Genetic Analysis of Herd Life in Canadian Dairy Cattle on a Lactation Basis Using a Weibull Proportional Hazards Model

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ABSTRACT

The objectives of this study were to identify the most important factors that influence functional survival and to estimate the genetic parameters of functional survival for Canadian dairy cattle. Data were obtained from lactation records extracted for the May 2002 genetic evaluation of Holstein, Jersey, and Ayrshire breeds that calved between July 1, 1985 and April 5, 2002. Analysis was performed using a Weibull proportional hazard model, and the baseline hazard function was defined on a lactation basis instead of the traditional analysis of the whole length of life. The statistical model included the effects of stage of lactation; season of production; the annual change in herd size; type of milk recording supervision; age at first calving; effects of milk, fat, and protein yields calculated within herd-year-parity deviations; and the random effects of herd-year-season of calving and sire. All effects fitted in the model had a significant effect on functional survival of cows in all breeds. Milk yield was by far the most important factor influencing survival, and the hazard increased as the milk production of the cows decreased. The hazard also increased as the fat content increased compared with the average group. Heifers that were older at calving were at higher risk of being culled, and expanding herds were at lower risk of being culled compared with stable herds. More culling was found in unsupervised herds than in supervised herds. The heritability values obtained were 0.14, 0.10, and 0.09 for Holstein, Jersey, and Ayrshire, respectively. Rank correlation between estimated breeding values (EBV) obtained from the current national genetic evaluation of direct herd life and the survival kit used in this study ranged from 0.65 to 0.87, depending on the number of daughters per sire. Estimated genetic trend obtained using the survival kit was overestimated.

(**Key words:** Canadian dairy breed, survival analysis, functional herd life)

INTRODUCTION

Longevity is a highly desirable trait that considerably affects overall profitability (Congleton and King, 1984; Allaire and Gibson, 1992). With increased longevity, the mean production of the herd increases because a greater proportion of the culling decisions are based on production, and the proportion of mature cows, which produce more milk than young cows, is increased. Further, the economic importance of herd life compared with milk production is considered higher than other nonproduction traits (Rogers and McDaniel, 1989; Van Arendonk, 1991; Allaire and Gibson, 1992; Dekkers, 1993).

Longevity can be measured in several ways (VanRaden and Klaaskate, 1993; Brotherstone et al., 1998; Vollema and Groen, 1998), and genetic evaluation systems are not standardized across countries, making the comparison of sire rankings difficult. In Canada, for instance, the survival of cows in each of the first 3 lactations is recorded as a binary trait and evaluated with a multiple-trait linear animal model in which survival in each lactation is considered as a separate trait (Jairath et al., 1998). However, linear models are not optimal for analysis of binary traits (Kalbfleisch and Prentice, 1980). In addition, survival times typically have a skewed distribution, and analysis using traditional linear models may not be appropriate. Moreover, with the current genetic evaluation of herd life (Jairath et al., 1998), a 2-yr opportunity window is used to determine whether a subsequent calving occurred. This results in a lag time of ≥ 2 yr when evaluating the survival of each daughter. Further, at the time of genetic evaluation of a cow, we know only the lower bound of each animal's productive life, and excluding such records or considering them as complete would lead to a bias. Survival analysis using a proportional hazard model as suggested by Smith and Quaas (1984) is an alternative method for evaluation of sires based on the length of productive life of their daughters. Ducrocq et al. (1988)

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showed that proportional hazard models could be used for the analysis of length of productive life. Ducrocq and Solkner (1998) developed the survival kit typically used by animal breeders for large populations. Survival analysis combines information on uncensored and censored records, which enables a proper statistical treatment of censored records and accounts for the nonlinear characteristic of longevity data. It also offers several advantages over the linear model that is currently used in Canada, including 1) precision can be increased by accounting for differences in days of productive life between cows that survive for the same number of lactations, 2) censored records eliminate the need to wait for 2 yr before using a lactation record, and 3) higher estimates of heritability are yielded in comparison with the linear model, suggesting increased reliability of sire EBV.

In view of its advantages, routine genetic evaluation of sires based on survival analysis was implemented in several European countries, including France (Ducrocq, 1999), Germany (Pasman and Reinhardt, 1999), The Netherlands (Vollema et al., 2000), Italy (Schneider et al., 2000), and Switzerland (Vukasinovic et al., 2001). In these countries, genetic evaluation of sires for survival of their daughters is based on fitting the model with stage by lactation as a time-dependent covariate. Stage of lactation is included in the model to account for changes in culling risk within lactation (Ducrocq, 2002). The sole baseline hazard function cannot account for these changes over time. Roxstrom et al. (2003), however, reparameterized the model and defined the baseline hazard function on a lactation basis. The results showed a better overall fit of the model and also a reduced number of stages of lactation.

The objectives of this study were 1) to assess the most important factors influencing the herd life in Canadian dairy breeds, 2) to estimate genetic parameters for longevity, and 3) to compare sire EBV between the results of the survival kit and the current genetic evaluations for herd life in the Holstein breed.

MATERIALS AND METHODS

Data were obtained from lactation records extracted for the May 2002 genetic evaluation of Holstein, Jersey, and Ayrshire breeds. The first 10 lactation records on cows that calved from July 1, 1985 to April 5, 2002 were used for parameter estimation. Length of productive life t was defined as time (days) from one calving to the next calving, death, or culling, and the record is censored if the cow has a next calving. Censored records represented cows being sold, exported, or leased to another herd or cows still in the herd. A lifetime record was considered to be completed (uncensored) if the cow

received a termination code, indicating that she was either culled or died for any reason. Cows changing herds during their productive life were considered right censored. Records associated with missing sire identification, incorrect calving dates, age at first calving outside the 18- to 40-mo range, and records from herds with <30 cows in Holstein and 20 cows in Jersey and Ayrshire were excluded from the analysis. Detailed description of the data sets used for parameter estimation for each breed is shown in Table 1.

The following model was used:

$$\lambda(t) = \lambda_{0,s}(t) \exp\{x'_m(t)\beta + z'_m u\}$$

where $\lambda(t)$ is the hazard of a cow, i.e., her probability of being culled at time t given she is alive just before t ; $\lambda_{0,s}(t) = \lambda\rho(\lambda t)^{\rho-1}$ is the Weibull baseline hazard function with scale parameter λ and shape parameter ρ and t is the time in days from one calving to the next calving for each stratum; β contains the covariates affecting the hazard with $x'_m(t)$ being the corresponding design vectors and u the vector of random variables with associated incidence vector z'_m .

The fixed covariates included in the model were as follows: time-dependent effect of stage of lactation in days (1 = 0 to 80; 2 = 81 to 235; 3 >235); effect of year and season of calving with year of calving from 1985 to 2002 (seasons of calving were January–March, April–June, July–September, and October–December); effect of season of production with the same definition as seasons of calving; effect of the annual change in herd size with 3 classes (decreasing = for a decrease in herd size of <–5%; nearly unchanged = no appreciable change $\geq$ –5% to $\leq$ 10%; and increasing = for increasing in herd size of >10%); effect of the type of milk recording supervision with 3 classes (unsupervised, supervised, and unknown = records that do not fulfill the minimum criteria set by the milk recording agency); effect of age at first calving in months; and effects of milk, fat, and protein yields. The latter effects were calculated as within herd-year-parity deviations with 3 classes for each: low = cows producing <0.4 SD below the herd-year-parity average; average = cows producing between 0.4 SD below and 0.6 SD above the herd-year-parity average; and high = cows producing >0.6 SD of the herd-year-parity average.

The random effects included were the effect of herd-year-season class that was assumed to follow a log-gamma distribution, and its effect was algebraically integrated out according to Ducrocq and Casella (1996). The genetic effect of the cow's sire is assumed to follow a multivariate normal distribution with mean zero and variance $A\sigma^2_s$, where σ^2_s is the variance among sires and A is the relationship matrix. Herd-year-season ef-

Table 1. The structure of the data sets used for parameter estimation in Holstein, Ayrshire, and Jersey breeds.

Breed	Minimum herd size	Sire: minimum number of		Number of life time records	Pedigree data (sires)
		Daughters	Herds		
Holstein	30	30	20	536,478	2090
Ayrshire	20	10	5	92,627	682
Jersey	20	10	5	43,794	551

fect was algebraically integrated out and only the variance was estimated. Heritability value was calculated as $h^2 = 4\sigma^2_s / (1 + \sigma^2_{hys} + \sigma^2_s)$ according to Yazdi et al. (2002).

One baseline hazard function, $\lambda_{0,s}(t)$, was defined for each lactation (subscript 0 designates a baseline hazard and subscript s relates to stratum s). A detailed description of the model and survival analysis of longevity data in dairy cattle on a lactation basis was described by Roxstrom et al. (2003) and Ducrocq (2002). Genetic parameters obtained from the Weibull model were used to estimate the breeding values of sires. Genetic evaluation was carried out using the entire lactation of cows. A total of 34,893 sires with daughters in 16,777 herds were included in the genetic evaluation for Holsteins. The corresponding figures for Jersey were 2478 and 847, respectively, and for Ayrshire were 2923 and 1436, respectively. The analyses were performed using the survival kit (Ducrocq and Solkner, 1998). Rank correlation among sire EBV from the current genetic evaluation of direct herd life in Canada and EBV obtained from the survival kit were computed.

RESULTS AND DISCUSSION

A total of 73.4, 78.5, and 74.4% of the lactation records were right censored for Holstein, Jersey, and Ayrshire breeds, respectively. The mean censoring time and failure time, respectively, for uncensored records after first calving in the Holstein breed were 368 and 266 d. The corresponding figures for Jersey were 369 and 248 d, respectively, and for Ayrshire were 378 and 259 d, respectively. In all breeds, all effects included in the model were highly significant ($P < 0.001$). The most important change in log likelihood was observed for the effect of milk yield.

The results for fixed effects were all expressed as relative culling risks, defined as the ratio between estimated risk of being culled under the influence of certain environmental factors ($\exp(\beta_i)$ for level i) and the average risk (or reference risk), which is usually set to one ($\beta_i = 0$). Values >1 indicate higher culling risk associated with that environmental factor. Relative culling risks <1 indicate lower culling risks (i.e., increasing effect of

environmental factor on longevity). For example, if the relative culling risk for a given class is 2, it means that a cow in that class has twice the risk of being culled compared with a cow in the reference class for that effect. Conversely, if the relative culling risk for a given class is 0.5, then a cow in that particular class has a 50% less chance of being culled than a cow in the reference class.

Within herd-year-parity, milk yield deviations had the greatest influence on the culling rate. Figure 1A illustrates the relative culling risks for milk yield in the 3 breeds. The relative culling risk for cows producing 0.4 SD below the herd-year-parity mean had higher risk of being culled than average producers for milk in all breeds. High-producing cows for milk are less likely to be culled compared with the average producers in all breeds. The influence of within herd-year-parity protein yield deviations follows the same trend as that of milk yield. The relative culling risk for cows producing 0.4 SD below the herd-year-parity mean have a higher risk of being culled than do average producers for protein in all breeds. Similar results were reported by Vukasinovic et al. (2001) and Vollema and Groen (1998) and Ducrocq (1999). However, fat yield cows producing 0.4 SD below the herd-year-parity mean are less likely to be culled compared with the average producers. Cows producing above the herd-year-parity average for fat yield are more likely to be culled, particularly in Jersey breed, compared with the average producer, which is likely the result of fat-based quota system that exists in Canada.

Within each class of production, differences exist between breeds in relative culling risk for milk, fat, and protein yields (Figure 1). For instance, in Jerseys, the relative culling risk for cows producing 0.4 SD for milk production below the herd-year-parity mean are at a higher risk of being culled than the Holstein and Ayrshire breeds. On the other hand, the relative culling risk for those cows producing 0.4 SD below the herd-year-parity mean for fat production are at a lesser risk of being culled, and those cows producing 0.6 SD for fat production (Figure 1C) above the herd-year-parity average are at a high risk of being culled compared with the other breeds. Figure 1B also shows that in Jersey

Figure 1. Estimates of the relative risk of culling (RRC) within herd-year-parity class of standardized milk, protein, and fat production for Holstein (black bars), Ayrshire (white bars), and Jersey (gray bars) breeds.

cows producing 0.4 SD below the herd-year-parity mean for protein production are twice as likely to be culled compared with Holstein cows. This might be due to the fact that Jersey cows are known for their lower milk production but higher percentage of fat content compared with other breeds, and the focus in Canadian Jerseys is to increase protein content, not fat percentage. Consequently, farmers want to put more emphasis on culling on those cows producing low milk and protein yield and high fat content. Similar trends are observed in France for Holsteins, where cows in extreme classes for fat percentage are at a higher risk of culling (V. Ducrocq, 2004, personal communication).

The effect of age at first calving did not have a large influence on the length of productive life, although a linear increase of relative culling risk was observed as age at first calving increased (Figure 2). The risk of being culled was higher for older heifers than heifers

calving at an age between 24 and 28 mo in all breeds. Late calvings are presumably caused by some problems associated with herd management, fertility, or other health problems, and these factors are likely to increase the risk of culling. Moreover, cows with delayed calvings are less profitable owing to higher rearing costs. Figure 2 also shows a trend toward a higher risk of culling for cows first calving at <21 mo of age; presumably, younger cows are at a greater risk for dystocia (Martinez et al., 1983). In studies of Ducrocq (1994) and Ojango et al. (2002), the effect of age at first calving was not significant. However, Ducrocq (1998) and Rogers et al. (1991), found that productive life decreased with an increased age at first calving.

The change in herd size had the least impact on the change in the log likelihood compared with the other main effects. The annual change in herd size was associated with relatively higher risk of culling in shrinking herds compared with stable herds. Those herds with annual increase in size had also lower culling rates than the stable herds in Holstein and Jersey breeds (Table 2). However, the differences among the 3 classes were small in all breeds. Similar results were reported by Ducrocq (1999) and Pasman and Reinhardt (1999). However, Durr et al. (1999), analyzing the Quebec data, observed that the relative culling risk for both shrinking herds and expanding herds was high compared with the stable herds.

The relative culling risk associated with the type of milk recording supervision for Holstein and Ayrshire breeds shows that cows in unsupervised herds had 1.12 and 1.21 times higher risk of being culled than cows in supervised herds, respectively (Table 2). This result indicates that culling decisions in Canadian Holstein and Ayrshire dairy breeds differ according to the type of milk-recording supervision. Presumably, this is related to the fact that supervised herds desire official lactation records and genetic indexes, as they are interested in the sale of breeding stock. In the Jersey breed, however, the difference between the two types of milk recording was negligible.

Table 2 also shows a systematic difference in relative culling risk among seasons of production in Holstein and Jersey breeds. Cows were 22 and 25% more likely to be culled just before the end of quota year (April to June) than after the beginning of the new quota year (July to September) in Holstein and Jersey breeds, respectively. No appreciable difference was observed in relative culling risk across seasons of production in Ayrshires.

Genetic Parameters

The estimates of sire variances, heritabilities, and the shape and scale parameters of the Weibull model

Figure 2. Estimates of the relative risk of culling (RRC) at age of first calving for Holstein (—○—), Ayrshire (—△—), and Jersey (—×—) breeds.

are presented in Table 3. The sire variances obtained in this study ranged from 0.039 to 0.046 across the 3 breeds, indicating that no appreciable differences existed in sire variance across the breeds. The sire variances obtained in this study are slightly different from those estimates obtained by Boettcher et al. (1999) and Durr et al. (1999), possibly owing to differences in the selection of data. Roxstrom et al. (2003) and Ducrocq (2002) also reported similar sire variances. Sewalem and Kistemaker (2001), working on the same data but fitting only one baseline hazard function for the entire length of life, also reported a similar sire variance (0.049). As shown in Table 3, the shape and scale parameters are slightly different across the breeds, which may indicate that there is a different overall change in

culling risk over time in each population. However, both Weibull parameters are consistent within the range of literature reports (Ducrocq and Solkner, 1998; de Jong et al., 1999; Durr et al., 1999; Roxstrom et al., 2003).

The heritability values found in this study (ranging from 0.09 to 0.14) are within the range of studies using the Weibull model (Ducrocq and Solkner, 1998; de Jong et al., 1999; Durr et al., 1999; Roxstrom et al., 2003). The higher herd-year-season variance in Jersey and Ayrshire breeds compared with the Holstein breed may be because these breeds are smaller in population size and if a sire has few daughters in several herds, and this may cause an inflation of the environmental variances or it may be due to breed characteristics.

Using the parameters obtained from the analyses, breeding value for sires were estimated, and results are presented only for the Holstein breed. Sires were compared with the same number of observations (i.e., number of daughters uncensored for survival analysis and number of daughters survived for the current genetic evaluation of direct herd life). The rank correlation between EBV obtained from the survival kit and the current genetic evaluation of direct herd life ranged from 0.67 to 0.87, depending on the number of daughters per sire (Figure 3). The rank correlations increased as the number of daughters increased. Boettcher et al. (1999) and Durr et al. (1999) reported a correlation of 0.72 and 0.66, respectively, between sire EBV estimated using the current Canadian official rating for herd life and EBV estimated from a Weibull model. These correlations are less than the result found in the present study. Moreover, the present study includes all lactations instead of the first 3 lactations used in the previous studies.

Table 2. Relative culling risk for different groups of herd size variation, type of milk recording, and season of production in Holstein, Ayrshire, and Jersey breeds.

Effect	Breed		
	Holstein	Ayrshire	Jersey
Herd size variation			
Decreasing	1.06	1.13	1.08
Nearly unchanged (stable)	1.00	1.00	1.00
Increasing	0.99	1.03	0.96
Type of milk recording			
Unsupervised	1.14	1.21	1.02
Supervised	1.00	1.00	1.00
Unknown	1.57	1.65	1.46
Season of production ¹			
July–September	1.00	1.00	1.00
October–December	1.09	1.04	1.01
January–March	1.16	1.01	1.12
April–June	1.22	1.05	1.25

¹Quota year commences in July of each year.

Table 3. Estimates of the Weibull shape parameter (ρ), scale parameter (λ), gamma parameter (γ), sire and herd-year-season variances, and heritability for Holstein, Ayrshire, and Jersey breeds.

Lactation no.	Breed					
	Holstein		Ayrshire		Jersey	
	ρ	λ	ρ	λ	ρ	λ
1	1.68	0.0013	1.78	0.0013	1.58	0.0016
2	1.78	0.0016	1.89	0.0015	1.67	0.0017
3	1.68	0.0017	1.90	0.0017	1.55	0.0018
4	1.61	0.0020	1.80	0.0018	1.49	0.0020
5	1.54	0.0022	1.75	0.0020	1.34	0.0022
6+	1.43	0.0028	1.65	0.0024	1.29	0.0028
γ	3.967		1.9190		2.453	
σ^2_{hys}	0.28649		0.6792		0.5016	
σ^2_{s}	0.046		0.039		0.040	
h^2	0.14		0.09		0.10	

The mean estimated breeding value for longevity of Holstein sires using the Weibull model and the current genetic evaluation for direct herd life is presented in Figure 4. The genetic trends for both methods increased steadily over years. The estimated genetic gain for functional herd life for the 1985 to 1995 birth year was 0.062 and 0.014 for the survival kit and the current herd life, respectively. Moreover, the genetic trend per year obtained from the Weibull model using the survival kit was higher than the genetic trend obtained from the linear animal model, and this higher genetic trend is particularly exaggerated for young bulls. The overestimation of genetic trend obtained from the survival kit may be related to the fact that the model assumes that the baseline hazard function within each lactation is constant over time. Ducrocq (2004, personal communication) observed the same overestimation of

genetic trend with a similar model. The latter model proved to be better for an indirect validation approach (Ducrocq et al., 2003). The possible explanation may be the fact that with increased milk production and increased calving interval caused by poor fertility animals might be subject to culling later within lactation. This later culling not being accounted for in model might have resulted in an overestimation of the genetic trend.

Even so, rank correlation of EBV obtained from the 2 methods was relatively low if one considered that they referred to different definitions of the same trait. This shows that there is a difference between the 2 methods of analyzing longevity data but it does not show which method is a better approach than the other. Generally, the use of a better model, which dissociates the additive genetic variance from the environmental variance, would result in a higher heritability value of a trait. Survival analysis generally provides better fit to the survival data because of their ability to properly account for censored and truncated records, their ability to account for the skewed distribution of survival data, and the way-time dependent covariates were accommodated may be the factors that contributed for the sire re-rankings. Moreover, analysis of failure-time data on a lactation basis has also given a better fit of the model and reduced computing time (Ducrocq, 2002; Roxstrom et al., 2003). On the other hand, the linear-animal model approach seems simple to implement; however, it may be less appropriate for the analysis of survival data.

Figure 3. Rank correlation of sire estimated breeding values obtained from the survival kit (Ducrocq and Solkner, 1998) and the current genetic evaluation for direct herd life in Canada (Jairath et al., 1998) for Holsteins.

CONCLUSIONS

Survival analysis on a lactation basis was successfully used to describe the longevity data of Canadian dairy breeds for genetic evaluation of herd life. This approach leads to a simpler data handling, reduced

Figure 4. Genetic trends of longevity (in genetic standard deviations) using the survival kit (—○—; Ducrocq and Solkner, 1998) and the current genetic evaluation for direct herd life in Canada (—■—; Jairath et al., 1998) for the Holstein breed. EBV = estimated breeding value.

number of elementary records, and hence, reduced computational time compared with a survival analysis across lactations. In all breeds, all effects fitted in the model had a significant effect on longevity, and milk yield was one of the largest contributing factors for culling. In all breeds, cows that produce low milk and protein yields were at a higher risk of being culled, while low-producing cows for fat content were at lower risk of being culled compared with the average group. Heifers calving >28 mo of age were at higher risk of being culled. Cows in shrinking herds were also at higher risk of being culled compared with cows in stable herds. Cows were likely to be culled before the end of the quota year in Holsteins and Ayrshires. More culling was found in unsupervised herds compared with supervised herds. The heritability values found were slightly different among the 3 breeds ranging from 0.09 to 0.14. Rank correlation between the national evaluations for direct herd life and EBV from the survival kit ranged from 0.65 to 0.87, which implied that the 2 methods would necessarily result in different genetic selection responses. However, the correlation obtained in the present study was slightly higher than previously reported results. Genetic trends obtained from the survival kit were overestimated particularly for young bulls.

REFERENCES

- Allaire, F. R., and J. P. Gibson. 1992. Genetic value of herd life adjusted for milk production. *J. Dairy Sci.* 75:1349.
- Boettcher, P. J., L. K. Jairath, and J. C. M. Dekkers. 1999. Comparison of methods for genetic evaluation of sires for survival of their daughters in the first three lactations. *J. Dairy Sci.* 82:1034–1044.
- Brotherstone, S., R. F. Veerkamp, and W. G. Hill. 1998. Predicting breeding values for herd life of Holstein-Friesian dairy cattle from lifespan and type. *J. Anim. Sci.* 67:405–411.
- Congleton, W. R., Jr., and L. W. King. 1984. Profitability of dairy cowherd life. *J. Dairy Sci.* 67:661–674.
- de Jong, G., A. R. Vollema, S. van der Beek, and A. Harbers. 1999. Breeding value for functional longevity in the Netherlands. *Proc. Int. Workshop on EU Concerted Action Genetic Improvement of Functional Traits in Cattle (GIFT); Longevity*, Jouy-en-Josas, France XX:68–72.
- Dekkers, J. C. M. 1993. Theoretical basis for genetic parameters of herd life and effects on response to selection. *J. Dairy Sci.* 76:1433–1443.
- Ducrocq, V. 1994. Statistical analysis of length of productive life for dairy cows of the Normande breed. *J. Dairy Sci.* 77:855–866.
- Ducrocq, V. 1999. Two years of experience with the French genetic evaluation of dairy bulls on production-adjusted longevity of their daughters. *Proc. Int. Workshop on EU Concerted Action Genetic Improvement of Functional Traits in Cattle (GIFT); Longevity*, Jouy-en-Josas, France XXI:60–67.
- Ducrocq, V. 2002. A Piecewise Weibull mixed model for the analysis of length of productive life of dairy cows. *Proc. 7th World Congr. Genet. Appl. Livest. Prod.*, Montpellier, France XX:04.
- Ducrocq, V., and G. Casella. 1996. A Bayesian analysis of mixed survival models. *Genet. Sel. Evol.* 28:505–529.
- Ducrocq, V., I. Delaunay, D. Biochard, and S. Mattalia. 2003. A general approach for international evaluations robust to inconsistencies of genetic trends in national evaluations. *Proc. Int. Tech. Workshop*, Beltsville, MD XXX:101–111.
- Ducrocq, V., R. L. Quaas, E. J. Pollak, and G. Casella. 1988. Length of productive life in dairy cows. 1. Justification of a Weibull model. *J. Dairy Sci.* 71:3061.
- Ducrocq, V., and J. Solkner. 1998. The Survival Kit, V3.12: A package for large analyses of survival data. Pages 447–450 in *Proc. 6th World Congr. Genet. Appl. Livest. Prod.*, Armidale, Australia.
- Durr, J. W., H. Monardes, and R. I. Cue. 1999. Genetic analysis of herd life in Quebec Holsteins using Weibull models. *J. Dairy Sci.* 82:2503–2513.
- Jairath, L., J. C. M. Dekkers, L. R. Schaeffer, Z. Liu, E. B. Burnside, and B. Kolstad. 1998. Genetic evaluation for herd life in Canada. *J. Dairy Sci.* 81:550–562.
- Kalbfleisch, J. D., and R. L. Prentice. 1980. *The Statistical Analysis of Failure Time Data*. John Wiley & Sons, Inc., New York, NY.

- Martinez, M. L., A. E. Freeman, and P. J. Berger. 1983. Genetic relationship between calf livability and calving difficulty of Holsteins. *J. Dairy Sci.* 66:1494–1502.
- Ojango, J. M. K., V. Ducrocq, and G. E. Pollott. 2002. Length of productive life for Holstein-Friesian cows raised on large-scale farms in Kenya. *Proc. 7th World Congr. Genet. Appl. Livest. Prod.*, Montpellier, France I:33.
- Pasman, E., and F. Reinhardt. 1999. Genetic evaluation for length of productive life of Holstein Cattle in Germany. *Proc. Int. Workshop on EU Concerted Action Genetic Improvement of Functional Traits in Cattle (GIFT)*. Longevity, Jouy-en-Josas, France XXI:55–59.
- Rogers, G. W., G. L. Hargrove, J. B. Cooper, and E. P. Barton. 1991. Relationships among survival and linear type traits in Jerseys. *J. Dairy Sci.* 74:286–291.
- Rogers, G. W., and B. T. McDaniel. 1989. The usefulness of selection for yield and functional type traits. *J. Dairy Sci.* 72:187.
- Roxstrom, A., V. Ducrocq, and E. Strandberg. 2003. Survival analysis of longevity in dairy cattle on a lactation basis. *Genet. Sel. Evol.* 35:305–318.
- Schneider, M. P., F. Canavesi, and A. B. Samore. 2000. Genetic evaluation for functional herd life in Italian Holstein. 51st Annu. Mtg. EAAP, Den Haag, The Netherlands 6:34.
- Sewalem, A., and G. Kistemaker. 2001. Genetic evaluation of herd life in Canadian dairy cattle. Technical report to the genetic evaluation board. Online. Available: <http://cgil.uoguelph.ca/dcbgc>. Accessed Jan. 1, 2004.
- Smith, S. P., and R. L. Quaas. 1984. Productive lifespan of bull progeny groups: Failure time analysis. *J. Dairy Sci.* 67:2999–3007.
- Van Arendonk, J. A. M. 1991. Use of profit equations to determine relative economic value of dairy cattle herd life and production from field data. *J. Dairy Sci.* 74:1101–1107.
- VanRaden, P. M., and E. J. H. Klaaskate. 1993. Genetic evaluation of length of productive life including predicted longevity of live cows. *J. Dairy Sci.* 76:2758–2764.
- Vollema, A. R., and A. F. Groen. 1998. A comparison of breeding value predictors for longevity using a linear model and survival analysis. *J. Dairy Sci.* 81:3315–3320.
- Vollema, A. R., S. van der Beek, A. G. F. Harbers, and G. de Jong. 2000. Genetic evaluation for longevity of Dutch dairy bulls. *J. Dairy Sci.* 83:2629–2639.
- Vukasinovic, N., J. Moll, and L. Casanova. 2001. Implementation of a routine genetic evaluation for longevity based on survival analysis techniques in dairy cattle populations in Switzerland. *J. Dairy Sci.* 84:2073–2080.
- Yazdi, M. H., P. M. Visscher, V. Ducrocq, and R. Thompson. 2002. Heritability, reliability of genetic evaluations and response to selection in proportional hazard models. *J. Dairy Sci.* 85:1563–1577.