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# Genetic determination of mortality rate in Danish dairy cows: A multivariate competing risk analysis based on the number of survived lactations

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## ABSTRACT

Dairy cow mortality has been steadily increasing during the last 2 decades in Denmark. This study aims to verify whether genetic mechanisms might be contributing to this increase. To do so, the records of 880,480 Holstein, 142,306 Jersey, and 85,206 Red Danish dairy cows calving from 1990 to 2006 were retrieved from the Danish Cattle register. Two causes of culling of cows were considered: death and slaughtering. Bivariate competing risk genetic models with a sire model structure were used to describe the death and the slaughtering rates simultaneously. The models included 2 random components: a sire random component with pedigree representing the sire genetic effects and a herd-year-season component. Moreover, the level of heterozygosity and the sire breed proportions were included in the models as covariates to account for potential nonadditive genetic effects due to the massive introduction of genetic material from other populations. The correlations between the sire components for death rate and slaughter rate were negative and small for the 3 populations, suggesting the existence of specific genetic mechanisms for each culling reason and common concurrent genetic mechanisms. In the Holstein population, the effects of the changes in the level of heterozygosity, breed composition, and the increasing genetic trend acted in the same direction, increasing the death rate in recent years. In the Jersey population, the effects of the level of heterozygosity and the breed proportion were small, and only the increasing genetic trend can be pointed as a genetic cause to the observed increase in the mortality rate. In the Red Danish population, neither the time-development pattern of the genetic trend nor the changes in the level of heterozygosity and breed composition could be causing the observed increase in the mortality; thus, nongenetic factors must be causing this negative development.

**Key words:** longevity, genetic trend, survival model

## INTRODUCTION

Dairy cow mortality has been steadily increasing during the last 2 decades all over the world. For example, the mortality rate increased from 2.6 to 5.7% in the United States from 1996 to 2007 (Garry, 2009), and in Ireland from 3.3 to 4.4% between 2002 and 2006 (Maher et al., 2008). In Denmark, cow mortality increased from an average of 2% in 1990 to approximately 3.5% in 1999 (Thomsen et al., 2004), and to 4.9% in 2005 (Thomsen and Sørensen, 2008). Cow mortality, therefore, constitutes a problem of animal welfare and farm economy. Several herd-level risk factors for mortality have been identified, such as herd size, SCC, and milk yield (Thomsen and Houe, 2006; Thomsen and Sørensen, 2009; Alvåsen et al., 2012). Moreover, concerns exist that historic breeding objectives focusing on production traits with negative genetic correlation to functional and health traits may have contributed to the observed increase in cow mortality. The goal of this work was to verify whether these concerns are well founded by studying in detail 3 populations of dairy cows, namely Holstein (**HOL**), Jersey (**JER**), and Red Danish (**RDC**), under production in Denmark. This task was not straightforward for 2 main reasons: the presence of incomplete observations and the presence of nonadditive genetic effects.

In the analyses presented here, we distinguish 2 causes of culling of cows: death and slaughtering. Our primary interest was to characterize the risk of dying and slaughtering will be seen here just as a competing cause of culling. The longevity of cows under production is, to the best of our knowledge, operationally defined by pooling the culling due to death and the culling due to slaughtering together. As a consequence, the large amount of evidence accumulated in the literature of the presence of genetic determination of culling rates (Ducrocq, 1994; Vollema and Groen, 1996; Caraviello et al., 2004) cannot be used to characterize the genetic determination of culling by death. In this paper, we propose a methodology that allows distinguishing these 2 causes of culling and to determine to which extent the genetic mechanisms involved with these culling causes

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overlap. We anticipated that we would show evidence of genetic determination of both causes of culling cows in the 3 populations studied; furthermore, the overlap of the genetic mechanisms involved in the 2 causes of culling would be small.

Although good-quality registers are available for the 3 Danish populations of dairy cows studied, part of the information on death culling is incompletely observed. Indeed, cows under production can leave the herd by causes different than death (e.g., export or slaughter not due to euthanasia) and, therefore, the time of death of these animals is only known to be larger than a certain observed time (i.e., we have right censuring). Moreover, some of the factors known to affect the risk of deaths vary along time and it is important to account for that when modeling these data. Finally, some animals entered the study already at an advanced age (late entry); these animals should be included in the analysis if we want to properly evaluate the number of animals at risk of dying at a certain time point. These problems can be circumvented by using statistical methods of survival analysis (Andersen et al. 1997; Kalbfleisch and Prentice, 2002; for a general overview and for applications in animal breeding see Ducrocq et al., 1988; Giolo and Demétrio, 2011). However, the survival analysis techniques currently used in animal evaluation require the censoring mechanism to be noninformative (i.e., the probability of censoring should not depend on any of the explanatory variables used in the model to describe the distribution of the time to death). Our results will show that, as one might suspect, common factors exist affecting both the time to death and the probability of a cow being slaughtered, so we clearly have informative censoring, which rules out the use of the standard techniques of survival analysis without proper adaptation. We will introduce here a statistical methodology based on multivariate competing risk models that circumvent the problem of informative censoring and still well represent the genetic scenario in a way that resembles the representation based on Gaussian linear mixed models classically used in quantitative genetics. We will simultaneously model the time-development of the probability of dying and the probability of being slaughtered (conditional on survival up to a given time) using a suitable bivariate model. This will allow us to properly characterize the quantitative genetic determination of the culling rate of cows due to death (accounting for the removal due to slaughtering) and to access the degree of overlap of the additive genetic mechanisms related to the 2 causes of culling of dairy cows in each of the 3 populations studied.

The second complication of this study was the presence of nonadditive genetic factors affecting the culling rates of dairy cows. Both the level of heterozygosity and the breed composition varied along time in our study. Moreover, the observed patterns of variation in recent years were not the same for the 3 populations studied. The models implemented here account for these genetic factors and allow us to estimate their effects. We anticipated that we would detect non-negligible effects of those factors on the culling rates associated with death (and on the culling rates due to slaughtering). Therefore, although these genetic effects are transitory (in the sense that they are not necessarily directly passed to the offspring) they should be taken into account when analyzing the time development of the mortality rate of dairy cows.

In summary, this paper aims to present a methodology to access possible genetic causes of the observed increase in mortality rate in dairy cows, which includes additive genetic effects, changes in the breed composition, and variations in the level of heterozygosity. This will be illustrated using the HOL, JER, and RDC populations of dairy cows under production in Denmark.

## MATERIALS AND METHODS

### *Data Editing*

The data used were provided by the Danish Knowledge Centre for Agriculture (Aarhus, Denmark) and contained records of all the calf births that occurred from 1990 to 2006 for the HOL, JER, and RDC dairy cattle populations. The data consist of 1 record per calving for each cow and included the following information: culling day and reason (dead or slaughtered) if the animal was culled, age at the first calving, calving year and season, herd year size (number of calf births in that particular herd year class), and coefficient of heterozygosity and sire breed composition (gene proportion of different breeds that compose the sire). The coefficient of heterozygosity and the sire breed proportions were included in the data to account for potential effects of the massive introduction of genetic material from other populations.

We considered in this study only the herds with more than 30 calves per year and that presented a stable or increasing herd size over the period in study. This data editing was done to avoid possible distortions due to the fact that the decision of culling a cow must be influenced by the herd situation. To do so, a simple linear regression of the herd size against the year was fitted and the herds with significant decreasing size, at a level of 5%, were excluded from the study. Cows with age at first parity lower than 540 d or larger than 1,280 d and cows with unknown sire were eliminated. After this editing, the data set included records on 880,480

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