

## **ESTIMATE THE GENETIC PARAMETERS AND ANALYSIS OF CULLING REASONS IN IRANIAN HOLSTEIN DAIRY CATTLE**

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### **SUMMARY**

Many animals are culled from the herd on dairy farms annually due to health problems, and this involuntary culling causes significant economic losses to the dairy industry. This study aimed to identify the trend of culling reasons and lifespan and estimate their genetic parameters. The cow history records and pedigree files of 11 large commercial dairy farms with cows culled from 1995 to 2015 were used. It is estimated that 18.6% of cows are culled voluntarily by farmers, while 81.4% of cows leave the herd involuntarily. Three main reasons for involuntarily culling were reproductive problems (25.9%), death and others (16.7%), and infectious diseases (14.3%). Over time, the distributions of culling reasons have altered with a reduction in "death and others", suggesting a better or more precise diagnosis of culling reasons and improvement in dairy farm recording systems. The average lifespan of cattle was 4.42 years with heritability of 0.14. The heritabilities of culling reasons were very low and ranged from 0.03±0.02 (metabolic and digestive disorders) to 0.08±0.03 (mastitis and udder problems). The significance of the maternal effect for some traits like mastitis indicates that it may be possible to improve an individual's health and, therefore, farm profitability genetically.

### **INTRODUCTION**

Dairy cows are expected to remain economically useful in their herds for a much shorter period of time than the natural lifespan of cows, which is approximately 20 years. The length of lifespan from birth until culling (Hu *et al.* 2021) varies from 4.9 years in US (De Vries 2017), to 6.3 years in UK (Pritchard *et al.* 2013) or 6.75 years in Australia (Wondatir Workie *et al.* 2021). An increase in lifespan can increase profitability by reducing the annual costs of replacement of cows, which indicates the economic importance of lifespan for dairy farmers.

Farmers have several reasons for culling cows from their herds which can be generally classified as voluntary or involuntary culling (Weigel *et al.* 2003). Compared to voluntary culling, which is based on optimal economic decisions, the involuntary culling occurs when farmers have to remove their productive, profitable cows due to illness, injury, infertility, or death (Wondatir Workie *et al.* 2021). Due to improvements in genetic trends for fertility and adding health disorders such as mastitis as well as longevity in the selection index for dairy cattle, culling rate is expected to change over time. In addition, it might be possible that some genes related to health disorders that lead to culling in dairy cattle pass over the generations. The objective of this study was to estimate the trend and genetic parameters of lifespan and culling reasons of dairy cattle.

### **MATERIALS AND METHODS**

The cow history records of 11 commercial dairy farms in Iran, which included cows culled between 1995 to 2015 were extracted from an on-farm record-keeping software. The variables extracted included herd, parity number, cow ID, birth date, culling date, culling reason, and the ID of sire and dam (for known parents). Data was edited by SQL Server Management Studio

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(Microsoft, 2012). Cows with missing parity numbers, birth dates, culling dates, unknown dam, milk period >10, date of birth greater than their dams' birth date, or missing culling details were removed from the original dataset. Culling reasons were categorized into seven groups as described in Table 1. Cow lifespan was calculated as the interval between birth date and culling date. The final dataset used for this study was 67,287 records of 13,616 heifers and 53,671 cows. For the analysis of culling reasons and estimation of the genetic parameters, each culling reason was considered as a different phenotype as a binary variable (1 or 0) indicating whether a cow left the herd for that reason or not. The trend of culling reasons over time was plotted in R using ggplot2 package (Wickham 2016).

Using ASReml (Gilmour *et al.* 2015), a binomial model with a logit link function was applied to the dataset to estimate the genetic parameters of each culling reason. For lifetime, however, a continuous model was used in which the data were tested for normality using Shapiro-Wilk test and then log- transformed to approach normality. A range of systematic effects, including herd, year of birth, the season of birth, year of culling, season of culling and their interactions and milk period were tested for significance for each trait (results not shown). Four combinations of random effects for direct genetic, maternal genetic, and maternal permanent environmental effects were compared via univariate analysis for each trait separately. The covariance between direct genetic and maternal genetic effects was ignored. The four models including 1) direct animal genetic effect, 2) direct and maternal effect, 3) direct and maternal permanent environmental effect, and 4) model including all above random effects were tested and then compared using likelihood ratio tests (LRT) between the full and reduced models.

**Table 1. Description of the culling reason (and their proportion) of used dairy cattle in this study**

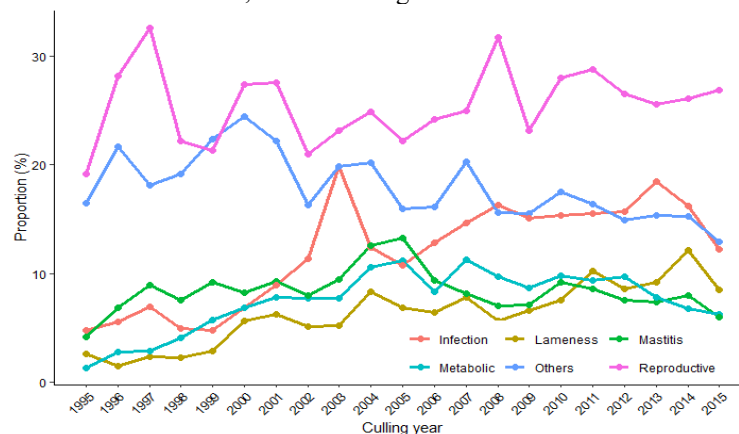
Group	Descriptions	Proportion (%)
Voluntary	Low milk production, old age, dairy purpose	18.6
Reproductive problems	Infertility, recurrent abortions, mummy (wax) abortion, stillbirth, ovarian cysts, uterus problems (rupturing, bleeding, infections, and diseases)	25.9
Feet and leg disorders	Lameness, joint infection, dislocation and fracture of the hands, legs and hip, crippling, hoof diseases and spinal cord injuries	7.8
Mastitis and udder problems	Mastitis, protracting and rupturing ligaments of the gland, complete teat-cistern obstruction, udder gangrene and bleeding	8.3
Metabolic and digestive disorders	Bloating, acidosis, ketosis, fatty liver, milk fever, displaced abomasum, obstruction and twisting of gut, omasum accumulation, abomasum and rumen, diarrhea	8.4
Infectious diseases	Leucosis, foot-and-mouth disease, brucellosis, pneumonia, tuberculosis, black leg, Bovine Johne's disease, lung and liver infections/abscess, Bovine Viral Diarrhea Virus (BVDV)	14.3
Death and others	Death, peritonitis, injury, blindness, toxication	16.7

## RESULTS AND DISCUSSION

According to data available over 21 years, 18.6% of cows were culled voluntarily by farmers. This was less than that reported (27.1%) by Ghaderi-Zefrehei *et al.* (2017), who studied the culling reason in one farm in Iran. The main reason for involuntarily culling was reproductive problems (RP) which accounted for almost a quarter (25.9%) of culling reasons (Table 1). The other major involuntary reasons for culling the cows from the herd were "death and others" (D&O) (16.7%), and

infectious diseases (14.3%) (Table 1). RP and infectious diseases have been reported as the most significant reasons of culling the dairy cows in Iran (e.g., Ghaderi-Zefrehei *et al.* 2017). The remarkable percentage of culling due to RP can be explained by the genetic selection performed on milk yield for many years and negative association exists between these traits (De Vries and Risco 2005). Regarding infectious diseases, Holstein cows are expected to be sensitive to some pathogens in Iran. Furthermore, this study is also included the heifers that have not calved and are mainly culled due to infectious diseases, and reproductive abnormalities not becoming evident until after first calving. The average lifespan was 4.42 years, which is close to US (4.9 years, De Vries 2017) and German dairy cattle (~5 years, Martens and Bange 2013), but lower than Australian cows (6.75, Wondatir Workie *et al.* 2021).

The trend of major involuntary culling reasons for Holstein cows over the period of 21 years is presented in Figure 1. Although there were fluctuations, the level of culling for RP remained high throughout the whole study period. Over the time, culling for D&O showed a downward trend, suggesting better, or more precise, diagnosis of culling reasons and improvement in dairy farm recording systems. There was an increase in involuntary culling of animals due to infectious diseases over time, with a sudden rise in 2002. Factors that may have led to this observation may be increasing the density of animals, which may result in disease spread; improved diagnosis of the culling reason over time (part of this group might come from the D&O group); decreased immunity caused by selection for low somatic cell counts; and the emergence of new diseases.



**Figure 1. Proportion of involuntary culling reasons by year of culling**

For all traits, maternal permanent environment effects were not significant (Table 2). For culling due to "mastitis and udder problems"(M&U), RP and D&O, the maternal genetic effect had small effects with significant likelihood ratio tests (LRTs), and because of the nature of dam effects on reproduction traits, it was retained in the model. Based on the results, heritabilities of culling reasons were low, ranging from 0.03 (metabolic and digestive disorders) to 0.08 (M&U) (Table 2). The heritability for lifespan was higher (0.14) which agrees with Van Pelt *et al.* (2015), however the definition of this trait differed (time from first calving to the last test date for milking production in Van Pelt *et al.* (2015) and time from birth to culling in this study). There is a lack of study on genetic parameters for culling reasons, however the heritability of some of these traits like clinical mastitis (0.01 to 0.42; Nash *et al.* 2000) and lameness (0.15 to 0.22; Weber *et al.* 2013) has been reported.

## CONCLUSIONS

This study shows that 81.4% of culling is out of the farmer's control (involuntary culling). Over time, culling reasons have altered with a reduction in "death and others" suggesting the better or

more precise diagnosis of culling reasons and improvement in dairy farm recording systems. Despite fluctuations, the rate of culling for Reproductive problems remained high throughout the study indicating the need for improving fertility management and consequently reproductive efficiency. Although the heritabilities of culling reasons were low, our results suggest that some opportunity may exist for genetic improvements in individual's health (e.g., mastitis and reproductive problems) in Iranian Holsteins and therefore improve animal welfare and farm profitability.

**Table2. Genetic variance ( $\sigma^2_g$ ), maternal variance ( $\sigma^2_m$ ), direct heritability ( $h^2$ ), maternal heritability ( $m^2$ ) (and their standard error (SE)) and likelihood ratio tests (LRT) and degrees of freedom (df) for the selected model when running a univariate animal model**

Trait <sup>1</sup>	$\sigma^2_g$ (SE)	$\sigma^2_m$ (SE)	$h^2$ (SE)	$m^2$ (SE)	LRT <sup>2</sup>	df <sub>3</sub>
F&L disorders (%)	0.17 (0.04)		0.05 (0.03)		0	0
M&U problems (%)	0.27 (0.04)	0.01 (0.03)	0.08 (0.03)	0.00 (0.02)	213 ***	1
M&D disorders (%)	0.11 (0.03)		0.03 (0.02)		0	0
Reproductive problems (%)	0.15 (0.02)	0.01 (0.01)	0.04 (0.02)	0.01 (0.01)	116 ***	1
Infectious diseases (%)	0.15 (0.02)		0.04 (0.02)		0	0
Voluntary (%)	0.30 (0.03)		0.08 (0.02)		0	0
Death and others (%)	0.16 (0.02)	0.02 (0.02)	0.05 (0.02)	0.00 (0.02)	149***	1
Lifespan (yrs) <sup>4</sup>	0.02 (0.00)		0.14 (0.01)		0	1

<sup>1</sup> All traits except lifespan were fitted in the binomial model on the logit scale ( $\sigma_{2e}=3.29$ ). F&L= Feet, and leg; M&U= Mastitis and udder; M&D = Metabolic and digestive.

<sup>2</sup> \*\*\*  $P < 0.001$ , \*\*  $P < 0.01$ , \*  $P < 0.05$ ,  $P < 0.1$ , ns or non-significant.

<sup>3</sup> df- the difference in the number of parameters between full and reduced models as 0, 1, 2 –for the base model (direct random effect), when maternal genetic effects or maternal permanent environmental effects or both were added.

<sup>4</sup> Lifestyle is reported as genetic standard deviation ( $\sigma_g$ ) instead of genetic variance ( $\sigma^2_g$ ).

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