

# GENETICS AND BREEDING

## Genetic Evaluation for Longevity of Dutch Dairy Bulls

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### ABSTRACT

Parameters needed for survival analysis of longevity records of cows to predict breeding values of their sires were estimated with data on Dutch Black and White and Red and White cows. The heritabilities of functional productive life were 0.041 and 0.036 on the log scale for Black and White and Red and White cows, respectively. Although the heritabilities and other parameters differed between both breeds, the resulting breeding values were hardly affected: the correlation between breeding values of Red and White bulls using either Red and White parameters or Black and White parameters was 0.992. Genetic correlations between the direct breeding value for functional longevity (based solely on longevity of sires' daughters) and breeding values for conformation, health, and fertility traits were calculated. Several alternative selection indices were investigated using these correlations. Based on the resulting reliabilities, it was concluded that the Dutch breeding value for functional longevity should be based on longevity, rump angle, teat placement, udder depth, feet and legs, and somatic cell count. The index was expressed on a scale with average of 100 and a standard deviation of 4 points (at 80% reliability). The economic value was Dfl. 65 per genetic standard deviation, which was 0.46 times the economic value of INET (Net Milk Revenue Index). For the breeding value for functional longevity that was first published in August 1999, slight modifications in the model were made.

**(Key words:** longevity, conformation traits, genetic parameters, economic value)

**Abbreviation key:** **BW** = Black and White, **DPS** = durable performance sum, **DU** = durability index, **RR** = risk ratio, **RW** = Red and White.

### INTRODUCTION

Breeding for an increased lifespan of dairy cows should aim for increased potential longevity (e.g., 6,

24). Farmers can use the extra space for selection to cull more heavily on production (20). Considering that voluntary culling is mainly determined by low production, functional longevity is an appropriate measure for involuntary culling and, thus, for potential longevity (2, 18).

Information on longevity can be easily obtained from milk recording records. To allow breeding organizations to make use of this information, a breeding value for functional longevity has to be predicted. The best method for analyzing longevity records is survival analysis, because this method allows the proper use of censored records and the use of time-dependent covariates (26). Censored records are records for which the actual length is not known because, for instance, the cow was still alive at the time of data collection or because it was moved to a nonmilk recording herd. Excluding such records from the analysis would bias the results. Inclusion of time-dependent covariates allows for a proper correction for, for instance, the effects of herd or production. Instead of assuming one class of an effect to hold for the entire longevity period of a cow, an effect can change over time. For instance, if a cow starts a new lactation a new effect of production can be assigned.

Until recently, the use of survival analysis was limited to small data sets. With the assumption of a Weibull hazard function for the baseline hazard (5) and the release of a computer program designed for large-scale analysis of survival data (8), survival analysis can be used for national evaluations for longevity.

Although survival analysis allows the inclusion of censored records and thus yields an unbiased breeding value prediction for young sires, its reliability mainly depends on the number of uncensored daughters. For a young bull, this number will be low. To increase the reliability, predictive traits such as conformation, health, or fertility can be used (24). The relative weighting of this indirect information to the direct information on longevity of daughters will be different for each sire, depending on the amounts of information available.

In this paper, the methodology used to predict breeding values for functional longevity of dairy bulls in the Netherlands is presented. Parameters that were needed to predict such a breeding value were estimated

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for both Black and White (**BW**) and Red and White (**RW**) cows. The possibility of a joint evaluation of BW and RW cows was investigated by comparing the ranking of sires in separate runs for BW, RW, and a combined run. The economic value of functional longevity was calculated for Dutch circumstances. Genetic correlations between functional longevity on one hand, and conformation, fertility, and health traits on the other hand were estimated. These correlations were used to find the set of traits that could be used as indirect predictors of the breeding value for functional longevity.

## MATERIALS AND METHODS

### Data

Data were obtained from the Dutch milk recording scheme and included cows with a test-day record on or after January 1, 1988. Data were collected until January 1999, so the study period covered 11 yr. Cows were required to be at least 640 d old at first calving. If the first calving of a cow was before the starting date of the study, the record was considered to be left truncated. Records of cows that were still alive at the time of data collection were considered to be right censored. Also records of cows that were moved to another milking herd were considered to be right censored. If this herd was participating in the milk recording scheme a new, left truncated record for that cow was started from that point in time. If the date of first calving was unknown, it was assumed that a cow first calved on 800 d of age, which is the Dutch average (17).

Different data sets were made according to different purposes of analysis, listed in Table 1. The purpose of

the first analysis was to determine which fixed effects were significant in the model of analysis. Because a sire effect had to be included anyway, this effect was not included in the model. Given limited computing capacity, the data were restricted on the number of daughters per sire, and data on a total of over 2.7 million cows were used to determine the significance.

For parameter estimation, the sire effect had to be included in the model. That made it necessary to reduce the data by an extra selection on herd. Herds were required to have data throughout the study period and the preceding 2 yr. Only data from herds with at least 150 cows in the data set, covering 11 yr, were allowed. With an average length of productive life of 3.2 yr of Dutch cows, this means that only herds with at least 43.6 milking cows on average were included. The average herd size in The Netherlands is 52.8 (17). Data that were used for parameter estimation of BW and RW comprised records on 118,282 and 252,226 cows, respectively.

For all three data sets that were used to predict breeding values, only restrictions on the number of daughters of a bull were set. The number of sires in the analysis of all dairy cows (14,158) is less than the sum of the number of sires in both the BW (10,493) and RW (4789) analysis, because some sires had a sufficient number of daughters both in the BW and in the RW population and thus were included in all three analyses. The Dutch BW population mainly is a cross between Dutch Friesian and Holstein Friesian cattle, as is the RW population a cross between Meuse-Rhine-Yssel and Holstein Friesian cattle. Of all the BW calves born in 1998, 99% had  $\geq 50\%$  Holstein Friesian genes. Of all

**Table 1.** Purpose of analysis, data edits, number of cows, and number of sires for different data sets.

Purpose	Data edits	Number of cows	Number of sires
Significant effects in model	$\geq 100$ daughters per bull	2,728,973	...
Parameter estimation BW <sup>1</sup>	$\geq 100$ daughters per bull $\geq 150$ cows per herd herd 13 y in data since 1986	118,282	2904
Parameter estimation RW <sup>2</sup>	$\geq 100$ daughters per bull $\geq 150$ cows per herd herd 13 y in data since 1986	252,226	2152
Breeding value prediction BW	$\geq 25$ daughters per bull	2,962,447	10,493
Breeding value prediction RW	$\geq 25$ daughters per bull	1,155,552	4789
Breeding value prediction all dairy cows	$\geq 25$ daughters per bull	4,134,449	14,158

<sup>1</sup>BW = Black and White cows.

<sup>2</sup>RW = Red and White cows.

RW calves born in that year, 71% had  $\geq 50\%$  Holstein Friesian genes (17).

### Model

The hazard function was modeled as in Ducrocq et al. (5):

$$\lambda(t, z(t)) = (\lambda_0(t) \exp(z'(t)\beta)) \quad [1]$$

where  $\lambda(t, z(t))$  = hazard function,  $\lambda_0(t)$  = baseline hazard function, and  $z(t)$  is a vector of (possibly time dependent) fixed and random effects with corresponding parameter vector  $\beta$ . The baseline hazard function is only dependent on time, assumed to be the same for each animal, and to follow a Weibull distribution as in Ducrocq et al. (5). The Weibull distribution is described by two parameters:  $\rho$  and  $\lambda$ , which are associated with the shape and intercept, respectively (13). Both were estimated during analysis.

The effects in the model were sire; genetic group of dam; age at first calving; change in herd size; lactation value in the first, previous, and current lactation; the interaction between parity and stage of lactation; and the interaction between herd and yearseason. Each effect is described separately.

Because of limited computing capacity, the number of classes in a model analyzed by survival analysis is restricted. In practice, no animal model can be used for large data sets, and thus a sire model was chosen. Relationships between bulls were identified through their sires and maternal grandsires. If the sire of a bull or his maternal grandsire was unknown, a genetic group was included in the pedigree. This genetic group was based on the breed of the bull and the expected year of birth of its sire or maternal grandsire. Sires were expected to be born 6 yr before their sons, and maternal grandsires were born 10 yr before the grand offspring. The sire effect of the cow was included as a random class variable, independent of time and was assumed to follow a multivariate normal distribution.

To account for the effect of the dam of a cow, a genetic group based on the breed and year of birth of the dam was included. The genetic group was modeled as a class variable that was independent of time.

Several studies showed a significant effect of age at first calving on the longevity performance of a cow. Usually, an older age at first calving is associated with an increased hazard (19, 26). Age at first calving was expressed in days and modeled as a linear continuous variable, which was independent of time.

The change in herd size was included to account for the change in hazard of a cow when, for instance, a herd is expanding because an extra milk quota has

been bought, or when a farmer quits milking and starts selling his cows. Change in herd size was calculated as the number of cows on January 1 of one year minus the number of cows on January 1 of the next year, divided by the number of cows on January 1 of the next year. The resulting figure was grouped into five classes:  $<-0.3$ ,  $<-0.1$ ,  $<0.1$ ,  $<0.3$ , and  $>0.3$ . An additional group for "unknown" was added, which was used for all herds in the last year of the data available for that herd. Change in herd size was modeled as a class effect that changed on January 1 of each year, or when a cow was moved to another herd.

Lactation value is a management index that compares phenotypic performances of cows within a herd for production of milk, fat, and protein. It is standardized for lactation length, season of calving, and age at calving. Milk, fat, and protein are weighed according to their economic values. The herd average per test day is 100 (11). During a cow's lactation the lactation value of her last test day is stored. So when a cow has finished a lactation, the lactation value of her last test day within that lactation is stored. The lactation values in the current lactation and in the previous lactation were modeled as class variables that changed at every calving. Lactation value in the previous calving was added because lactation value in the current lactation might be influenced by diseases and fertility problems. Knowing that production in one lactation is correlated to production in the next, the lactation value in the previous lactation could give a better correction for voluntary culling. The lactation value in the first lactation was included in the model to investigate whether a farmer considered this figure when making culling decisions. It was modeled as a class variable that was independent of time. A lactation value below 60 was given the value 60, and a lactation value over 150 was given the value 150. The values in between were all separate classes. Missing values were grouped into one class. A separate class was made for a lactation value in the previous lactation if the cow was in its first lactation. By inclusion of this within-herd, phenotypic measurement of production, the longevity of cows was adjusted for voluntary culling and, thus, the best alternative available to measure functional longevity (2, 20).

Parity was modeled as a class effect that changed at each calving. Stage of lactation was also modeled as a class effect, and changed at calving, 60 d after calving, 180 d after calving, and 300 d after calving. Parity and stage of lactation were combined into an interaction term.

Herd was modeled as a random class variable. Yearseason was a class variable that changed for each cow on January 1, April 1, July 1, and October 1 of each calendar year. The interaction between yearseason and

herd was included in the model integrated out of the likelihood during the analyses (4, 6), and assumed to follow a log-gamma distribution.

## Methods

Survival analysis was performed using the Survival Kit developed by Ducrocq and Sölkner (8). The theory implemented in this program was extensively described in Ducrocq and Casella (4). The significance of effects was tested by a likelihood ratio test comparing the full model with models excluding one effect at a time.

The heritability of functional length of productive life on the log scale was calculated as (4):

$$h_{\log}^2 = [4 \times \text{var}(\text{sire})] / [\text{var}(\text{sire}) + \text{var}(\text{herd} \times \text{year} \times \text{season}) + \text{var}(\text{e})] = [4 \times \text{var}(\text{sire})] / [\text{var}(\text{sire}) + \text{trigamma}(\gamma) + (\pi^2/6)], \quad [2]$$

where  $\gamma$  = estimated gamma parameter for the interaction between herd, year, and season;  $\text{trigamma}(\gamma)$  = variance of this interaction, calculated as the second derivative of the logarithm of the gamma function; and  $\pi^2/6$  = variance of the extreme value distribution. The heritability on the log scale was transformed to one on the original scale, computing approximated variances on the numerator and the denominator of the heritability. These approximations were obtained using the first terms of a Taylor expansion of the sire effect and of the sum of all random effects around their means on the log scale. The resulting formula was (3)

$$h_{\text{orig}}^2 = h_{\log}^2 / [\exp\{\nu/\rho\}]^2 \quad [3]$$

with

$$\nu = \text{digamma}(\gamma) - \ln(\gamma) - \text{Euler's constant}, \quad [4]$$

where  $\text{digamma}(\gamma)$  was calculated as the first derivative of the logarithm of the gamma function;  $\text{digamma}(\gamma) - \ln(\gamma)$  = expectation of the interaction between herd, year, and season; and  $-\text{Euler's constant}$  (Euler's constant = 0.5722) = mean of the extreme value distribution. The heritability on the original scale should be interpreted as the heritability that would have been estimated in the absence of censoring but using both censored and uncensored records for a proper estimation of each effect.

The estimates for class effects were expressed as risk ratios (RR). The RR was the ratio of the hazards of two individuals differing only by the level of one effect, all others being assumed equal. The estimate of one class within each effect was arbitrarily set to zero, and the

other classes within that effect were expressed relative to this one. Thus, the RR of a particular class of an effect could be calculated as the {exponent of estimate of b} divided by the exponent of {0} if all classes within the effect were evaluated at the same point in time. If the classes are evaluated at different points in time, the baseline hazard function ( $\lambda_0(t)$  in equation [1]) should be taken into account as well (10).

The question whether BW and RW bulls could be evaluated in a joint analysis was addressed by calculating two correlations: the correlation between breeding values of RW bulls which were predicted using BW parameters and using RW parameters, and the correlation between breeding values of RW bulls which were predicted using only data on RW cows and using data on all dairy cows. Genetic trends were calculated as the average predicted breeding value for functional longevity per year of birth of the bulls.

The economic value of functional longevity was calculated using the dynamic programming model of Van Arendonk and Dijkhuizen (21). This program optimized the replacement and insemination policy on dairy farms. Involuntary culling was modeled and the relative chance of involuntary culling was one of the input parameters. From [1] it follows that an animal with a breeding value of  $u$  has a relative risk of being culled of  $\exp(u)$ . By setting the relative chance of involuntary culling to  $\exp(u)$  the effect of a genetic change can be studied. The value of  $u$  was set to  $+1/2$  and  $-1/2$  the genetic standard deviation. For both situations, the effect on herd income was computed and the effects were averaged. Herd income was expressed as net income per cow per year and annualized with a discount rate of 4% and a planning horizon of 20 yr.

From the model, the economic value of involuntary culling is calculated per genetic standard deviation per average cow. Economic values of production traits are standardized to the variance of the production in the first lactation. To standardize the economic value from the dynamic programming model to the same base of the production traits, the economic value of protein yield was computed with the dynamic programming model as well. The economic value for involuntary culling was then standardized as

$$\text{EVS}(\text{inv.cull.}) = \frac{\text{EV}(\text{inv.cull.})}{(\text{EV}(\text{prot.}))} \times (12 \times 13.7), \quad [5]$$

where EVS = the standardized economic value, EV = economic value per unit genetic standard deviation, 12 = economic value for protein yield as used in the calculation of INET (12), and 13.7 = genetic standard deviation of protein yield on the current BW basis.

**Table 2.** Input parameters for the base situation for the calculation of the economic value of functional longevity.

Parameter	Value
Kg milk adult cow	10,000
Fat percentage	4.42
Protein percentage	3.46
Adult weight cow (kg)	620
Calf weight (kg)	42
Price kg milk <sup>1</sup>	-0.04
Price kg fat	8.00
Price kg protein	12.00
Price feed per kVEM <sup>2</sup>	0.35
Price per kg slaughter weight	4.10
Price calves per kg	6.42
Price replacement heifer	2000
Discount rate per year	0.04

<sup>1</sup>Prices are all in Dutch guilders.

<sup>2</sup>VEM = Voeder Eenheid Melk ("Feed Unit Milk"), one kVEM compares with 6.9 kJ of net energy (22).

The relation between production level per herd and variance was derived from the breeding value prediction for production traits in the Netherlands. The breeding value prediction includes a correction for heterogeneity of variance per herd. The relation between level of production and variance could be approximated by a simple linear regression, which was used in the dynamic program.

Table 2 contains the parameter values for the base situation. Prices were taken from the study of Koenen et al. (14). The production of 10,000 kg of milk of an adult cow corresponds to a heifer production of 7370 kg. For this base situation, the economic value of protein yield and involuntary culling was calculated by changing the protein percentage from 3.46 to 3.4946% (+ 1%), and changing the relative risk of culling into 0.85 and 1.15. The change of the relative risk from 1 to 0.85 is equal to a change of 0.575 genetic standard deviation on the original scale, and the change in relative risk from 1 to 1.15 is equal to a change of 0.494 genetic standard deviation on the original scale.

The estimates of the sire effects were correlated with the sires' national breeding values for log-SCC, milking speed, temperament during milking, interval calving to first insemination, nonreturn at 56 d after insemination, calving ease direct effect, calving ease maternal effect, stature, chest width, body depth, rump angle, rump width, muscularity, rear leg set (side view), claw diagonal, fore udder attachment, front teat placement, teat length, udder depth, udder height, suspensory ligament, frame, and the descriptive traits overall score for udder and overall score for feet and legs. Only predicted breeding values of sires born from 1986 to 1989 were used. Sires were required to have a minimum reliability of 40% for all traits, including functional longevity. The reliability of the breeding value prediction for func-

tional longevity was calculated using the method of Meyer (15), based on the number of uncensored records of daughters, thus yielding an approximation of the true reliability. For the calculation of the correlations in BW cattle, predicted breeding values of 954 bulls were used. For RW cattle predicted breeding values of 397 bulls were used, and for all dairy cattle predicted breeding values of 1343 bulls were used. Correlations between predicted breeding values were corrected for their reliabilities by the method of Blanchard et al. (1). Furthermore, a stepwise regression procedure was used to determine the importance of each trait for the prediction of functional longevity.

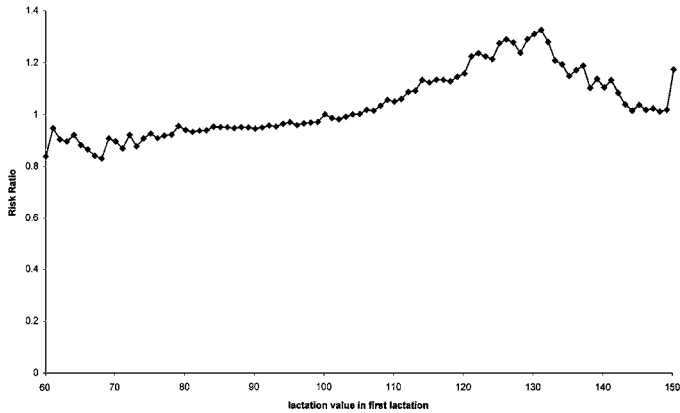
The approximated genetic correlations were used to compare different selection indices for sires for functional longevity based on both longevity information and health, fertility, and conformation information of daughters. The weighting of different traits into the index depends on the amount of information that is available for each trait, and will thus be different for different bulls. Indices were calculated for the situation in which the breeding value for conformation traits was based on information from 60 daughters, for SCC and interval calving to first insemination from 100 daughters, and for longevity from 30 daughters. This is the information that is on average available when the first daughters of a bull have finished their first lactation. It was assumed that all traits had equal genetic variance and that the phenotypic variance was dependent on the genetic variance and the heritability. For conformation traits the heritability used was 0.30, for SCC 0.15, for interval calving to first insemination 0.06 and for functional longevity 0.10. Indices were compared based on their reliabilities.

## RESULTS AND DISCUSSION

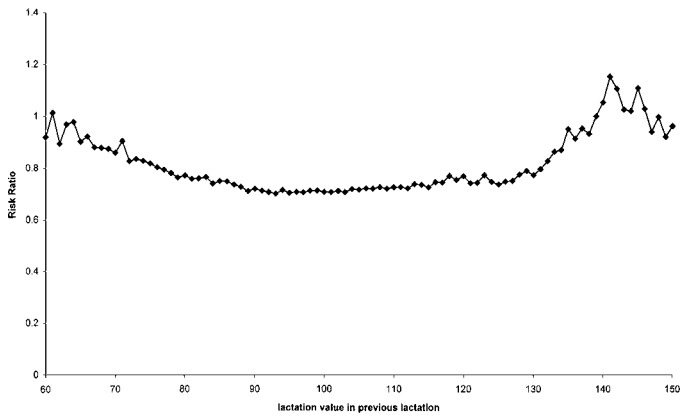
### Effects in the Model

All effects in the model were found to be significant ( $P < 0.01$ ). The estimate for the continuous effect of age at first calving was  $0.673 \times 10^{-3}$ , indicating that cows that were older at first calving had a higher risk of being culled, as was also found in other studies (9, 19, 26).

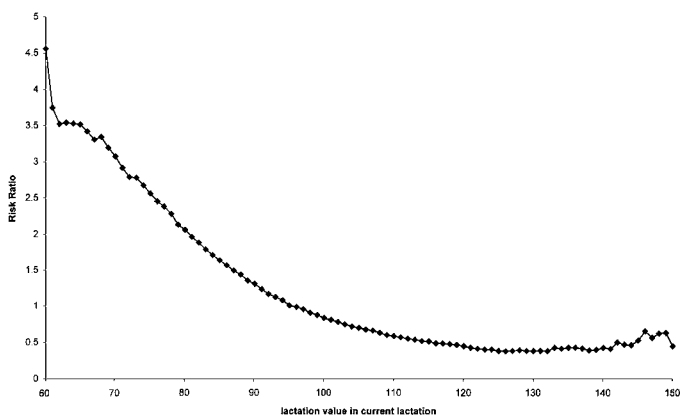
The RR associated with the three different lactation values are visualized in Figures 1 through 3. The classes 60 and 150 contain values below or equal to 60 and over or equal to 150, respectively, which caused the deviant RR for these classes. Figure 1 contains the RR of lactation value in the first lactation. After correction for all other effects in the model, a higher lactation value in the first lactation was associated with a higher risk of being culled, until a threshold was reached at 131 with a RR of 1.32, after which the RR decreased. This result was the opposite of what was expected. Cows



**Figure 1.** Risk ratios for lactation value in the first lactation.



**Figure 2.** Risk ratios for lactation value in the previous lactation.



**Figure 3.** Risk ratios for lactation value in the current lactation.

that produced more in their first lactation compared to their herdmates were at a higher risk of being culled, unless they produced so much that their risk declined.

Figure 2 contains the RR of lactation value in the previous lactation. The RR decreased with increased lactation value, until the lowest RR of 0.71 was reached at a lactation value of 90. RR stayed 0.71 until a lactation value of 105, after which it increased to 1.14 at lactation value 141. This result seemed more logical: cows producing more in their previous lactation compared to herdmates were at a lower risk of being culled, until they produced too much and their risk increased.

Figure 3 contains the RR of lactation value in the current lactation. The range of RR for this lactation value was much larger than for the other two lactation values. The cows with a lactation value of 60 or below were at a 4.6 times higher risk of being culled than their herdmates with a lactation value of 95 (RR = 1). The RR was decreasing with higher lactation values, until the optimum was reached at lactation value 130 with a RR of 0.38. Cows with a lactation value in the current lactation higher than 130 were at a slightly higher risk of being culled, also possibly because of their increased risk for diseases or fertility problems.

From Figures 1 through 3 it can be concluded that although all three lactation values were significant, the lactation value in the current lactation had by far the largest impact on survival. Whether it makes sense to include all three lactation values is debatable, because for many cows, the lactation value in the first lactation will be equal to either the lactation value in the previous lactation or the lactation value in the current lactation, which may explain the strange estimates for lactation value in the first lactation.

Table 3 contains the RR associated with different classes of change in herd size. As expected, the RR of cows decreased with increasing herd sizes, although the RR of the class with the largest herd increase (>30%, RR = 0.85) was a bit higher than that of the class with moderate increase (>10%, RR = 0.84).

### Parameters

Table 4 contains the estimates of the parameters from the survival analysis for both BW and RW cattle. The

**Table 3.** Risk ratios (RR) for different classes of change in herd size.

Change in herd size	RR
<-30%	1.64
>-30% and <-10%	1.20
>-10% and <10%	1.00
>10% and <30%	0.84
>30%	0.85

**Table 4.** Estimates of parameters from survival analysis for Black and White (BW) and Red and White (RW) dairy cattle.

Parameter	BW	RW
$\rho^1$	1.49	1.84
$\gamma^2$	4.19	1.57
hys-variance	0.27	0.88
Sire variance	0.020	0.023
$h^2_{\log}$ <sup>3</sup>	0.041	0.036
$h^2_{\text{orig}}$ <sup>4</sup>	0.11	0.098

<sup>1</sup>Parameter of baseline hazard function.

<sup>2</sup>Parameter of hys-variance.

<sup>3</sup>Heritability on logarithmic scale.

<sup>4</sup>Heritability on original scale.

estimates of  $\rho$  were 1.49 and 1.84, respectively. A  $\rho$  larger than one indicates that the baseline hazard increased over time. In a study with data from Danish Holstein cows, Neerhof et al. (16) found a  $\rho$  of 0.97 for functional length of productive life, which was low compared with other estimates from the literature. Ducrocq et al. (6) estimated a  $\rho$  of 1.355 for functional length of productive life of US Holstein cows. Ducrocq (3) used a value of 2 for  $\rho$  for the evaluation of French dairy bulls, and for the evaluation of Swiss Holsteins, Vukasinovic (27) used a  $\rho$  of 1.53. In a subset of the data used in the present study, Vollema and Groen (26) found a  $\rho$  of 1.37 for data from small farms, and 1.38 for data from large farms.

The  $\gamma$  parameter, which is a measure for the variance of the effect of herd  $\times$  year  $\times$  season, differed substantially between BW and RW cows (4.19 and 1.57, respectively). The variance due to herd  $\times$  year  $\times$  season was larger among RW than among BW cows. The sire variance in BW cows was slightly lower than in RW cows. The resulting heritabilities were comparable between BW and RW cows: 0.041 and 0.036 on the log scale for BW and RW cows, respectively, and 0.11 and 0.098 on the original scale. The differences in sire variances and herd  $\times$  year  $\times$  season variances apparently compensated each other. Vollema and Groen (26) used data on BW cows from one region of the Netherlands and found heritabilities of approximately 0.02 and 0.06 on the log and original scale, respectively, which were low compared with results from other studies. Dürer et al. (9) estimated heritabilities of 0.08 and 0.15 on the log and original scale, respectively, using data on Quebec Holsteins. Ducrocq and Sölkner (7) estimated heritabilities of 0.11 and 0.22 on the log and original scale, respectively. Neerhof et al. (16) found estimates of 0.055 and 0.22. Vukasinovic (27) found estimates of 0.072 and 0.184, respectively. Compared with these Canadian, French, Danish, and Swiss estimates, the heritability of functional length of productive life of Dutch dairy cows is rather low.

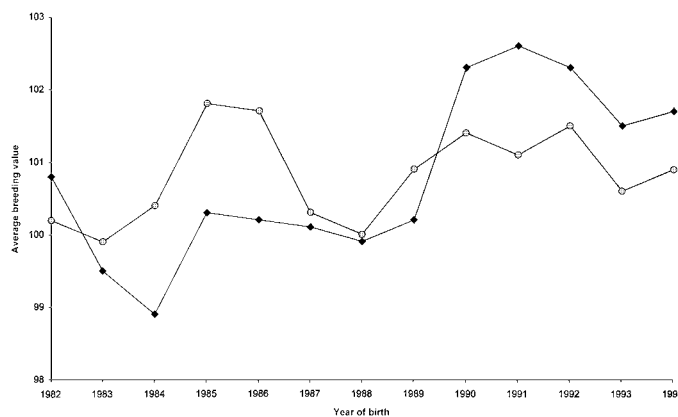
## Breeding Values

Despite the different parameters for BW and RW, the correlation between breeding values of RW bulls estimated using BW parameters and using RW parameters (see Table 4) was 0.992. Thus, the effect of the difference in parameters was very small. The correlation between breeding values of RW bulls estimated with data from RW cows and with data from all dairy cows, based on BW parameters, was 0.964. We concluded that predicting breeding values for all dairy bulls in one joint analysis was justified.

If BW and RW cattle had to be analyzed separately, breeding values of BW and RW bulls could not be compared directly with each other. Furthermore, some bulls would have both a BW and a RW breeding value for functional longevity. Although one joint analysis requires a lot of computational effort, this disadvantage is outweighed by the advantages.

## Genetic Trends

Figure 4 contains the genetic trends for BW and RW bulls. The average reliability of the breeding value for functional longevity was over 75% for both BW and RW bulls, except for the bulls born in 1992, 1993, and 1994, when the average reliabilities were decreasing to 70, 60, and 55%, respectively. From 1983 to 1989, RW bulls had a higher genetic potential for functional longevity than BW bulls. From 1990 onwards, the average breeding value was highest for BW bulls and the pattern was the same for BW and RW bulls. The difference between BW and RW was then approximately 0.8 point on the relative scale. Although no clear pattern can be seen throughout the whole period of analysis, the conclusion that the genetic trend is not decreasing seems justified.



**Figure 4.** Genetic trend for functional longevity for Black and White (◆) and Red and White (○) cattle.

**Table 5.** Economic values (EV, in Dutch guilders) of involuntary culling and protein yield for different alternatives.

Prod. cow (kg)	Prod. heifer (kg)	Replacement costs <sup>1</sup>	Change in RR	Change in income/kg protein	$\sigma(\text{protein})^2$	EV(protein)	EV(inv.cull.)	EV(protein)/EV(inv.cull.)	EVS(inv.cull.)
8000	5896	2000	1 → 0.85	14.42	13.03	187.9	73.0	0.39	63.9
8636	6365	2000	1 → 0.85	14.24	13.70	195.1	74.8	0.38	63.0
10,000	7370	2000	1 → 0.85	14.28	15.04	214.8	79.9	0.37	61.2
10,000	7370	2000	1 → 0.93	14.28	15.04	214.8	84.0	0.39	64.3
10,000	7370	2000	1 → 1.15	14.28	15.04	214.8	92.6	0.43	70.9
12,000	8844	2000	1 → 0.85	14.44	16.81	242.7	90.5	0.37	61.3
10,000	7370	2500	1 → 0.85	14.06	15.04	211.5	94.5	0.45	73.5
10,000	7370	1800	1 → 0.85	14.36	15.04	215.9	73.5	0.34	55.9

<sup>1</sup>Cost of a replacement heifer.

<sup>2</sup>Genetic standard deviation of protein yield.

## Economic Value

Table 5 contains the economic values per genetic standard deviation for different alternatives. All costs and economic values were expressed in Dutch guilders per cow per year. It appeared that the economic value of involuntary culling was not completely linear: an increase in involuntary culling cost more than a decrease.

The economic value of involuntary culling increased with increasing production level, as did the genetic standard deviation of protein yield. The ratio between the economic value of involuntary culling and of protein yield was hardly dependent on the level of production. As a result, the standardized economic value of involuntary culling (EVS(inv.cull.)) was nearly independent of the level of production as well. This had two major implications: 1) the breeding value for functional longevity, which is a measure for involuntary culling, could be weighted in the breeding goal with the same economic value for all production levels, and 2) because the economic value of functional longevity increases linearly with the genetic standard deviation of protein yield, the economic value has to be adjusted with every change in the base for the breeding value prediction for production traits.

The economic value of involuntary culling was strongly dependent on the cost of a replacement heifer. The economic value increased when the difference between the cost of a replacement heifer and the benefit from a slaughter cow increased. Van Arendonk (20) came to the same conclusion.

From data shown in Table 5, it was concluded that the economic value of functional longevity was around 65 Dutch guilders per genetic standard deviation. The economic value of the main production index in The Netherlands, the INET (Net Milk Revenue Index), has an economic value of 140 Dutch guilders per genetic standard deviation (12). The ratio between the economic values for functional longevity and production

was thus 1:2.15. VanRaden and Wiggins (23) made an overview of the relative economic values of herd life and production from the literature, and concluded that the ratio between both values was on average 1:2.5, which was in line with their own estimate. All estimates were expressed on a genetic standard deviation basis.

## Correlations with Health, Fertility, and Conformation Traits

Table 6 contains the approximated genetic correlations between functional longevity on one hand, and health, fertility, and conformation traits on the other hand for BW, RW, and all dairy bulls. Because the

**Table 6.** Genetic correlations between risk of involuntary culling on one hand, and health, fertility, and conformation traits on the other hand for Black and White (BW), Red and White (RW), and all dairy bulls (All).

Trait	BW	RW	All
Log-SCC	0.23	0.31	0.24
Milking speed	-0.14	0.01	-0.10
Temperament	-0.14	-0.06	-0.07
Interval calving to first AI	0.14	0.10	0.16
Nonreturn at day 56	-0.15	0.15	-0.15
Calving ease (direct)	0.11	0.18	0.15
Calving ease (maternal)	0.02	-0.08	-0.08
Stature	0.04	-0.15	0.06
Chest width	0.44	0.51	0.41
Body depth	0.41	0.20	0.41
Rump angle	-0.25	0.26	-0.11
Rump width	0.27	0.33	0.29
Muscularity	0.27	0.43	0.20
Rear legs set (side view)	-0.01	-0.01	0.00
Claw diagonal	-0.25	-0.13	-0.20
Fore udder attachment	-0.28	-0.47	-0.30
Front teat placement	-0.23	-0.30	-0.14
Teat length	0.14	0.29	0.19
Udder depth	-0.38	-0.50	-0.38
Udder height	-0.19	-0.41	-0.14
Suspensory ligament	-0.27	-0.38	-0.20
Frame	0.07	-0.13	0.09
Udder (overall score)	-0.48	-0.51	-0.33
Feet and legs (overall score)	-0.34	-0.20	-0.20

estimate of the sire effect from model [1] was used, a positive correlation indicated that a higher score for the trait was associated with a higher risk of being culled, and thus a shorter functional length of productive life. Correlations were different between BW and RW for some traits. Milking speed in BW was slightly correlated with functional longevity ( $-0.14$ ), while in RW it was not ( $0.01$ ). The correlation with nonreturn at 56 d was opposite in BW and RW cows:  $-0.15$  and  $0.15$ , respectively. A large difference between correlations with rump angle was found:  $-0.25$  for BW, and  $0.26$  for RW cows. Also the correlations with frame were opposite:  $0.07$  for BW, and  $-0.13$  for RW cows.

Correlations between risk of involuntary culling and chest width and body depth were strong, and positive: a high breeding value for chest width or body depth was associated with a high risk of involuntary culling, and thus a short functional length of productive life. In practice, chest width and body depth are believed to have a positive relation with longevity. This might be true if longevity is not adjusted for production, and if a higher score for chest width and body depth is associated with a higher production. Results from this study should be interpreted that if two cows have the same production, the one with the highest score for chest width or body depth has a higher risk of being culled. From this analysis, it can not be concluded whether the higher risk of being culled is because, for instance, a higher risk of displaced abomasum or because a farmer might be disappointed in a strong cow that does not produce as much as herd mates with the same scores for chest width and body depth.

As demonstrated in Vollema and Groen (25), genetic correlations between conformation and longevity traits can change substantially during time, especially in an upgrading population. In The Netherlands, the upgrading of BW cattle with Holstein genes mainly took place in the 1980s, while the upgrading process of RW cattle started later. Also, the RW population now contains fewer Holstein genes than the BW population (17), and it is expected that the percentage of Holstein genes will increase in the coming years. The correlations as estimated from the BW bulls were used to compare selection indices to choose an indirect way of predicting breeding values for functional longevity, because they were expected to reflect the correlations in the present population.

### Indirect Prediction

In the stepwise regression, traits were added to the model according to the amount of variation in functional longevity each trait explained, adjusted for variation that was already explained by a correlated trait. The

breeding values of BW bulls for functional longevity were best explained by their breeding values for the following traits (in order of explained variation): chest width, feet and legs, rump angle, log-SCC, milking speed, suspensory ligament, fore udder attachment, muscularity, interval calving to first insemination, stature, rump width, behavior, teat length, front teat placement, udder depth, and rear udder height. The breeding values used in this regression analysis were from BW AI-bulls born between 1986 and 1989. From other analyses (results not shown) it appeared that the results from the stepwise regression were highly dependent on the data set used.

Table 7 contains the genetic correlations between the traits that were further investigated in the alternative selection indices. Table 8 contains weighting factors and reliabilities of these alternative selection indices for functional longevity. For a bull whose first breeding values are predicted, the highest reliability of the breeding value for functional longevity was  $0.57$ , combining direct information on longevity of his daughters and information on nine other traits. When three traits (teat length, suspensory ligament, and interval calving to first insemination) were omitted, the reliability stayed the same (alternative 2, see Table 8).

When indices 3 to 8 were compared with index 2, omitting chest width, rump angle, and feet and legs appeared to have the highest impact on the reliability of the index. Omitting front teat placement, udder depth, or log-SCC had a much smaller effect. Based on these results, index 2 seemed a logical choice. However, because it was not clear if the genetic correlation between functional longevity and chest width was a causal relationship and also because the relationship between chest width and production needs further investigation, chest width was dropped from the index and indices 9 to 13 were calculated. It appeared that omitting chest width had no effect on the relative effect of omitting one of the other traits. Indices 14 and 15 were added to show that replacement of front teat placement by teat length and replacement of udder depth by suspensory ligament resulted in lower reliability. Therefore, we concluded that the combined index for functional longevity should be based on direct information on longevity of daughters, and on indirect information on rump angle, teat placement, udder depth, feet and legs, and log-SCC. For an average bull's first breeding value prediction the index would have a reliability of  $0.54$ . An index based solely on longevity information of daughters would have a reliability of  $0.45$  for an average young bull. With an increasing amount of information on the longevity of a sire's daughter becoming available, the indirect prediction becomes rapidly less important and the reliability increases.

**Table 7.** Genetic correlations among traits used in alternative selection indices (CHW = chest width, RUA = rump angle, FTP = front teat placement, TEL = teat length, UDD = udder depth, SUL = suspensory ligament, FAL = feet and legs, SCC = log-SCC, ICI = interval calving to first insemination, DIR = breeding value for functional longevity, directly predicted from daughter information).

	RUA	FTP	TEL	UDD	SUL	FAL	SCC	ICI	DIR
CHW	-0.10	-0.08	0.26	-0.44	-0.17	-0.02	0.03	-0.05	-0.41
RUA		-0.19	0.07	0.00	-0.10	-0.07	0.00	0.16	0.25
FTP			-0.39	0.30	0.44	0.24	-0.05	-0.19	0.23
TEL				-0.20	-0.15	-0.03	0.09	0.20	-0.14
UDD					0.35	0.20	-0.38	-0.14	0.38
SUL						0.37	0.03	0.01	0.27
FAL							0.06	-0.10	0.34
SCC								0.05	-0.23
ICI									0.14

## DU and DPS

The index for functional longevity was expressed on a scale with average 100 points, and a standard deviation of 4 points at a reliability of 80%. It was now called **DU**: durability index. Because DU aims to be independent of production, it was logical to add it to the already existing index for production (INET). The sum was called **DPS** (durable performance sum), and was calculated as

$$\text{DPS} = \text{INET} + (\text{DU} - 100) * \text{EVP}, \quad [6]$$

where DU = breeding value for functional longevity, also called durability; and EVP = economic value per point durability. With 100% reliability, the standard deviation of DU would be about 4.5 points, so the economic value per point DU was Dfl. 65/4.5 = Dfl. 14.44.

## CONCLUSIONS

From the production traits, the lactation value in the current lactation had the highest impact on survival.

The effect of using BW parameters for breeding values of RW was negligible, as was the effect of using all dairy data instead of only RW data. One simultaneous analysis could be used for all dairy bulls. The genetic trend for functional longevity was not decreasing. The economic value of functional longevity under Dutch circumstances was Dfl. 65 per genetic standard deviation. The combined index for functional longevity should be based on direct information on longevity of daughters and on indirect information on rump angle, teat placement, udder depth, feet and legs, and log-SCC. On average, the reliability of the first breeding value for functional longevity of an AI test bull was 0.54.

## APPLICATIONS

In August 1999, the first national proofs of Dutch bulls for DU were published. Four changes were made in the model used for survival analysis: 1) the effect of age at first calving was implemented as a class variable instead of a continuous variable, with 28 classes: 640 to 669 d, 670 to 684 d, 685 to 699 d, ..., 1060 to 1074

**Table 8.** Index weights and reliabilities for alternative selection indices for breeding value prediction of functional length of productive life (CHW = chest width, RUA = rump angle, FTP = front teat placement, UDD = udder depth, FAL = feet and legs, SCC = log-SCC, TEL = teat length, SUL = suspensory ligament, ICI = interval calving to first insemination, DIR = breeding value for longevity, directly predicted from longevity of daughters, REL = reliability).

	CHW	RUA	FTP	UDD	FAL	SCC	TEL	SUL	ICI	DIR	REL
1	-0.39	0.32	0.15	0.11	0.28	-0.19	0.03	0.10	-0.11	0.66	0.57
2	-0.36	0.30	0.18	0.14	0.31	-0.18				0.67	0.57
3		0.32	0.17	0.29	0.28	-0.14				0.71	0.54
4	-0.38		0.13	0.14	0.29	-0.17				0.71	0.54
5	-0.36	0.27		0.19	0.33	-0.17				0.68	0.56
6	-0.41	0.30	0.21		0.32	-0.21				0.67	0.56
7	-0.33	0.28	0.23	0.20		-0.14				0.71	0.54
8	-0.34	0.30	0.18	0.21	0.29					0.68	0.56
9			0.11	0.30	0.26	-0.13				0.76	0.51
10		0.29		0.33	0.30	-0.13				0.73	0.53
11		0.32	0.24		0.31	-0.21				0.74	0.52
12		0.30	0.21	0.33		-0.11				0.75	0.51
13		0.31	0.17	0.34	0.26					0.72	0.53
14		0.30		0.31	0.30	-0.13	-0.10			0.72	0.53
15		0.33	0.18		0.28	-0.21		0.16		0.73	0.52

d, 1075 d and up; 2) the lactation value in the first lactation was removed from the model, because for many cows this was the same as the lactation value in the previous or current lactation; 3) a fixed, time dependent effect of year  $\times$  season was added for a better correction for trends; and 4) instead of a genetic group for the dam of a cow, the effect of maternal grandsire was included in the model, with unknown maternal grandsires being replaced by genetic groups in the same way as in the pedigree. Apart from information on longevity of daughters, also information on rump angle, front teat placement, udder depth, feet and legs, SCC, and interval calving to first insemination was included in the breeding value. The latter trait was added to the index because it was thought a fertility trait should be included. The economic value that was used to add DU to INET, resulting in DPS, was rounded to Dfl. 15 per point DU.

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