

Genetic Variation in Functional Longevity and its Relation to Mastitis Resistance in Danish Holsteins

J. Jensen, I.R. Korsgaard, H.J. Neerhof, A. Vollema, P. Madsen, and V. Ducrocq

Danish Institute of Agricultural Sciences, Research Centre Foulum, DK-8830 Tjele, Denmark

and

Wageningen Institute of Animal Sciences, PO 338, 6700 Wageningen, The Netherlands

and

Institut National de la Recherche Agronomique, F-78352 Jouy-en-Josas Cedex, France.

Abstract

Mastitis resistance is expected to be an important component of survival in dairy cows. Longevity records of 97,275 Holsteins from 661 herds were analysed using survival analysis methods. The first model included effects of whether the cow had had mastitis in a specific period or not. The risks of cows being culled due to mastitis treatments were modelled for varying periods after the treatment date. The model also included a correction for production and thus we define longevity as functional longevity. Genetic parameters for functional longevity were estimated in a second model without effects of mastitis included. Both models included a random sire effect.

A model where a mastitis treatment was assumed to have an effect on culling risk until the end of the current lactation, had the highest likelihood, compared to models where mastitis had an effects in other time periods after a treatment. In this model a cow with a mastitis treatment had a 1.69 times higher risk of being culled than a healthy herdmate.

In the second model the heritability of functional longevity on the original scale was estimated as 0.216. Simple correlations between breeding values for functional longevity and the estimated breeding value for mastitis resistance from the national system for evaluation of breeding values was around -0.4. This indicates that better mastitis resistance is genetically correlated with a lower risk of being culled and thus a longer functional length of productive life.

1. Introduction

Health traits are important parts of total economic merit in dairy cattle (Groen et al., 1997) and are expected to be an important element in decisions on culling of individual cows. It is therefore expected that there are strong relations between health and longevity.

In Scandinavian countries, where a national health recording system is in place, health traits can be selected for directly, but elsewhere; other sources of information must be used. One obvious possibility would be to use longevity. Culling due to low milk production is very important in dairy cattle and longevity is therefore usually corrected for production in order to obtain an approximate measure of culling due to other reasons than production; i.e. involuntary culling. Such a measure

is usually called “functional longevity” (Dekkers, 1993).

Only mastitis was included in the study as a health trait, since this is the most important disease in dairy production systems (Madsen et al, 1987, Milian-Suazo et al, 1988, Lyons et al, 1991, Nielsen et al, 1996). However, other diseases could also have an important influence on culling decisions.

The objective of this study was:

- To study the effect of a mastitis incidence on culling risk.
- To estimate the genetic variation in functional longevity.
- To study the genetic relationship between functional longevity and mastitis resistance.

This paper reports parts of a larger study that will be published elsewhere (Neerhof et al. 1999).

2. Material and Methods

2.1 Data

Data on 97,275 Holstein cows from 661 herds was included in the analysis. The herds selected had continuously been included in the health recording system for more than 5 years and the herds had used AI-sires only. The study period covered the period from beginning of 1990 until the end of 1996. Dentine et al (1987) found that culling policies differed between grade and registered herds. Therefore breeding herds were not included in the study. Breeding herds were defined as herds that had sold at least one young bull to an AI-organisation during the study period. Cows with an age at first calving less than 540 days was excluded. Records were regarded as right censored if the cow

was alive at the end of the study period or was sold to a herd not included in the study.

The cows were daughters of 4,414 bulls and after tracing sires and maternal grandsires the total number of bulls in the pedigree file was 5,357.

An incidence of mastitis was defined as a veterinary treatment due to mastitis, dry period mastitis, mastitis due to teat lesions and acute mastitis. These are all treatments of clinical mastitis.

Length of productive life, defined as the number of days between first calving and culling, was used as a measure of longevity. The data included right censored, uncensored and left-truncated records.

2.2 Statistical models

For comparison of different ways of including mastitis treatment in the model, the hazard function, $\lambda_i(t)$, of length of productive life of animal i , $i=1, \dots, n$, was modelled as:

$$\lambda_i(t) = \lambda_0(t) \exp\{z_{1i}(t) + z_{2i}(t) + z_{3i}b_3 + z_{4i}b_4 + z_{5i}(t)b_5 + z_{6i}(t) + h_i(t) + s_j\} \quad [1]$$

where $\lambda_0(t)$ is the baseline hazard function, which is only dependent on time and is assumed to follow a Weibull distribution, as in Ducrocq et al. 1988.

The function $z_{1i}(t)$ is a piecewise constant function, that changes whenever animal i enters a new parity, i.e:

$$z_{1i}(t) = \begin{cases} b_{11} & \text{if animal } i \text{ is in its first parity at time } t \\ \dots\dots\dots & \\ b_{17} & \text{if animal } i \text{ is in its seventh or higher parity at time } t \end{cases}$$

Parities 7 and up were pooled together into one class.

Similarly, $z_{2i}(t)$ is a piecewise constant function, that changes whenever animal i enters a new parity * stage of lactation class, i.e. $z_{2i}(t) = b_{2kl}$ if animal i is in its k 'th parity and l 'th stage of lactation at time t with $k=1, \dots, 7$ and $l=1, \dots, 4$. Changes in stage of lactation are defined to occur at calving, 60, 180, and 300 days after calving.

z_{3i} is the age at first calving of animal i , and b_3 , is the corresponding regression parameter. Age at first calving ranged from 540 to 1319 days in the data set.

z_{4i} is the proportion of Holstein genes of animal i , and b_4 is the corresponding regression

parameter. The proportion of Holstein genes ranged from 0 to 1.

The production in the previous lactation, relative to herd mates, was included as $z_{5i}(t)$ with corresponding regression parameter b_5 . Production in the current lactation was not included because a cow with a disease might have a lower production due to that disease. Production was defined as the 305-days energy corrected milk production (ECMP) and calculated as Sjaunja et al. 1990.

$$ECMP = 0.25 * M + 12.2 * F + 7.7 * P \quad [2]$$

where M was the 305 d milk production, F was the 305 d fat production, and P was the 305 d protein production (all expressed in kg). The ECMP of each

cow in each lactation was divided by the average ECMP within herd, year of calving, and lactation to obtain a phenotypic measure for production relative to a cow's herdmates. Lactation 3 and up were pooled together into one class for calculating the averages. For cows with less than 45 milking days and without an extended record, an average production (1.00) was assumed. In the first lactation all relative productions were set to 1.00. Thus $z_{5i}(t)=1.00$ if animal i is in its first parity at time t . If animal i is in its m 'th lactation, $z_{5i}(t)$ is the relative production in lactation $m-1$, with $m=2, 3, \dots$. The relative production compared to herdmates ranged from 0.04 to 1.82.

Beaudeau et al. 1995 found no significant influence of occurrence of mastitis in the previous lactation on a cow's risk of being culled due to occurrence of mastitis in the current lactation. Therefore, the first way of including mastitis was to declare a cow "diseased" from the first treatment of mastitis in a lactation until the start of the next lactation. The second way of including mastitis was to declare a cow "diseased" from a treatment until a number of days afterwards. If there was a retreatment within that period, the period was lengthened from that date with the same number of days. Different numbers of days were used: 10, 100, 200, 400, and 800 days. These different ways of including mastitis were compared based on the maximum likelihood of the resulting models. It has to be emphasised that not the period during which the cow is diseased is modelled, but the period during which that disease occurrence is expected to have an effect on the farmers decision whether to cull the cow or not. When the number of days is small, only acute disposal is studied.

$z_{6i}(t)=b_{6n}$ if animal i in the n 'th class of disease period (as previously defined) at time, t , where $n=1$ if a cow is not diseased, and $n=2$ if a cow is in a disease period.

$h_i(t)=h_j$ if animal i is in the j 'th class of the interaction between herd, year, and season. Four seasons were distinguished, changing on the first of January, April, July and October of each year. The interaction between herd, year, and season was assumed to follow a log-gamma distribution and was integrated out of the likelihood during the analyses (Ducrocq and Casella, 1996, Ducrocq et al. 1988).

The vector of sire effects (s_j) was assumed to follow a multivariate normal distribution. Relationships between sires were identified through their sires and maternal grandsires.

Sire transmitting abilities for functional longevity was estimated in model [1] but without effects of mastitis treatments included. The estimates of the sire effects (s_j) were used as transmitting abilities and correlated to the national proof for mastitis resistance (Nielsen et al., 1996).

Survival analysis was performed using the Survival Kit developed by Ducrocq and Sölkner (Ducrocq and Sölkner, 1998) and the estimates were expressed as risk ratios (RR). Heritability of functional longevity was expressed both as heritability of log functional length of productive life and was also transformed to the original scale using a Taylor series approximation.

3. Results and discussion

3.1 Phenotypic relationships between functional longevity and mastitis

The -2 log-likelihood of the different ways of modelling the effect of mastitis on culling risk is shown in Table 1.

Table 1. Comparison of different ways of modelling the effect of mastitis occurrence on the risk of being culled (RR) of a cow compared to a healthy cow.

Model	RR of mastitis	-2 log likelihood ^{*)}
1.Until end of lactation	1.69	0
2.Until 10 d after occurrence	1.23	3037
3.Until 100 d after occurrence	1.50	2229
4.Until 200 d after occurrence	1.56	1373
5.Until 400 d after occurrence	1.59	545
6.Until 800 d after occurrence	1.56	639

^{*)} -2 log likelihood for the first model is subtracted.

The models have the same number of parameters and can therefore not be compared using likelihood ratio tests. However, the model in which a mastitis incidence affects the culling risk until the end of the lactation had the largest likelihood, and therefore this was assumed to be the best model among those studied. The model where a mastitis

incidence was considered to have an effect only in a 10-d period after treatment had the lowest likelihood. It seems unlikely that a cow should be culled immediately after being treated for mastitis. In addition, due to rules on retention times after treatment with antibiotics, a cow cannot be slaughtered immediately after treatment with antibiotics. Milan-Suazo et al. (1988) also concluded that many cows with a diagnosis of mastitis were kept for relatively long periods after treatment. The risk ratio for the most likely model was 1.69, which also was the highest ratio among the models studied. This means that a cow with a mastitis treatment had a 1.69 larger risk of being culled than a cow with all other conditions than mastitis in the model the same.

There is a clear effect of an incidence of mastitis on the risk of being culled. This risk is increased for the remainder of the lactation. Models assuming a short-term risk had lower likelihood than other models.

3.2 Heritability of functional longevity

From the model without mastitis included, the estimated heritability on the log scale was 0.0548. When transformed to the original scale the estimate was 0.216. This was similar to an estimate of 0.217 based on French Holstein data (Ducrocq and Sölkner, 1998), but was much lower than an estimate of 0.064 based on Dutch Holstein data (Vollema and Groen, 1998).

The estimate indicates that considerable genetic variation in functional longevity exists in the Holstein population.

3.3 Genetic relationship between functional longevity and mastitis resistance

Out of the 5,357 bulls in the analysis 2,746 had an official breeding value for mastitis resistance. Out of these, 125 bulls had more than 50 daughters with uncensored records in the data used in the survival analysis. For these bulls the correlation between transmitting ability for functional longevity and the breeding value for mastitis resistance was -0.37 . This means that daughters of bulls with a high breeding value for mastitis resistance had a lower risk of being culled, and thus a longer functional length of life. If the bulls were

required to have at least 100 uncensored records, the number of bulls was 79 and the correlation was -0.48 . Nielsen and Pedersen (1995) calculated correlations between breeding values for Danish bulls for different longevity traits and mastitis resistance. They required the bulls to have at least 70 first crop daughters and obtained correlations that ranged from 0.22 to 0.33, which is comparable to the results of the present study.

There seems to be a substantial genetic correlation between mastitis resistance and functional length of productive life.

4. Conclusions

- There is a clear effect of an incidence of mastitis on the risk of being culled. This risk is increased for the remainder of the lactation.
- There is considerable genetic variation in functional longevity in the Holstein population.
- There is a substantial genetic correlation between mastitis resistance and functional length of productive life in the Holstein population.

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