

## EFFECT OF BREEDING PROGRAMS ON THE FUNCTIONAL LONGEVITY OF IRANIAN HOLSTEIN COWS

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### ABSTRACT

This study aimed to determine the effect of breeding programs on the functional longevity of Iranian Holstein cows. For this purpose, records of 538,873 animals collected by the Animal Breeding Center of Iran from 1990 to 2013 were used. Functional longevity was calculated from the difference between the first calving date and the last recording date. Animals that were alive in the herd or their culling date was unavailable, and less than one year had passed from their last recording were considered censored data, accounting for 34.23% of the records. The effect of milk production, herd size, interaction between lactation period and stage, herd-year-season of calving, Holstein gene percentage, and age at first calving were evaluated, and significant effects were included in the maternal grandsire model on genetic evaluation of longevity. The survival probability in different levels of effects was calculated by *cmprsk* package, and genetic evaluation of longevity was performed using *Survival kit* software. All effects were significant on the functional longevity, and thus the culling risk had a decreasing trend with increasing herd size changes and age at first calving, which increases with the increment of Holstein gene percentage. The culling risk decreased with increasing lactation, and animals were more likely to be culled in the first lactation. Direct heritability of longevity was estimated at 0.15, indicating good genetic diversity for breeding this trait. The effect of breeding programs with estimated breeding values for milk, fat, and protein production showed that the culling risk for higher genetic production potential tended to increase.

**Keywords:** Culling risk, Dairy cattle, Functional longevity, Holstein gen percentage.

## INTRODUCTION

Functional longevity is one of the essential objects in the dairy cattle industry. The number of calving for each animal increases with the increment of longevity, and more heifers will be produced for sale while providing replacement animals (Byun, 2012). In addition, it increases average herd production due to a higher production of adult rather than young animals (Sewalem et al., 2004). Therefore, increasing the functional longevity will significantly increase the net profit of herds. The final goal of selection programs in dairy cows is to maximize genetic gain for productive traits. The selection of animals only for milk production has caused unfavorable genetic responses for traits related to health, longevity, fertility, and environmental sensitivity (Brito et al., 2021). Therefore, it is necessary to include functional longevity and physical body traits in the selection criteria (Brito et al., 2021). The replacement of dairy cows is essential to dairy cattle farm management. Replacement decisions include culling low-performance dairy cows and their replacement with suitable heifers (Nor et al., 2014). A large part of the replacements involves voluntary culling of productive cows for slaughter, which is defined as the culling of productive cows from the herd due to the decision of farmers (Fetrow et al., 2006). It has been reported that culling for the individual slaughter of cows is associated with older calving age, high age at first calving, complications of calving and long calving interval, low production level, and health indicators such as high somatic cell count in milk, very high or low fat-protein ratios in the first lactation (Pritchard et al., 2013; Rilanto et al., 2020). These factors can be considered risk factors associated with animal culling (Kulkarani et al., 2021).

A common method for analyzing longevity data is survival analysis (Forabosco et al., 2009), which is due to a more accurate time scale (day instead of month, year, or lactation period), the ability to deal with live cows as censored, and effectively study time-dependent variables (Smith and Quaas, 1984). Analysis of longevity is typically performed based on the sire and maternal grandsire models (Forabosco et al., 2009). However, the heritability of this trait is very low (Van Pelt et al., 2015) and leads to incorrect phenotypic predictions of individual survival based on parental information alone. Survival analysis is a set of statistical methods for analyzing data in which an event variable such as death and disease occurs (Clark et al., 2003). The trait used in this analysis is time, which can

be the year, month, week, or day. Survival time is defined in a specific known period. Censoring occurs when information about the survival time of an animal is incomplete (Kleinbaum and Klein, 2012).

It was reported that longevity decreased from 1980 to 2000 in dairy cows in 38 states east of the Mississippi River, and thus annual survival rates decreased by 4 and 6.3% in the second and third lactation, respectively (Pinedo et al., 2010). In the study of hazard risk for the survival of Dutch dairy cows, it was reported that production level, calving period, high fat-protein ratio, and average insemination for all calving were directly related to survival time, while the number of somatic cell count and low fat-protein ratio were negatively associated with survival (Kulkarani et al., 2021).

The heritability of longevity has been reported to be 0.038 to 0.210 in different studies (Mészáros et al., 2008; Potocnik et al., 2011; Jenko et al., 2013; Musingi, 2019); in the range of 0.002-0.031 using random regression for Dutch dairy cattle (Van Pelt et al., 2015); in the range 0.06-0.09 using the linear model and 0.05-0.18 using the threshold model for Brazilian Holstein cows (Kern et al., 2014). The objective of the present study was to evaluate the active strategies in breeding programs of Holstein cattle and their impact on maintaining or increasing the functional longevity of Iranian Holstein cows.

## MATERIALS AND METHODS

The present study used data of 538,873 Holstein cows collected by the Animal Breeding Center of Iran from 1990 to 2013. Data included production records (milk, fat, and protein), reproduction (herd information, year and season of calving, birth data, calving date, parity), and pedigree file. Firstly, data were edited using Visual FoxPro 9.0 software (Karyono, 2007). The pedigree structure of the data is presented in Table 1.

The studied trait in this study included functional longevity. Functional longevity was calculated from the difference between the first calving date and the last recording date. The time interval was defined in two different ways: (i) animals whose last recording date was the culling date, which was considered as a complete record; and (ii) animals whose last recording was unknown, which was considered as an incomplete record (right censoring data, 36.5% of the total data). Table 2 shows the descriptive statistics of functional longevity data.

The following model was used to evaluate breeding programs on functional longevity (Rokouei et al., 2010):

**Table 1. Pedigree structure used for Iranian Holstein cows.**

Animals	Number of animals
Individuals	749,992
Dams	655,170
Sires	673,729
Individuals with offspring	444,244
Individuals with no offspring	305,748
Sire founders	2,130
Dam founders	57,601

**Table 2. Descriptive statistics of functional longevity data for Iranian Holstein cows.**

Parameter	Average	Minimum	Maximum
Longevity of the culled animals (d)	1,458	126	5,497
Longevity of the censored animals (d)	1,077	84	5,465

$$h_{ijklmnop}(t) = h_0(t) \exp[hys_i(t) + h_{var j}(t) + p_k(t_1, t_2) + m_l(t) + \beta_1 AFC_m + \beta_2 HF_n + G_o + S_p],$$

where  $h_{ijklmnop}(t)$  is the hazard function for a given cow at time  $t$ ;  $h_0(t)$  is the Weibull baseline hazard function with scale parameter  $\lambda$  and shape parameter  $\rho$ ;  $h_0 = \lambda\rho(\lambda t)^{\rho-1}$ ;  $hys_i(t)$  is the time-dependent random effect of herd-year-season, which is assumed to have an independent distribution, following a log-gamma distribution (four seasons were considered for each year);  $h_{var j}(t)$  is the fixed time-dependent effect of the herd size change classes (changes  $\leq -5\%$ ,  $-5\% < \text{changes} \leq 5\%$ ,  $5\% < \text{changes} \leq 15\%$ ,  $15\% < \text{changes} \leq 35\%$  and changes  $> 35\%$ );  $p_k(t_1, t_2)$  is a time-dependent combined effect of lactation number and stage of lactation (Lactation stage includes less than 90 days, between 90 to 150 days, between 150 to 270 days, between 270 to 365 days and more than 365 days);  $t_1$  days after first calving and  $t_2$  days after current calving with changes at 270 and 380 days per parity. The  $m_l(t)$  is the time-dependent fixed effect related to 305-d mature-equivalent milk production within herd-year, which was included to account for voluntary culling based on milk production. Cows were classified into five groups based on milk production (groups 1 to 5 are cows with a milk production of  $< -1.5$  SD, between  $-1.5$  and  $< -0.5$  SD, between  $-0.5$  and  $< 0.5$  SD, between  $0.5$  and  $< 1.5$  SD, and  $> 1.5$  SD than the average of the herd-year of calving production, respectively).  $\beta_1$  and  $\beta_2$  are the time-independent regression of age at first calving (AFC) and Holstein gene proportion in % (HF);  $G_o$  is the genetic group for breeding values of milk production traits and age at first calving;

$S_p$  is a time-independent random effect of sire, assuming multivariate normal distribution with mean vector 0 and covariance matrix  $A\sigma_s^2$ , where  $A$  is the additive genetic relationship matrix, and  $\sigma_s^2$  is an additive genetic variance of sire.

Heritability ( $h^2$ ) was estimated for the longevity trait as follows:

$$h^2 = \frac{4\sigma_s^2}{\sigma_s^2 + 1}$$

where  $\sigma_s^2$  is the variance between sires.

For genetic grouping of animals based on estimated breeding values of milk, fat, protein, and age at first calving traits, firstly, the (Co) variance components and genetic parameters of traits were estimated by ASReml software based on the next single trait model:

$$y_{jk} = \mu + HYS_j + \beta_1 AFC_k + a_k + e_{jk}$$

where  $y_{jk}$ : the record of animal  $k$ ;  $\mu$ : mean of trait;  $HYS_j$ : the effect of herd-year-season of calving;  $\beta_1$ : regression of age at first calving.  $a_k$  and  $e_{jk}$  are the random effects of the direct genetic and residual, respectively. Then, the breeding values of milk, fat, protein, and age at first calving traits were calculated at first calving and grouped based on breeding values. The grouping was done in such a way that the breeding values of the cows in each herd were considered, and the animals were divided into five groups. The packages of Survival (Therneau, 2018) and Cmprsk (Fine and

Gray, 1999) were used to determine the effect of factors on longevity and calculate the culling risk of animals at different times of various levels of factors. Estimation of the variance component of longevity and the culling risk for different groups of breeding values was performed by Survival kit software (Meszaros et al., 2013).

## RESULTS AND DISCUSSION

Analysis of factors affecting functional longevity showed that all the studied factors, including changes in herd size, lactation stage, milk production, interaction between lactation period and stage, Holstein gene percentage, age at first calving, and estimated breeding value for milk, fat, protein, and age at first had a significant effect on longevity. Fig. 1 shows the changes in the functional longevity of animals based on the longevity function of all animals. The functional longevity change function can be divided into three periods, which are related to the population up to 500 days, between 500 to 3,000 days, and after 3,000 days of age, respectively. High data density is related to the period up to 500 days of age, and many animals had been culled from the herds in the third stage. Curve changes after 3,000 days showed slight decreasing changes, with a

more decreasing slope before 3,000 days of age.

In the study of risk factors for the longevity of Dutch dairy cows under changes in agricultural policies (milk quota period, post-milk quota period, and phosphate regulation period), the average longevity for all breeding cows was 3,087 days. The median predicted longevity for these three policies was 1,911; 1,897 and 1,792 days, respectively (Kulkarani et al., 2021).

The heritability of functional longevity for Iranian Holstein cows was calculated to be 0.15 using of Weibull model. In addition, estimated sire variance and herd-year-season variance were 0.04 and 0.091, respectively. The heritability of functional longevity: 0.085 for the United States (Ducrocq et al., 1988); between 0.022 to 0.023 for the Netherlands (Vollema and Groen, 1998); 0.092 for Canada (Dürr et al., 1999); 0.069 for Sweden (Strandberg and Roxström, 2000), and 0.116 for Germany (Buenger et al., 2001) were estimated using of the same model (Weibull model).

Sewalem et al. (2004) estimated the heritability of longevity for Canadian Holstein cows using the Weibull model, and reported a range of 0.03-0.05, which was lower than our findings in the present study. A value of 0.14 was reported for Slovenian Holstein cows (Potonik et al., 2011), while M'hamdi et al. (2014) reported a heritability

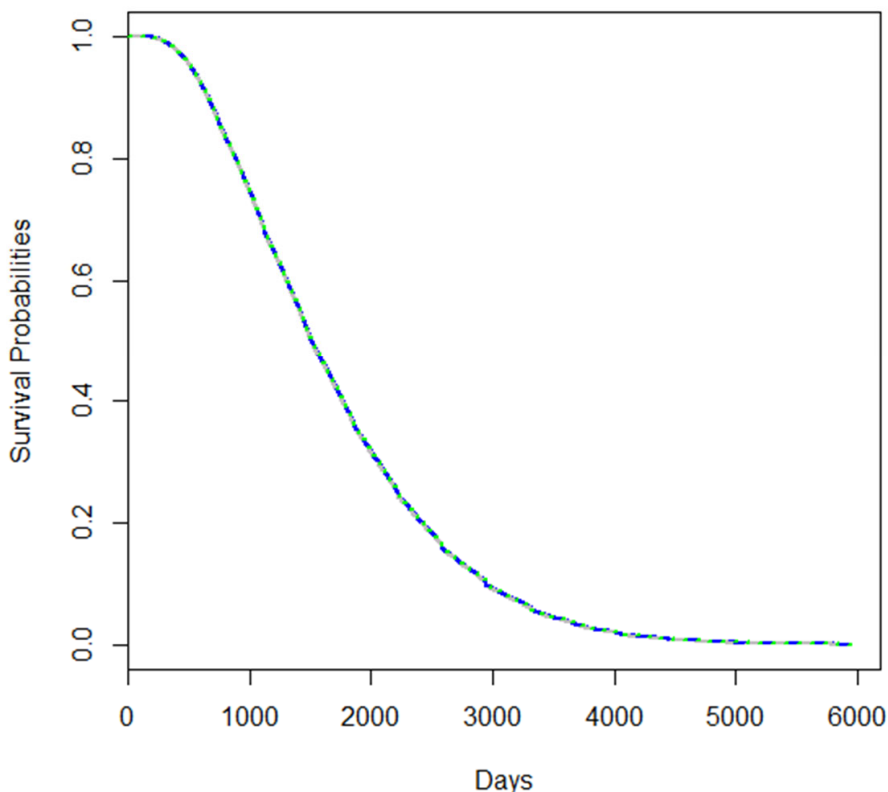


Fig. 1. Longevity changes of Iranian Holstein cows.

of functional longevity of 0.19 for Tunisian Holstein cows. Furthermore, Strapáková et al. (2014) estimated a heritability of longevity 0.13 for Slovakian Holstein cows using the sire model. A comparison of the results shows that the estimated heritability (0.15) corresponds to the range of the recent studies. In some populations (Strapáková et al., 2014), the variance between sires (0.05) and herd-year-season (0.3) was higher than our findings.

In a study of survival for the crossbreed calves, the range of heritability for survival from 1 to 30 and 30 to 200 days of age was reported to be 0.045 to 0.075 (Davis et al., 2019). Estimated heritability monthly survival using a random regression model varied from 0.002 to 0.031 (Van Pelt and Veerkamp, 2014; Van Pelt et al., 2015). Survival was also studied for female Holstein calves from birth to first calving, birth up to 305 days, birth to culling, and first calving to culling,

and heritability for these traits were reported at 0.009, 0.007, 0.141, and 0.162, respectively (Weller et al., 2020). In a study conducted in Kenya, the functional longevity of Sahiwal herds was studied as the time between birth or the first calving to the last lactation record, number of lactation periods, total lactation days, total milk production periods, survival from birth to 44, 56, 80, 92, 104 and 128 months and from the first calving to 12, 36, 60, 84 and 96 months. Heritability was reported to be higher for longevity-related survival (0.084-0.119) than for longevity related to productive life (0.038-0.097). Also, the heritability of survival from the first calving to the defined ages (0.090-0.119) was found to be higher than the survival from birth to the desired ages (0.084-0.104) (Musingi, 2019).

The relative culling risk for different lactation at different stages of lactation is shown in Fig. 2. Although the comparison of lactation stages should be made within each period, the effect

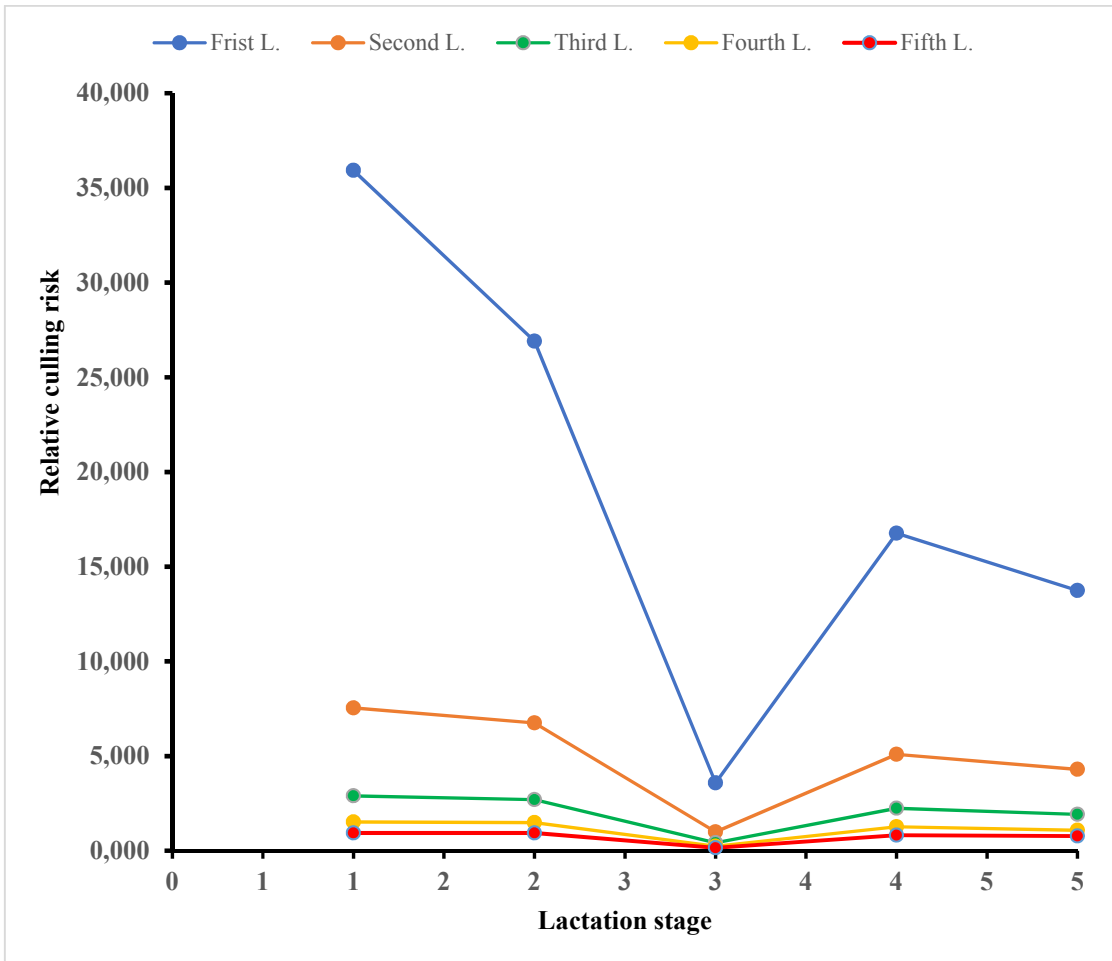


Fig. 2. The effect of lactation period (L: lactation) and stage (Lactation stage includes less than 90 days, between 90 to 150 days, between 150 to 270 days, between 270 to 365 days and more than 365 days) on the culling of Iranian Holstein cows.

of lactation on culling in the first lactation was significant, suggesting a decision to cull heifers after the first lactation. In general, culling risk was high in the first stage of all periods, which can indicate that the decision of breeders to cull is mostly based on milk production during the first four months of lactation and health problems associated with calving. In addition, culling in the first stage of lactation may be due to high stress on the animal to reach peak milk production, making a negative balance of energy, and as a result, the occurrence of metabolic diseases such as acidosis and mastitis. As shown in Fig. 2, the highest culling risk was related to the first stage (1 to 90 days) and decreased in the following stages. Therefore, the culling risk in the first stage is about ten times higher than in the third stage. These results are consistent with those reported by Dadpsand Taromsari (2006). Culling in the late stages of lactation is likely to indicate a decision to cull after the cow has dried up and faced issues such as infertility and mastitis.

The effect of milk production on the relative culling risk is shown in Fig. 3. Animals with incomplete or non-standard milk production were considered as a basis, and other groups were compared. Groups with a production of 1.5 standard deviations less than the average herd

had a lower culling risk than the other groups. However, compared to other groups, a higher culling risk was observed in the fourth group, which was opposite to the results of Dadpsand Taromsari et al. (2006).

The culling risk of cows in the first group was about 18% lower than that of the fifth group. In general, the culling risk has increased with the increment in milk production. High milk production due to the mismatch between energy needs and energy intake creates a negative energy balance in cows, which causes weight loss and a decrease in the body condition score at the beginning of lactation (Lucy, 2001). Raguz et al. (2011) reported a slight reduction in the culling risk with increasing milk production. The culling risk of the high-producing cows in the herd is higher than low-producing cows due to sensitivity to environmental conditions (Weigel et al., 2003). These results highlight the effect of milk production on the selection of Holstein herds because most of the selections made in the last decades have been based on milk production.

The effect of herd size changes on the relative culling risk is shown in Fig. 4. The annual change in herd size significantly affects the relative culling risk. In other words, the herd factor, which depends on factors such as feeding method,

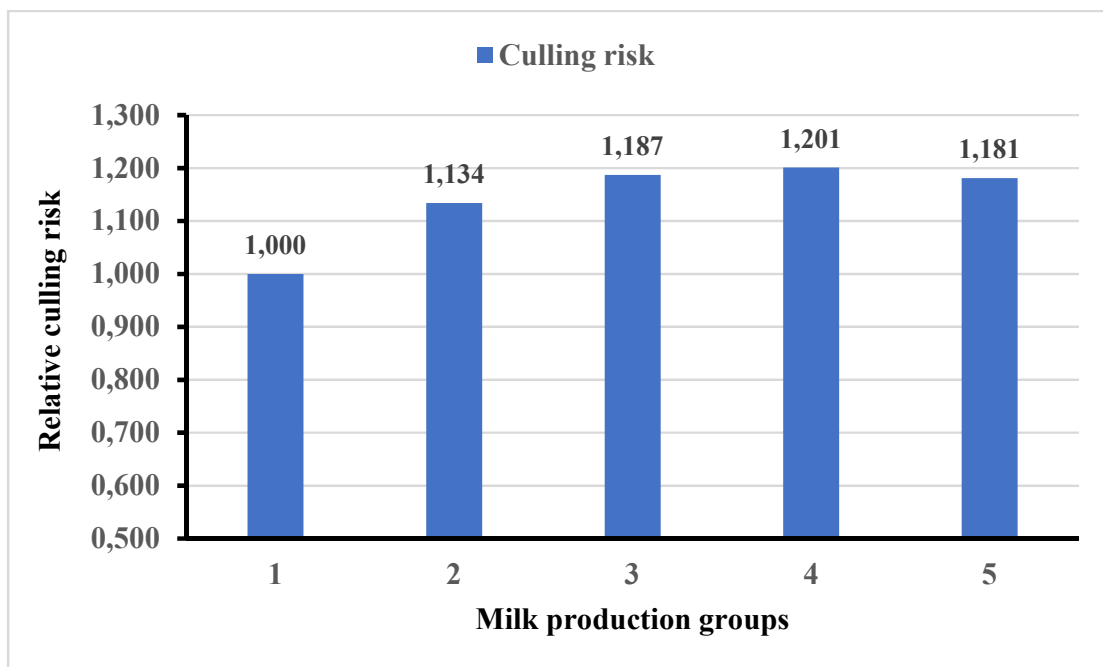


Fig. 3. The effect of milk production (groups 1 to 5 are cows with a milk production of < -1.5 SD, between -1.5 and < -0.5 SD, between -0.5 and < 0.5 SD, between 0.5 and < 1.5 SD, and > 1.5 SD than the average of the herd-year of calving production, respectively) on the relative culling risk.

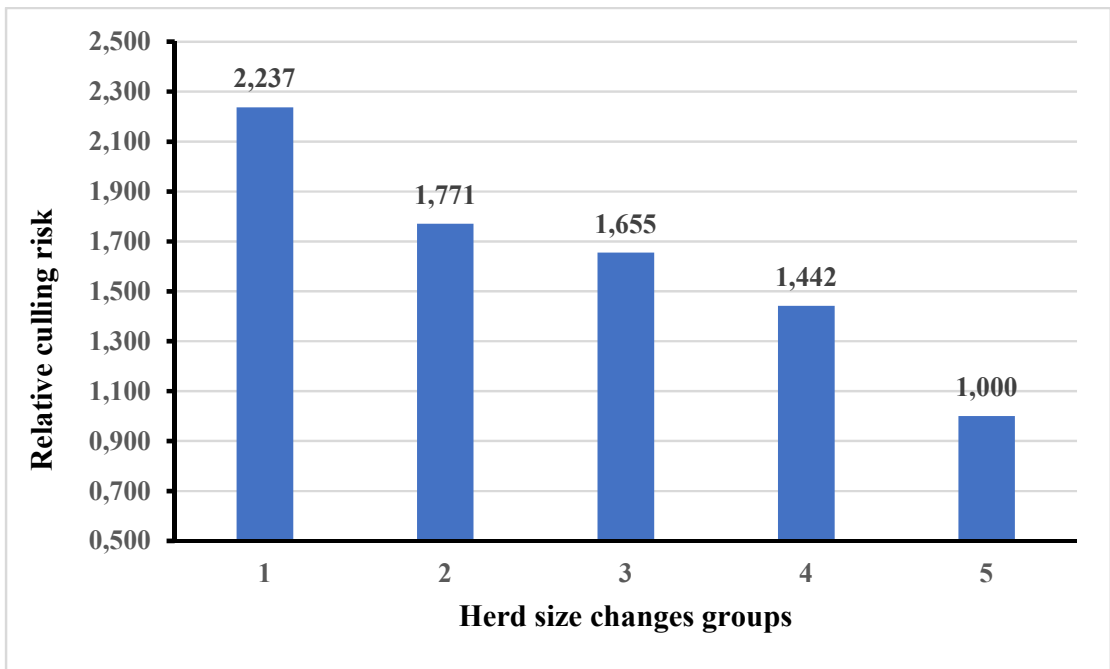


Fig. 4. Effect of herd size changes (1 to 5 shows changes  $\leq -5\%$ ,  $-5\% < \text{changes} \leq 5\%$ ,  $5\% < \text{changes} \leq 15\%$ ,  $15\% < \text{changes} \leq 35\%$  and changes  $> 35\%$ , respectively) on the relative culling risk.

management program, and weather conditions, directly affects animal culling. The culling risk was significantly reduced in a change of more than 35% compared to last year. The culling risk in the first group ( $< -5\%$ ) was higher than in the other groups. In line with the policy of increasing the herd population during the year, efforts are made to preserve animals, and animals are removed from the herd only by voluntary culling.

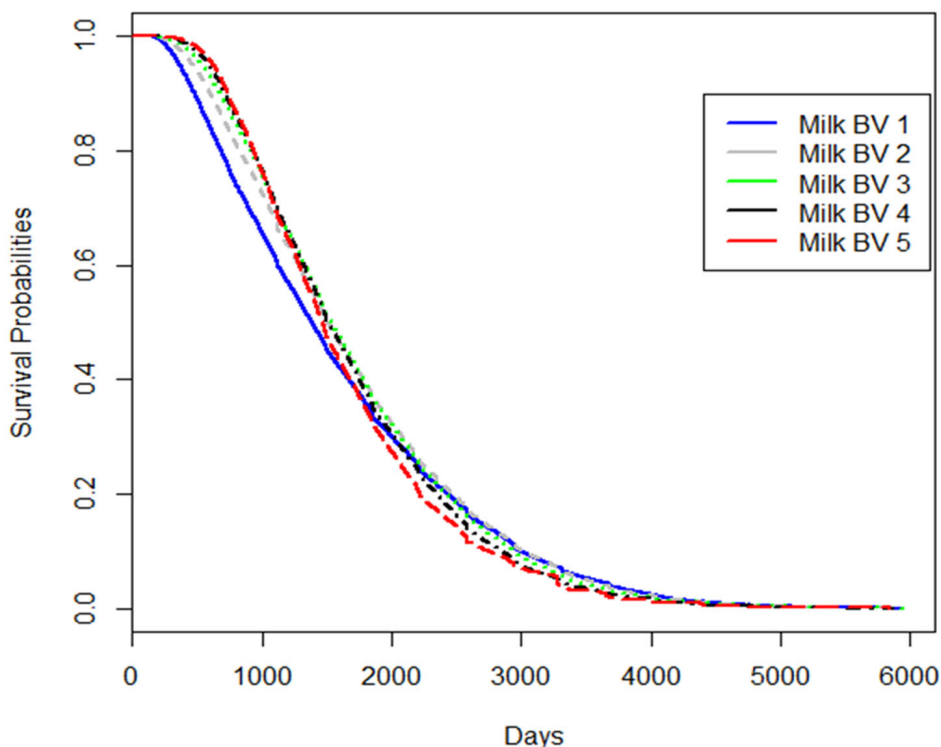
Weigel et al. (2003) reported similar results and stated that low-producing cows were 4.2 times more likely to be culled than the average risk in the group with minor changes, while high-producing cows were only 0.5 times more likely to be culled. After increasing herd changes, the culling risk of the low-producing cows decreases the relative risk to 2.6 times, and the culling risk of the high-producing cow increases the average to 0.7 times. Culling criteria, such as disease prevalence, price changes, and milk rations, also change over time (Potocnik et al., 2011).

Reduced culling by increasing the number of cows has also been mentioned by other researchers (Meszaros et al., 2008; Bonetti et al., 2009). Raguz et al. (2011) studied Croatian dairy cows and reported that animals, especially the Simmental breed, had a higher culling risk in larger herds than in smaller herds. However, a slight increase was observed in Holstein cows. Potocnik et al. (2011) also considered herd dynamics as one of the factors affecting the relative culling risk.

Expanding herd size changes reduce the culling risk, and change decrement decreases the culling risk.

In the present study, the Holstein gene percentage and age at first calving were considered as covariates. Due to the negative coefficient ( $-0.001589$ ), an inverse relationship was observed between Holstein gene percentage and functional longevity. The culling risk has also increased with adding Holstein gene percentage. Increasing the age of the first calving reduced functional longevity (regression coefficient,  $-0.006854$ ), which is consistent with the results of many other researchers. Zavadilova et al. (2011) reported a high effect of age at first calving on reducing functional longevity. Conversely, Raguz et al. (2011) found a weak effect of age at first calving on functional longevity. Decreasing calving age increases the number of calves, and consequently increases the amount of milk produced during functional longevity and makes the herd more profitable.

The functional longevity curve trend for five groups of milk breeding values is shown in Fig. 5. In the initial part of the graph, up to the age of 1,800 days, animals with low breeding values had a high culling risk. In general, animals with low genetic potential were voluntarily removed in this section. However, this trend changes after 1,800 days, and animals with higher breeding values do not last well in the herd and are forced



**Fig. 5. Functional longevity curve for five groups of milk breeding values (BV 1 to BW 5 indicates low to high breeding value).**

to be culled. As a result, animals with lower breeding values are more durable in the herd.

Fig. 6 shows the functional longevity curve for the five groups of fat breeding values. As can be seen, in the initial part of the graph, i.e., up to 1,400 days, animals with low breeding values are more likely to be culled. In general, animals with low genetic potential were voluntarily culling in this section. However, this trend changes after 1,400 days and livestock with higher breeding value does not last well in the herd and are forced to be culled.

The functional longevity curve for five groups of breeding values of protein was shown in Fig. 7. Animals with low breeding values have a higher culling up to the age of 1,200 days. However, this trend changes after 1,200 days, and animals with higher breeding values do not have good durability in the herd and are forced to be culled. Since breeding programs focus on milk and fat production and the correlation of milk protein content with milk and fat production, the trend of protein changes is similar to Figs. 5 and 6.

Fig. 8 shows the functional longevity curve for five groups of age at first calving breeding values. As can be seen, the curve has two parts. In the first part, cows of an older age at first calving have a lower culling risk due to the development of physical dimensions and physical structure

of the animal, and more tolerance for the first calving and stress of milk production. In the second part, the animal that gave calving at a younger age than the average calving age had more durability and less culling risk, but these animals did not have much durability in the herd. It can be observed that the functional longevity of the animal increases with decreasing age at first calving. Decreased age at first calving positively affects milk production throughout life (Zavadiłova et al., 2011). Nilforooshan and Edriss (2004) reported a slight positive phenotypic correlation (0.052) between age at first calving and longevity. M'hamdi et al. (2014) observed a linear increase in the culling risk with increasing age at first calving and reported a low risk for animals that give calving at a younger age.

Gill and Allaire (1976) stated that the ideal age at first calving to maximize performance was 22.5 to 23.5 months. Increased culling risk at older ages is related to fertility and calving problems. Nilforooshan and Edriss (2004) reported a negative correlation (-0.093) between age at first calving and functional longevity. Age at first calving is an important and influential factor in milk production and its composition. Estimated heritability is low for age at first calving, which indicates that this trait is more affected by environmental conditions such as management



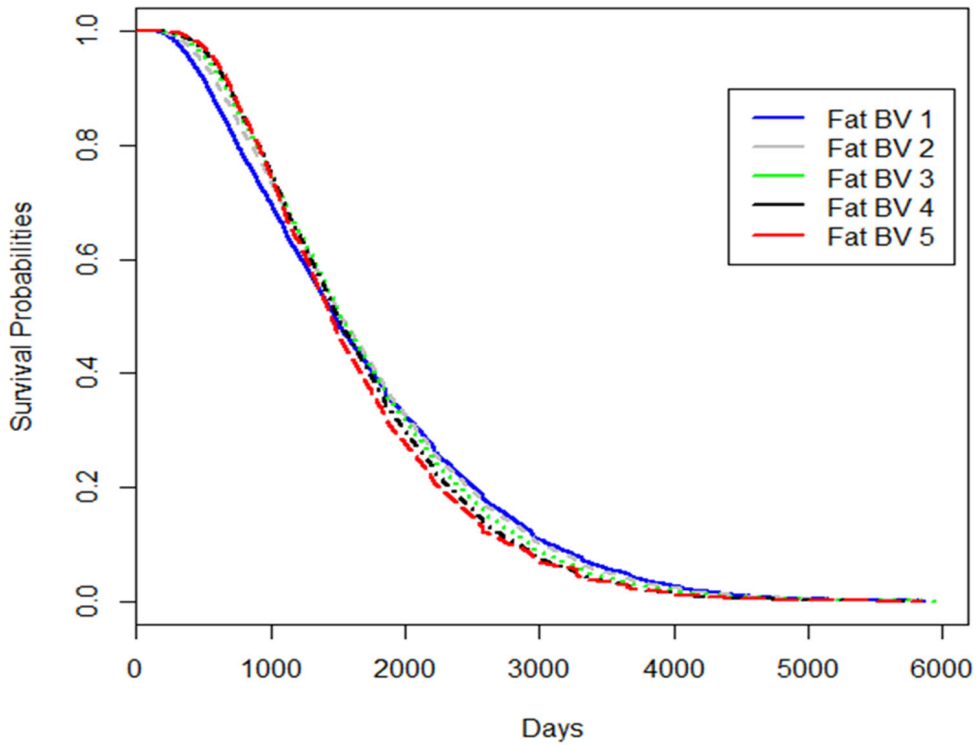


Fig. 6. Functional longevity curve for five groups of fat breeding values (BV 1 to BW 5 indicates low to high breeding value).

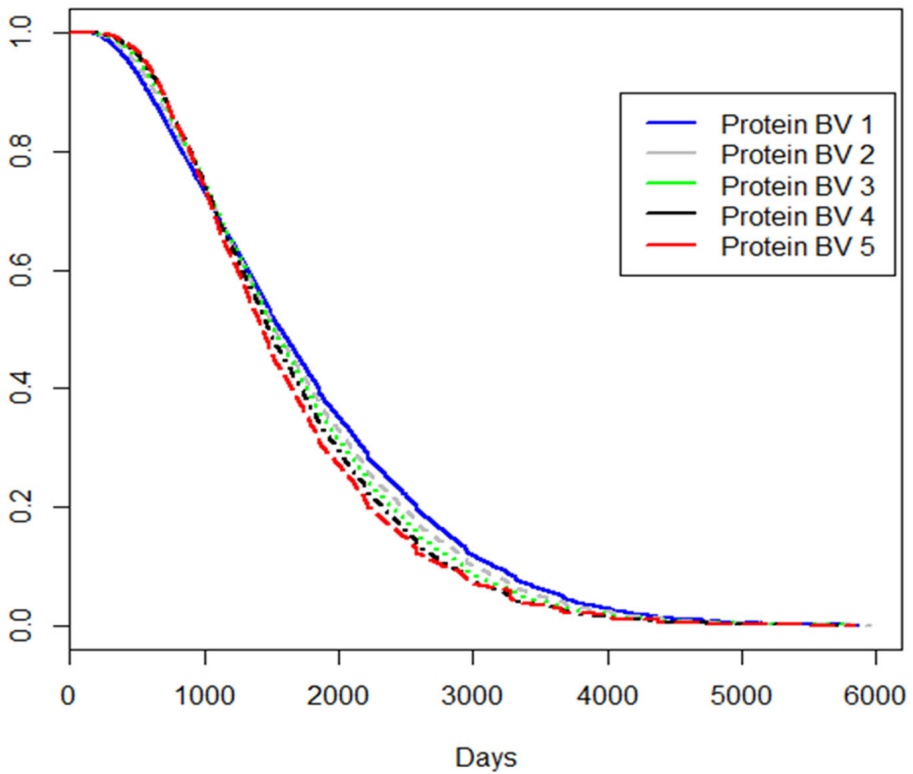


Fig.7. Functional longevity curve for five groups of protein breeding values (BV 1 to BW 5 indicates low to high breeding value).

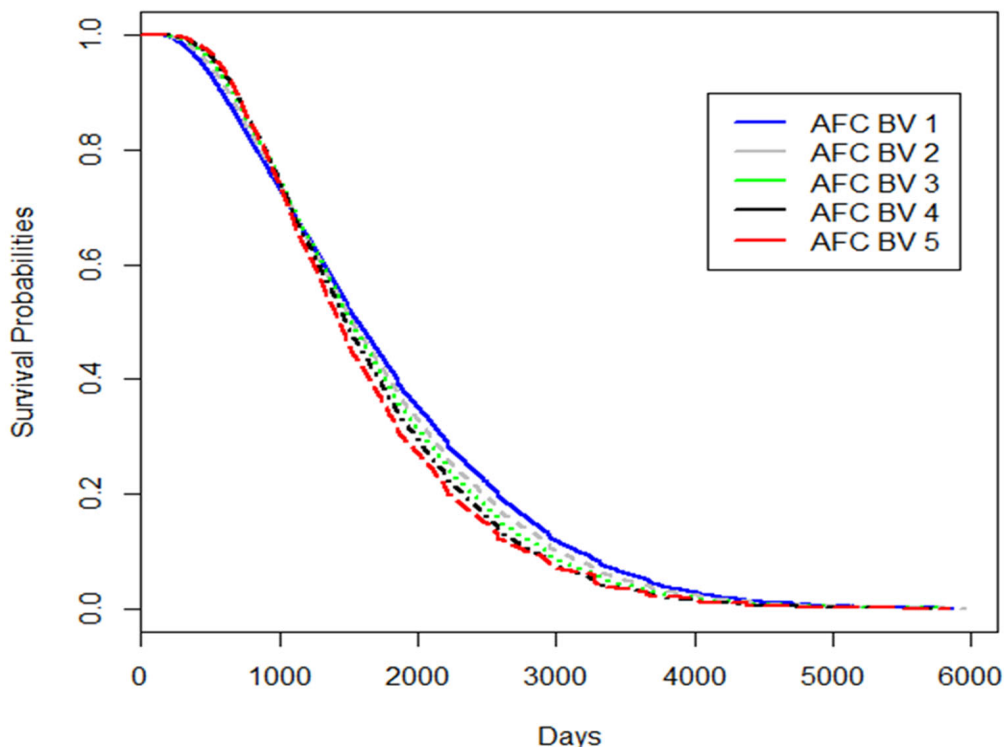


Fig. 8. Functional longevity curve for five groups of age at first calving breeding values (BV 1 to BV 5 indicates low to high breeding value).

and nutrition. Excessive reduction of age at first calving has a negative effect on milk, fat, and protein production traits, while the decrease of the age at first calving to less than 22 months should be avoided.

Table 3 shows the culling risk for the five groups of breeding values of production traits and age at first calving. Culling risk increased as animal breeding values were higher in the second to fifth groups of milk breeding values. Therefore, the culling risk for the second to fifth groups has increased by 4, 9, 12.8, and 17.3%, respectively. Compared to the first group, the second to fifth groups of fat and protein breeding values also had an increasing trend. The range of increase based on the fat and protein breeding values in the second to fifth groups varied from 0.7 to 4.5% compared to the first group. The culling risk for breeding value age groups at first delivery did not show a regular trend. Animals in the second group had the lowest culling risk, whereas the fourth, second, fifth, and first groups had the highest culling risk.

The results showed that the impact of active breeding programs in recent decades has caused changes in the functional longevity of Iranian Holstein cows. The effect of these programs on

production traits showed a fixed and declining trend. Animals with more significant genetic potential for production traits showed an increasing culling risk trend. Although the functional longevity curves of these animals have a lower culling risk than groups with lower genetic potential before 1,000 days, the culling risk of these animals has increased over time. This indicates a more unfavorable status compared to low genetics potential group, and thus the best group for the breeding value of milk trait has a culling risk 20% higher than the low genetics potential group.

## CONCLUSIONS

The results showed that the culling risk increased with the increment of the breeding values (genetic potential) of productive traits. Therefore, considering the importance of animal longevity and its relationship with farm economics, more attention should be paid to this trait in breeding programs for Iranian Holstein cows. In addition, the estimated heritability of 0.15 for functional longevity shows genetic diversity, while this trait can be improved through breeding programs.

**Table 3. Culling risk based on five groups of breeding values of milk, fat, protein, and age at first calving**

Breeding value's group	1	2	3	4	5
Milk	1	1.041	1.091	1.128	1.173
Fat	1	1.015	1.030	1.031	1.045
Protein	1	1.037	1.043	1.035	1.007
Age at first calving	1.005	1	1.007	1.010	1.005

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