the information needed to select directly for increased

herd life of their cows. To help accommodate those breeders with a more accurate tool with which to select for longevity, Canada implemented in 1996 a genetic evaluation of dairy sires for longevity or herd life of their daughters (Jairath et al. 1998).

2. Current Genetic Evaluation for Herd Life

2.1. Underlying scientific principles

Longevity can be recorded and expressed in a variety of ways. Van Arendonk (1986) proposed that selection to increase longevity should emphasize increasing resistance of cows to involuntary culling, in part because culling for production would limit realization of increases in actual lifespan of cows. In

Canada, data collected about culling reasons is not considered reliable enough to accurately distinguish voluntary and involuntary culling. As an alternative, in Canada herd life is adjusted for production, yielding an evaluation of so-called “functional” herd life (**FHL**) (Ducrocq et al. 1988). Dekkers (1993) demonstrated that FHL, although not equivalent to resistance to involuntary culling, is superior to unadjusted herd life when selecting for profitability.

Herd life is a complex trait, with many genetic and environmental influences. One factor that contributes to the complexity is that herd life is a lifetime trait. Influences on a given cow’s phenotype are likely to change as she ages. For example, herd dynamics change from year to year, due to fluctuations in milk and feed prices, weather, heifer inventory, and other factors. The herdmates of a given cow will change due to culling and differences in calving intervals, so a cow’s contemporary group changes continually. In addition to changes across a cow’s lifetime in the environmental influences on longevity, genetic influences may also differ. Different genes may be expressed at varying levels across a cow’s lifetime. Different correlated traits that affect herd life may play a greater role in resistance to involuntary culling at different ages. For example, Boettcher et al. (1997) found that feet and leg traits had a more profound effect on survival to five years of age than on survival through the first lactation. Jairath and Dekkers (1994) observed that genetic correlations among survival in the first three lactations were only moderately high (0.60 to 0.75), indicating that survival was a different genetic trait in each lactation. Boettcher et al. (1999) recently reported estimates that were greater (0.84 to 0.91) but still less than unity. To accommodate these differences, the Canadian genetic evaluation models survival as different traits in the first 3 lactations, assigning cows to different contemporary groups for each subsequent calving.

Cows do not fully express their longevity until they are finally culled from the herd. This fact presents a major obstacle in the genetic improvement of longevity and the genetic evaluation of sires for herd life of their daughters. Genetic improvement is fastest for traits that are expressed early in life. Because of the current rapid genetic trend in yield traits, by the time the initial daughters of most commercial AI sires have finally finished their productive lives, many of these bulls will have been replaced in active service by younger bulls with higher EBV for yield.

Two options can be used to help circumvent the problem of delayed data expression. First, actual lifespan can be replaced by a different measure of herd life that can be recorded relatively early in life. One approach is to record stayability or survival up

to a certain chronological age or milestone, such as to a given number of lactations. Short and Lawlor (1992) reported genetic correlations of stayability to second calving, 54 months, and 84 months,; with total productive lifespan. All correlations were relatively high (≥ 0.73) and most were above 0.90. These results indicate that early measures of herd life can be efficiently used to select indirectly for total lifespan. The Canadian evaluation is based on survival in first, second, and third lactations, so bulls will have a progeny test for longevity at about the same time that they initially receive their test for yield traits.

The second option is to perform indirect selection for longevity by using information about non-survival traits that are genetically associated with herd life. As stated earlier, some Canadian breeders have supported balanced breeding for both production and type because they believed that type traits influenced longevity. Many researchers (e.g. Boldman et al. 1992, Boettcher et al. 1997, Jairath and Dekkers 1994, Schneider et al. 1999, and Short and Lawlor 1992) have studied the relationship between conformation traits and measures of longevity. In general, udder traits have the strongest relationship with FHL, with feet and leg traits also being of some importance. Dairy character traits were highly correlated with unadjusted herd life. Because conformation traits are usually evaluated during the first lactation, this information can be used to provide an early predictor of herd life.

Boldman et al. (1992) developed a procedure for predicting sire transmitting abilities for herd life based on the conformation of their daughters. Their calculations indicated that a battery of 18 type traits could predict transmitting abilities for herd life with a reliability of up to 0.56. Visscher (1994) demonstrated that this estimate of reliability is biased upward, but a procedure based on the work of Boldman et al. (1992) has been adopted by the US and used in their genetic evaluations for herd life. Genetic evaluations for herd life in Canada also incorporate information about conformation, but only includes 4 traits, which decreases the overestimation of accuracy. In Canada, the prediction of transmitting ability for herd life based on conformation traits is called “indirect” herd life (**IHL**) and the prediction based on observed daughter survival is called “direct” herd life (**DHL**).

2.2. Data and models

2.2.1. Direct herd life

Data for the Canadian sire evaluation for DHL are taken from the records used for the national genetic evaluation for lactational production traits. Data are edited to include records with years of first calving

≥1980. In addition, only records of survival within the first three lactations are included. Additional edits require all cows to have a first lactation record, a minimum age at first calving, and for all production records to be within reasonable ranges. Finally, the production evaluation includes only lactational records with ≥ 90 days in milk and this requirement was maintained for DHL. In contrast to the production evaluation, which is performed quarterly, the sire evaluation for DHL is performed only twice per year (February and August). Evaluations are calculated for 5 breeds. The most recent evaluation for Holsteins included records from 1,652,884 daughters of 80,197 sires. Among these sires, 5900 met the various eligibility requirements for official publication. The EBV for cows are not maintained in any national database or published.

Survival in lactations 1 to 3 are analyzed as separate traits by using a multiple-trait linear animal model. The following model equation is used:

$$Y = HY + RHS + AGE + FAT + PROT + PROT * RHS + A + e$$

where Y is the observation for survival in a given lactation (0/1), HY is the fixed effect of herd-year of calving; RHS is the fixed effect of the interaction among herd registry status, change in herd size, and season of calving; AGE represents linear and quadratic regressions of survival on age at calving in first lactation; FAT represents linear, quadratic, and cubic regressions of survival on normalized fat yield in first lactation, expressed as a deviation from herd year average; PROT is the equivalent for protein yield, PROT*RHS is the linear regression of survival on PROT within each of the RHS groups; A is the random additive genetic effect, and e is the random residual.

For a given lactation, survival is recorded as 1 if the cow had a recorded calving date in the following lactation and 0 otherwise. Precise culling dates are not always identified, so a cow was considered culled if she had no subsequent calving date recorded within two years of her most recent calving date. An important distinction exists between these survival traits and stayabilities. With stayabilities, cows that do not survive to a given lactation will be considered to not have survived to all later lactations. However, with this survival trait, cows that do not survive a given lactation are recorded as missing in all subsequent lactations. In other words, survival in a given lactation is conditional upon survival through the previous lactation. On average, conditional survival is about 75% in lactation 1, 71% in lactation 2, and 66% in lactation 3.

Herd-years are based on the traditional quota year in Canada, which runs from July to June. Culling

patterns differ with respect to season of calving, registration status of cows and herds (e.g. Boettcher et al. 1997 and Dentine et al. 1987), and within herds that are expanding or decreasing in size. Therefore, these factors are accounted for by grouping animals and herds with similar characteristics and estimating an effect associated with these characteristics. The inclusion of an interaction of this effect with PROT accounts for different degrees of culling for production. Sixty RHS classes were established by crossing 4 registry groups, 5 herd-size-change classes, and 3 seasons. Cows from herds with >90% and <10% registered cows formed two registry groups. Registered and grade cows from the remaining herds formed the other two groups. Herds were grouped if they increased in size by either >25% or >10%, changed by <10%, or if they decreased in size by either >10% or >25%. Seasons are from July to October, November to February and March to June.

The relationship matrix for the most recent Holstein evaluation included 3,228,383 animals and 55 unknown parent groups. The heritabilities and genetic correlations for survival in each lactation were estimated by Boettcher et al. (1999) and are shown in Table 1. Residual variances and correlations depend on whether records for lactations 2 and 3 are present or missing and whether records were from official or unofficial milk recording programs. Records from unofficial programs receive 60% of the weight that official records receive.

Table 1: Heritabilities¹ and genetic correlations² of survival in lactations 1 to 3 used in the Canadian genetic evaluation of direct herd life.

	Lactation		
	1	2	3
Lactation 1	0.04		
Lactation 2	0.85	0.04	
Lactation 3	0.84	0.91	0.04

¹Heritabilities on diagonal.

²Genetic correlations on off-diagonal.

Solving the corresponding mixed model equations yields sire EBV for three traits, FHL in lactations 1, 2, and 3 (FHL₁, FHL₂, and FHL₃). The three EBV are combined across lactations such that,

$$DHL = b_1 * FHL_1 + b_2 * FHL_2 + b_3 * FHL_3,$$

where b₁, b₂, and b₃ are weights calculated using a selection index that considered survival in lactations 1 to 10 in the aggregate genotype. Estimates for the weights from this procedure were similar for all three lactations, so equal weights are used for b₁, b₂, and b₃. Table 2 has correlations among EBV from lactations 1, 2, and 3, and overall DHL (Jairath et al. 1998). Standard deviations of EBV for individual lactations were approximately 0.04.

Table 2: Correlations among EBV from lactations 1, 2, and 3 and overall DHL.

	Lactation		
	1	2	3
Lactation 2	0.88		
Lactation 3	0.86	0.97	
Overall DHL	0.95	0.98	0.97

2.2.2. Indirect herd life

The sire EBV for IHL are based on combining sire EBV for four conformation traits: Mammary System (**MS**), Feet and Legs (**FL**), Frame and Capacity (**FC**), and Rump (**R**). All four traits are composite traits accounting for several related traits. For example, MS includes udder depth, median suspensory ligament, and udder texture. Weights for the 4 traits were computed using selection index methodology where increased FHL was the selection goal. Genetic correlations with FHL were assumed to be 0.57, 0.23, 0.20, and 0.19, for MS, FL, FC, and R, respectively. These values were based on an unpublished study by Z. Liu (1994), for which the data were primarily (80%) from registered cows. Based on these parameters, the optimal index gave relative weights of 9.3, 2.4, 1.4, and 0.2, to MS, FL, FC, and R. However, to account for expected future changes in dairy housing in Canada, where sound feet and legs are expected to be of increased importance, the chosen index was

$$\text{IHL} = 8*\text{MS} + 4*\text{FL} + 1*\text{FC} + 1*\text{R}.$$

This index was found to be only slightly less accurate than the optimal index (Jairath et al. 1998). This combination of traits explained 36% of the genetic variation in FHL.

2.2.3. Combined herd life

Sire EBV for DHL and IHL are combined using the MACE (Schaeffer 1994) procedures that are currently used to calculate international rankings of sires. All Canadian sires with official EBV for conformation traits are included in the analysis. Sire EBV for DHL and IHL are deregressed by using a modification of the approach of Banos et al. (1994) that accounts for the overall mean. For details on this procedure, see Jairath et al. (1998). Deregressed EBV are then used as data in a multiple-trait analysis of DHL and IHL. For this analysis, heritabilities of DHL and IHL are assumed to be 0.04 and 0.18, respectively. Residual correlations of DHL and IHL are assumed to be zero, although some cows will contribute to EBV for both DHL and IHL of their respective sires. This assumption tends to increase the emphasis on IHL in the index, relative to the

optimal index. However, actual impacts of this assumption on the accuracy of the index were found to be minor (Jairath et al. 1998).

The analysis of deregressed EBV yields multiple trait estimates of DHL and IHL. These new EBV are then recombined based on the following index:

$$\text{CHL} = b_D * \text{DHL} + b_I * \text{IHL},$$

where CHL is combined herd life and b_D and b_I are respective weights for the new multiple trait EBV for DHL and IHL. The b_i were determined from selection index procedures, assuming genetic correlations with CHL of 0.9 and 0.6 for DHL and IHL, respectively. The resulting weights were 2.46 for DHL and 0.16 for IHL. Table 3 has correlations between EBV for IHL, DHL, and CHL (Jairath et al. 1998). In spite of the vastly greater weight on DHL versus IHL, the correlations of each with CHL are relatively similar.

Table 3 Correlations between EBV for direct herd life (DHL), indirect herd life (IHL) and combined herd life (CHL).

	DHL	IHL
IHL	0.37	
CHL	0.80	0.79

This result occurs for several reasons. First, the weight on DHL is much greater because the variability in DHL is much lower than for IHL (sire variances are 0.0062 versus 0.018). Second, the relative contribution of DHL and IHL depends upon the amount of information available for each. Because cows are classified for conformation during their first lactations and DHL includes the first 3 lactations, most bulls, particularly recent progeny test bulls, will have more daughter information for IHL than for DHL. In addition, because the heritability of the index of conformation traits is greater than of DHL (0.18 versus 0.04) the same number of daughters yields more information about IHL than DHL. Finally, the correlation structure of CHL, DHL, and IHL plays a role. The CHL in Canada is not the same genetic trait as DHL, being genetically correlated by only 0.90. This feature of the evaluation is in contrast to the evaluation implemented in the US (VanRaden and Wiggans 1995), where “indirect” conformation data is also used to increase the accuracy of the “direct” prediction. With the US evaluation, the direct trait is the same as the combined trait, so EBV for herd life are based almost entirely on direct information for sires with many daughters. However, because of the correlation structure used in Canada, the weight in the CHL on the conformation index will never drop below about 0.25, even when the reliability of DHL reaches 100% (Jairath et al. 1998).

This feature has been justified by the importance of type traits in Canada. First, from a “scientific” standpoint, improved conformation of udders, feet and legs, and rumps can have benefits in addition to increased longevity, such as more efficient milking, decreased treatments for locomotive problems, and easier calving, respectively. Second, from a “marketing” perspective, the acceptance by Canadian breeders of the herd life evaluations was expected to be greater with a slight overemphasis on conformation traits.

2.3. Publishing and use of EBV

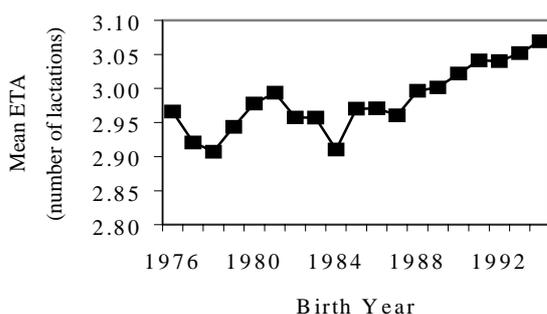
2.3.1. Expression of sire ETA for herd life

Only evaluations for CHL are officially published in Canada and only for bulls. Most cows have solutions for DHL from the mixed model equations and EBV for the conformation traits contributing to IHL, but the two values can not be easily combined by using the same blending procedure that is used for bulls. The results for bulls are expressed as predicted transmitting abilities for the number of lactations that daughters are expected to survive, after adjustment for production, standardized to a base of 3 lactations. The EBV range from 2.22 to 3.40 with a standard deviation of 0.15. Figure 1 shows the genetic trend in Canada for CHL, with mean ETA of bulls plotted against year of birth. The trend is generally positive, particularly in the recent years. This overall upward trend is likely to largely reflect gains in IHL due to increased genetic trend for type traits, rather than significant increases in DHL (Jairath et al. 1998).

2.3.2 Use of ETA for herd life

Yield traits are of primary importance for dairy producers, so the recommended use of ETA for herd life is their incorporation into selection indexes that

Figure 1: Genetic trend in mean sire ETA for combined herd life.



include yield traits and other traits of economic importance. To this end, ETA for herd life are now

included in the Total Economic Value (TEV) in Canada, an index for sire selection (Dekkers 1995). The economic value of increased FHL was estimated by using the dynamic programming model of Van Arendonk and Dijkhuizen (1985). The value of a 1% decrease in involuntary cull rate was worth about \$3 per cow in first lactation and decreased with age. Across all ages, the value was about \$12.70 per cow (Dekkers 1995). Based on these results, herd life was assigned a weight of 4 in the TEV, relative to 10 for production and 1.5 for udder health. Among the current top 10 bulls ranked for TEV, only one has an ETA for herd life that is below average.

3. Possible future changes to the Canadian genetic evaluation for herd life

In the future, the procedure for genetic evaluation of herd life in Canada is expected to change with the availability of new information and different statistical approaches for the analysis of longevity data. Already, since 1996 the evaluation has changed slightly, to incorporate new estimates of genetic parameters (Boettcher et al. 1999) that were estimated by using more data than were the original values (Jairath and Dekkers 1994).

The anticipated changes will likely occur in two areas. The first area concerns the data available for analysis and the second addresses the statistical models for estimation of breeding values.

3.1. Data entering the evaluation

For simplicity, The genetic evaluation of herd life in Canada began as an adjunct of the lactational evaluation for production traits. This procedure was efficient, because little additional editing of the data was required for implementation of the herd life evaluation. However, some limitations resulted, causing the removal of some potentially important records and delay in the use of others, both of which may have affected the reliability of sire ETA for herd life. One of the major deficiencies of the data for the production evaluations was the requirement for 90 days in milk for the inclusion in the database. The primary disadvantage resulting from this restriction is systematic elimination of all information about cows that are culled within the first 90 days of their initial lactation. For example, if daughters of a given sire were particularly prone to mastitis at or around the time of first calving and this trend caused a high rate of early culling, no record of these culls would exist in the database. The 90 day restriction also causes delays in the inclusion of records from all lactations into the data for the herd life evaluation. The presence of a new lactation record indicates survival of the previous lactation. A

cow culled in the first 90 days of a lactation would be identified as a non-survivor, although she actually survived to start that lactation. However, no record of her culling would exist, meaning that a delay of approximately 1 year would result before her record of non-survival was entered into the database, according to the rules of the editing procedure. Another deficiency in the production database was that, although termination dates for lactations were recorded, termination reasons were not recorded consistently. In many instances, a dry date may not be distinguished from a culling date, resulting in a delay for inclusion of the record into the database for herd life.

In February 1999, a genetic evaluation based on a test day model was officially adopted for production traits in Canada (Jamrozik et al. 1997). For several reasons, this adoption has the potential to improve the quality of the data in the genetic evaluation for herd life. First, all tests after 5 days of lactation will be included in the database. Minimum requirements for length of lactation will apply only to the official publication of EBV, rather than to the inclusion of data in the evaluation. Thus, the 90-day restriction will no longer affect inclusion of records from cows culled early in their lactation. Second, Canadian milk recording agencies have developed new streamlined recording procedures to help smoothly implement the test day evaluation. These changes may increase the precision to which data about culling is recorded, decreasing the delay for inclusion of data into the evaluation for herd life. Alas, the implementation of the test day evaluation for production has recently demanded the bulk of the attention and resources from the Canadian Dairy Network, which calculates and publishes genetic evaluations in Canada, so these changes to the herd life evaluation will slowly be adopted in the future.

3.2. Statistical models for evaluation

Currently, a linear model is being used for genetic evaluation of a binary survival trait. Clearly, this approach does not represent the most statistically appropriate procedure.

Boettcher et al. (1999) compared some of the properties of the current analysis to other procedures that are more appropriate in theory. The first alternative was the threshold model (Gianola 1982), which assumes that the observed categorical trait is controlled by continuous underlying variability and fixed thresholds that determine into which category an individual's phenotype will fall. Boettcher et al. (1999) reported that heritability estimated (on the underlying scale) by the threshold model for herd life was greater than by the linear model, which could lead to increased selection accuracy, although the difference was negligible when both heritabilities

were expressed on the underlying scale. However, the threshold model was limited to the sire model (at least for correct estimation of variance components) and required more computing time than did the linear model. Also, correlations of sire EBV from the linear and threshold model were very high (0.98), indicating little opportunity for major benefits by adopting the threshold model.

A second approach for the analysis of herd life that has received considerable attention recently is survival or failure time analysis (Ducrocq et al. 1988). Survival analyses are non-linear statistical procedures that model the probability of survival or culling at time t , conditional upon survival up to time t . Several researchers (Boettcher et al. 1999, Dürr et al. 1997, and Schneider et al. 1999) have applied survival analysis to Canadian data for longevity of dairy cattle. Survival analysis has several attractive qualities in addition to its superiority over the linear model for statistical appropriateness for longevity data. First, survival analyses can readily account for censored data, which are common for longevity traits. In the current evaluation of herd life in Canada, cows must reach some milestone, such as culling or recalving, in order for their records to be included in the evaluation. Cows that are between these milestones when the data is collected for evaluation have censored records that are simply not included under the current procedures. However, the survival analysis can incorporate the information that the cow was alive at the time of data collection. This additional source of information may increase the accuracy of sire EBV. Survival analyses can also incorporate time-dependent covariates for explanatory factors that change across the lifetime of the cow. For example, cows may change their contemporary group as they move from one lactation to another or from one stage to another within a lactation. Factors that change across lactations are accounted for in the Canadian evaluation by the multiple trait definition of survival in each lactation, but additional traits would be required to account for changes within lactations. The survival analysis also tends to give greater estimates of heritability than does the linear model when both estimates are expressed on the linear scale (Boettcher et al. 1999), suggesting increased reliability of sire EBV and increased selection accuracy. Boettcher et al. (1999) also reported slightly lower correlations between sire EBV from survival analysis and the linear model (0.90 to 0.94) than between the linear model and threshold model (0.98). Therefore, noticeable and potentially meaningful differences in sire ranking would result with a change from a linear model to a survival analysis. Finally, software for survival analysis is readily available (Ducrocq and Sölkner 1994) and well tested with dairy cattle data.

Genetic evaluation with a survival analysis may have some disadvantages relative to the linear model, however. First, computing requirements tend to be greater, both in terms of memory and time. This factor may limit genetic evaluation with survival analysis to a sire model rather than an animal model. Animal models are the standard for genetic evaluation of production traits and are preferred over sire models because they help account for nonrandom mating. Because herd life receives much less emphasis in selection than does production, nonrandom mating with respect to herd life is likely to be less common than for production, for which assortative mating is often practiced. An animal model was shown to yield slightly biased estimates of genetic variance when using the survival analysis (Ducrocq and Casella 1996) but this may not necessarily equate to bias or reranking of sires.

A second potential drawback of the survival analysis is that the common approach based on days of productive life assumes that survival is the same genetic trait throughout life. Results of Jairath and Dekkers (1994) and Boettcher et al. (1999) indicated that genetic correlations between survival in lactations 1, 2, and 3 were less than unity. Theoretically, genetic effects could be modeled as time dependent covariates or perhaps with random regression approaches (e.g. Jamrozik et al. 1997), but the application of such a model may be difficult. One option that will be explored in Canada to account for differences in genetic traits across the lifetime is a multiple-trait analysis that combines a survival analysis with a linear or threshold model. Korsgaard et al. (1998) developed a Bayesian procedure for survival analysis and reported that the procedure could be extended to include correlated quantitative or categorical traits. Survival analysis would be applied to days of productive life over a cow's complete lifetime and another trait expressed early in life, such as survival through first lactation would be analyzed with a linear or threshold model.

3.3. Opinions of Canadian breeders

Results of research on the survival analysis have been presented to leaders of the dairy breeding industry in Canada and feedback from breeders and A.I. companies has been positive. Appealing factors are the reported higher estimates of heritabilities and the potential to include information about survival in lactations >3. Although survival in the first 3 lactations accounts for >65% of the economic value of lifetime survival (Dekkers 1995), is highly correlated with survival in later lactations, and is recorded earlier than is information about later lactations, Canadian breeders put a high perceived value on cows that can withstand culling for many lactations. Also, additional support for survival

analyses stem from their adoption by other countries for analysis of longevity (Ducrocq and Sölkner 1998). International evaluation of sires for production traits is common practice and the future application of cross-country evaluation for functional traits will be simplified if all countries employ similar procedures in domestic evaluations.

Some breeders have expressed interest in the evaluation of lifetime milk production rather than, or in addition to, the simple number of days, months, or lactations survived. A survival analysis would be ideal for such an application. Alternatively, information in addition to production could be accounted for with an analysis of a profit or relative net income trait, such as that developed by Weigel et al. (1995). These traits are expected to have heritabilities of magnitudes between production and longevity traits and are expected to be robust (Meuwissen and Goddard 1997).

The precise future of the Canadian evaluation for herd life is unknown, but will be directed by results of research both in Canada and across the globe.

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