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Genetic analysis of longevity traits for Holstein cows in Iran

Hani Rezaee¹, Saeed Zerehdaran^{*1}, Hossein Naeemipour Younesi², Majid Sarmad³

¹ Department of Animal Science, Ferdowsi University of Mashhad, 91779 Mashhad, Iran.

² Department of Animal Science, University of Birjand, 97191 Birjand, Iran

³ Department of Statistics, Ferdowsi University of Mashhad, 91779 Mashhad, Iran

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Present study aims to estimate genetic parameters for traits related to longevity for of Holstein cows in Iran. Five traits were defined to evaluate longevity consisting of number of days from first calving to the end of first lactation or culling (HL1), number of days from first calving to end of second lactation or culling (HL2), number of days from first calving to end of third lactation or culling (HL3), number of days from first calving to the end of the fourth lactation or culling (HL4) and number of days from first calving to the end of the fifth lactation or culling (HL5). Required information was obtained from the data collected by the National Breeding and Improvement of Animal Production Center of Iran, during years 1987-2014. To estimate heritability and breeding values, DMU software was used. Genetic trends were also calculated based on the mean of annual breeding values. Heritability estimates for HL1 to HL5 were 0.018, 0.088, 0.11, 0.085 and 0.05, respectively. The highest breeding value for longevity was predicted in HL2 (+100.18 days) and the lowest value for this trait was predicted in the HL5 (-82.73 days). Genetic trend, based on the annual mean of breeding values for studied traits, increased during first years and decreased afterwards. The obtained genetic trend for HL1 was different from other traits and showed a steady pattern during years of study. According to heritability estimates and genetic trend of traits related to longevity, culling cows in after the first calving and regardless of the future performance of cows in the next calving will result in a population of cows unable to express their actual life span. However, optimal herd life and maintaining the genetic reserves related to this trait will be obtained through keeping cows for longer times in the herd and letting them produce until the fourth or fifth year after the first calving. Then cows could be culled, by taking other important traits such as milk

^{*}Corresponding authors: zerehdaran@ferdowsi.um.ac.ir

production and disease resistance into account. It will certainly reduce the replacement costs and increase the profit of dairy farms. Therefore, in order to improve longevity, it is suggested that culling at age of fourth or fifth year after the first calving should replace the current culling policy in dairy farms of Iran.

KEYWORDS: breeding value / heritability / Iranian Holstein / longevity

Attention to traits such as fertility, health and composition of udder, longevity and survival has been increased for selecting dairy cows in recent years [Clasen et al. 2017]. However, Human intervention such as unnatural housing and management conditions and exclusive emphasize on genetic selection for production-related traits before the 1980s are the main factors caused reduced length of life of dairy cattle [Fraser 2008, Knaus 2009, Oltenacu and Broom 2010, Egger-Danner et al. 2015]. The economic importance of longevity has been mentioned in several studies. Wischer et al. [2000] demonstrated that the economic value of this trait is equal to half of the economic value of milk protein percentage. Brandts et al. [1996] reported that the economic value of longevity is equal to one third of the economic value of milk production. Direct genetic improvement could be done by including longevity trait in the selection index. Biological capabilities of cows are much longer than the amount of time they spend in the industrial herds and therefore improving longevity is feasible. Herd life is defined by the time period which a cow allows to stay in the herd for production and the ability of a cow to avoid from culling in an unsatisfactory conditions for maintaining health and productivity. Schuster et al. [2020] demonstrated that culling is referred to as leaving out a cow from the herd regardless of reason, destination, and condition. Culling is generally due to decrease in milk production and fertility or disease [Rezaee et al. 2006, Nienartowicz-Zdrojewska et al. 2009, Shahdadi et al. 2017, Clasen et al. 2017, Schuster et al. 2020]. Thus, herd life as a compositional trait, is greatly influenced by production and functional traits [Clasen et al. 2017]. This trait is generally determined by the culling decisions and influenced by production and survival [Rezaee 2001, Nienartowicz-Zdrojewska et al. 2009]. Consequently, longevity can be expressed based on health and fertility traits, and is extremely dependent on the owner's managerial decisions. Therefore, it is difficult for an owner or breeder to define a measurable phenotype and directly select animals for longevity. This will ultimately lead to the selection of cows with unrealistic longevity and completely dependent on the farmer's opinion [Clasen et al. 2017, Rezaee 2001]. Nienartowicz-Zdrojewska et al. [2009] studied culling reasons from 1909 to 2006 in Polish Friesian (Black-and-White) cows. In this study, cows culled because of their age (the highest longevity) showed the highest lifespan yield. These cows differed significantly from other cows culled due to other reasons. The highest lactation capacity (lactation peak) was obtained in the third and fourth lactation parities. Accordingly, it is assumed that a cow with more calving, shows decreased functional traits. A study on genetic aspects of herd life in Iranian cows was conducted by Dadpasand Taromsari et al. [2006] using survival analysis. They reported that the risk of culling daughters of sires with low breeding values is almost four times higher than elite sires. The genetic and phenotypic trend of herd life in Holstein cows in Iran was also investigated by Amirpour Najafabadi et al. [2017] using survival analysis and sire model. They reported that it is possible to improve this trait through selecting superior cows. Nowadays, culling a cow before reaching the highest ability of milk production frequently occurred [Classen et al. 2017]. Improving herd life will increase the maturity and the average of herd age. Increase in herd life will consequently increase herd production, the possibility of voluntary culling and also intensity of selection and will the cost of replacement [Rezaee 2001, Shahdadi et al. 2017, VanRaden and Wiggans 1995, McCullough and Di Lorenzo 1996]. However, some limitations such as low heritability, measurability of trait in dams only, unavailability of trait to measure before culling, as well as undesirability of specific analysis and evaluation methods leads to the fact that genetic improvement of longevity is still low in Iran [Rezaee 2001 and Heydarpour 1998]. In most of previous studies only one definition of herd life was used and analyses were generally conducted on animals in the first calving with no attention to the longevity status of the animals in subsequent calvings [Rezaee 2001, Rezaee et al. 2006, Compton et al. 2017, Heise et al. 2016]. In the study done by Clasen et al, longevity was defined and evaluated as five traits based on the Nordic Herd Genetic Evaluation (NAV) [Clasen et al. 2017]. Using several definitions to assess longevity trait leads to investigate longevity of cows at older ages. As a result, the likelihood of the biasness of results will be minimized due to the higher likelihood of traits appearing at older ages compared to what emerged at the first calving and before maturity. Clasen et al. [2017] estimated the genetic parameters of longevity in mixed-breed cows in Denmark. Heritability estimates ranged from 0.022 to 0.090. They concluded that low heritability of these traits is due to immediate culling cows by farmers. Heise et al. [2017] studied the genetic structure of longevity in German Holstein cows. They estimated heritability of 18 survival traits for first 3 parities from 0.017 to 0.027. Previous researches [Rezaee 2001, Brotherston and Hill 1991] similarly indicated the same policy of culling in dairy farms over many years. In a study by Sasaki, herd life assessment models were investigated and it was reported that using Hazard function model for genetic evaluation of this trait is more practical [Sasaki 2013]. However, differences between estimated values of Hazard function and simple and multiple linear models are not clear. Sasaki demonstrated that using longevity and its correlated traits, through direct and indirect evaluation may increase the reliability of estimates [Sasaki 2013].

Present study aimed to estimate the genetic parameters and breeding values for the longevity of Holstein cows in Iran based on first five calving periods and suggest the best time to select cows for this trait.

Material and methods

Data was obtained from the National Breeding and Animal Production Improvement Center of Iran. Pedigree information (animal, sire, and dam numbers) and functional information consisting age at first calving, date of birth, herd, season, date of first to fifth calving, date of lactation periods and date of culling for each animals were available (Tab. 1). Data was edited using FOXPRO [1998] and SAS 9.2 [2008] software and files were prepared to be analysed using DMU software [Madsen and Jensen 2010]. The longevity traits in this study were defined according to the Nordic Herd Genetic Evaluation-NAV in which longevity traits were defined as 5 traits consisting number of days from first calving to end of first lactation or culling (HL1), number of days from first calving to end of second lactation or culling (HL2), number of days from first calving to the fourth lactation or culling (HL3), number of days from the first calving to the end of the fifth lactation or culling (HL5). These definitions were used because they fully fit the longevity of dairy cows in Iran, in which cows with complete lactations or those which had the opportunity to perform it, were selected.

Low heritability for longevity shows that this trait is more affected by environmental factors. Therefore, an appropriate model considering these factors is necessary for analyzing this trait. Based on previous research done by Sasaki [2013] appropriate model for predicting heritability and breeding value for longevity traits is as following:

$$y_{iik} = \mu + HYS_i + b_1(Age - Age) + b_2(Age - Age)^2 + a_i + e_{iik}$$

In this model, represents each of the five longevity traits, μ is the mean of studied trait, is the combined fixd effect of the ith Herd-Year-Season of first calving, b₁ and b₂ are fixed linear and quadratic regression coefficients on age at first calving, a_j is random effect of jth animal and e_{ijk} is the random residual effect.

DMU software was used restrict maximum likelihood (REML) technique for estimating fixed and random (genetic and non-genetic) components. Breeding values were also estimated through animal model using best linear unbiased production (BLUP). SPSS [2007] software was used to evaluate significant genetic trends for studied traits. The inbreeding level of animals was also investigated using CFC software [Sargolzaei *et al.* 2006].

Results and discussion

The means of the studied traits were 315, 715, 1098, 1461 and 1828 days, respectively (Tab. 1). Estimated values indicate that most cows have completed their current lactation period. In other words, cows were allowed to complete their lactation period for one year after calving, which indicates that most cows were culled after completing the current lactation period and only on the basis of production. This indicates that decrease production is the most important reason of culling in Iranian cows by their owners. The estimated mean of this study were consistent with the results of Clasen *et al.* [2017] and Nienartowicz-Zdrojewska *et al* [2009] in Denmark and Poland.

Trait	HL1	HL2	HL3	HL4	HL5
Animals with pedigree	501808	377763	266757	176911	107634
Animals with record	403349	289470	189642	115552	64575
Number of inbred animals	716	407	207	92	35
Numbers of fixed effects (HYS)	39343	33319	26304	20190	14757
Mean longevity (day)	315.74	715.38	1098.35	1461.49	1828.10
Standard deviation longevity	143.97	210.77	264.90	352.23	435.92

Table 1. Descriptive information for longevity traits

HL1 – days from first calving until the end of first lactation or culling. HL2 – days from first calving until the end of second lactation or culling. HL3 – days from first calving until the end of third lactation or culling. HL4 – days from first calving until the end of fourth lactation or culling. HL5 – days from first calving until the end of fifth lactation or culling.

Table 2. Heritability estimates and variance components for longevity traits

Trait	HL1	HL2	HL3	HL4	HL5
Heritability	0.018	0.088	0.11	0.085	0.05
Standard Error	0.0015	0.004	0.005	0.007	0.007
Additive genetic variance	247.8	2824.49	5466.94	7250.38	6608.54
Residual variance	13293.05	29138.5	46336.1	72814.1	124448.08
Phenotypic variance	13540.85	31962.99	51803.04	85466.48	131056.62
Average inbreeding coefficients	0.0003	0.0002	0.0002	0.0001	0.00008

 $\rm HL1$ – days from first calving until the end of first lactation or culling. $\rm HL2$ – days from first calving until the end of second lactation or culling. $\rm HL3$ – days from first calving until the end of third lactation or culling. $\rm HL4$ – days from first calving until the end of fourth lactation or culling. $\rm HL5$ – days from first calving until the end of fifth lactation or culling.

Heritability estimates along with genetic and phenotypic variances for longevity traits are shown in Table 2. Heritability estimates ranged from 0.018 to 0.1. HL1 showed the lowest and HL3 showed the highest heritability estimates. Current heritability estimates were in the range of values estimated by Heydarpour [1998] for dairy cows in Iran. In another study done by Rezaee et al. [2004], estimated heritability for longevity was reported to be 0.002 in Holstein cows in Iran. Similarly, in a research done by Mohammadi [2003], heritability of longevity in Holstein cows was reported to be low. In the study of Rezaee and Farhangfar [2006], heritability of this trait for registered cattle was much higher than non-registered cattle, which indicated that nonregistered cattle were more affected by the environment compared to registered cattle. In a study done by Harris *et al.* [1992], estimated heritability for longevity in Guernsey cattle was 0.02 for cows with 48-month-old and 0.72 for cows with 72-month-old. In another study on dairy bulls and heifers in the UK [Mrode et al. 2000], heritability of this trait was estimated to be 0.66. Heritability for longevity in Brown Swiss cows in Italy was also estimated to be 0.06 [Samore et al. 2010]. Changes in heritability estimates for longevity traits in Holstein cows in Iran was presented in Figure 1. In this figure, an increase in heritability form HL1 to HL3 and then a decrease from HL3 to HL5 were occurred. Heritability estimates for HL4 (0.085) and HL2 (0.088) were close, while heritability for HL1 was lower than other traits. The amount of additive

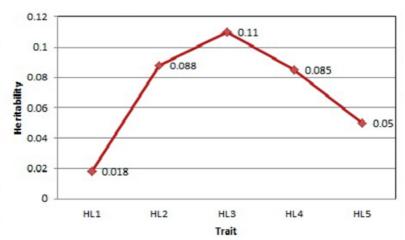


Fig.1. Heritability estimates for longevity traits. HL1 - days from first calving until the end of first lactation or culling; HL2 - days from first calving until the end of second lactation or culling; HL3 - days from first calving until the end of third lactation or culling; HL4 - days from first calving until the end of fourth lactation or culling; HL5 - days from first calving until the end of fifth lactation or culling).

genetic variance also increased from HL1 (247.8) to HL4 (7250.38) and then reduced in HL5 (6608.54). Decrease in additive genetic variance in HL5 could be due to increase in culling at this age and the implication of managerial decisions. In fact, there was an attempt to reduce this effect with considering Herd-Year-Season of first calving as a combined fixed effect, in the calculations. However, it seems that the reduction of genetic variance in longevity traits could be due to managerial decisions and the opinion of ranchers and owners of dairy cows. Increase in culling at fifth lactation could explain why estimated inbreeding coefficient is lower for HL5 compared to other longevity traits. Clasen et al. [2017] in Danish cows reported that the amount of additive genetic variance increased from first to fifth lactation, resulting in greater heritability in the fifth lactation. Completing physiological growth and approaching the age of maturity which finalizes the biological characteristics of the animal are the main reasons behind increase in additive genetic variance for longevity traits. It means, as animal gets older, the chance of culling by the owner would be much lower and consequently, the genetics share of the animal would be higher. Regarding the status of the observations, decrease in the proportion of genetics for longevity in the fifth calving is again due to increase in culling at this age due to managerial decisions.

These results suggested that if a cow is selected for longevity based on its performance in the first calving, which is generally the case, the inheritance of this trait and its occurrence in the following years will be different based on the actual physiological condition of the animal. In fact, increasing the chance of a cow to stay in herd will improve the heritability of the longevity traits. Therefore, culling a cow based on inappropriate decisions of a farmer and other managerial conditions will reduce the heritability of the longevity and the rate of improvement for this trait.

The mean and range of changes in the predicted breeding value of cows for the studied traits were presented in Table 3. The highest average for breeding value was observed in HL3 (+0.45 days) and the lowest average was found in HL5 (-0.61 days). The highest breeding value was found in HL2 (+100.18 days) and the lowest breeding value was found in HL5 (-82.73 days). Standard deviations for studied traits were increased from HL1 to HL5 and the highest rate of variation were observed in HL4 and HL5. Present results are consistent with the results obtained by Shahdadi *et al.* [2017]. They found similar genetic and phenotypic trend of longevity traits for dairy cows in Iran. They also suggested that including longevity in breeding programs would lead to obtain optimal results for this trait. A similar result was also reported by Jairath *et al.* [1998].

 Table 3. Means, standard deviation (SD), maximum and minimum of predicted breeding value for longevity traits

Traits	Mean	SD	Maximum	Minimum
HL1	-0.4071	6.6182	86.9489	-36.9710
HL2	0.1258	13.5159	100.178	-67.9368
HL3	0.4486	17.4870	79.2844	-71.9099
HL4	-0.0008	19.7371	82.1360	-76.1681
HL5	-0.6051	19.4475	82.6725	-82.7306

 $\rm HL1$ – days from first calving until the end of first lactation or culling. $\rm HL2$ – days from first calving until the end of second lactation or culling. $\rm HL3$ – days from first calving until the end of third lactation or culling. $\rm HL4$ – days from first calving until the end of fourth lactation or culling. $\rm HL5$ – days from first calving until the end of fifth lactation or culling.

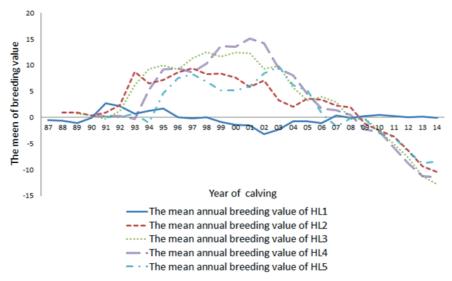


Fig. 2. Annual mean of breeding value estimates of longevity.

The trends of the annual mean of estimated breeding values for longevity traits in different years are shown in Figure 2. The rate of change for the first trait was different from other traits so that for HL1 was almost constant (close to zero) during studied years. While in the traits that were related to other parity, the trend was generally first increasing and then decreasing. There was an increasing trend for HL2, (+93.43) until 1997 and then a decreasing trend was observed afterwards. For HL3, the trend was increasing until 1998 (13.53) and then a downward trend was observed. Regarding HL4 and HL5, increasing trend continued until 2001 (15.12) and 2003 (9.70), and then reduction was started. According to Figure 2, decreasing trend for longevity traits continued until the end of 2014. The breeding value of all except HL1 from 2009 onwards tended to be negative. This was while the trend of HL1 adjective was increasing during these years. This difference appears to be due to further culling in first parity cows. Therefore, the remaining cows have more breeding value.

HL2 to HL5 showed almost the same trend in later years, which is quite different from the HL1 trend, due to the culling of cows in their first calving or keeping them for other parties. Culling cows in the first calving and regardless of the future performance of cows in the next calvings and at the same time, attention only to the productive and functional traits, will result a community of cows unable to show the actual amount of longevity. It reduces the longevity of cows in the herd and increases the cost of replacement for the owner. In fact, there is a high probability that cows that have a high potential in terms of longevity will be culled and it decrease genetic progressing for longevity traits.

The results of this study showed that optimal herd life and preservation of genetic reserves related to this trait it will be achieved by keeping cows in the herd for a longer time and allowing them produce up to the fourth or fifth year after the first calving. Then cows could be culled, by taking other important traits such as milk production and disease resistance into account. Therefore, in order to improve longevity, it is suggested that culling at age of fourth or fifth year after the first calving should replace the current culling policy in dairy farms of Iran

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