

GENETIC PARAMETERS FOR MORTALITY OF REPLACEMENT HEIFERS DURING THE FIRST YEAR IN THE NETHERLANDS

A.G.F. Harbers, M.J.G. Boemaars and M.H.F. de Werd

NRS, PO Box 454, 6800 AL Arnhem, The Netherlands

INTRODUCTION

Functional longevity in dairy cattle is a trait that receives much attention in the durable performance sum (DPS), the Dutch total merit index (Vollema *et al.* 2000). In this index functional longevity is a measure of involuntary culling of lactating cows. Stillbirth, defined as a calf that dies just prior to, during or within 24 hours after parturition, is another trait for which a genetic evaluation is available (Harbers *et al.* 2000). Parameters for the period between birth and first lactation are not available in the Netherlands. The economic importance of this stage is substantial: the costs of raising replacement heifers represents 15 to 20% of the total milk production costs (Heinrichs 1993). The average costs of replacing a heifer during the first year are € 250 (PR 2000).

Mortality is a stayability trait measuring whether or not an animal is alive at a certain age. It is therefore a binary trait and it does not contain complete information (Vollema 1998). Mortality of calves occurs mainly during the first month of life according to Olsson *et al.* (1993). They report an overall mortality of 2.1% during the first 3 months of which 1.3% occurs in the first month. Heinrichs (1993) reports mortality of calves from birth to 1 year of age to be from 6 to 20%. A mortality rate of 8.1% during the whole rearing period was found in a survey among 959 Dutch farmers (Mourits 2000).

Mortality of replacement heifers can be used as a trait within the durable performance sum and thus become part of the breeding objective. Besides an economic importance breeding objectives must have a genetic component. The trait could also be used as a predictor of a breeding objective trait with a low reliability, when the genetic correlation between predictor and breeding objective is high and the predictor has a high reliability early in the life of the animal. A third option is to monitor the population. This gives the tools for a quick reaction if the genetic trend is undesirable.

The objective of this study was to estimate phenotypic and genetic parameters for mortality of replacement heifers from 3 days to 1 year of age in the Netherlands and to evaluate the possible use of the trait in a breeding program.

MATERIALS AND METHODS

Trait definition. Five mortality traits were defined. The first trait was mortality within 14 days of age (MOR3-14). For each female calf alive at 3 days of age this trait was scored as a failure if she was culled before or at 14 days of age, otherwise she got a success score. The second trait was mortality within 30 days of age (MOR15-30). Animals culled before 15 days of age did not get a score for this trait. Animals alive at 15 days of age got a failure score if the animal was culled before or at 30 days of age. The other three traits were mortality within 90 days of age (MOR31-90), mortality within 365 days of age (MOR91-365) and mortality within 365 days of age for all animals alive at 3 days of age (MOR3-365). The first four traits measure

mortality in different time periods within the first year and the last trait measures overall mortality in the first year.

Definition of the traits were based on the major culling reason in each time period. During the first 14 days enteritis caused by *E. Coli* is the main culling reason. Enteritis caused by pathogens other than *E. Coli* is the major culling reason in the second half of the first month after birth. In the second and third month of life respiratory diseases largely affect culling. After the third month calves are culled for various reasons.

Data editing. Data from calves born from March 1st 1993 to March 1st 1999 were used. Female calves born and raised in the same herd were considered to be replacement heifers. Only herdbook registered Holstein Friesian replacement heifers with a gestation length between 260 and 300 days were considered. Calves had to be alive at day 3 after birth. Death at day 1 is considered stillbirth (Harbers *et al.* 2000) and death at day 2 was excluded because of data quality. Finally, records from herds with less than 20 replacement heifers per year or from sires with less than 60 daughters were discarded. The total dataset contained 1,486,335 records. A dataset with breeding values for stillbirth and functional longevity of the sires was available based on the latest routine evaluation of these traits.

Statistical analyses. The binomial observations were analysed with single trait sire models with fixed effects: parity of the dam (7 levels), herds size (12 levels), gestation length (8 levels), month x year of birth (72 levels) and herd x 3 year period (10780 levels). Random effects were sire and residual. The number of sires with at least 60 records was 2287. Pedigree of each sire was traced back two generations. The pedigree file included 2454 bulls in total. Contemporary groups were defined as all replacement heifers born within a herd during a 3 year period. This was done to ensure that contemporary groups were large enough.

Variance components were estimated with ReML assuming a normal distribution of the trait. Heritabilities on the binomial scale were transformed to heritabilities on the continuous scale (Dempster and Lerner 1950). Genetic correlations between the mortality traits and between functional longevity, stillbirth and MOR3-365 were approximated using the method of Calo *et al.* (1973) including bull solutions with a reliability of at least 70% ($n = 44$).

Economic analysis. The economic value of mortality was based on the average replacement costs of heifers culled in their first year. The extra selection response due to inclusion of mortality in the breeding goal was determined by calculating the economic value per genetic standard deviation per cow per year and comparing it to the response obtained with the current traits in DPS (Vollema *et al.* 2000).

RESULTS

Statistical analyses. Table 1 shows the unadjusted means of the five different mortality traits and the relative contribution of each time period. Mortality within 14 days of age accounted for 27% of the total mortality in the first year. In the first month of life 44% of the overall mortality in the first year occurs, reflecting the importance of the first month of life.

Estimates of genetic parameters are in Table 2. Heritabilities on the binomial scale are less than 0.01 for all mortality traits. This heritability is an underestimate of the heritability on the continuous scale because of the discrete nature of the data. On the continuous scale heritabilities range from 0.03 to 0.06.

Approximated genetic correlations between the mortality traits range from 0.48 to 1.00. Adjacent time periods have genetic correlation of 0.82 or higher. MOR3-365 has approximated

genetic correlations of 0.88 or higher with each of the other traits. The high genetic correlations can be due to autocorrelation because MOR3-365 is the sum of the 4 individual traits. The most distant time periods, MOR3-14 and MOR91-365, have a correlation of only 0.48 indicating that these traits are genetically different.

Approximated genetic correlations between overall mortality and stillbirth and overall mortality and functional longevity are favourable at 0.26 and -0.34, respectively. These correlations show that overall mortality on the one hand and stillbirth and functional longevity on the other hand are genetically different.

Economic analysis. With a genetic standard deviation of 0.01 (see Table 2) and replacement costs of € 250 the economic value per genetic standard deviation is € 2,50 per replacement heifer. In the Netherlands 45% of all new-born calves are raised as replacement heifers. The economic value per genetic standard deviation per cow per lactation is therefore € 1,13 (€ 2,50*0,45). Including mortality in the breeding goal increases overall selection response with less than 0.1%.

Table 1. Percentage of mortality per time period and the relative contribution¹ of each time period in the overall mortality in the first year.

Traits	Percentage	Relative contribution
MOR3-14	1.4%	27%
MOR15-30	0.9%	17%
MOR31-90	1.2%	23%
MOR91-365	1.7%	33%
MOR3-365	5.2%	100%

¹Relative contribution is calculated as mortality in the specific time period divided by the overall mortality in the first year.

Table 2. Estimates of genetic parameters of mortality¹.

Traits	MOR3-14	MOR15-30	MOR31-90	MOR91-365	MOR3-365	h_n^2 ²	σ_g
MOR3-14	.006±.0005					.064	.003
MOR15-30	.88	.003±.0003				.043	.001
MOR31-90	.60	.82	.003±.0003			.037	.002
MOR91-365	.48	.75	.89	.003±.0003		.029	.002
MOR3-365	.88	1.00	.97	.94	.009±.0028	.039	.010

¹Heritability estimates on the diagonal with standard error of estimates, approximated genetic correlations below the diagonal.

² h_n^2 = Heritability transformed to the continuous scale.

DISCUSSION AND CONCLUSIONS

In this study, mortality in the first year (5.2%) is lower than reported by Heinrichs (1993). Mourits (2000) found a higher mortality of replacement heifers compared to this study. She considered mortality in the whole rearing period which is 26 months in the Netherlands while this study is limited to the first 12 months of the rearing period. Olsson *et al.* (1993) found a lower mortality in the first 3 months compared to this study (2.1% vs 3.5%). The relative

contribution of mortality in the first month within the first 3 months for this study and Olsson *et al.* (1993) is similar (66% vs 62%). Incidence of mortality of replacement heifers in the first year is low and it largely relates to the first month of life.

Until now no estimates for the genetic components of mortality of replacement heifers were presented. This study gives a first impression of the genetic components. Future studies may use more advanced techniques, like a threshold model or survival analysis, to account better for the nature of the data. Genetic correlations may be estimated with a multiple trait analysis to reduce sampling errors. The value of an evaluation for mortality of replacement heifers may be better assessed with these techniques. Results of this study indicate that mortality of replacement heifers does have a genetic component but heritabilities are low even after transformation to the continuous scale. Correlations between mortality in different time periods in the first year are moderate to high and favourable (0.48 to 1.00). However, the approximated genetic correlations probably have large sampling errors due to the low number of bulls used to estimate the correlations. Mortality in the first year can be regarded as genetically the same trait as mortality in the individual time periods. Correlations with stillbirth and functional longevity are low but favourable (0.26 and -0.34, respectively). The correlation of -0.34 is of the same magnitude as the best predictors currently used in the longevity analysis in the Netherlands (Vollema *et al.* 2000). Besides a reasonable correlation a predictor trait should have a high reliability early in the life of the animal as well. The average daughter group size of 120 of Dutch AI bulls and the estimated heritabilities in Table 2 show that the latter requirement will not be easily fulfilled.

The genetic standard deviation shows that the mortality of the offspring of the most extreme sires will differ 6%. Therefore the trait could be used to monitor the population.

Based on the very low increase in overall selection response (< 0.1%) found in this study it was concluded that mortality of replacement heifers is not a breeding objective trait. Based on the low reliability it was concluded that it can not be used as a predictor of functional longevity.

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