Breeding value for functional longevity in the Netherlands

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Abstract

In August 1999, the first official index for longevity will be published in The Netherlands. This index will be estimated using both information on longevity of sires' daughters (direct breeding value), and information on sires's breeding values for functional traits (indirect breeding value). The index aims to be an overall measure for the functionality, or ability to delay involuntary culling, of the daughters of a bull. As more information on the longevity performance of daughters becomes available, the weighting on the direct breeding value will be heavier.

The direct breeding value is predicted using survival analysis techniques as programmed in the "Survival Kit". Data on cows is available through the milk recording and I&R databases. In the model, the baseline hazard is assumed to follow a Weibull distribution. The model furthermore includes the effects of age at first calving; the interaction between parity and stage of lactation; the interaction between herd, year, and season; production compared to herdmates; change in herd size; lactation value of cow; genetic group of maternal granddam; maternal grandsire; and sire. The pedigree file contains sires and maternal grandsires of bulls. The heritability estimated on log-scale is 0.04. When a young sire has longevity information on 30 daughters, the reliability of the direct index only will be 0.43.

Regression techniques and selection index theory were used to identify which breeding values for functional traits explain most variation in direct breeding values for functional longevity. Traits that are suitable for including in the indirect breeding value are rump angle, teat placement, udder depth, feet and legs, somatic cell count (on log-scale) and interval calving – first insemination. Adding the information on conformation (60 daughters), fertility traits and SCC (100 daughters) to the direct information on longevity (30 daughters) increases the reliability of the combined index to 0.55. As the relative weighting of each source of information is dependent on the number of daughters, it will be determined for each bull separately.

1. Introduction

In August 1999, breeding values for longevity will be published for the first time in The Netherlands. This index will be estimated using both information on longevity of sires' daughters (direct breeding value), and information on sires' breeding values for functional traits (indirect breeding value). The index aims to be an overall measure for the functionality, or ability to delay involuntary culling, of the daughters of a bull.

This paper describes the method of estimation a breeding value for longevity in The Netherlands and how this breeding value is combined with breeding values for functional traits.

2. Estimation of breeding values for longevity

2.1 Data

Lactation data of herdbook registered cows are used. The data contain Black and White cows and Red and White cows. Lactations with calving date January 1988

and onwards are used for the genetic evaluation. Cows calving for the first time younger than 640 days are discarded. Cows moving herds during a lactation get in the milk recording system an extra part lactation. By this milk production realised in different herds can be taken into account. Further data from the Identification and Registration system is used to keep track of the movings of cows in more detail. This data reveals if a cow culled from a milk recording herd went to a slaughterhouse or to a non-milk recording herd, i.e. this data reveals if a cow died or not. In the first case a record is uncensored while in the second case the record is censored.

2.2 Method

Breeding values are estimated with the survival analysis using the Survival Kit developed by Ducrocq and Sölkner. The hazard function is modelled as:

$$\lambda(t,z(t)) = \lambda_0(t)\exp\{z(t)'b\} \qquad [1]$$

where $\lambda(t,z(t))$ is the hazard function of an individual depending on time t, $\lambda_0(t)$ is the baseline hazard function assumed to follow a Weibull distribution, and z(t) is a vector of (possibly time dependent) fixed and random effects with corresponding parameter vector b.

The following effects are included in the model:
- herd*year*season: random class effect, time dependent;
- parity*stage of lactation: class effect, time dependent;
- herd size change: class effect, time dependent;
- age at first calving: continuous effect, time independent;
- lactation value: class effect, time dependent
- sire: random class effect, time independent;
- maternal grandsire: random class effect, time independent;
- genetic group maternal granddam: class effect, time independent.

Herd*year*season

Four seasons are distinguished, changing on the first of January, April, July and October each year. Further this effect changes when a cows changes herd. The effects of herd and year*season are combined into an interaction term, which is absorbed during analysis and is assumed to follow a gamma distribution.

Parity*stage of lactation

Parity changes at the beginning of each lactation; parity number 7 and higher are treated as one class. Stage of lactation changes at calving and at 60, 180 and 300 days after calving.

Age at first calving

The effect of age at first calving (expressed in days) is assumed to be linear with herdlife and being constant during the cows' life.

Herd size change

Herd size change is computed by comparing the number of cows present on the 1st of January with the number of cows in the same herd one year later on the 1st of January. Eight classes are distinguished: herd which stopped during that year, herds decreasing with more than 50%, herds decreasing with 30-50%, herds decreasing with 10-30%, herds staying about the same size (-10% to +10%), herds increasing with 10-30%, herds increasing with more than 50% and herds having data in current year (so no increase or decrease can be determined).

Lactation value

Lactation value is a management figure to compare phenotypic performances of cows within a herd. This figure is presented to the farmer after each milk recording and is a combination of milk, fat and protein yield weighted with economic weights. It is a relative figure with the herd mean set to 100. A cow having a lactation value of 110 is 10% better than her herdmates. Three different lactation values are used as effect in the model: the lactation value of current (time dependent changing at beginning of lactation), previous (time dependent changing at beginning of lactation) and first lactation (time independent) are used to correct for the effect of production on herdlife. The lactation value of previous lactation is added to the model to correct in case the

cow was sick during the last milk recording. Figures 1,2 and 3 show the estimated effects of the three different lactation values. Lactation value of the current lactation clearly hat the largest effect.

Sire and maternal grandsire

The sire and maternal grandsire effect are assumed to follow a multinormal distribution. Relationships between sires and maternal grandsire are identified through their sires and maternal grandsires.

Genetic group maternal granddam

To take into account the effect of maternal granddam on a cows' herdlife genetic groups are formed based on the breed code of the maternal granddam and year of birth of the cow.

2.3 Parameters and model test

Based on a data set of Black and White cows parameters were estimated. Rho, gamma and heritability were estimated. The model mentioned above was used, except leaving out the maternal grandsire effect. Data on 118,282 cows originating from 2904 sires was used. The estimates are in table 1.

All effects in the model were significant.

Table 1 Parameters estimated on Black and White cows.

Parameter	
Rho	1.49
Gamma	4.19
Herd*year*season variance	0.27
Sire variance	0.020
Heritability (log-scale)	0.041
Heritability (original scale)	0.11

Table 2. Genetic correlation between functional longevity and other functional traits based on two data sets: Black&White bulls born between 1986 and 1989 and between 1990 and 1994.

Trait	Correlation with functional longevity	
	1986-1989	1990-1994
Somatic cell score	-0.23	-0.36
Rump angle	0.25	0.19
Feet&legs	0.33	0.33
Udder depth	0.38	0.36
Teat placement	0.23	0.25
Chest depth	-0.41	-0.23
Interval calving-1st insemination	-0.14	-0.37

3. Predictors for longevity

As it takes a long time before breeding values for functional longevity for get high reliabilities the possibility to predict functional longevity from other functional traits was analysed. Stepwise regression and selection index calculations shoed that the best predictors were: somatic cell score, rump angle, teat placement, udder depth and feet and legs score (table 2).

Chest depth could also be used as predictor but the correlation with functional longevity over time was not stable. The fertility trait 'interval between calving and first insemination' had a rather promising genetic correlation with functional longevity for the bulls born between 1990 and 1994 but the correlation was much lower for the bulls born between 1986 and 1989.

The reliability of the EBV for a bull with first crop daughters at the end of first

lactation increases by 10% when information on the five predictor traits is added to the functional longevity information. The functional longevity index based on longevity data only has a reliability of 0.43 while the index using also predictor traits reaches up to 0.54 assuming a first crop of 100 daughters of which 30 daughters are culled at the end of the first lactation. The breeding values for functional longevity and the predictors are combined using a selection index. The weight of a breeding value in the index depends on the amount of information the breeding value is based on. For every bull separate index weights are computed when combining the information.

Figure 1 Effect of lactaton value of current lactation on longevity.

RR for LV of current lactation
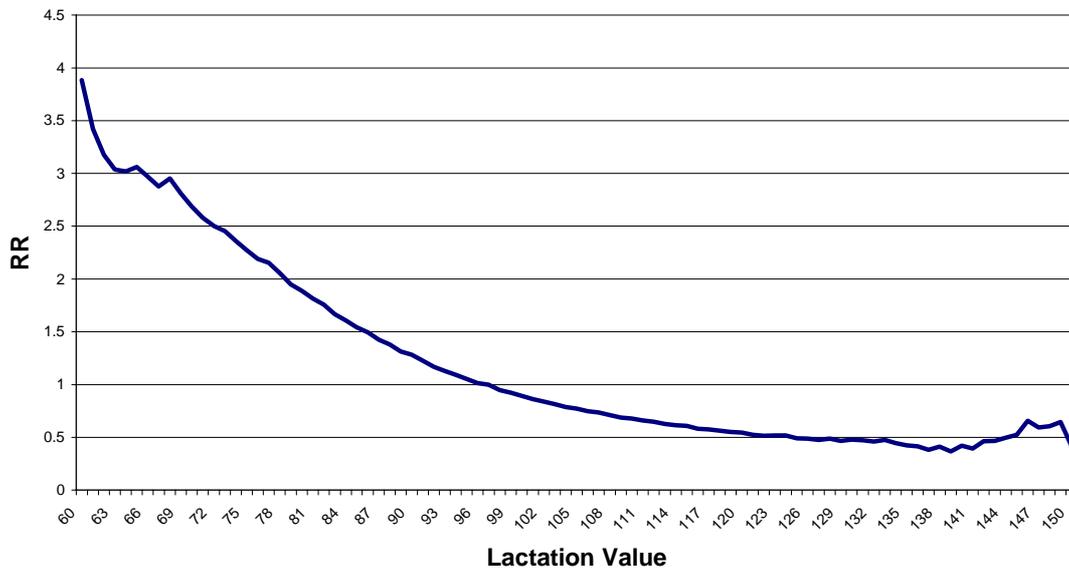
Figure 2 Effect of lactaton value of previous lactation on longevity.

RR of LV of previous lactation
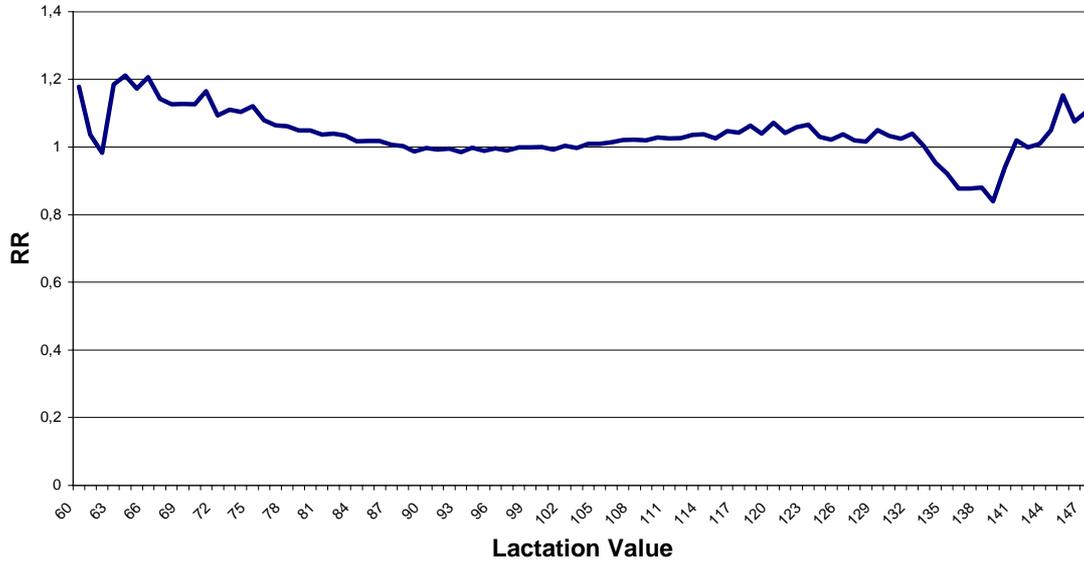
Figure 3 Effect of lactaton value of first lactation on longevity.

RR for LV of first lactation