LENGTH OF PRODUCTIVE LIFE OF DAIRY COWS:
II. VARIANCE COMPONENT ESTIMATION AND SIRE EVALUATION

V. DUCROCQ[1], R. L. QUAAS and E. J. POLLAK

Department of Animal Science

G. CASELLA

Biometrics Unit

Cornell University

Ithaca, NY, 14853

[1] Permanent address: Station de Génétique Quantitative et Appliquée

C.N.R.Z.,I.N.R.A.,78350, Jouy-en-Josas, France

ABSTRACT

Estimates of the genetic component of the cows' true stayability and of an approximation of their functional stayabilities were computed from length of productive life records of 83,338 grade Holstein daughters of 2,182 sires. True stayability is defined as the aptitude of a cow to delay culling whereas functional stayability refers to the ability to delay involuntary culling. The probability of a cow being culled is described using two Weibull models with time-dependent covariates. The first one includes fixed herd x year and stage of lactation x lactation number effects and a random sire effect. In the second model, a within herd x lactation level of milk production is included in order to correct the sire effects for the major source of voluntary disposal. Such a model, actually characterizing "milk-corrected" stayability, is a first step toward a functional

stayability evaluation.

The empirical Bayes estimates of the sire variance component are very similar for both models. Rigorously speaking, phenotypic variance of length of productive life cannot be computed because of the presence of time-dependent covariates in the models. If this problem is ignored, a "pseudo-heritability" of 8.5% is obtained for both traits. The correlation between the two sire evaluations is only 0.74. Milk yield is favorably related to true stayability, but slightly opposed to milk-corrected stayability. Functional stayability is presented as an appealing and economically important secondary trait to consider in breeding programs, as a complement to the current production traits.

Key words: Holstein-Friesian, empirical Bayes methods, sire evaluation, stayability, sire variance component, nonlinear model, Weibull model, length of productive life.

INTRODUCTION

In an earlier paper (10), two definitions of stayability were introduced: **true stayability** characterizes the aptitude for a cow to remain in her herd and **functional stayability** represents the ability to delay involuntary disposal. Both traits are of interest for the dairy breeder : the former is an indirect measure of the overall excellence of the cow, as viewed by the dairyman (11, 15) whereas an improvement of the latter would allow better and more profitable cows to live longer and therefore more low producers to be voluntarily culled (18).

Smith (16) reviewed the main objections to direct selection of AI sires on stayability of their daughters: it has been reported that stayability measures have a low heritability, and a high positive correlation with milk yield and that, consequently, the strong selection on milk yield should generate a significant positive correlated response on stayability. Also, because stayability is often

measured later in life than first lactation milk yield, its inclusion in breeding programs would increase the current generation interval and reduce genetic progress on milk production.

Most estimates of heritabilities for stayability measures reported in the literature range from 0.02 to 0.08 (9). But recent results suggest that it may be possible to detect a higher genetic variability when proper statistical methods are used (6,7) and when a continuous measure of stayability is employed rather than the usual measures such as survival to a fixed age or to a fixed lactation number (16,17). Furthermore, the use of a continuous measure like Length of Productive Life (LPL) or age at disposal, which does not limit evaluation to those sires whose daughters have reached a given age threshold - e.g. 48 months - may allow the consideration of stayability in breeding programs without a drastic change in the current generation interval. Finally, involuntary culling is obviously not reduced by selection on milk yield and voluntary disposal is more likely to be influenced by the *relative* - rather than the absolute - level of production of the cow within her herd: better producing cows live longer but higher *average* milk production is not synonymous with higher *average* stayability: an indirect improvement of true stayability through selection on milk production seems hopeless.

The above considerations give new prospects to a sire evaluation for stayability. Moreover, it has been shown that Weibull regressions (5, 13) with time-dependent covariates allow efficient modeling and statistical treatment of dairy cows LPL data (10). The objective of this paper is to apply such models to the estimation of sire variance component and sire effects for true and functional stayabilities.

MATERIALS and METHODS

Models

The two models considered are straightforward extensions of the regression models presented in Ducrocq et al. (10). They are based on the concept of hazard function (5, 13) which characterizes the relative culling rate of the cow. If T denotes the failure time of a cow, her hazard $\lambda(t)$ at time t is defined as:

$$\lambda(t) = \lim_{\delta \to 0} \frac{\text{Prob}\,[\,t \le T < t + \delta \mid T \ge t\,]}{\delta} \qquad [1]$$

Ducrocq et al. (10) showed that the analysis of length of productive life data can be performed using a particular type of "proportional hazard" models for which the hazard $\lambda(t)$ of a cow at time t is expressed as the product of a baseline Weibull hazard function $\lambda_0(t) = \lambda p\,(\lambda t)^{p-1}$ for some λ and p and a positive function $e^{z_i \cdot \beta}$ of the covariates of interest z_i. With respect to the models used in (10), a sire effect is simply added to detect differences in true and milk-corrected stayabilities of the daughters of different sires.

The hazard of a daughter of sire q is written:

$$\lambda(t) = \lambda p\,(\lambda t)^{p-1}\,\exp\{\,h_j(t) + g_{kl}(t) + s_q\,\} \qquad \textbf{(model A)} \qquad [2]$$

where : λ and p are respectively the location and the shape parameters of the baseline Weibull hazard function.

$h_j(t)$ is the jth time-dependent herd x year effect which changes on January 1, each year;

$g_{kl}(t)$ is the time-dependent stage of lactation x lactation number (SL x LN) effect corresponding to the kth stage of lactation (from day 0 to day 29 after parturition, from day 30 to 249, or from day 250 to the beginning of the next lactation) and lth lactation number, (lactation 1, 2, 3 and more);

s_q is a time-independent sire effect. Here, s_q is a measure of the

transmitting ability of sire q for *true* stayability.

The following model is also considered:

$$\lambda(t) = \lambda p \, (\lambda t)^{p-1} \, \exp \{ h_j(t) + g_{kl}(t) + r_m(t) + s_q \} \quad \textbf{(model B)} \qquad [3]$$

where $r_m(t)$ is the within herd x lactation level of production (WHLP) effect associated with the mth class of milk production. Nine classes are defined as in Ducrocq et al. (10). Since their analysis concludes that there is no interaction between lactation number and WHLP effects, first and later parities are ranked together: The effect $r_m(t)$ characterizes for each cow the influence on stayability of her *relative* level of milk production, based on her 305 days Mature Equivalent (305ME) record. A tenth class is also defined for cows with unknown 305ME record.

For model B, sire effects reflect genetic differences for reasons for disposal other than milk production (milk-corrected stayability). Since low milk yield is by far the major reason for voluntary disposal, s_q mainly measures the genetic component of involuntary culling, i.e., functional stayability.

Variance Component Estimation

A sire variance component and sire effects were estimated for models A and B using an empirical Bayes approach (2, 3): first, the sire variance component of a specific prior distribution is obtained, after integrating out the sire effects. Then, these effects are estimated as the modes of an appropriate posterior distribution.

The hazard $\lambda(t \,; z_m, q)$ of a daughter m of a sire q at time t can be written as:

$$\lambda(t \,; z_m(t), q) = \{ \lambda p \, (\lambda t)^{p-1} \, e^{z_m(t)'\beta} \} \, w_q \qquad [4]$$

where $w_q = e^{s_q}$ is the relative culling rate corresponding to the effect of sire q (here, $z_m(t)$ and β designate the effects other than the sire effect). Similarly, it is possible to isolate w_q in the expression of the survivor function at y_m, the

censoring time or the failure time of cow m. Conditionally on w_q, the likelihood of a daughter m of sire q is either (5):

a) $S(y_m ; z_m(y_m), q)$ if cow m is censored;

b) $f(y_m ; z_m(y_m), q) = \lambda(y_m ; z_m(y_m), q) \, S(y_m ; z_m(y_m), q)$ if m is uncensored.

Thus, by pulling together all the cows which are conditionally independent given q, it is possible to get the contribution to the likelihood $g_q(y_m | \beta, p, \lambda, w_q)$ of all the LPL records (y_m) of the daughters of sire q (for details, see (9)).

Now assume that the relative culling rate w_q for sire q follows a gamma distribution with parameters γ and γ, i.e., constraining without loss of generality the expectation of w_q to be 1. The density function of such a distribution is:

$$\pi(w_q | \gamma) = \frac{\gamma^\gamma \, w_q^{\gamma-1} \, e^{-\gamma w_q}}{\Gamma(\gamma)} \qquad [5]$$

Several reasons justify this critical choice: gamma distributions are popular among Bayesians because they can describe - or approximate - a wide variety of distribution shapes. Also, gamma distributions have an algebraic form which is not too complex and which may allow an analytical solution of otherwise difficult problems. As it will be seen, this is the case here. A log-gamma prior for a sire effect s_q may be unfamiliar to animal breeders. Normal or multivariate normal distributions for sire effects have been always considered as almost compulsory priors for genetic effects - such as s_q - in a quantitative genetics context, as a result of the polygenic model and the law of large numbers. However, it is seldom asked on *which scale* these genes combine their effect additively. Here, which of w_q, s_q, log s_q or whatever function of s_q should be considered normally distributed? The answer is not known a priori. The flexibility of the gamma distribution precludes the need for an arbitrary choice on this subject.

By application of the Bayes theorem, the contribution of all the daughters of sire q to the posterior density $\pi_q(\gamma, \beta, p, \lambda, w_q | y_m)$ can be derived and the

nuisance parameter w_q can be integrated out in order to obtain the contribution to the marginal posterior density $\pi_q (\gamma, \beta, \rho, \lambda \mid y_m)$. It is the choice of the gamma prior for w_q which makes this integration possible. Then, assuming that the sires are unrelated and summing all these elementary contributions over all the sires, we obtain the marginal posterior density $\pi (\gamma, \beta, \rho, \lambda \mid y)$ given the data vector y (9). Estimates of $\theta' = (\gamma, \beta', \rho, \lambda)'$ are obtained as the mode of $\log \pi (\gamma, \beta, \rho, \lambda \mid y) = \log \pi (\theta \mid y)$. The maximization of this nonlinear function is performed using a standard multivariate Newton's algorithm (8). It must be noted that effects in β are also nuisance parameters but it seems impossible to integrate them out algebraically. Then, "losses in degrees of freedom" resulting from the estimation of β are not accounted for. This should not be a serious problem since β does not include too many parameters.

For large samples, $\pi (\theta \mid y)$ is approximately multivariate normal with mean $\hat{\theta}$ and variance-covariance matrix V, where V is the inverse of a matrix with element (v, v') equal to :

$$-\left[\frac{\partial^2 \log \pi(\theta \mid y)}{\partial \theta_v \partial \theta_{v'}} \right]_{\theta = \hat{\theta}}$$

((2), p224)   [6]

Large sample standard errors of the elements in θ are computed as the square root of the diagonal elements of V.

Sire Evaluation

Once the prior distribution of the sire effect is known, estimates of sire values can be derived in two ways:

The posterior density $\pi(\theta, w \mid y)$ - where w is the vector of sire effects w_q - can be maximized assuming that the estimates of $\theta' = (\gamma, \beta', \rho, \lambda)$ are already known from the previous analysis. Thus w maximizes $\log \pi(w \mid y, \theta = \hat{\theta})$.

Alternatively, only the gamma parameter γ can be retained from the empirical Bayes estimation described previously and new estimates are computed for β, ρ and λ by maximizing log $\pi(\beta, \rho, \lambda, \mathbf{w} \mid \mathbf{y}, \gamma = \hat{\gamma})$.

These two methods should give similar results if the amount of information available to evaluate β, ρ and λ is large, i.e., if $\pi(\theta, \mathbf{w} \mid \mathbf{y})$ is reasonably peaked around the mode $\hat{\theta}$ of the marginal density $\pi(\theta \mid \mathbf{y})$ (for details, see (9)). An approximate expression of the variance of w_q is also given in (9).

Data Set

The data set includes LPL records of *grade* cows freshening for the first time after January 1, 1981. All records from the 899 New-York State herds with at least 20 observed failures (uncensored records) over the period 1981-1986 are selected. After editing abnormal records, this data set included 185,666 lactations from 87,338 cows. From these, 52.7% were still alive on March 1, 1986 and 8.6% had been sold for dairy purposes. These two categories of records (61.3%) are considered as censored. The proportion of such records is quite large and as a consequence, some herd-year "subclasses" included only censored records. The corresponding herd-year effect estimates are $-\infty$. Cows in those herd-years all have a hazard of 0 and do not contribute to the comparison between their sires. The situation is different for cows censored in herd-years for which some actual failures have been observed: they were at a lower risk than those which failed and this can be partly attributed to the effect of their sire.

Herd size varies from 20 to 658 (average: 97). A total of 2,182 sires are represented with an average of 40 daughters (15 uncensored daughters). The distribution of cows across sires is extremely unbalanced: 655 sires have no uncensored daughters and 34 sires have more than 500 daughters (63.1% of the total number of daughters). This distribution is unavoidable: a few sires have

been used intensively in the grade population after a favorable progeny test.

RESULTS and DISCUSSION

Estimation of the sire variance component

The Weibull models as described in [2] and [3] are overparameterized (9). This overparameterization is broken by arbitrarily setting λ to 1, the second SL x LN effect to 0 (and the fifth WHLP effect to 0 for model B). The maximization of the log-posterior density $\log \pi(\theta \mid y)$ is performed using Newton's algorithm (8). The matrix of second derivatives of $\log \pi(\theta \mid y)$ for the Weibull models A and B is easy to compute and very sparse. For example, in contrast with the Cox's regression, the herd x year block of this matrix is diagonal (9).

[table 1 here]

Convergence is very fast and is obtained after respectively 5 and 6 iterations for models A and B. A value of $\hat{\rho} = 1.387 \pm 0.003$ is obtained for model A whereas $\hat{\rho} = 1.355 \pm 0.003$ for model B. Estimates of elements of β are given in table 1, with their large sample standard error of prediction. These estimates are consistent with the results presented in (10). In particular, the presence of an interaction between lactation number and stage of lactation is confirmed: first parturition cows are at a higher risk than older cows during the early part of their lactation .

The parameter γ of the gamma distribution of the sire relative culling rate w_q converges to 55.0 ± 10.4 for model A and 55.4 ± 10.5 for model B.

It can be shown that the moments of the distribution of s_q are:

$$\hat{E}(s_q) = \hat{E}(\log w_q) = \Psi(\hat{\gamma}) - \log \hat{\gamma} = -0.009$$

$$\hat{Var}(s_q) = \hat{Var}(\log w_q) = \Psi^{(1)}(\hat{\gamma}) = 0.0183$$

for model A, where $\Psi(.)$ and $\Psi^{(1)}$ are the digamma and trigamma functions ((1), p258-260; (13), p26). Therefore, $\Psi^{(1)}(\hat{\gamma})$ is the sire variance component familiar to animal breeders. For model B, almost identical results are obtained since the parameter γ is virtually unchanged. The density of the distribution of w_q for model A - gamma(55,55) - is presented in figure 1. This distribution is slightly skewed to the right whereas the distribution of $s_q = \log w_q$ is almost symmetric. Indeed, when γ is large, the log-gamma distribution tends toward a normal distribution ((13), p26). This property proves *a posteriori* that the sire effects s_q are approximately normally distributed.

(figure 1 here)

To evaluate the heritability of stayability, the phenotypic variance of the logarithm of LPL needs to be computed. Unfortunately, many records are censored : a simple computation of this variance using raw data would be meaningless. When a Weibull regression model is used with time-*independent* covariates, the phenotypic variance of log T (where T = failure time) is given by:

$$var(\log T) = \frac{1}{\rho^2}\left[\frac{\pi^2}{6} + \Psi^{(1)}(\gamma) \right] \qquad (9) \qquad\qquad [7]$$

Therefore, if the fact that covariates are time-dependent is ignored, a "pseudo-heritability" can be defined on the log scale as:

$$\hat{h}^2 = \frac{4\,\hat{var}(s_q)}{\hat{var}(\log T)} \qquad\qquad [8]$$

Then, $\hat{h}^2 = 0.085$ for true *and* milk-corrected stayability. This value is rather low but seems consistent with estimates from the literature. In any case, since it is not known whether var(log T) in [7] is a (large?) overestimate or underestimate

of the true value accounting for the time-dependency of the covariates, this value of $\hat{h}^2$ is difficult to interpret. More work needs to be done on this subject.

More interestingly, figure 1 shows that the sire relative rate ranges approximately from 0.65 to 1.3. This means that the daughters of some sires have, at any time and during all their productive life, a probability to be culled twice as large as for daughters of some other sires. If these daughters are in a herd with an "average" culling rate and have a regular calving interval, the estimates of SL x LN effects can be used to compute any value of a "predicted" survivor curve. For example, if an average calving interval of one year is assumed, consider the step function $g(t)$ for the SL x LN effects which takes the values indicated in table 1 and with jumps at x_j, $j = 0, 1, ... J-1$ where:

$$x_j = 365 \, k \qquad \text{if } j = 3k;$$

$$x_j = 365 \, k + 30 \qquad \text{if } j = 3k+1$$

$$x_j = 365 \, k + 250 \qquad \text{if } j = 3k+2.$$

Assuming $h(t) = 0$ for all t, and with $x_J = t$, we have for sire q :

$$\hat{S}(t;q) = \exp\left[-w_q \sum_{j=0}^{J-1} e^{g(x_j)} (x_{j+1}^p - x_j^p) \right] \qquad [9]$$

If the relative culling rate corresponding to sires X and Y are, say, $w_q = 0.8$ for X and $w_q = 1.2$ for B, 70% and 59% (respectively) of their daughters will be still alive after 2 years of productive life and 42% and 27% after 4 years. These fairly large differences in survival rates are graphically presented in figure 2 and illustrate the importance of genetic variability for stayability.

[figure 2 here]

The similarity of the sire variance component for true and milk-corrected

stayability is quite surprising. Previous attempts to estimate the heritability of stayability after correcting for differences in milk production indicated that heritability was significantly reduced (2, 14, 19). At least three interpretations may explain these results:

i) The WHLP effects in model B do not reflect any characteristic of genetic origin and therefore do not modify the variability of LPL due to the sire. Yet, this explanation does not seem tenable: it is well known that cows from sires of high genetic merit for milk production rank higher on average on 305ME production and have a longer LPL.

ii) The genetic variability of milk-corrected stayability may not be as low as previously indicated. In contrast with the studies where a reduction of heritability was observed when milk yield was taken into account, the correction used here is based on *relative* milk production within herd and may reflect more adequately the voluntary culling practices than those based on *absolute* production, allowing a better detection of sire differences for other disposal reasons.

iii) Futhermore, a negative correlation may exist between the different genetic components of true stayability: if s, s^* and s^{**} denote respectively the sire component of true stayabilty, of stayability "due to superior milk production" and of mik-corrected stayability, we may write $e^S = e^{S^*} e^{S^{**}}$ and so, var(s) = var(s^* + s^{**}). But results for model 2 suggest that var(s^* + s^{**}) ≈ var(s^{**}). Hence, var(s^*) + 2 cov(s^*,s^{**}) ≈ 0 and therefore cov(s^*, s^{**}) < 0.

A more precise knowledge of the phenotypic variance of log T when censoring and time-dependent covariates are present is needed to assess this hypothesis.

Sire Evaluation

Sire relative culling rates w_q are evaluated assuming that either γ only or β, ρ, λ and γ are known, i.e., by maximizing either the log-posterior density $\log \pi(\beta,$ $\rho, \lambda, w \mid y, \gamma = \hat{\gamma})$ or $\log \pi(w \mid y, \gamma = \hat{\gamma}, \beta = \hat{\beta}, \rho = \hat{\rho})$.

Estimates obtained for β and ρ in the latter case are extremely close to those presented in table 1. Moreover, the correlation between the two sets of sire effects is 0.9982 for model A and 0.9985 for model B: the two methods of sire evaluation are virtually equivalent and only the first set of solutions $\hat{w}_q$ is used hereafter.

A Spearman's rank correlation of 0.80 is obtained between the sire estimates for models A and B. Most sires have very few daughters and their estimates are quite insensitive to the model chosen. When the set of estimates is limited to the 153 sires with at least 20 uncensored daughters, the rank correlation is 0.73. Figure 3 shows the relationship between the two sire evaluations for these 153 sires. They are far from being identical.

The average change in sire effects $\hat{s}_q = \log \hat{w}_q$ when model B is used instead of model A is 0.00 (range: -0.32 to +0.24) and 50% of the estimates increase or decrease by more than 0.04.

[figure 3 here]

These differences between the two evaluations invalidate the interpretation i) given previously for the similarity of the sire variance components obtained for the two models: obviously, the sire effects in models A and B do not measure the same genetic characteristics. This is also illustrated in table 2 for some bulls with many daughters. Their ranking greatly varies with the model selected.

[table 2 here]

Correlation with other traits

Table 3 presents correlations between sire estimates s_q for true and milk-corrected stayability and Northeast AI Sire Comparison (NEAISC) evaluations for sires with at least 5 uncensored daughters in our data set. These correlations give some indication on the genetic correlations between the two stayability traits and production traits. Note that a negative correlation describes a *favorable* relationship between these traits: a negative value of s_q corresponds to a desirable (low) culling rate. As expected from earlier studies (for a review, see (9)), milk yield and true stayability are favorably associated. The relationship between the two traits is also apparent in figure 4 for the 153 sires with at least 20 uncensored daughters. When differences in milk production are accounted for, the correlation between the sire evaluations obtained using model B and for milk production is unfavorable, but small (figure 5). If the sire effect in model B actually characterizes his genetic merit for a trait close to functional stayability, this unfavorable relationship would suggest that a slight antagonism exists between milk production and biological fitness.

(figures 4 and 5 and table 3 here)

The correlation between the current NEAISC stayability evaluation and the true stayability sire effect studied here is rather low. Some sires rank very differently on both evaluation. If the analysis of LPL using model A is correct, the use of the current evaluation on survival to 48 months of age in breeding program would be rather inefficient in improving length of productive life.

Type appraisals have been often presented as an indicator of functional stayability, though many studies showed that the only part which may actually affect stayability is the udder (for a review, see (4) and (9)). Type evaluations were not available for all the sires studied here but some of them are presented in table 2 and indicate that a type evaluation is a very poor predictor of milk-

corrected stayability. For instance, bulls A, B, and C have similar milk-corrected stayability evaluation though their PDT (Predicted Difference for Type) evaluations vary from elite (+2.02) to extremely low (-3.03). It is striking that a bull with a very unfavorable PDT ranks among the best for milk-corrected stayability.

CONCLUSION

This study clearly demonstrates the feasibility of a large scale sire evaluation for stayability based on sophisticated nonlinear statistical methods which account for the peculiar nature of survival data and for the presence of censored records. Controversial issues which may require further investigations before the implementation of such an evaluation include the following:

i) Should the registered and grade populations be treated alike? Since registered and grade cows are not culled at the same time nor for the same reason, it is expected that the baseline survivor curves and the sire effects would be different for the two groups. Separate analyses seem unavoidable.

ii) How should the estimates of the sire effects be presented to the dairymen and the bull studs in an intuitively understandable form, easy to interpret? In particular, an expression of genetic merits increasing with improved stayability is desirable to avoid confusion. Some alternatives are examined in (9).

iii) Which of the two stayability evaluations should be preferred? True stayability is a measure of the actual average length of productive life of the progeny of a sire and as such, gives an indication on the total profitability of his daughters. It is consistent with the current routine stayability evaluations computed at Cornell University for the northeastern states of the US and at Guelph University for Canada. However, the actual *new* information brought by LPL data is included in the *functional* sire evaluation - which is approximated here by "milk-corrected" stayability of the sires'daughters. The current

evaluations on production traits - and type appraisal for registered breeders - supply to the dairyman a precise measure of the increase in returns that he might expect from the use of a superior sire. The next element that he might need is an indicator of how much the *costs* - e.g. replacement costs, health costs, reproductive costs - associated to his future progeny may vary. A functional stayability evaluation would give a crude and indirect, yet global, simple and intuitive indication on how these costs may vary between daughters of different sires.

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Table 1 : Estimates of "fixed" effects in model A and B : a summary

	Model A	Model B	SEP[1]		Model B	SEP[1]
ρ	1.387	1.355	±0.003			

	Model A	Model B	SEP[1]		Model B	SEP[1]
average herd x year effect	-9.90	-9.94				

LN[1]	SL[1]	SL x LN effects		SEP[1]		WHLP[1]	WHLP effects	SEP[1]
1	1	0.09	-0.04	±0.05		1	-0.61	±0.02
1	2	0	0			2	-0.48	±0.02
1	3	0.23	0.32	±0.02		3	-0.37	±0.02
2	1	-1.83	-1.77	±0.08		4	-0.26	±0.02
2	2	-0.31	-0.27	±0.02		5	0	
2	3	0.24	0.39	±0.02		6	0.12	±0.02
≥3	1	-1.52	-1.38	±0.07		7	0.38	±0.02
≥3	2	-0.37	-0.31	±0.02		8	0.81	±0.02
≥3	3	0.28	0.35	±0.02		9	1.60	±0.02
						10	-1.22	±0.04

[1] : SEP : large sample standard error of prediction

LN : Lactation number

SL : Stage of lactation

WHLP : Within herd x lactation level of milk production

Table 2. Some sire relative culling rates $\hat{w}_q$ for models A and B

Sire	number of daughters	$\hat{w}_q$ Model A (true)	Model B (milk-corrected)	NEAISC[1] Milk (kg)	NEAISC[1] survival at 48 mo (%)	PDT[2]
A	4,074	0.74	0.82	+410	79	-3.03
B	884	0.83	0.81	-90	77	0.79
C	113	0.96	0.84	-110	80	2.02
D	5,099	0.91	1.01	+480	77	-0.39
E	5,214	0.91	0.89	+230	75	-0.49
F	1,010	1.26	0.99	-110	69	0.08
G	629	1.29	1.26	-110	68	-0.95
H	1,445	0.99	1.37	+838	74	-0.30

[1] : NEAISC: Northeast AI Sire Comparison

[2] : PDT : Predicted Difference for type

1 -   Figure 1. Density function of a gamma function with parameters 55 and 55.

2 -

3 -   Figure 2. Survivor curves S(t) for different values of the sire relative culling rate

4 - w_q (w_q = log s_q) ; assumptions : calving interval = 1 year ; herd x year effect =

5 -   average.

6 -

7 -   Figure 3. Estimates of the sire effect s_q = log w_q in model A (true stayability) and

8 -   model B (milk-corrected stayability) for the 153 sires with at least 20 uncensored

9 -   daughters.

10 -

11 -   Figure 4. True stayability sire evaluation (Model A) vs NEAISC milk evaluation for

12 -   the 153 sires with at least 20 uncensored daughters.

13 -

14 -   Figure 5. Milk-corrected stayability sire evaluation (Model B) vs NEAISC milk

15 -   evaluation for the 153 sires with at least 20 uncensored daughters.
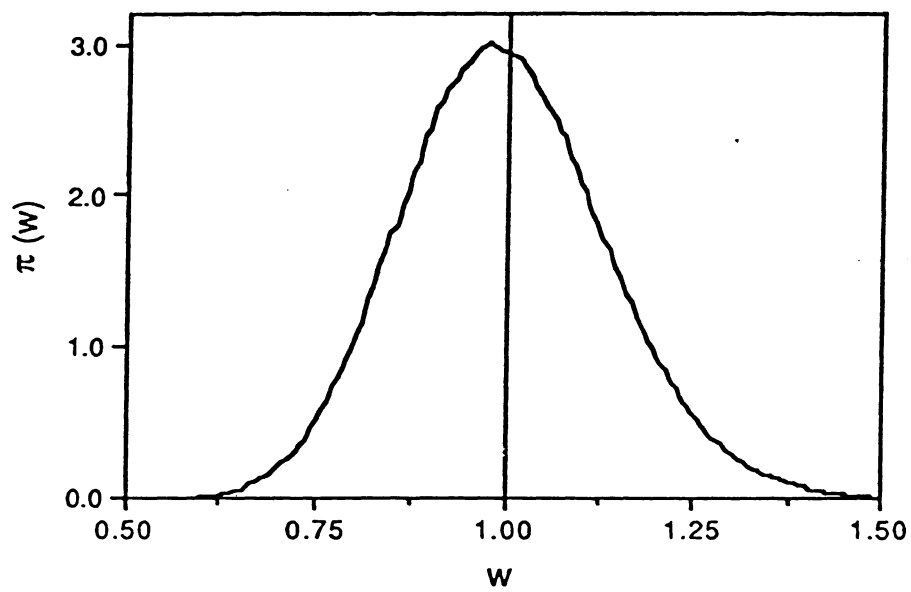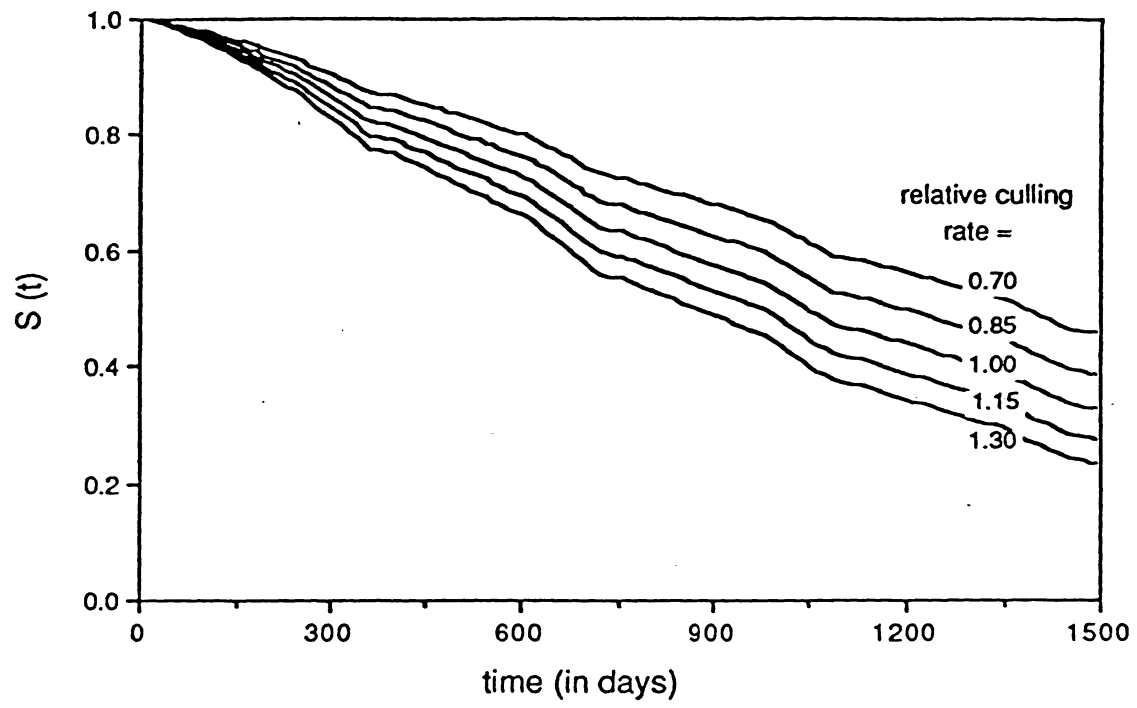
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Figure 1

Figure 2

Figure 3

Figure 4
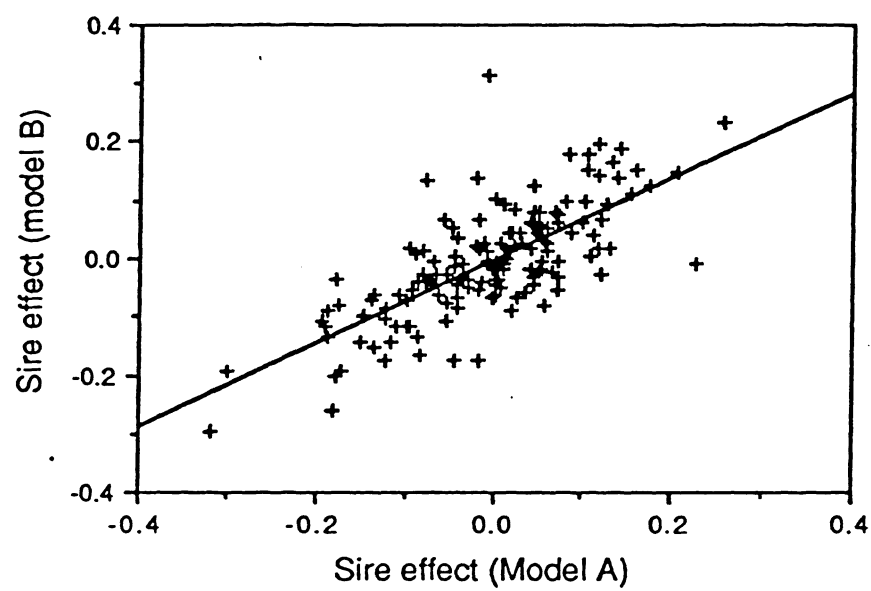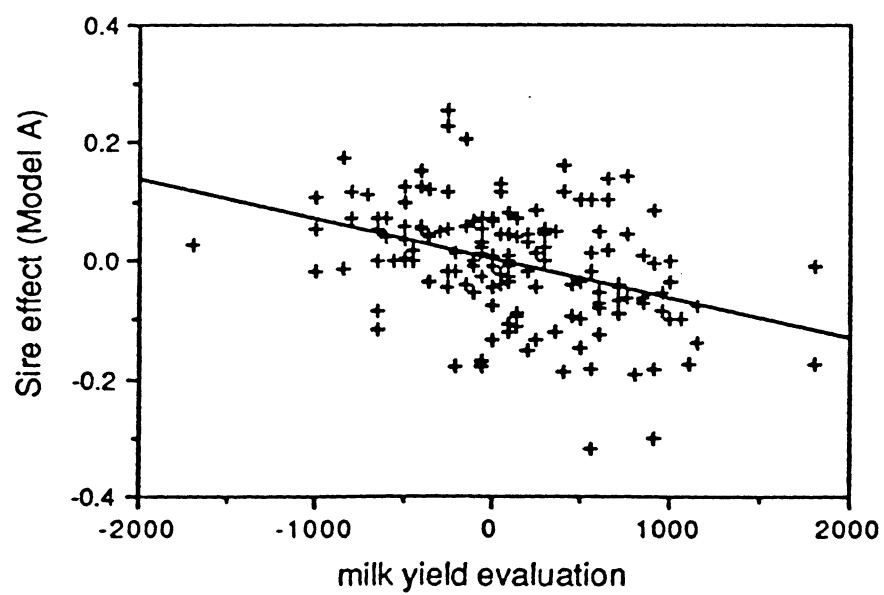

Figure 4

Figure 5

Figure 5