

E-19 Breeding value for Longevity (LON)

▪ Introduction

The life span of a dairy cow indicates how long a cow has been able to prevent being replaced due to a shortcoming. In other words, how satisfied her cattle breeder is with her. A cattle breeder considers many traits when determining his culling policy. Roughly, these traits can be divided into production, fertility, health and workability. As cows are kept for the purpose of producing milk, replacement based on an unsatisfactory production is called voluntary culling, and replacement based on other traits is called involuntary culling. In practice, the reason that a cow is culled is seldom due to only one of these two. A cow that is not in calf following insemination and with a low milk production is more likely to be culled than another cow that is also not yet in calf, but that has a higher production of milk.

The actual life span of a dairy cow depends upon the cattle breeder's decision to have it culled. Assuming that a constant number of cows are kept in a herd throughout the years, one can easily calculate the actual life span on an operation using '1/replacement percentage'. The replacement percentage is the number of heifers divided by the total number of dairy cows. In this way, the life span is expressed in terms of the number of lactations. The same applies on a national level. According to the Annual Statistics, the replacement percentage has been just above 30% for years now. This means that the average realised productive life span has equalled 3.3 lactations during this time. The average number of milking days of all of the lactations, including the incomplete records, is 300 days. The following Table presents information concerning the life span of the cows included in the milk recording system that have been culled from 1989 up to and including 2005. The productive life span, this is the period between the first calving date and the culling date, is expressed in the number of days.

Table 1. The productive life span of cows included in the milk recording system and that were culled in the period 1989 – 2005

year	days	year	days	year	days
1989	1217	1994	1171	2000	1108
1990	1183	1995	1206	2001	1132
1991	1201	1996	1161	2002	1147
1992	1175	1997	1133	2003	1183
1993	1179	1998	1150	2004	1207
		1999	1121	2005	1224

Because the cattle breeder determines the life span of a dairy cow, it is difficult to visualise the results of selection for longevity. As it is, the dairy farmer continues to select cows in his herd, which is mainly determined by the percentage of young heifers, compared to his dairy herd, which he raises each year. Because of this selection based on longevity will not give longer realised herd life. Selection on life span only gives a longer herd life in case the dairy farmer really decides to raise less young stock and starts milking less new heifers (lower replacement rate). With a constant replacement rate and a genetic improvement of the the herd, involuntary culling will be replaced by voluntary culling (on the population level).

The Dutch breeding value for Longevity (LON) is a figure that indicates how satisfactory the daughters of a certain bull function. It is a measure to rank bulls for the ability of their daughters to resist culling.

▪ Direct and indirect information

The milk recording data provides information concerning when a cow is calving for the first time and when her last test milking occurred. The productive life span can then be calculated as the difference between these two dates. This information is the *direct* information that is analysed in the breeding value estimation. As the heritability of Longevity is low (about 12%) and it may take quite some time before enough direct information is available concerning the life span of the daughters of a bull, information on correlated (predictive) traits is also used in the case of young bulls. This information is the *indirect* information. The definite breeding value for Longevity consists of two components: one based on the direct breeding value for Longevity (direct information), and one based on the breeding values for other traits (indirect information). The amount of information from both sources may vary per bull. For this reason, an estimation of the ratio of direct and indirect information for each bull is provided.

When the breeding value of a bull is calculated for the first time, the indirect information results in an increase in the reliability of approx. 20%. As a bull grows older, more direct information about life span becomes available and so the indirect information becomes less significant.

▪ Direct breeding value estimation

a. Data

The direct breeding value estimation is based on the direct information concerning the life span of the herd book daughters of a bull. The productive life span is calculated from the data from the milk recording system: the number of days between the first calving and the last test milking. If a cow is transferred to a different herd that participates in the milk recording system, then this has no effect whatsoever on the calculation of her life span. As it is, there are two effects to be considered in the season in which the transfer occurs: the first on the first herd and the second on the other herd. Both HYS-effects (herd*year*season effects) are taken into account. If she is transferred to a herd that is not participating in the milk recording system, then her definite life span will not be known, but her life span up until that moment, which is a minimum value of the definite life span, will be known.

A cow must be at least 640 days old when calving for the first time in order to contribute to the breeding value of a bull. In addition, she is to have had a test milking after January 1, 1988.

b. Survival analysis

The direct life span data is analysed using the survival analysis. The methodology of the survival analysis is characterised by the following: 1. the animals of which the definite life span is not (yet) known are also included in the analysis, 2. it allows for an exact adjustment for interfering effects, and 3. the chance of culling can be modelled per parity and within parity for lactation stage.

The survival analysis does not examine the life span, but rather the likelihood of culling. Life span and chance of culling are closely connected.

As long as cows are still alive, their actual life span remains unknown. The data of such cows cannot be included in methodologies such as those used in the breeding value estimation for other traits. If the data were to be included, it would mean that the breeding value for the life span would be continually underestimated, especially in the case of young bulls. After all, a young bull has young daughters by definition. If the method only analyses the data of the daughters that have already been culled, then this data will always concern daughters that were replaced at a young age. This will mean a low breeding value, independent of how many daughters are still alive.

The survival analysis also considers the data of the daughters that have not (yet) been replaced. This is possible because the analysis considers the likelihood of culling, rather than the life span itself. A cow that is still alive has not been replaced in the competition with her herd mates and this provides information on her life span compared to that of her herd mates. In this way, one can obtain a usable breeding value for Longevity for a young bull as well.

The second advantage of the survival analysis is the precise modelling. It is assumed in traditional methodologies that the influence of any interfering effect is continuous. In the survival analysis, it is possible to incorporate a time component (the effect is time-dependent). An example: the effect of the herd*year*season*parity (HYS) is incorporated in the breeding value estimation for production (Chapter E-7, Handbook CRV). Depending upon the operation and the date of calving, a HYS-effect is defined for each parity; one that applies to that particular parity, that is to say, during the entire lactation period. Where the life span is concerned, it is obvious that a single HYS-effect for the entire life of a cow may be too long. For example, the quota system will cause the culling policy (and therefore the life span) in the beginning of the calendar year to differ from the other seasons.

Survival analysis offers the opportunity to alter the HYS per season. The HYS-effect also changes if a cow is transferred to another herd. Figure 1 presents an example of a time-dependent HYS-effect in the form of a diagram. The likelihood of culling due to the HYS-effect varies with each season. Even if the cow is transferred from one herd to the other (at the end of May), the HYS-effect on the likelihood of culling will change. It is also possible to model other effects with a time component in the same way, so that the adjustment for these interfering influences is very precise.

Besides the two advantages mentioned, the survival analysis does have one disadvantage. Due to the complexity of the calculation method, one will require a great deal of computer capacity in order to estimate a limited number of animal effects. In addition, there is too little information available concerning cows to allow one to estimate a reasonably reliable breeding value for the female part of the herd. This is why a sire-maternal grandsire model is used for the breeding value estimation, instead of an animal model.

The survival analysis is conducted using the "Survival Kit". This is a set of programs written by Vincent Ducrocq and Hans Sölkner for the purpose of estimating both the necessary parameters as well as the breeding values for large populations (Ducrocq and Sölkner, 1998).

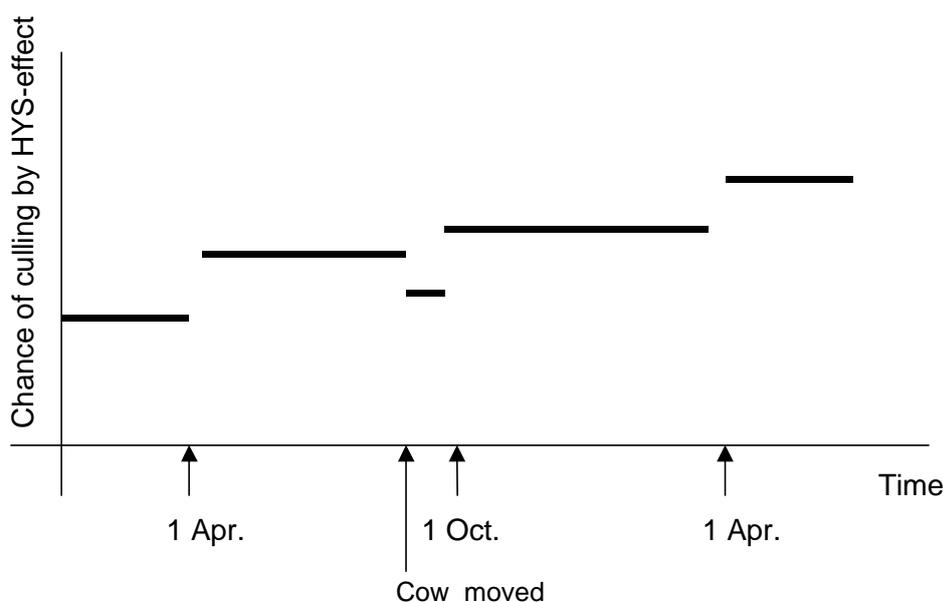


Figure 1. Example of the time dependent HYS-effect for a cow, transferred from one herd to an other (at the end of August)

Table 2. Parameters (rho's) of the Weibull distribution estimated per parity-lactation stage class

Parity	1	2	3
Lactation stage			
0-30 days	1,48	1,42	1,32
31-190 days	1,02	1,39	1,32
191-250 days	0,98	1,17	1,09
251-330 days	1,23	1,36	1,21
> 331 days	1,94	1,77	1,38
Dry period	0,00	0,00	0,00

c. Statistical model

The model for the direct breeding value estimation for Longevity is:

$$Y_{ijklmnopqrs} = \text{HYS}_i + \text{PARSTA}_j + \text{PARY2M}_k + \text{HSA}_l + \text{FCA}_m + \text{HETER}_n + \text{RECOM}_o + S_p + \text{MGS}_q + \text{GG}_r + e_s$$

in which:

- $Y_{ijklmnopqrs}$: Likelihood of culling a cow;
- HYS_i : Herd*Year*Season category i , in which two classes per year. This random class effect is time dependent and changes when a cow is transferred, and on April 1 and October 1 of each year. It is assumed that the dispersion follows the gamma distribution (see Table 2 parameters);
- PARSTA_j : Parity*Lactation Stage Class j . The parities are divided in Parity 1, parity 2, parity 3 and higher. The stages changing by 30, 190, 250 en 330 days. The dry cows have their own class. The Weibull distribution is used for the PARSTA effect. The phenotypical chance of culling is presented in figure 2. The rho's from July 2004 are presented in table 2.
- PARY2M_k : Parity*Year*2month Class k . This 2 month class effect is time-dependent, changing on the 15^e of the odd months, starting in January 1988 for 10 parity classes.
- HSA_l : Herd Size Alteration Class l . The HSA is a time-dependent class effect and is calculated by comparing the number of cows present in a herd on January 1st, with the number of cows on the same herd on January 1st, one year earlier. Seven classes are distinguished between: shrinkage between 90 and 50%, shrinkage between 50 and 30%, shrinkage between 30 and 10%, neither shrinkage nor growth over 10%, growth between 10 and 30%, growth over 30%, and herds that were terminated (more than 90% shrinkage).
- FCA_m : Age at the time of the first calving m , expressed in days. This effect is categorised in classes of 15 – 30 days, depending upon the number of animals per class. This effect is measured independent of the time, that is to say, it is assumed that the effect of FCA remains the same during the entire life span of a dairy cow;
- HETER_n : Heterosis effect p : divided in 10 classes, with steps of 12,5%;
- RECOM_o : Recombination effect q : divided in 10 classes, with steps of 6,25%;
- S_p : Sire effect r , thus half of the additive genetic effect or half of the breeding value of the sire, as a time-dependent random class effect (see Table 3 for the heritability);
- MGS_q : Maternal Grand Sire effect s , thus quarter of the additive genetic effect or quarter of the breeding value of the maternal grand sire, as a time-dependent random class effect (see Table 3 for the heritability);
- GG_r : Genetic Group s of the maternal grand dam (the dam of the dam), based on her breed and the daughter's year of birth, as a time-dependent random class effect;
- e_s : Residual term t , anything that is not explained by means of the model.

The change in the size of a herd is incorporated because a herd that is expanding will adopt a replacement policy that is totally different from that of a herd that is cutting back. The age at the time of the first calving is shown to have an effect on the life span of dairy cows. Cows that are relatively old at the time of the first calving have a shorter life span than cows that are relatively young. With every thirty

days, the likelihood of culling increases by approx. 2.5% for a cow that calves for the first time. This effect continues throughout the life of the cow, as the effect is incorporated independent of time.

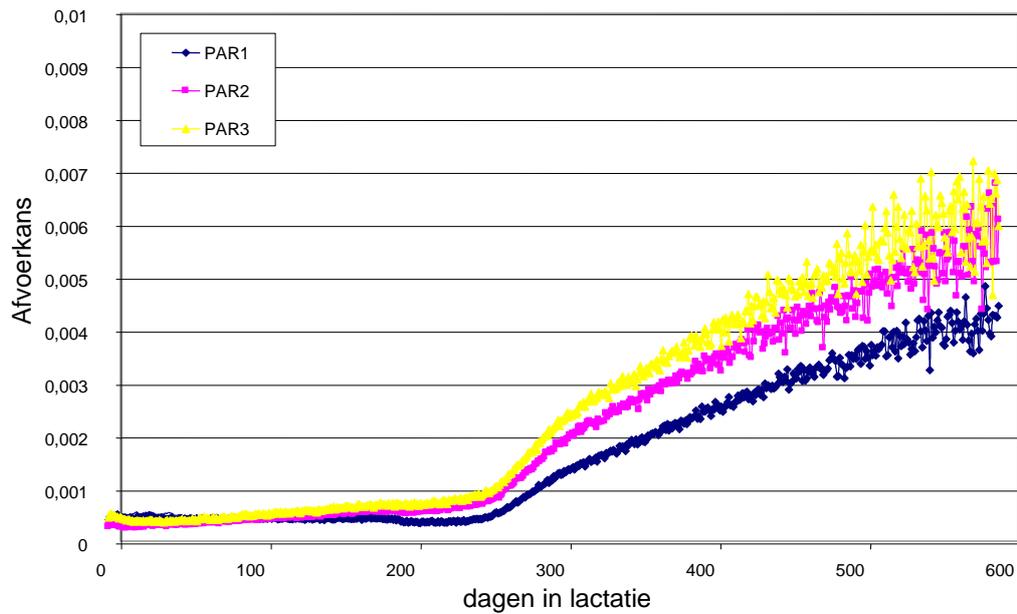


Figure 2. Relative likelihood of culling per lactation per lactation stage

Figure 2 illustrates the likelihood of culling during the lactation period. The diagram shows that the likelihood of culling in the case of two-year-olds does not strongly depend upon the stage of lactation, but that the chance sharply increases in the second stage during subsequent lactation periods.

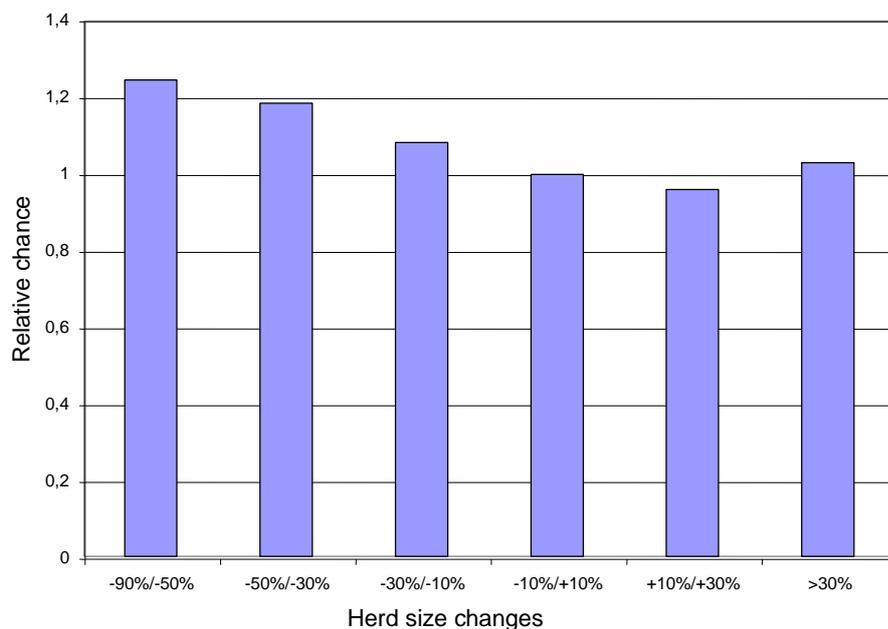


Figure 3. Likelihood of culling per change in herd size

Figure 3 illustrates the change in the likelihood of culling in the event that the size of the herd changes.

The estimated maximum heterosis effect is a longer productive life span of 130 days. This longer life span resulting from heterosis is equal to 45% of the genetic standard deviation of longevity. For milk production the estimated heterosis effect in the breeding value estimation is 148 kg milk, which is about the same as 21% of the genetic standard deviation of milk production.

The estimated maximum recombination effect (50% recombination) is a 35 days shorter productive life span. This shorter life span is equal to 13% of the genetic standard deviation of longevity. For milk production the estimated recombination effect (50% recombination) in the breeding value estimation is –62 kg milk, which is about the same as 9% of the genetic standard deviation of ilk production.

From the heterosis and recombination estimation for longevity can be concluded that heterosis relatively has bigger effect and recombination has a smaller effect compared with milk production.

An extensive sire model is used for the breeding value estimation: the ‘sire-maternal grandsire model’. The breeding value of the bull is not estimated via the information of the daughters alone, but also with information on the granddaughters via the female bloodline and the bull’s family relationships. If the ancestors of bulls are unknown, then these are incorporated in the relationship matrix using genetic groups, which are defined on the basis of the breed and the year of birth. There is optimal consideration for the genetic merit of the dam of the cow through the maternal grandsire and a genetic group for maternal grand dam, which are included in the model. The genetic group of the maternal grand dam is determined on the basis of her breed and year of birth. In this way, the results are adjusted for any selective use of certain bulls.

d. Parameters

Table 3. Parameters that are used for the breeding value estimation for Longevity

Parameter	Value
Gamma	4.95
Heritability (original scale)	0.12

▪ Indirect breeding value estimation

a. Reliability

Essentially, the breeding value for Longevity is estimated using data on the life span of the daughters and granddaughters of a certain bull. However, the reliability of the breeding value estimation of a bull depends upon the heritability that applies for the trait for which a breeding value is being estimated, and on the amount of information that is available. The heritability for Longevity is not very high: 0.10. In comparison: the heritability for milk production is 0.59. This means that in order to obtain a certain degree of reliability in the breeding value estimation for Longevity, one will require more information than in the case of milk production. Particularly where young bulls are concerned, the available information is scant. The reason is that the amount of information depends upon the number of daughters that have already been culled.

b. Predictors

Which is why indirect information is used, in addition to the direct information concerning the life span. Breeding values are calculated for a whole range of predictive traits (type, somatic cell count, fertility). In the case of young bulls, these breeding values are used to increase the reliability of the breeding value for Longevity. In the case of older proven bulls, the indirect information does not contribute anything new to the breeding value for life span.

c. Weighing factors predictive traits

There are a number of traits that show a correlation to longevity. Here, the most important are those that, combined, provide the best prediction. The traits of which the breeding values, in addition to the direct information concerning Longevity, are incorporated in the estimation of the breeding value Longevity are the following:

- udder depth
- locomotion
- somatic cell count (on a logarithm scale)

Table 5. Genetic correlation between Longevity and predictors

trait	correlation
udder depth	0.22
locomotion	0.24
log-somatic cell count	0.44

The weighing factors that are used to weigh the predictive traits in the breeding value for Longevity depend upon the heritabilities of the traits, the correlation between the traits and the amount of information that is available per trait.

The extent to which the predictive traits contribute to the estimated breeding value for Longevity largely depends upon the number of daughters for which culling data is already available.

Incomplete records

Up until 1999, the percentage of incomplete records was often used as a measure for the life span inheritance of bulls. Not entirely justifiably, as the percentage of incomplete records was not adjusted for any interfering effects, and was therefore certainly not a breeding value. The correlation between the percentage of incomplete records and the breeding value for functional life span is 0.4. Therefore, the percentage of incomplete lists does indicate something about the genetic merit towards trouble-free functioning, but by far not everything. The information that was used in calculating the percentage of incomplete records is also used in the breeding value estimation for Longevity. With the arrival of the new breeding value for Longevity, the percentage of incomplete records will no longer be published.

▪ Publication

The breeding value for Longevity is presented as a complete breeding value, expressed in days. The standard deviation of the breeding value Longevity is 270 days. The breeding value for Longevity is published for an AI sire if the reliability is 30% or more.

In addition, a maximum of 70% of the daughters or granddaughters may have a first calving date prior to January 1, 1988. This in order to prevent the situation in which only a very selected group of offspring is analysed, for which possibly a different selection policy was used from that of the larger part of the offspring. This would result in an incorrect breeding value estimation; this particularly concerns bulls born before 1984. In the case of these bulls, a breeding value is calculated on the basis of the expectation values and the predictors.

▪ Basis

Breeding values for longevity traits of bulls are published on 3 bases: a Black&White base, a Red&White base and a Local base. The definitions of these bases are as follows:

Black&White base (Z):

AI bulls born in 2001 and 2002 with at least 87.5% HF blood and 12.5% or less FH blood, with Black&White color and an official breeding value for the concerning trait;

Red&White base (R):

AI bulls born in 2001 and 2002 with at least 87.5% HF blood and 12.5% or less FH blood, with Red&White color and an official breeding value for the concerning trait;

Local base (Y):

AI bulls born in the period from 1998 until 2002 with at least 87.5% MRIJ blood and 12.5% or less HF blood and an official breeding value for the concerning trait.

Every 5 years, in a year divisible by 5, the reference year for the base is moved 5 years. The base differences are shown in Table 6.

Table 6. Base differences for Longevity

	Z → R	R → Y	Z → Y
Longevity	140	162	302

▪ Literature

Van Arendonk, J.A.M., 1985. Studies on the replacement policies in dairy cattle. II. Optimum policy and influence of changes in production and prices. *Livestock Production Science*, vol. 13, pag. 101.

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