Introduction

Longevity (also called herd life or survival) is a trait with a significant impact on the profitability of dairy cows (Allaire & Gibson 1992). Improved longevity can result in decreased replacement costs and a higher proportion of mature cows in a herd. Ability of a cow to withstand involuntary culling is called functional longevity, and this trait is usually a subject of genetic improvement. Many different terms and statistical models have been used to describe the likelihood that an animal will remain in the herd longer than the other animals. Genetic evaluation models for survival traits are not standardized across populations, which makes the comparison of sire rankings difficult (INTERBULL 2007). Exact or approximated date of culling of a cow is usually a basis for definition and expression of survival traits. From this date, several different measures of survival could be derived. They include age at disposal, survival to a given age or in predefined time period (e.g. lactation), defined as binary (with values of 0 or 1) traits.

Proportional hazard (PH) model (Ducrocq et al. 1988) has been adopted by a majority of countries for the analysis of survival traits in dairy cattle. This model attempts to estimate the probability that an animal will remain in the herd longer than a randomly selected cow.
animal will survive to time \( t \) given that it has survived to time \( t-1 \). Implementations of this model are restricted to a single-trait sire model, and the Weibull function is used for modelling the baseline hazard. Advantages of PH models include accounting for censoring and the possibility of time-dependant environmental effects in the model. Only one genetic effect (sire effect) is usually fitted for each animal during its whole lifetime.

The second most popular genetic evaluation model for survival is a multiple-trait (MT) animal model, with traits defined as a survival (0 or 1) to certain end-points or within certain time intervals in a cow’s lifetime (Madgwick & Goddard 1989). The Canadian model for herd life (Sevalem et al. 2007) includes five correlated traits defined as: survival from first calving to 120 days in milk (DIM), from 120 to 240 DIM, from 240 DIM to second calving and survival through third and fourth lactations. Linear models are usually used for the analysis of these binary traits. Censored records are either not included in the analyses or treated as missing data in the model.

A longitudinal generalization of multiple-trait models for survival can be achieved through a random regression (RR) model proposed by Veerkamp et al. (1999). Binary observations (0 = culled, 1 = survived) are assigned to each discrete unit in the cow’s lifetime, such as per lactation or per month after first calving. A linear model with RRs for an animal genetic effect can be fitted to this data for genetic evaluation purposes. Breeding values for survival can be generated for both cows and sires and for each point on the trajectory. Veerkamp et al. (1999) showed that a RR model for survival traits was relatively robust to censoring of the data.

Galbraith (2003) applied the above models to the analysis of survival data to Canadian Ayrshire and Jersey breeds and concluded that different models gave different rankings of animals, but could not determine which model was better for genetic improvement. Comparison of competing methodologies for survival data is difficult because of the differences in trait and model definitions.

The objective of this research was to compare the three methods: MT, RR and PH models, for genetic evaluation of survival in dairy cattle through a simulation study. Models were ranked according to accuracy of sire evaluation, estimated as the correlation between true and estimated breeding values (EBV) for survival traits. Predictive abilities of different models were assessed through correlations between EBV and the proportion of sire’s daughters that survived to a given time.

**Material and methods**

**Simulation**

The empirical survival curve for the Canadian Jersey breed (Galbraith 2003) describes the probability that a cow is alive in a given month after the first calving. A plot of this curve for months from 1 to 100 after first calving is given in Figure 1. The same Figure shows the plot of genetic variance for survival of Jersey cows in months 1 to 100 after the first calving, estimated from the RR model (Galbraith 2003). Those two curves were the input parameters for the simulation of survival data in this study. Permanent environmental (PE) effects for survival were assumed to have the same variance as genetic effects. Heritability for survival was constant in each month after first calving, implying that the residual variance followed the shapes of the genetic and PE monthly variances.

![Figure 1](image-url)  
**Figure 1** Empirical survival curve and genetic variance of survival by month after first calving.
animal. Trait X (approximating a continuous production trait) was normally distributed with mean 0, heritability of 0.3 and a phenotypic variance equal to 100. The second, uncorrelated trait, Y, was the time of culling of an animal, defined in the interval from 1 to 100 months after the first calving. Simulation of phenotypes for X consisted of generating additive genetic and residual components from standard normal distributions. For time of disposal, Y, the overall additive genetic (a), PE (p) and residual (e) components were simulated for each animal as variables from a normal distributions with mean zero and variance of 1. An animal-specific threshold for the i-th month was defined as follows:

$$T(i) = H(i) + a \sigma_a(i) + p \sigma_{PE}(i) + e \sigma_e(i),$$

where $\sigma_a(i)$, $\sigma_{PE}(i)$ and $\sigma_e(i)$ are genetic, PE and residual standard deviations for hazard in the i-th month respectively. Variable $G(i) = a \sigma_a(i)$ will be referred to as the true genetic value for the hazard. A random deviate ($d$) from a standard normal distribution N(0,1) was subsequently generated for a given animal. The month of culling for an animal was defined as the smallest $i$ for which the value of $T(i)$ was not smaller than $d$.

Several other binary phenotypes corresponding to survival in different time intervals from 1 to 100 months after the first calving were further generated based on the value of month of culling for a given cow, following Canadian genetic evaluation model for survival traits (Sevalem et al. 2007). Finally, a month of culling was used to define a 100 elements vector of 0 and 1 for each cow, determining whether she was alive (1) or dead (0) in a given month after the first calving for the RR model.

Three levels of heritability (0.100, 0.050 and 0.025) of survival and two levels of number of females per generation (2000 and 4000) were considered in the simulation. Number of males per generation was equal to 100 in each case. Starting from the base generation of 2100 or 4100 animals, 19 generations of selection and mating were simulated. The length of each selection and mating cycle was set to 13.2 months, which was the length of the average calving interval for Canadian Jerseys (Miglior & Van Doormaal 2005). Selection of males and females was based on phenotypes for trait X that was available for both sexes. Survival was therefore independent of trait X and can be treated as a functional survival. Sires were assigned to dams randomly. Semen supply was assumed to be unlimited and the best sires were selected across generations regardless of age. The top surviving females in the population for the trait X were used as dams in the next cycle of matings. Each mating resulted in one progeny with sex ratio equal to 0.5. Twenty one replicates were generated for each of the six scenarios (i.e. three heritability levels times two female population size levels). Simulation scenarios will further be denoted as $h^2xY$, where $x$ stands for the heritability level and $y$ is the number of females per generation. For example, $h^2(0.100)$ F(2000) is the simulation scenario with $h^2 = 0.100$ and female population size equal to 2000.

Estimation of breeding value

Three models were applied to the simulated survival data for the purpose of estimating breeding values for sires. Only survival data on females were used following schemes practiced in dairy cattle breeding. The models were as follows:

**Proportional Hazard model**

$$h_{ik}(t) = h_0(t) \exp(\mu_j + s_i),$$

where $h_{ik}(t)$ is the hazard of the k-th daughter of the j-th sire in the j-th generation, i.e. her probability of being culled at time $t$ given she was alive just before $t$, $h_0(t)$ was a Weibull baseline hazard function, $\mu_j$ is the fixed effect of the j-th generation, $s_i$ was the random (normally distributed) effect of the i-th sire. The PH model does not include a residual term because in the survival model the residual variability is modelled through the survival distribution. Data for this model were month of culling for cows. Censored records (i.e. cows still alive at the moment of analysis) were included. Sire and maternal-grand sire relationships were used to account for covariances between sires.

**Linear Multiple-Trait (MT) animal model**

$$y_{ij} = \mu_j + a_{ik} + e_{ijk},$$

where $y_{ij}$ is the observation for survival (0 or 1) of the i-th trait of the k-th cow, $\mu_j$ is the fixed effect of the j-th generation for trait i, $a_{ik}$ is the random additive genetic effect of cow k for trait i and $e_{ijk}$ is random residual effect. All random effects of the model were assumed to be normally distributed. Traits ($i = 1–5$) were as follows: survival from first calving to 120 DIM, survival from 120 to 240 DIM, survival from 240 DIM to second calving, survival through second lactation and survival through third lactation.
Survival in each of the five traits was coded as 0 if the cow was culled during that time period, or as 1 if the cow survived that time period. If the cow did not have an opportunity to begin or complete a given time period, then the observation was missing. Observations for different traits were correlated through genetic and residual effects. All covariances between animals were accounted for by a full additive relationship matrix.

**Random Regression animal model**

\[ y_{jkt} = \sum_{m=0}^{4} \beta_{jm} z_{tm} + \sum_{m=0}^{4} q_{km} z_{tm} + \sum_{m=0}^{4} p_{km} z_{tm} + \epsilon_{jkt}, \]

where \( y_{jkt} \) is the survival observation (0 or 1) on cow \( k \) at month \( t \) after first calving, \( \beta_{jm} \) are fixed regression coefficients specific to \( j \)th generation, \( q_{km} \) are random additive genetic coefficients specific to cow \( k \), \( p_{km} \) are random PE coefficients specific for cow \( k \), and \( \epsilon_{jkt} \) is the random residual effect for each observation and \( z_{tm} \) are covariates. All random effects of the model were assumed to be normally distributed. Orthogonal Legendre polynomial of order four were used for all fixed and RRs. The selection of order of polynomials for fixed and RR was based on the results of Galbraith (2003). Each cow had up to 100 binary observations for each of 100 months after the first calving. Censored records were treated as missing data in the model. Residuals for different months were assumed uncorrelated, and a different residual variance was allowed for every month after the first calving. All additive relationships among animals were included in the analyses.

Covariance components for each model were estimated using the same models and the first replicate of the simulated data, for three levels of heritability and the scenarios with 2000 females per generation only. Covariances were kept constant for genetic evaluation models for replicates two through 21. The Survival Kit (Ducrocq & Sölkner 1994) was used for the PH model. Covariances for MT and RR models were estimated using Gibbs sampling. Posterior means of 100 000 samples after 20 000 burn-in iterations were used as estimates. Standard Gaussian assumptions were applied to a Bayesian specification of MT and RR models.

Estimates of breeding values for sires for all simulation scenarios and all 20 replicates were obtained for all three models. The Survival Kit (Ducrocq & Sölkner 1994) with constant parameters was used for the PH model. Estimates for_MT and RR models were obtained as Best Linear Unbiased Predictors (BLUP), using the iteration on data method.

**Comparison of models**

Two groups of sires of cows, with a minimum of 20 or 100 daughters with survival data, were selected for model comparison purposes. Within each model and simulation scenario, EBV were correlated with true breeding values (TBV) for each replicate, and correlations were averaged across replicates. Empirical standard deviations of average correlations were also obtained. EBV were calculated for five different time points in a cow’s life, corresponding to the thresholds in the MT model. They were 120 DIM after first calving, 240 DIM after first calving, second, third and fourth calvings. TBV for sire \( q \) at time \( t \) was equal to \( \alpha_q \sigma_q(t) \). EBV were solutions for \( s_q \) from the PH model, solutions for \( d_{tq} \) from the MT model and solutions for \( \sum_{m=0}^{4} q_{km} z_{tm} \) from the RR model. TBV for survival corresponded to the probability of culling at a given time. Larger EBV from the MT and RR models denoted higher probabilities of survival of daughters at a given point in time, and thus correlations between EBV and TBV should be negative for those two models. EBV from the PH model represented the probability of culling for a cow, and therefore, were expected to be positively correlated with the TBV. To make comparisons easier to follow, all correlations were expressed in absolute values where the higher is the correlation, the better is the model. Correlations between TBV and EBV can be used as a measure of accuracy of the genetic evaluations for each model.

Another comparison criterion was based on the percentage of a sire’s daughters that survived to each of the five described end-points. Those proportions were correlated with EBV for survival within model and simulation scenario for two groups of sires, with minimum of 20 or 100 daughters in the data. Average correlations (with standard deviations) across replicates were estimated. Correlations were expressed in absolute values and can serve as a tool to examine the predictive abilities of the three models.

Finally, EBV for sires from the different analyses were correlated to quantify differences in rankings of sires between models.

**Results**

**Data characteristics**

Average number of cows with records per replicate for simulation scenario \( h^2(0.100)F(2000) \) was
19 023, with a standard deviation (SD) of 76.3. Scenario $h^2(0.100)F(4000)$ gave on average 37 986 (SD = 157.7) cows with records. Proportions of censored cows were 13.2% (SD = 0.5) for scenario $h^2(0.100)F(2000)$ and 13.3% (SD = 0.4) for scenario $h^2(0.100)F(4000)$. Average number of sires of cows for scenario $h^2(0.100)F(2000)$ was 596 (SD = 22.9) with an average number of daughters per sire equal to 31.5 (SD = 1.2). Corresponding numbers for scenario $h^2(0.050)F(2000)$ were 633 (SD = 16.4) and 59.6 (1.7) respectively. Scenarios for other levels of heritability for survival had similar numbers of cows, censored cows, sires and average number of daughters per sire per replicate. In each replicate for simulations with 2000 and 4000 breeding females per generation, total numbers of animals were 41 100 and 80 100 respectively.

Average month of culling after first calving ranged from 34 (SD = 26.6) in generation five to 39 (SD = 27.8) in generation 18, for the data set used for estimation of covariance components and simulation scenario $h^2(0.100)F(2000)$. Averages for the production trait (X) for the same data set increased from 0.2 (SD = 10.3) in generation two to 9.2 (SD = 10.2) in generation 20, with relatively constant variance across generation. Overall phenotypic survival curve for this data set was very similar to the empirical survival curve used to simulate the data. Absolute differences between simulated and expected frequency of alive cows were not larger than 0.04 for any given month after the first calving. Similar patterns were observed for other scenarios, with slightly larger differences between simulated and expected survival curves for the two smaller levels of heritability.

Average (by replicate) number of sires with at least 20 daughters was equal to 283 (SD = 12.4) for scenario $h^2(0.100)F(2000)$ and 491 (SD = 15.4) for scenario $h^2(0.100)F(4000)$ respectively. Respective averages for the 100 daughters minimum were 35 (SD = 6.2) and 120 (SD = 5.3).

### Genetic evaluation for survival traits

Average absolute correlations (with SD) across 20 replicates between TBV and EBV of sires for survival to five points in cow’s lifetime after first calving from PH, MT and RR models for simulation scenario $h^2(0.100)F(2000)$ are given in Table 1. The highest correlations (0.60 and 0.77 for sires with minimums of 20 and 100 daughters respectively) were for the PH model, followed by RR and MT evaluations. The values of PH correlations were the same for all five time points while correlations for the other two models increased in absolute terms with time. The range of correlations (between 120 DIM and fourth calving) was slightly larger for the MT model. Bigger daughter group size resulted in higher accuracies for MT and RR models. Correlations between TBV and EBV for scenarios $h^2(0.050)F(2000)$ and $h^2(0.025)F(2000)$ are given in Tables 2 and 3 respectively. Model rankings were similar at all heritabilities.

Accuracy of genetic evaluation for survival decreased with heritability, from 0.60–0.77 for $h^2 = 0.100$ to 0.40–0.55 for $h^2 = 0.050$, for the PH model. For all three heritability levels, larger progeny groups gave better accuracy of sire evaluation for all survival traits. Accuracy of sire evaluation increased with time for RR and MT models. Smaller progeny groups gave larger variability of accuracy, measured by empirical standard deviations across replicates, than larger progeny groups. Evaluations for survival to 120 DIM were the least accurate while evaluations for survival to fourth calving were more accurate.

### Table 1

<table>
<thead>
<tr>
<th>End-point</th>
<th>MT MIN = 20 (0.07)</th>
<th>MIN = 100 (0.15)</th>
<th>RR MIN = 20 (0.07)</th>
<th>MIN = 100 (0.12)</th>
<th>PH MIN = 20 (0.05)</th>
<th>MIN = 10 (0.08)</th>
</tr>
</thead>
<tbody>
<tr>
<td>120 DIM</td>
<td>0.27</td>
<td>0.35</td>
<td>0.42</td>
<td>0.59</td>
<td>0.60</td>
<td>0.77</td>
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<tr>
<td>240 DIM</td>
<td>0.46</td>
<td>0.59</td>
<td>0.48</td>
<td>0.65</td>
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<td></td>
</tr>
<tr>
<td>2nd calving</td>
<td>0.49</td>
<td>0.61</td>
<td>0.52</td>
<td>0.68</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3rd calving</td>
<td>0.49</td>
<td>0.58</td>
<td>0.59</td>
<td>0.74</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4th calving</td>
<td>0.52</td>
<td>0.60</td>
<td>0.60</td>
<td>0.75</td>
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</tr>
</tbody>
</table>

DIM, days in milk.
showed the highest level of accuracy in the case of MT and RR models. Accuracy of the RR model reached the level of the PH model for survival to the fourth calving.

Absolute correlations (with SD) across 20 replicates between TBV and EBV of sires for survival to five points in cow’s lifetime after the first calving from PH, MT and RR models for scenario $h^2(0.050)F(4000)$ are given in Table 4. A larger female population resulted, in general, in slightly higher accuracy of genetic evaluation for all five survival traits. Similar patterns were observed at all heritability levels (results not shown). Ranking of models and time trends in accuracy were, in general, the same as those for scenarios with female population size per generation equal to 2000.
Absolute values of the correlation (with SD) between EBV from RR, MT and PH models and percentages of sire daughters (PSD) that survived to each of the five end-points for simulation scenario $h^2(0.050)F(2000)$ are shown in Table 5. Rankings of models were different from rankings based on correlations between TBV and EBV for survival. The best overall was the RR model, with the exception of 120 and 240 DIM and 100 daughters per sire, when the highest correlations were from the MT model. Model MT gave better prediction of survived daughters than the PH model for the first three time points in the cow’s lifetime. Similar rankings of models were obtained for the other two levels of heritability of survival (results not shown). For all simulation scenarios, correlations between PSD and EBV for survival from the PH model showed relatively large changes in time, from approximately 0.3 for 120 DIM to approximately 0.8 for the fourth calving, compared with less variable correlations for the two other models. This indicated relatively poorer performance of the PH model in prediction of PSD earlier in a cow’s life. Similarly to correlations between TBV and EBV, correlations between PSD and EBV decreased, in general, with decreasing heritability level. Correlations were larger for sires with larger number of daughters. There were practically no differences between prediction ability of models for scenarios with 2000 or 4000 females per generation.

Different models gave different rankings of sires with respect to survival of daughters to five end-points in cows’ life. Table 6 shows absolute values of correlations between EBV from PH, RR and MT models for simulation scenario $h^2(0.050)F(2000)$. Evaluations from MT and RR models gave more similar rankings than EBV from the other pairs of models. Estimates from the RR model were more similar to MT evaluation (except of the third and the fourth calvings) than to PH evaluations. On the other hand, EBV from the PH model were more like evaluations from the RR model. Only correlations between RR and PH evaluations showed an increasing trend in time. Other results (not shown) indicated a slight decrease in correlations between EBV from different

<table>
<thead>
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<th>End-point</th>
<th>Model</th>
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<th>MIN = 100</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>MT</td>
<td>RR</td>
<td>PH</td>
</tr>
<tr>
<td>120 DIM</td>
<td>0.66 (0.03)</td>
<td>0.73 (0.04)</td>
<td>0.28 (0.07)</td>
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<tr>
<td>240 DIM</td>
<td>0.64 (0.03)</td>
<td>0.76 (0.02)</td>
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<td>0.85 (0.04)</td>
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<td>0.76 (0.02)</td>
<td>0.92 (0.04)</td>
</tr>
<tr>
<td>4th calving</td>
<td>0.63 (0.04)</td>
<td>0.80 (0.02)</td>
<td>0.89 (0.04)</td>
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</table>

DIIM, days in milk.

<table>
<thead>
<tr>
<th>End-point</th>
<th>Models</th>
<th>MIN = 20</th>
<th>MIN = 100</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
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<td>MT-PH</td>
<td>RR-PH</td>
</tr>
<tr>
<td>120 DIM</td>
<td>0.79 (0.02)</td>
<td>0.56 (0.06)</td>
<td>0.57 (0.04)</td>
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<tr>
<td>240 DIM</td>
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<td>0.72 (0.05)</td>
<td>0.67 (0.03)</td>
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<tr>
<td>2nd calving</td>
<td>0.76 (0.02)</td>
<td>0.68 (0.05)</td>
<td>0.71 (0.03)</td>
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<tr>
<td>3rd calving</td>
<td>0.78 (0.02)</td>
<td>0.72 (0.03)</td>
<td>0.78 (0.02)</td>
</tr>
<tr>
<td>4th calving</td>
<td>0.70 (0.03)</td>
<td>0.72 (0.04)</td>
<td>0.81 (0.02)</td>
</tr>
</tbody>
</table>

DIIM, days in milk.

Table 5 Absolute values of correlation coefficients (standard deviations in brackets) between estimated breeding values from random regression (RR), multiple-trait (MT) and proportional hazard (PH) models and percentages of sire daughters that survived to each of the five end-points ($h^2 = 0.050$), two levels of minimum number of daughters per sire (MIN = 20 and MIN = 100) and number of females per generation equal to 2000

Table 6 Absolute values of correlation coefficients (standard deviations in brackets) between estimated breeding values from random regression (RR), multiple-trait (MT) and proportional hazard (PH) models, for five end-points ($h^2 = 0.050$), two levels of minimum number of daughters per sire (MIN = 20 and MIN = 100) and number of females per generation equal to 2000
models with lower level of heritability. There was no trend in relationships between EBV from different models for the two different levels of female population size.

**Discussion**

Comparison of models for analysis of survival traits in livestock animals is difficult because different traits are usually analysed by different models. The stochastic simulation approach, in which true genetic potential for survival is known, seems to be one way to assess the accuracy of different models for survival. The simulation used in this study was based on empirical parameters of the Canadian Jersey population (Galbraith 2003) and did not involve any particular model. Thus, none of the compared models was favoured through the assumptions of the simulation. The empirical survival curve and genetic variances in the interval from 1 to 100 months after the first calving were the only crucial parameters of the simulation. Genetic and PE variances were kept constant for different levels of heritability of survival. Smaller values of $h^2$ were therefore achieved by increasing the level of the residual variance at each month. Selection on an uncorrelated trait facilitated the generation of functional survival data independent of a production-dependent trait. No environmental effects were simulated which meant that the simulated populations were homogeneous in terms of management and culling practices.

Covariance components were estimated only once for each model and heritability level and were kept constant for genetic evaluations. This followed a common practice of genetic evaluation systems, where parameters for the model are estimated periodically, on smaller subsets of the data. Genetic evaluation models are relatively robust to changes in covariance components (Schaeffer 1984; Strabel & Jamrozik 2002). Gibbs sampling could have been used for estimation of covariance components and the genetic evaluation simultaneously in MT and RR models, for each of 120 replicates. This approach, however, would require much more computing time in comparison with the BLUP analyses, and therefore seemed impractical for our purposes.

A linear model was assumed for binary traits (MT and RR models), and this may not be optimal in terms of statistical correctness. However, Meijering & Gianola (1985) showed no practical differences in rankings of individuals from either a linear or a threshold model when traits were binary.

Accuracy of evaluation, measured as the correlation between TBV and EBV, in five selected time-points of cow’s life favoured the PH model over the competing models at heritability of 0.100 or lower. The time points coincided with the definition of survival traits used in the MT model in Canada. Only one evaluation for a sire was obtained from the PH model while RR and MT models had different EBV for survival to different time points. Sire solutions from the PH model and relative risk factors associated with sire effects gave identical estimates of correlations between TBV and EBV. Accuracy of evaluation for RR and MT models increased with time, and the RR model approached the accuracy of the PH model for the most distant time point (fourth calving). Higher proportions of culled cows and larger variances can explain a time-dependant increase in accuracy for RR and MT models at later ages. Constant probability of culling over the entire time interval from 1 to 100 months after calving was a limitation of the PH model. Probability of involuntary culling for a cow is likely to be variable in time. Evaluations from the PH model could therefore be overestimated at the beginning and underestimated at end of the time-scale. Accounting for time-dependant sire effects in the PH model is theoretically possible (Veerkamp et al. 1999), but has not yet been implemented in the Survival Kit software. Both RR and MT models were animal models and as such they generate EBV for all cows and sires in the data. Evaluation of animals for survival to any point on the time scale was also possible in the RR model.

Prediction of future records was another criterion that was used for model comparisons in this study. Results indicated superiority of the RR model over MT and PH models. Both RR and MT models gave relatively stable values of correlations between PSD and EBV for survival, whereas the respective correlation for the PH model increased dramatically between 120 DIM and the fourth calving. Small values of correlations for the PH model at early time points were associated with relatively large values of sampling variances. This would suggest again the potential benefits of incorporating time-dependant sire effects in the PH model. Survival data used for calculating PSD was the same as the data utilized in the genetic evaluation model. An independent sample of daughters should theoretically be used for estimation predictive ability of the model. Data in this project, however, were generated by simulation, and no systematic fixed effects were modelled. Samples of new daughters should give practically the same
estimates of correlations. Furthermore, all models were compared on the same basis.

Rankings of sires provided by PH, RR and MT models were different, as indicated by correlations between EBV from pairs of models. This supported results of Galbraith (2003) where the same models were applied to real survival data in Canadian dairy breeds. Differences between rankings obtained in the current study were variable and depended on the particular time point for survival definition.

Conclusions

Stochastic simulation indicated that the PH model with the Weibull hazard function was the most accurate in terms of correlation between TBV and EBV for analysis of survival data in dairy cattle. RR and MT models gave lower accuracies of genetic evaluation, especially for survival in early stage of cow’s lifetime. Predictive ability of models, measured by correlation between EBV and the proportion of sire daughters that survived to certain age after first calving, favoured the RR model over its competitors. This would support potential benefits of using RR models for genetic evaluation of dairy cattle for survival traits.

Acknowledgements

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