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An improved model for the French genetic evaluation of dairy bulls on length of productive life of their daughters

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Introduction

A routine genetic evaluation of dairy bulls based on the length of productive live (LPL) of their daughters was implemented in France in June 1997 (Ducrocq, 1999). Since then, estimated breeding values (EBVs) for "Functional longevity", denoted LGF, are computed twice a year, in June and October. These EBVs characterise the effect of a bull on the culling risk of their daughters independently from their milk production level. LGF being at best a moderately heritable trait, the reliability of these EBVs are low for young sires when only the first lactation record of their first crop daughters are available. Since 2001, within the general framework designed to compute the French total merit index (ISU) for bulls and cows, LPL direct information has been combined with indirect information coming from early predictors of LPL: somatic cells count, fertility and some type traits (Ducrocq et al, 2001). The resulting EBVs, denoted LGFc ("c" for "combined") are now the only published ones. However, as the inclusion of direct information is done through "pseudo-records" and weights that are by-products of the direct LPL genetic evaluation, a proper genetic evaluation of LPL is as necessary as before.

Length of productive life is known from milk recording data and does not require the implementation of any extra recording system: when the cow is milk recorded, it means that she is still alive. However, the statistical analysis of LPL presents a major difficulty: when the cow is alive, we only have a lower bound of her actual LPL: its current value. Such a record is called "censored". The optimal use of all the available information - censored and uncensored records – requires the use of survival analysis techniques. These rely on the concept of hazard function which represents the instantaneous culling risk of a cow, t days after her first calving. This is a measure of her probability to be culled at t, given she was alive at t-1. The hazard function allows the inclusion of both censored and uncensored records within a unique modelling framework.
The model used for the genetic evaluation of LPL from 1997 to 2003 described the hazard function h(t) of a particular cow as (see Ducrocq, 1999 for details):

$$h(t) = h_0(t) * \exp\left\{\sum_m f_m(t) + hys_k(t) + s_i + 0.5\, mgs_j\right\} \qquad [1]$$

where:

- $h_0(t)$ is the baseline hazard function, i.e., a function describing how the hazard of the whole population is varying as this population is ageing. A parametric function, the Weibull hazard function, was chosen. The corresponding Weibull survivor function is a flexible extension of the decreasing exponential function. In practice, in the evaluation, one of the two Weibull parameters (the "shape parameter" known as "ρ") was assumed to be known ($\rho = 2$).
- $\sum_m f_m(t)$ is the sum of fixed environmental effects which increase or decrease the instantaneous culling risk. Some of these effects are considered as acting the same way during all the life of the cow (e.g., the age at first calving). But most of these effects are supposed to vary with time. They are treated as "time-dependent" effects. This permits a more precise modelling of the change in probability of being culled over time. From 1997 to 2003, these effects were: a year-season effect, a combined effect of the lactation number (6 classes) and stage of lactation (6 classes), a combined effect of herd size and variation of herd size from one year to the next, an effect of the within herd milk production class (10 classes) by year and an effect of the within herd fat percent and protein class (5 classes each).
- $hys_k(t)$ is a random herd-year-season effect. Given its flexibility and mathematical convenience, a log-gamma distribution with a single fixed parameter γ (in practice, $\gamma=4$) was assumed.
- $s_i + 0.5\, mgs_j$ represents the additive genetic contribution of the sire i and the maternal grand sire j of the cow. With this expression, a positive value corresponds to an increase in risk of culling, on an unnatural scale. This is why the EBVs published are multiplied by -1 and expressed in standard genetic deviation (as all functional traits in France): a positive EBV is then favourable.

All computations were done using a specific software, the "Survival Kit" (Ducrocq and Sölkner, 1998b). This software as well as statistical models similar to the one presented here are used in various European countries for dairy bulls national evaluation (Denmark, Germany, Italy, The Netherlands, Spain, Switzerland – see Interbull, 2004).

With time, it has appeared that the genetic trend in the French Holstein breed – about one genetic standard deviation in about 15 years (see figure 10)- was not plausible, given the trends observed on correlated earlier predictors such as mastitis resistance or female fertility. This dubious highly positive trend was also found in other breeds (in Normande but not in Montbéliarde) and other countries. In addition, genetic correlation estimates between countries obtained in a test run for international longevity genetic evaluation were overall disappointingly low (van de Lindé, 2003). However, until recently, there was no pertinent test to validate or unvalidate the LGF genetic trend. The validation tests proposed by Interbull do not take into account the specificities of survival analysis (nonlinear model, censoring). An approximate method was proposed (Ducrocq et al, 2003) and implemented

(Ducrocq, 2004). This method confirmed the overestimation of the genetic trend in Holstein and Normande. A new model had to be looked for, with the hope to get a more reasonable genetic trend. This paper describes this model. Only Holstein results are presented here.

Material and method

Data

LPL records from milk recorded Holstein cows that were daughters of AI sires with at least 5 daughters in herds with at least 5 cows were included in the analysis. Lactations started before January 1, 1988 were discarded. This date is also the threshold date chosen for incorporation of any record in the total merit index analysis (Ducrocq et al, 2001).

It is known that reasons for culling a cow are different in different lactations and even between early and late lactation. These culling reasons also have different genetic components. But one implicit assumption in model [1] is that the sire effect on culling probability remains the same over all the life of his daughters. Obviously, this is at best an approximation of the true situation. To buffer potentially large deviations from this assumption, it was decided to concentrate the evaluation on the risk of being culled in early life by considering as censored at her 6th calving the record of any cow still alive after 5 lactations.

Records from cows still alive on January 1, 2004 were also considered as censored as well as cows sold to other milk recording herds or cows in herds with a size decreasing by more than 50% in one year.

As a result, the analysed data file included 8,682,630 LPL records of daughters of 24,537 sires. 9.4% of these records were truncated, i.e., correspond to cows who calved for the first time before January 1988 but were culled or were censored after that date. In total, 31.1 % of the LPL records were censored.

The pedigree of AI sires was traced back on the male side only and a relationship matrix was created with a total of 25,250 animals, distributing unknown sires and maternal grand sires and all maternal grand dams in a total of 55 different groups, based on year of birth, sex and country of origin.

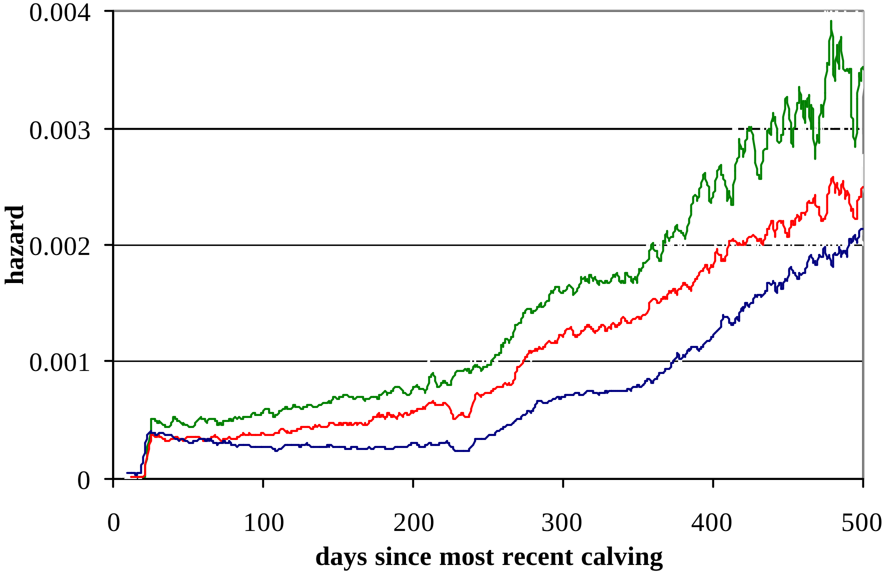
Model

Previous work (Ducrocq, 2002; Röxström et al., 2003) had shown the interest of a modelling of the baseline hazard function not over the entire productive life of the animals, but within lactation – and even within stage of lactation. To illustrate this, figure 1 presents an empirical within lactation estimate of the overall hazard function (derived from the Kaplan-Meier estimate of the survivor curve, Kalbfleisch and Prentice, 1980) among cows calving for the first time in 2000. Clearly, the pattern is very similar across lactations but with different slopes: first the hazard slowly increases to about 270 days, with a faster increase in second and third lactation. Then there is a sharp increase at the end of lactation with a different slope for very long lactations (>380 days). It was decided to use these cut points (day of calving, 270 days, 380 days and day when dried) to define periods within which a different Weibull baseline hazard would be used (as in Ducrocq, 2001). By more precisely describing how the hazard varies within and across lactation, the piecewise Weibull baseline replaces both the previous unique baseline and the lactation number by stage of lactation time-dependent effect of model [1]. In fact, this piecewise Weibull baseline was also defined separately for the successive years of calving (1988 to 2003). If τ denotes the number of days since the most recent calving, the new model can be written:

$$h(t) = h_{0,lnr}(\tau) * \exp\left\{\sum_{m*} f_{m*}(t) + hys_k(t) + s_i + 0.5\, mgs_j\right\} \qquad [2]$$

where $h_{0,lnr}(\tau)$ is the Weibull baseline for the nth period (1 to 4) of the rth lactation (1 to 5) started in year l (1988 to 2003). Both Weibull parameters are now re-estimated at each evaluation.

Figure 1: Within lactation estimate of the hazard function, based on the Kaplan-Meier estimate of the survivor function of cows born in 2000.



The other effects in the model are:

- as before:
  - an age at first calving effect (by classes of 1 month, between 20 and 42 months);
  - a herd size by variation in herd size interaction effect (herds with less than 5 cows, 5 to 19 cows with 3 subclasses of variation in herd size (decrease by more than 10%, stable size, increase by more than 10%), 20 to 49 cows and 50 cows or more with 5 "subclasses" of variation in herd size: decrease by more than 15%, by 5 to 15%, stable size, increase by 5 to 15%, by more than 15%);

- slightly different from before:
    - a within herd milk production class by year-season (instead of year), with 4 seasons (calendar trimesters). Note that the definition of this effect within year-season and of Weibull baselines within year leads to the exclusion from the model of a specific year-season effect as in [1]. Milk production classes were defined as before but using more accurate mature-equivalent 305 day milk production estimates for records in progress. Deviations of these productions from the herd-year-lactation average (lactation 1 vs 2 and more) were used to define 10 classes, from bottom 10% to top 10% within herd;
    - within herd fat percent and protein percent classes (5 classes each) by year, with a definition similar to milk production;
    - a random, log-gamma distributed herd-year effect (instead of herd-year-season): in small herds and herds with strong seasonality of calving, some herd-year-season cells corresponded to very few uncensored records (0 or 1), in which case the effect could not be considered as properly accounting for the herd culling policy. The log-gamma parameter is no longer fixed, but re-estimated during the analysis;
- new:
    - a region by year effect, to account for systematic differences in culling policies between regions due to varying production systems and markets. For the Holstein breed, 8 regions were defined;
    - a lactation number x stage of lactation by within herd milk production class effect, which accounts for the fact that poor producing cows are culled earlier in lactation.

Computational considerations

A move from a situation where the baseline was unique and defined with fixed parameters to one where several hundred Weibull shape parameters have to be estimated at the same time as the other effects was not possible to envision with the previous version of the "Survival Kit". Considerable effort was invested into the development of a more efficient approach to maximize the a posteriori density of all the parameters, given the sire variance (see Ducrocq and Casella, 1996, for details) The limited memory quasi-Newton algorithm of Liu and Nocedal (1989) was replaced by a full Newton algorithm with modifications to ensure positive definiteness of the Hessian matrix (Dennis and Schnabel, 1983) which is critical in the initial iterations. This had strong negative implications on the amount of RAM required (full storage of the Hessian matrix) and the CPU time per iteration but had extremely favourable consequences on convergence rate – usually 3 to 5 iterations, with a much stricter final convergence criterion. Overall computation time was reduced by more than an order of magnitude with the old model and by about 3 with the new, more complex model.

Estimation of genetic variance, genetic evaluation and validation tests

The complete data set was used to re-estimate the sire variance under the new model, using the procedure defined in Ducrocq and Casella (1996). With the new estimate, sire effects were computed and converted to LGF EBVs as before. The same genetic trend validation test as for the old model was implemented. Also, an evaluation was performed with the same data but ignoring all the information after January 1st, 2000, mimicking an identical genetic evaluation 4 years ago. Based on EBVs from 2000, bulls with daughters calving for the first time in 2000 were grouped into 6 classes and the Kaplan-Meier (Kalbfleisch and Prentice, 1980) survivor curve of these daughters was computed for each class. The comparison of these raw survivor curves obtained from data not included in the evaluation is the direct illustration of the effect of a selection based on LGF bull proofs.

Results

All effects in the new model were found to be highly significant. This is hardly surprising given the size of the data set, but all these effects strongly influence the risk of being culled. The γ parameter was estimated at $\gamma = 4.40$ i.e., the variance of the log-gamma herd-year effect is equal to $\Psi^{(1)}(\gamma) = 0.255$ where $\Psi^{(1)}(.)$ is the trigamma function (Kalbfleisch and Prentice, 1980).

The approach of Ducrocq and Casella (1996) led to a maximum a posteriori estimate of $\sigma_s^2 = 0.03468$. The standard error of this estimate was not computed because it was too computationally demanding. But for the Normande breed, with a similar data structure but a smaller data set (1.415 million records, 4165 sires), the characteristics of the approximate a posteriori distribution of the sire variance was extremely peaked and symmetric with a standard deviation of 0.00116. In other words, the sire variance estimate for the Holstein breed is certainly extremely precise. This variance value is much smaller than the previous value ($\sigma_s^2 = 0.0525$, Ducrocq and Sölkner, 1998a) but is more along the lines of other national evaluations (Interbull, 2004). This corresponds to an effective heritability of $h^2 = \frac{4\,\sigma_s^2}{\sigma_s^2 + \Psi^{(1)}(\gamma) + 1} = 10.8\%$ (from Yazdi et al., 2002). This heritability corresponds to the heritability of the trait in absence of any censoring. In fact, the "equivalent heritability", $h_e^2(t) = \frac{4\,\sigma_s^2}{\sigma_s^2 + \Psi^{(1)}(\gamma) + 1/p}$, where p is the proportion of uncensored records at time t, Yazdi et al, 2002) is lower and increases with time. Figure 2 illustrates this change in equivalent heritability during the first 3 years of productive life, using for p the Kaplan-Meier estimate of the animals born in year 2000. These values are useful to compute approximate reliabilities. For example, a sire with N daughters has on average N_u of them uncensored after days of productive life. The approximate reliability of his LGF proof based on his daughters only is then $R = \frac{N_u\ h^2}{(N_u\text{-}1)\,h^2 + 4} = \frac{N\,h_e^2}{(N\text{-}1)\,h_e^2 + 4}$.

Figure 3 represents the estimates of the Weibull shape parameter ρ over the years, lactations and periods. A ρ value larger than 1 corresponds to a hazard function increasing with time. The larger ρ is, the faster the increase. Clearly, the ρ value is relatively low during the first period, i.e., from 0 to 270 days of each new lactation with a value between 1.6 and 2.2 for lactations 2 to 5 and a markedly smaller value in lactation 1 (between 1.3 and 1.6). Whatever the lactation, a smooth decline of the ρ estimate with time is apparent. The decline is faster in lactations 2 and 3: the very similar estimates obtained for lactations 2 to 5 in the early nineties are more spread out in the most recent years. The second period of each lactation, from 270 to 380 days, is characterized by a fast increase in culling, with ρ estimates mostly above 4.5. Again, these ρ estimates exhibit a slightly decreasing trend with time, with a sharp fall during the last year. Also, these ρ values consistently decrease from one lactation to the next. from lactation 2 to 5. The same trends (over time and from lactations 2 to 5) are observed for the third period (after 380 days of lactation). During this third period, the ρ estimate for the first lactation remains at the same high level as for the second period, while it is more moderate (between 3 and 4) for the other lactations. For the fourth period (from the date when dried to the next calving) the risk of being culled is 0: it is known that a new calving occurred and therefore, the animals were not at risk. This level was chosen to avoid to give credit to cows - and their sires –with long dry period. In practice, the software takes a value of $\rho=1$ with the other Weibull parameter λ equal to 0 (or equivalently $\rho \log\lambda=-\infty$).

Figure 2: equivalent heritability as a function of number of days since first calving, derived using the Kaplan-Meier estimate of the survivor function of cows born in 2000.

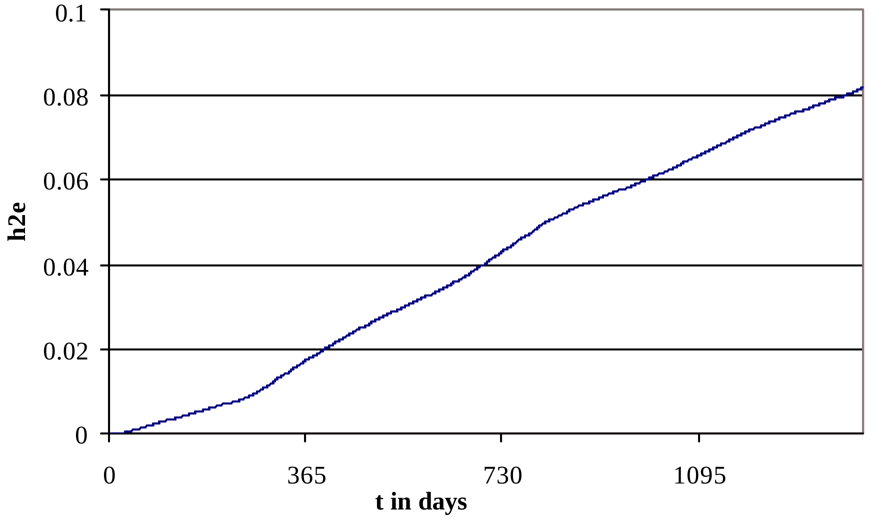
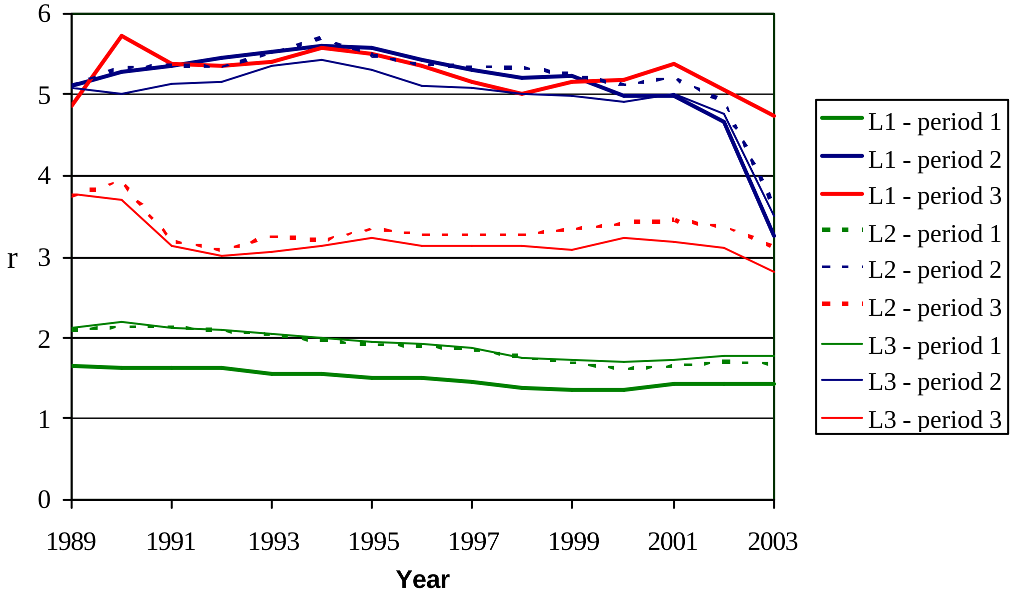


Figure 3: estimate of the Weibull parameter r as a function of lactation number (lactation 1 to 3 here), period within lactation (1: 0 to 270 days, 2: 271-380, 3:>380) and year.



In summary, the piecewise Weibull baseline clearly described the cyclic pattern of the hazard function over lactations: the hazard function in first lactation has its own characteristics, with an initially slow increase in risk over time, followed by a sharp increase which is maintained for very long first lactations. For the other lactations, the increase is initially a bit faster. The sharp increase at the end of a usual lactation length is similar to the first lactation, but for very long lactations, the risk of culling does not increase as fast. These results are consistent with those of Ducrocq (2002) in the Normande breed and with the raw hazard estimates displayed in figure 1, except that figure 1 gave the impression of a decrease in risk during the first period of the first lactation. This discrepancy can be attributed to the other effects in the model that also influence the raw estimates, in particular the within herd level of milk production effect. The last important finding in the description of the baseline is its smooth and systematic change over time towards a slower increase of the risk of culling for all lactations and all periods, although with different rates of change. It will be seen later that this change may be related to the overestimation of the genetic trend with the old model.

Figure 4 presents the estimates of the age at first calving effect. The risk of being culled increased with age at first calving. Although this trend is consistent with the solutions of the previous model and others studies, it appears that the increase in risk is more pronounced with the new model, with a quite low risk of being culling for very early calvers (before 24 months) and a flat trend for very late calvers (38 mo or more). Another result consistent with the old model is the sharp increase in risk of being culled in shrinking herds and the corresponding decrease in expanding herd, compared to stable ones (Figure 5). Some variation exists with herd size, especially for very small herds, but the estimate for this latter class is difficult to interpret, as any change in herd size is not really comparable to a similar change in bigger herds.

Figure 4: estimate of the relative risk of culling for the age at first calving effect (reference: 32 months).

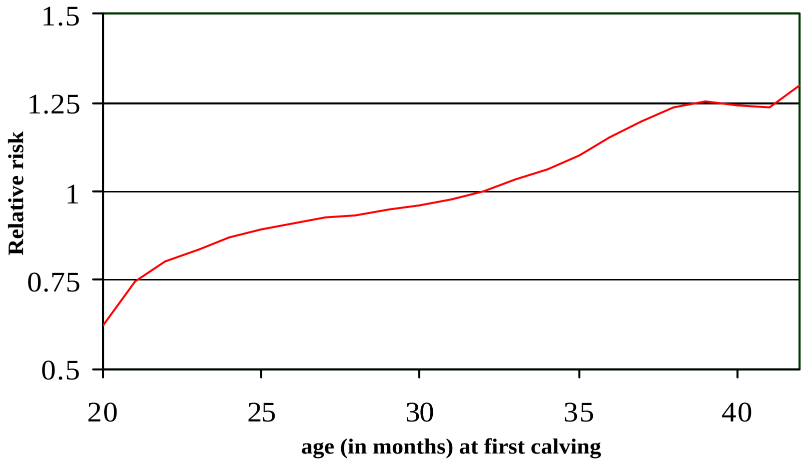


Figure 6 displays the region by year estimates, compared to region 1. Although the magnitude of the effect is not extremely large, systematic differences between regions clearly exist and must be accounted for. Regions 1 and 2 represent the western part of France (Bretagne, Loire valley) and the risk of being culled in these regions is about 20% larger than in regions 5 and 6 (southern half of France).

The estimates of the two effects dealing with within herd-year class of milk production were combined to construct figures 7 and 8. Figure 7 presents the year-season effects during the second period of the first lactation for the worst class of milk production. This effect has drastically changed over the years. In the early nineties, a first lactation cow in the worst class for milk production had her risk of being culled multiplied by 5 to 6 in fall and winter (first and last trimester of each year) compared to an average producer. In spring and summer, this risk was only multiplied by about 3.

Figure 5: estimate of the relative risk of culling for the herd size x variation of herd size effect (reference: stable herd size of 20 to 50 cows.

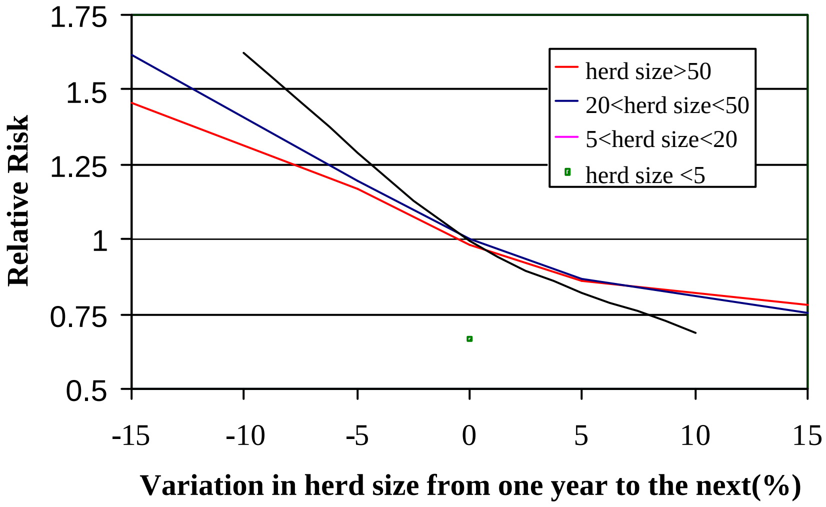


Figure 6: estimate of the relative risk of culling for the region x year effect (reference: region 1 for each year).

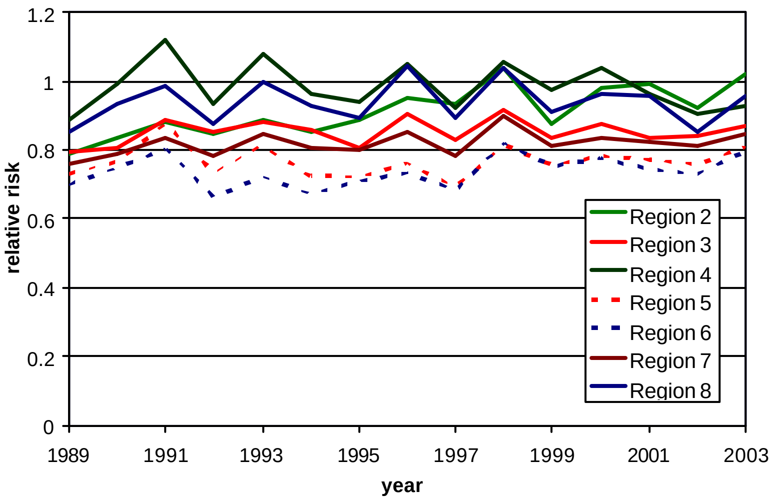


Figure 7: estimate of the relative risk of culling for the worst (bottom 10%) within-herd milk production class by trimester and year, during the second period (270 to 380 days) of lactation 1 (reference: average production class).

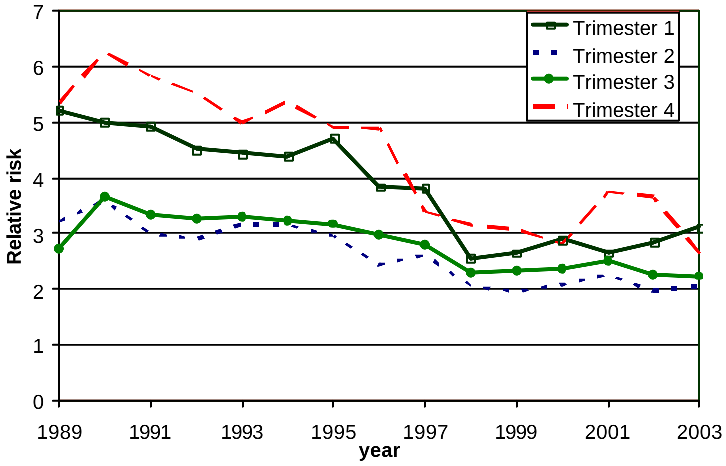
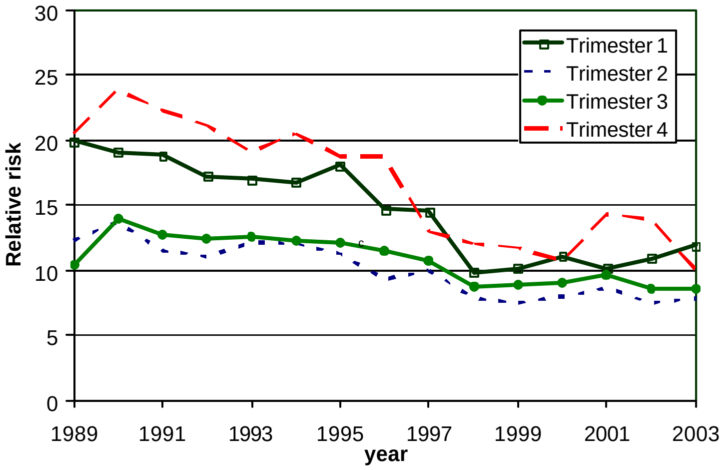


Figure 8: estimate of the relative risk of culling for the worst (bottom 10%) within-herd milk production class by trimester and year, during the first period ((0 to 270 days) of lactation 1 (reference: average production class).



The relative risk associated with production steadily decreased over the years to a value between 2 and 3 in the recent years with a similar, but much closer ranking across seasons. The drop was particular clear in 1998. Similar trends are observed for all periods and lactations, but with differences in the magnitude of relative risks. In particular, the first period – first 270 days – of the lactation is characterised by a huge relative risk of being culled for the worst producers (10 to more than 20 times the risk of an average producer in the early nineties, between 8 and 12 in the most recent years – Figure 8).

For within herd fat percent class (not shown), the risk of being culled was larger for the best class (relative risk with respect to the average class around 1.15 during most of the nineties) and smaller for the worst class (relative risk around 0.95). The amplitude is rather small but has been much smaller since 1998 (from 0.98 to 1.07), the worst class being then consistently at a slightly higher risk than the average class. Obviously, the emphasis on fat percent selection has changed over time.

Figure 9: estimate of the relative risk of culling for the worst (bottom 10%) within-herd protein percent production class (reference: average production class).

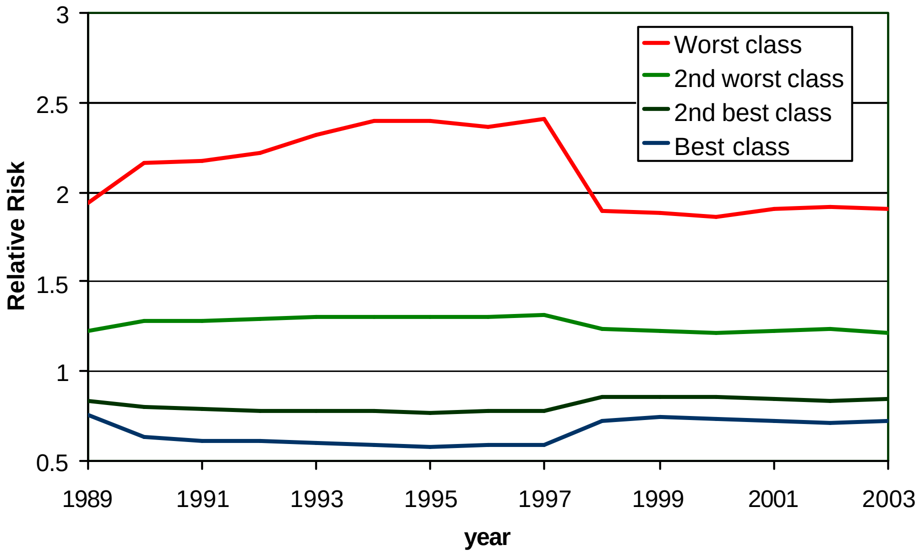
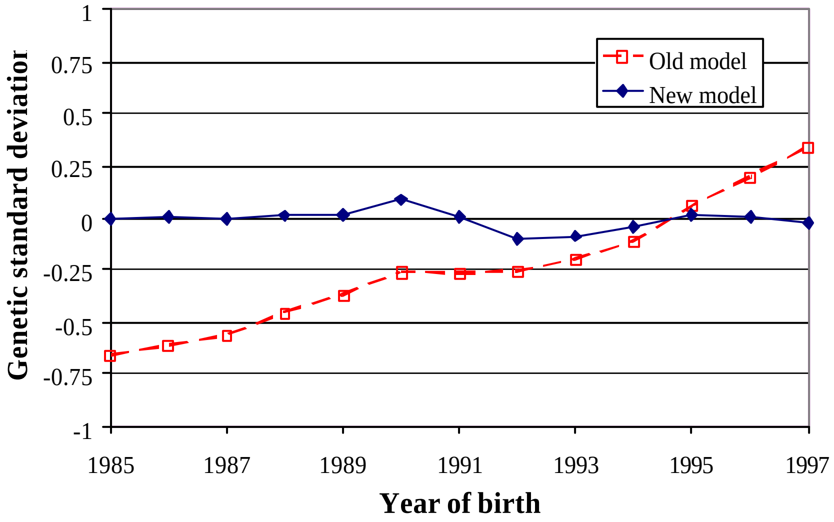


Figure 9 displays the estimated relative risk for the within herd protein percent class compared to the average class. The range of estimates was much broader than for fat percent: cows with very low protein percent (bottom 20%) were about twice more likely to be culled than average cows. On the other hand, cows with high protein percent had a low relative risk. The range was even larger in the early nineties, with a clear drop in 1998, as for fat percent and milk production. Clearly, there was a strong change around 1998 in the emphasis given to all production traits in the varying European economic context.

Figure 10: estimates of the genetic trend with the old and new models.



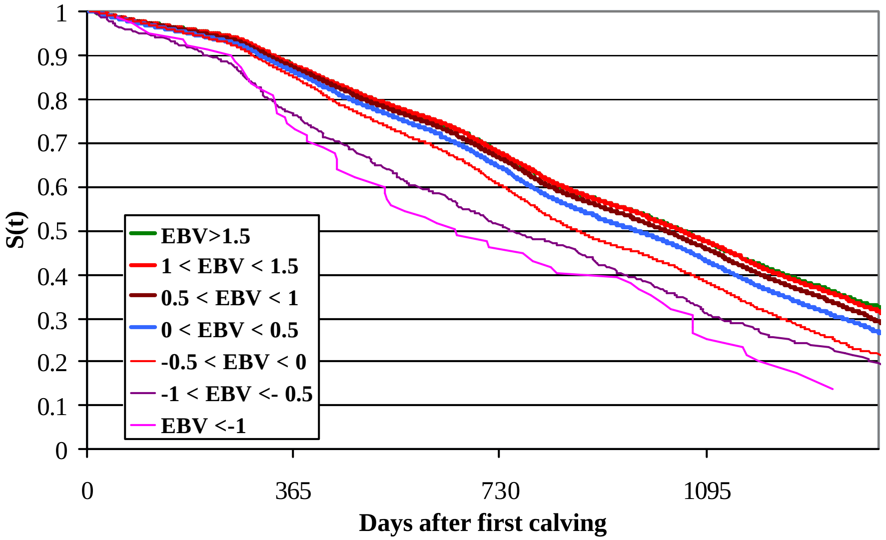
With the new model, the genetic trend obtained was virtually flat over the whole period (figure 10). The new LPL genetic trend makes more sense: selection on type or milking speed had only a limited impact on the unfavourable correlated responses known to occur on fertility and disease resistance when selection was mainly on production.

The trend validation test was much more satisfying: the regression coefficient estimate was -0.54% +/- 0.20% of sire standard deviation / year when sire were treated as fixed in the regression model, hence well below the +/-2% limit required by Interbull.

The correlation between old and new EBVs for bulls with a reliability above 0.70 was 0.86. This is low but this is largely explained by the change in genetic trend. Within year correlations between the 2003 and 2004 proofs were higher (0.89 to 0.93), despite a new trait definition (survival up to the end of lactation 5) and additional data.

An final validation was done by performing a sire genetic evaluation with all the data available until 2000 and then looking at the raw survivor curves of new daughters born in 2000. Only daughters of sires with a LPL EBV reliability of at least 0.50 in 2000 were considered. This represented 259,416 daughters of 147 proven sires. 7 groups were created based on the sires' EBV in 2000, by class of 0.5 genetic standard deviation. These groups were unbalanced: the worst group included only 1 sire and 79 cows. This was to be expected since most of the bulls with very negative LPL EBVs often had a bad type or somatic cells evaluation and were not kept as proven sires. On the other hand, the group for sires with EBVs between 0 and 0.5 contained 89,210 daughters of 74 bulls. The very best bulls group was also very unbalanced: it included 7 bulls and 10,710 daughters, but one of the bulls had 43% of the daughters. The raw survivor curves for the different groups are displayed in figure 11. Clearly, the group average EBVs and the corresponding survivor curves are ranked similarly. The range between extreme groups reaches about 23% of difference in survival, 600 days after first calving. Again, this number should be interpreted with caution as daughters of very bad bulls are barely represented. The difference between top groups is small, but widens with time and also with increasing EBV reliability in 2000 (not shown). The survivor curve for the daughters of the best group of bulls was not different from the group ranking second. In fact, the most represented bull in that group was obviously overestimated. His 2004 proof went down by about one genetic standard deviation. Overall, it can be concluded that bull selection on LPL EBVs is actually reflected in survival of their daughters.

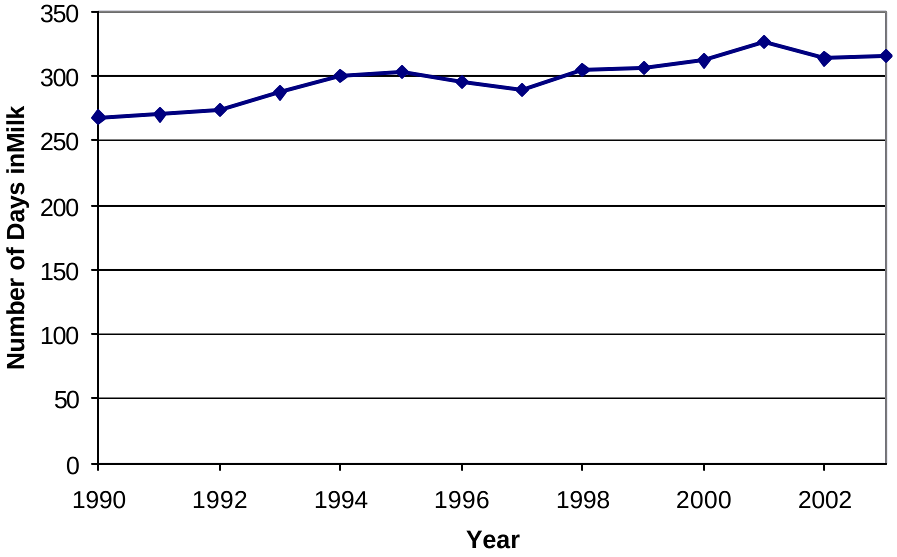
Figure 11: raw survivor curves of the daughters born in 2000 from bulls evaluated based on data collected until year 2000, grouped by LPL EBV of their sire.



Discussion and Conclusion

Our analysis of longevity data with survival models assumes a proportional hazard model. Deviations over time from strict proportionality across classes were accounted for through the inclusion of time-dependent covariates. Although possible in theory, these covariates cannot be chosen as continuous covariates because of computing cost constraints. For the same reasons, the baseline hazard functions cannot be left completely arbitrary as in a Cox model. It would be too computationally demanding for national genetic evaluations. The new model proposed is a compromise: it is much more flexible than the old model: the baseline is piecewise Weibull and is defined within lactation and year. This allows a finer level of description of the overall culling rate of the animals both during their lifetime and over the years. It is particularly important to account for the cyclic nature of the hazard, which is not related with the ageing of the animals, but with their reproductive (and lactational) cycle. The old model was trying to accommodate this through the inclusion of stage of lactation x lactation number effects. This was not as flexible. Moreover, the stages of lactation in the old model were defined rather arbitrarily (Ducrocq, 1999). It was far from optimal to have several short stages in early lactation – when the hazard evolves slowly and smoothly) and just one after 240 days of lactation. Finally, one of the Weibull parameters (ρ) was assumed to be fixed. Indeed, the new model reveals that the rate of increase of the hazard – estimated through ρ- has changed over time. Other effects also noticeably changed over time, either smoothly or abruptly. In particular, voluntary culling due to production characteristics appears to have decreased over time, with a large step around 1998.

Figure 12: average days in milk when culled for first lactation cows.



This highlights the very complex nature of survival data. Survival analysis deals with measures of time, but during that time, environmental conditions change continuously. Not surprisingly, chances of confounding between effects in the models are large, especially when they are time-dependent themselves. This is probably why the old model seemed to give sensible results for fixed effects although the genetic trend was grossly overestimated. Reasons for confounding with the previous model are perhaps numerous. But a potential one has been found : figure 12 shows the number of days in milk for first lactation cows that were culled. A continuous increase is observed. This is not surprising: with selection on yield and better management, average daily production has globally increased over time. This has led to a delay in the moment within lactation when a cow, for example, a sterile cow is considered as economically unsuitable and is culled. Such a change is not accounted for when a unique baseline is considered. As a consequence, even if the proportion of cows culled at each lactation is unchanged, younger sires with on average higher production EBVs may have been inadequately considered as improving the longevity of their daughters.

It is difficult to know where the inclusion of more time-dependent covariates should be stopped. There should be an optimum and a genetic trend passing the Interbull validation test is not the only nor the best criterion. Ubiquitous goodness of fit tests are not really available in survival analysis, in particular due to the censoring phenomenon (Klein and Moeschberger, 1997). More specific tests rely on assumptions that are not always perfectly suited, such as the hazards proportionality assumption. With huge data sets, this assumption is not really realistic and whatever the model, the test would probably lead to rejection. Furthermore, the tests proposed assume that all effects are fixed. Bayesian tests could perhaps be used but would again be difficult to implement on very large data sets. Hence, pragmatic compromises have to be found for practical implementation. This is the approach that was adopted here. Among the most obvious compromises that have been chosen, there are two that deserve special attention. They both concern the genetic component of the model:

First, as in the old model, a sire- maternal grand-sire model has been assumed. Some people feel very uneasy with the apparent impossibility to use an animal model. Once more, the main reason is the computational impossibility to implement it for large national applications. Although it can be tested for genetic evaluations of small populations, a survival animal model cannot be used for estimation of variance components, at least with the approach of Ducrocq and Casella (1996). It is true that the sire model is theoretically incorrect because ¾ of the genetic variation is not included in the model, that this part does not appear explicitly in the residual of the model and that the residual does not have the usual normal distribution. But the sire model is the only practical one: the part of the genetic variance not considered in the model is negligible compared with the large residual variance of the Weibull model. Simulation results (Meuwissen et al, 2002 and unpublished own simulations) clearly showed that a sire model approximation is very good, at least with the usual magnitude of the observed genetic variance. Of course, this is no longer the case when unrealistically large (more than 10 times the usual range) genetic variances are used in simulations which, furthermore, clearly favour the animal model (as in Damgaard et al, 2003). If cow solutions are desired, approximations have been proposed (Ducrocq, 2001).

The second assumption that is known to be invalid but was retained as a compromise is the choice of a time-independent sire effect. Culling reasons clearly vary within and across lactation (low milk production, type defects, milking speed, fertility, diseases) and consequently the genetic component of culling also vary. Considering culling in different periods as separate traits is a possibility (Ducrocq, 2002) but reduces the overall reliability of proofs. Including the sire effect as a discrete time-dependent effect for different periods with associated genetic correlations between periods and/or lactations is an alternative that should be investigated. The most appealing strategy would be to treat the sire effect as a continuous covariate (as in Veerkamp et al., 2001) but using within lactation random regression to account for the clear cyclic pattern). However this will remain once again beyond computational feasibility for a long time for large applications.

It must be acknowledged that the model used here only approximates the true nature of the LPL trait. But we have shown that selecting on the resulting EBVs should lead to a better cow survival. This should strengthen the interest for LPL evaluations in breeding programs.

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