Interpretive Summary:

Genetic determination of mortality rate in Danish dairy cows: a multivariate competing risk analysis based on the number of survived lactations. *By Maia et al*. The recent increase in cow mortality in Denmark can be partially explained by genetic causes. While evidences that there are genetic related mechanisms associated to the increase in the mortality of cows of the Holstein and the Jersey populations, no evidences were found of such deleterious genetic effects in the Red Danish population. Since the mortality rate of the Red Danish is also increasing, there must be non-genetic factors causing this negative development.

GENETIC CAUSES OF MORTALITY OF DAIRY COWS

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 two 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 form 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 two 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 in order to account for potential non-additive 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 act in the same direction increasing the death rate in the 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, there must be non-genetic factors causing this negative development.

Key Words: longevity, genetic trend, survival models.

INTRODUCTION

Dairy cow mortality has been steadily increasing during the last two decades all over the world. For example, the mortality rate increased from 2.6 to 5.7% in the US 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, the cow mortality increased from an average of 2% in 1990 to ~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, somatic cell count, and milk-yield (Thomsen and Houe, 2006; Thomsen and Sørensen, 2009; Alvåsen et al., 2012). There are, moreover, concerns 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 is to verify whether these concerns are well founded by studying in detail three populations of dairy cows, namely Holstein, Jersey and Red Danish, under production in Denmark. This task is not straightforward for two main reasons: the presence of incomplete observations and the presence of non-additive genetic effects.

In the analyses presented here, we distinguish 2 causes of culling of cows: death and slaughtering. Our primary interest is 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 evidences accumulated in the literature of the presence of genetic determination of culling rates (Vollema and Groen, 1996, Ducrocq, 1994; Caraviello et al., 2004) cannot be used to characterize the genetic determination of culling by death. In this paper, we will propose a methodology that allows to distinguish these two causes of culling and to determine at which extent the genetic mechanisms involved with these culling causes overlap. We

anticipate that we will find evidences of genetic determination of both causes of culling cows; however, the overlapping of them is small in the three populations studied.

Although good quality registers are available for the three 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 enter in the study already at an advanced age (late entry); these animals should enter in the analysis if we want to properly evaluate the number of animals at risk of dying in a certain time point. These problems can be circumvented by using statistical methods of survival analysis (Kalbfleisch and Prentice, 2002; Andersen et al. 1997 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 non-informative, *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, there are common factors 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 a 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 overlapping of the additive genetic mechanisms related the two causes of culling of dairy cows in the three populations studied.

The second complication of this study is the presence of non-additive genetic factors affecting the culling rates of dairy cows. Both the level of heterozygosity and the breed composition are varying along the time in our study. Moreover, the observed patterns of variation in the recent years are not the same for the 3 populations studied. The models implemented here account for these genetic factors and will allow us to estimate their effects. We anticipate that we detect non-negligible effects of those factors on the culling rates associated to 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 Holstein, the Jersey and the Red Danish populations of dairy cows under production in Denmark.

MATERIAL AND METHODS

Data editing

The data used was provided by the Danish Knowledge Centre for Agriculture and contained records of all the calve births occurred from 1990 to 2006 for the Holstein (HOL), Jersey (JER) and Red Danish (RDC) dairy cattle populations. The data consist of one 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

120 the first calving, calving year and season, herd year size (number of calve births in that particular herd
121 year class), coefficient of heterozygosity and sire breed composition (gene proportion of different
122 breeds that compose the sire). The coefficient of heterozygosity and the sire breed proportions were
123 included in the data in order to account for potential effects of the massive introduction of genetic
124 material from other populations.

125 We considered in this study only the herds with more than 30 calves per year and which
126 presented a stable or increasing herd size over the period in study. This data editing was done to avoid
127 possible distortions due to the fact that the decision of culling a cow must be influenced by the herd
128 situation. To do so a simple linear regression of the herd size against the year was fitted and the herds
129 with significant decreasing size, at level of 5%, were excluded from the study. Cows with age at first
130 parity lower than 540 days or larger than 1280 days and cows with unknown sire were eliminated.
131 After this editing the dataset included records on 880,480 HOL, 142,306 JER and 85,206 RDC dairy
132 cows. For each of the 3 breeds, a Sire Dam pedigree file for all sires with progenies in the edited data
133 was extracted from the Nordic Cattle Genetic Evaluation (NAV) pedigree file.

134 ***Breed proportion and heterosis***

135 The breed proportion and the coefficient of heterozygosity are currently considered in several models
136 by the NAV (see for example the report of the Nordic Cattle Genetic Evaluation of 2012). The
137 proportion of genes from different breeds carried by each animal was calculated by

$$b_i(p) = \frac{b_i(s) + b_i(d)}{2},$$

138 where $b_i(p)$, $b_i(s)$ and $b_i(d)$ are the proportion of genes from breed *i* in the progeny, the sire and the
139 dam, respectively. The coefficients of specific heterozygosity between the pair of breeds *i* and *j*, $\gamma_{ij}(p)$,
140 were calculated by (Lópes-Villalobos et al., 2010)

$$\gamma_{ij}(p) = b_i(s)b_j(d) + b_j(s)b_i(d).$$

141 The coefficient of general heterozygosity, referred below simply as the coefficient of heterozygosity for
142 the progeny *p,* is given by the sum of all the coefficients of specific heterozygosity for that animal.

143 ***The competing risk problem***

144 The longevity trait understood as a measure of the productive life of the cow was defined as the total
145 number of survived lactations until the culling day. As usual in survival analyses, the data includes two
146 types of incomplete records: a) *right censored*, comprised by cows that were still alive at the end of the
147 data collection period (07th January 2011) or cows moved to another herd or exported during the study
148 period and b) *late entry,* comprised by the cows that in the begin of the studied period had already
149 completed more than 1 parity, *i.e.*, the first parity occurred before 1990. For example, if a cow had the
150 first and the second parity before 1990 and further parities in 1990 or later, we considered only the
151 records from the 3rd parity and treated as a late entry data and although we know that this animal was
152 alive before 1990 we were not interest in computing the risk of culling at the previous years and
153 therefore we ignored the data previous to 1990. Note that the inclusion of the animals with late entry
154 data in the analyses allowed us to compute the correct culling risk in each year from 1990 to 2006.
155 Note also that there are no left censored animals (*i.e*. animals that were culled before 1990) in this
156 study because the animals culled before 1990 were not included in the dataset. This does not affect the
157 estimates of the hazard function at any time of the observation period because the left censored animals
158 would never be in the risk sets at any time in the observation period. The analyses were concentrated in
159 the longevity up to 6 parities, cows that completed 7 or more parities had the number of lactations
160 truncated at the sixth parity and were treated as right censored at the sixth parity.

161 In this study, we deal with a competing risk problem since the cows may be culled for one
162 of two possible reasons (Martinussen and Scheike, 2006), namely: death or slaughter. A cow was
163 registered as dead when the animals suddenly died or when the animals were euthanized. In order to
164 describe the competing risk models considered here, we define the random variables T, representing

the number of survived lactations and taking values in $\{1,2,3,4,5,6\}$, and J representing the culling cause. The *cause-specific hazard probability* (Kalbfleisch and Prentice, 2002) for the j^{th} culling cause is given, for t=1, …,6, by

$$\lambda_j(t) = P(T = t, J = j | T \geq t).$$

Here j is equal to 1 if the cow died and 2 if the cow was slaughtered. That is, $\lambda_j(t)$ is the probability of a cow to be culled for the j^{th} specific cause at the t^{th} lactation given that the cow had survived from all causes until the t^{th} lactation. The survival function is then defined by

$$S(t) = P(T > t) = \prod_{k \leq t} \left(1 - \lambda_{\cdot}(k)\right),$$

where $\lambda_{\cdot}(t) = \lambda_1(t) + \lambda_2(t)$, is the total hazard probability of be culled at the t^{th} lactation.

Multivariate mixed models

We handled the competing risk problem by using a bivariate discrete relative risk model with frailty components (**BFDRRM**). In the following description of the BFDRRM $\boldsymbol{U} = (\boldsymbol{U}_1, \boldsymbol{U}_2)$ is a set of random components (*i.e*. frailties as referred in the literature of survival analysis), assuming different effects for each specific cause and $X(t)$ represents a set of explanatory variables containing time-dependent and time-independent explanatory variables. According to the BFDRRM**,** the vector of the specific hazard probability functions for the i^{th} cow is given, conditionally on $\boldsymbol{U} = \boldsymbol{u}$, by

$$\begin{bmatrix} \lambda_{i1}(t|\boldsymbol{u}) \\ \lambda_{i2}(t|\boldsymbol{u}) \end{bmatrix} = \begin{bmatrix} \lambda_{01}(t)\exp(X_i'(t)\beta_1 + Z_i'\boldsymbol{u}_1) \\ \lambda_{02}(t)\exp(X_i'(t)\beta_2 + Z_i'\boldsymbol{u}_2) \end{bmatrix} \text{ for } t = 1,2,\ldots,6,$$

where $\lambda_{0j}(t)$ is the baseline hazard function for the specific-cause j at the lactation t and $\lambda_{ij}(t|\boldsymbol{u})$ is a short notation for $\lambda_{ij}(t|\boldsymbol{U} = \boldsymbol{u})$. The time independent explanatory variables included in the model were: age at first parity (first quartile, second to third quartile and fourth quartile), coefficient of heterozygosity and the sire breed proportion (proportion of Holstein-Friesian genes for HOL sires, US Jersey genes for JER sires and Holstein-Friesian, American Brown and Nordic Red genes for the RDC sires). The following time dependent explanatory variables were included in the model: the herd size

given by the total number of observed calve births per year (first quartile, second to third quartile and fourth quartile), the calving year and the calving season (first semester aggregating the winter and spring, and second semester aggregating summer and fall). We included in the model two random components (*i.e.* frailties): a sire random component $\boldsymbol{S}$ with pedigree representing the sire genetic effect and a herd-year-season component $\boldsymbol{H}$. We assumed that $(\boldsymbol{S}, \boldsymbol{H})'$ follow a multivariate normal distribution with mean equal to zero and covariance matrix given by

$$\boldsymbol{\Sigma} = \begin{bmatrix} \boldsymbol{\Sigma}_s \otimes \boldsymbol{A} & \mathbf{0} \\ \mathbf{0} & \boldsymbol{\Sigma}_h \otimes \boldsymbol{I} \end{bmatrix}.$$

Here $\boldsymbol{\Sigma}_s = \begin{bmatrix} \sigma_{s1}^2 & \sigma_{s12} \\ \sigma_{s12} & \sigma_{s2}^2 \end{bmatrix}$ represents the covariance matrix for the sire effect, $\boldsymbol{A}$ is a known relationship matrix given by sires' pedigree, $\boldsymbol{\Sigma}_h = \begin{bmatrix} \sigma_{h1}^2 & \sigma_{h12} \\ \sigma_{h12} & \sigma_{h2}^2 \end{bmatrix}$ represents the covariance matrix for the herd-year-season effect, and $\boldsymbol{I}$ is an identity matrix.

Inference

The bivariate discrete competing risk model may be seen as a sequence of multinomial trials (Kalbfleisch and Prentice, 2002), where each of the lactations is considered as a new trial and can be modeled via a multivariate binomial model with random components. To do so, we created a pseudo dataset containing one record for each of the observed lactations of each cow. Next we created two indicator variables Y_{it1} and Y_{it2}, where Y_{itj} receives the value 1 if the cow was culled by the reason j at the lactation t and 0 otherwise. Then, we assumed that $Y_{itj}|\boldsymbol{U} = \boldsymbol{u}$ were pseudo Bernoulli variables with probability of success equal to $\lambda_j(t|\boldsymbol{U} = \boldsymbol{u})$ and that $Cov(Y_{it1}, Y_{it2}|\boldsymbol{U} = \boldsymbol{u}) = 0$. Maia et al. (2013) showed that the distribution of the pseudo binomial variables could be approximated by a Poisson distribution as result of the classical approximation of the binomial distribution by the Poisson distribution applied when the probability of success is very small (*i.e.* the law of rare events). The use of this approximation avoided serious numerical and statistical instability, since the present problem

would be equivalent to perform inference with a Bernoulli model with the probability of success very close to zero. The model also included a dispersion parameter via quasi-likelihood estimation (Wedderburn, 1974; Breslow and Clayton, 1993; Jørgensen and Labouriau, 2012; Jørgensen et al. 1995). In this approach it is assumed that $\mathrm{Var}\left(Y_{itj}|\boldsymbol{U}=\boldsymbol{u}\right)=\phi_j\lambda_j(t|\boldsymbol{U}=\boldsymbol{u})$, where ϕ_j represents the parameter of dispersion for the j^{th} specific cause.

All the models were fitted using the software DMU version 6.0, release 5.1 (Madsen and Jensen, 2010; Madsen et al. 2010).

Heritability, breeding values and genetic trend

The marginal heritability for the relative risk of culling by each specific cause *j* at the lactation *t* is calculated by

$$h^2_{\lambda(t)} \approx \frac{\sigma^2_{u,j}}{\sigma^2_{u,j}+\sigma^2_{v,j}+\frac{\phi_j}{\lambda^*_j(t)}} \quad , \qquad (1)$$

where ϕ_j represents the dispersion parameter, and $\lambda^*_j(t)$ represents the hazard probability for the j^{th} cause evaluated at the predicted values of the random components. The formula (1) arises from a Taylor approximation of the total variance and theory of survival analysis (for details see Maia et al. 2013). More precisely, define, for each lactation $t = 1,2,\ldots,6$, for each individual $i = 1,\ldots,n_t$ at risk at the lactation t and the j$^{\text{th}}$ cause of culling ($j = 1,2$),

$$\hat{\eta}_{i,j}(t) = \log\left(\widehat{\lambda_{0j}(t)}\right) + \boldsymbol{X}^t_i(t)\widehat{\boldsymbol{\beta}}_j + \boldsymbol{Z}^t_{1i}\widehat{\boldsymbol{s}_j} + \boldsymbol{Z}^t_{2i}\widehat{\boldsymbol{h}_j}$$

as the estimated of the cause specific log hazard probability (the linear predictor) and the $\lambda^*_j(t) = \exp\left[\hat{\eta}_{i,j}(t)\right]$. The heritability was estimated at the overall median survival time t_m and the specific hazard probability for the specific cause *j* at the median survival time was estimated by

$$\tilde{\lambda}_j(t_m) = \exp\left[\bar{\eta}_j(t_m)\right],$$

where $\bar{\eta}_j(t_m) = n_{t_m}^{-1} \sum_{i=1}^{n_{t_m}} \hat{\eta}_{i,j}(t_m)$.

The genetic trend for each specific cause of culling was estimated by the mean of the sires estimated breeding values (**EBV**) by the birth year. Only EBVs of young bulls were considered in order to avoid the effect of very high selected sires. A bull for which the difference between its birth year and the birth year of its oldest daughter presented in the data is smaller or equal to 5 years was declared to be a young bull.

RESULTS AND DISCUSSION

The evolution of the mortality rate in the edited dataset is displayed in Figure 1. There, an almost linear increase is observed over the studied period for the 3 populations. This is in agreement with the increase in the mortality of cows in Denmark reported in Thomsen and Sørensen (2008) and is in line with the results obtained in other countries (*e.g*. Garry, 2009 and Maher et al., 2008).

The median survival times were 2 lactations for the RDC and the HOL populations and 3 lactations for the JER population. The proportions of censored data were relatively high (~15 - 22%, see Table 1), and the probability of a cow to survive 7 or more lactation were low (less than 3%, see Table 1). Figure 2 presents the proportions of dead, slaughtered and censored cows for each of the parities.

Applying the specially designed multivariate extension of the discrete relative risk model (BFDRRM) for competing risks described below allowed us simultaneously modelling the culling rate of cows related to death and the culling rate due to slaughtering. The estimates of the sire variances for slaughtering were almost equal for the 3 populations (~0.02 with SE ~0.001) and the marginal heritabilities for slaughtering (evaluated at the median survival probability) varied from ~3% to ~4% being slightly larger for the RDC population (see Table 2). On the other hand, the estimates of the sire variances for death varied considerably (largest for the RDC and smallest for JER). Moreover, the

marginal heritabilities for death are smaller than the heritabilities for slaughter for the HOL and JER populations and are larger than the heritabilities for slaughter for the RDC population (see Table 2). Furthermore, the correlations between the sire random components for death and the sire random component for slaughtering are negative but small for the 3 populations (although not statistically significant for the JER population, see Table 2), suggesting the existence of common concurrent genetic mechanisms related to the slaughtering and the death rates for the HOL and the RDC populations. On the other hand, since the absolute values of those genetic correlations are small, there must exist also predominant genetic mechanisms specific to each of the culling reasons.

The effects of the coefficient of heterozygosity on the hazard probability for death are all negative (see Table 3). However, the recent time-developments of the level of heterozygosity are not the same for the 3 populations (see Figure 3), therefore the impacts of changes in the coefficient of heterozygosity are different in the 3 populations. For instance, in the HOL population the level of heterozygosity decreased along the time, which contributes to generate a concomitant increase in the mortality rate of this population along the years. In contrast, in the RDC population the pronounced increase observed in the level of heterozygosity along the years acts as decreasing the mortality. In the JER population, although the level of heterozygosity increased along the years, the effect of the coefficient of heterozygosity on the hazard probability of death is small (and even not statistically significantly different from zero), therefore the positive influence of the increase in the level of heterozygosity on the mortality (if any) must also be small. Furthermore, the effects of the historical changes on the breed composition on the hazard probability for death resemble the effects of changes in level of heterozygosity discussed above. Indeed, for the HOL population the proportion of Holstein-Friesian has a positive effect on the hazard probability for death (see Table 4), which tends to increase the hazard probability for death for this population along the years because the proportion of Holstein-Friesian increased in the period of study (see Figure 4). The effects of changes in breed composition for

the JER and the RDC populations tend to be small and are not statistically different from zero (see Table 4).

The observed marginal genetic trends differ substantially for the slaughter and death related components of the longevity (see Figure 5 and Table 5). For slaughter, all the 3 populations showed a decreasing average sire genetic effect on the hazard probability, suggesting that the recent selection programs are contributing in improving this component of the longevity. On the other hand, the average sire genetic effect on the hazard probability to death showed a clear increasing trend for the HOL and the JER populations, suggesting that the recent selection programs are contributing to increase the mortality rate in those populations. Furthermore, the genetic trend for death is almost constant for the RDC population, with a small decrease in the last years, suggesting that the recent selection programs are essentially acting neutrally on the death related longevity for this population. Furthermore, the fact that there are qualitative differences in the genetic trends estimated for slaughter and death corroborates to the hypothesized existence of different specific determining genetic mechanisms related to the 2 culling causes in discussion.

In summary, in the HOL population the effects of the changes in the level of heterozygosity and breed composition act in the same direction as the increasing genetic trend for death; therefore all these effects tend to increase the mortality rate for the HOL population along the years. The case of the JER population occupies an intermediary position. In this population, the effects of the changes in the level of heterozygosity and breed composition are positive and small (if any), and only the increasing genetic trend can be pointed as a genetic cause to the observed increase in the mortality rate. In contrast, in the RDC population neither the time-development pattern of the genetic trend nor the changes in the level of heterozygosity and breed composition can be causing the observed increase in the mortality rate. This suggests that strong non-genetic causes of mortality of cows must be acting in the RDC population.

CONCLUSIONS

Our results suggest that the increase in the cow mortality occurred recently in Denmark can be partially explained by genetic causes. While evidences that there are genetic related mechanisms associated to the increase in the mortality of cows for the Holstein and the Jersey populations, no evidences were found of such deleterious genetic effects in the Red Danish population. Since the mortality rate of the Red Danish is also increasing, there must be non-genetic factors causing this negative development. Furthermore, multivariate methods using competing risk methods are required for properly discussing the type of questions we answered here because there are evidences of the presence of different specific genetic mechanisms related to culling due to slaughter and culling due to death. The multivariate discrete relative risk model for competing risks presented here is an example of such a technique. It would be interesting to perform investigations similar to the present study in other populations; the statistical tools for that are available now.

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366

367 **Table 1** – Some survival statistics.

	Holstein	Jersey	Danish Red
Median survival time	2	2	3
Probability of survival 7 or more parities	0.031	0.011	0.007
Proportion of censoring (%)	19.9	22.7	15.6

368

Table 2 – Estimates of the variance and correlations of random components from the competing risk model and the corresponding marginal heritabilities.

Component	Cause	Holstein		Jersey		Red Danish	
		Variance (SE)	Corr (SE)	Variance (SE)	Corr (SE)	Variance (SE)	Corr (SE)
S[1]	Death	0.155 (0.007)	-0.079 (0.031)	0.089 (0.013)	-0.094 (0.084)	0.436 (0.040)	-0.195 (0.072)
	Slaughter	0.022 (0.001)		0.022 (0.002)		0.020 (0.002)	
H[2]	Death	0.458 (0.006)	-0.261 (0.010)	0.414 (0.014)	-0.370 (0.025)	0.955 (0.031)	-0.458 (0.032)
	Slaughter	0.048 (0.001)		0.053 (0.002)		0.030 (0.002)	
Dispersion	Death	0.683 (0.001)	-	0.712 (0.002)	-	0.514 (0.002)	-
	Slaughter	0.649 (0.001)		0.693 (0.002)		0.623 (0.002)	
Heritability	Death	0.024		0.019		0.054	
	Slaughter	0.043		0.036		0.047	

[1] **S** represents the sire random component.
[2] **H** represents the herd-year-season random component.

372 **Table 3 –** Estimated mean effect of the coefficient of heterozygosity on the longevity for each culling reason

373 (asymptotic standard error in parenthesis).

Population	Death	Slaughter
Holstein	-0.212 (0.036)	0.032 (0.011)
Jersey	-0.013 (0.067)	-0.127 (0.025)
Red Danish	-0.266 (0.116)	-0.299 (0.033)

374

375 **Table 4 –** Estimated mean effects of the sire breed compositions on each specific culling rate (asymptotic
376 standard error in parenthesis).

Population	Breed	Death	Slaughter
Holstein	**Holstein-Friesian**	0.487 (0.107)	-0.095 (0.033)
Jersey	**US Jersey**	0.146 (0.128)	-0.016 (0.057)
Red Danish	**Holstein-Friesian**	0.303 (0.261)	-0.169 (0.061)
	American Brown	0.053 (0.218)	-0.003 (0.049)
	Nordic	0.208 (0.243)	-0.167 (0.599)

377

Table 5 – Spearman correlation between the estimated breeding values and the sire's birth year.

Population	Cause	Spearman correlation	P-value
Holstein	**Death**	0.25	<0.001
	Slaughter	-0.44	<0.001
Jersey	**Death**	0.24	<0.001
	Slaughter	-0.41	<0.001
Red Danish	**Death**	-0.03	0.283
	Slaughter	-0.53	<0.001

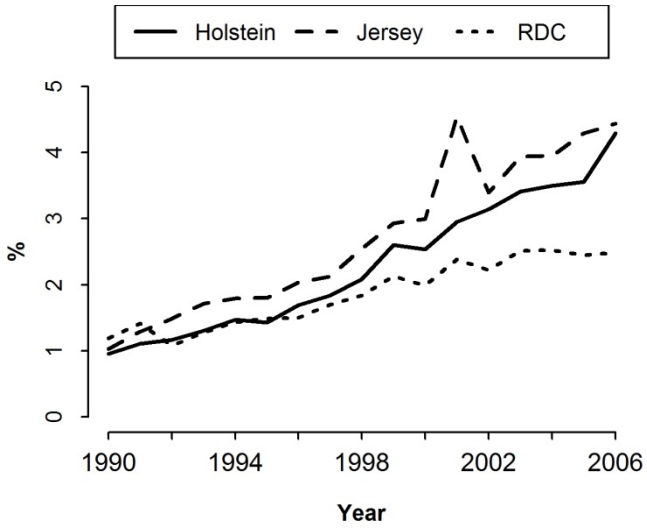

Figure 1 – Mortality rate evolution from 1990 to 2006.

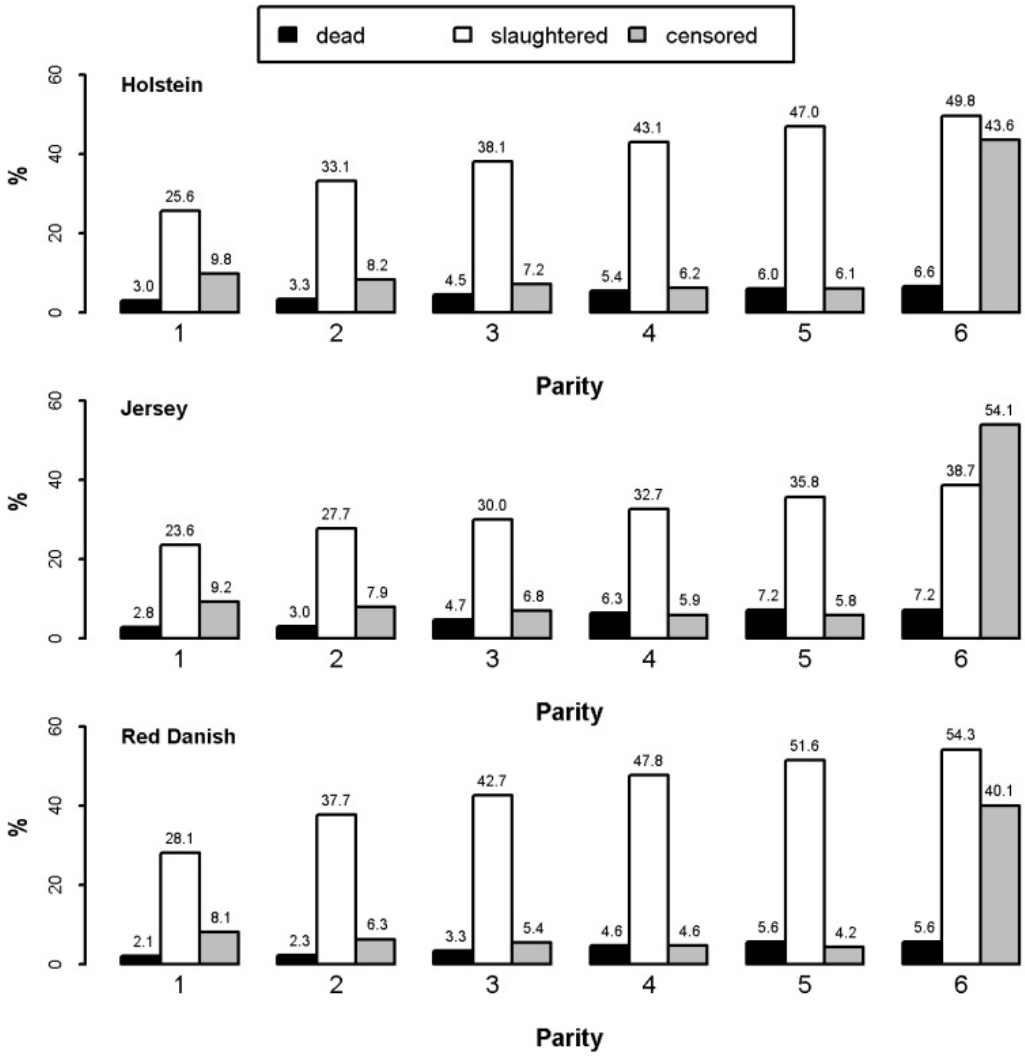

Figure 2 – Proportion of dead, slaughtered and censored cows per parity.

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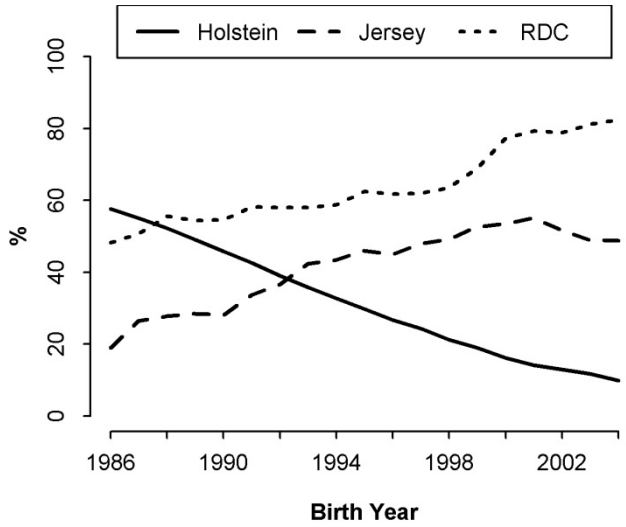

397 **Figure 3 –** Average coefficient of heterozygosity of the cows by birth year.

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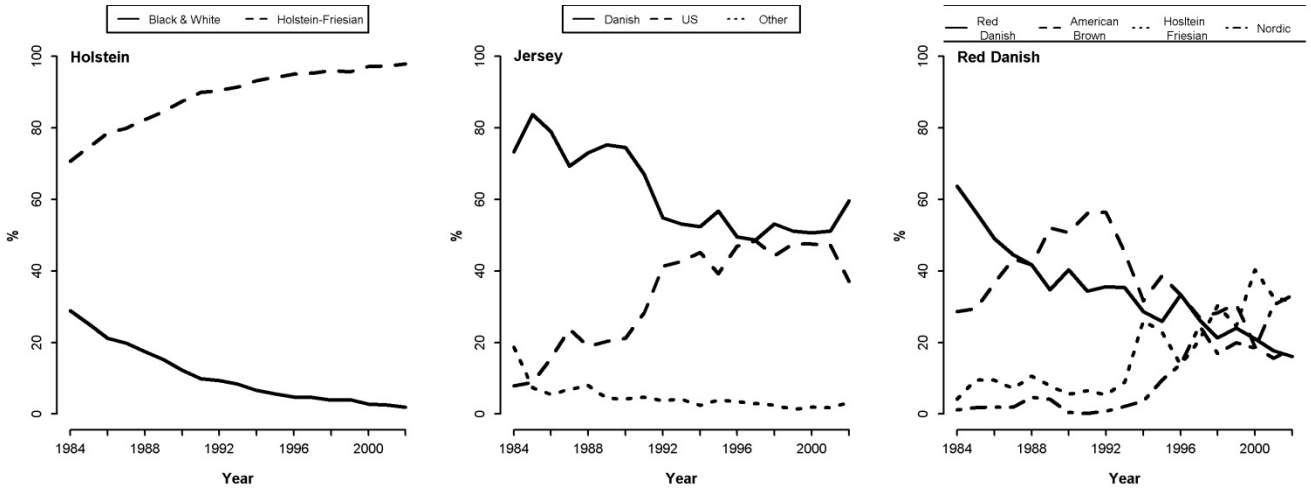

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401 **Figure 4 –** Average breed composition of the sires by the birth year.

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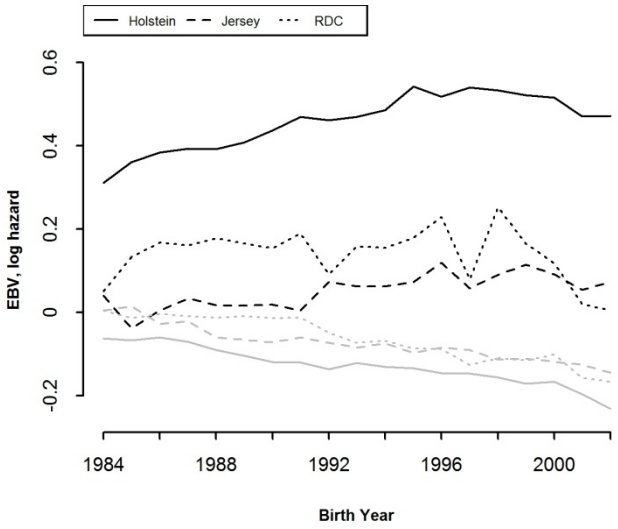

404

405 **Figure 5 –** Marginal genetic trends for the sire's estimated breeding values for death (black curves) and

406 slaughter (gray curves).