Analysis of culling records and estimation of genetic parameters for longevity and some production traits in Holstein dairy cattle

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ABSTRACT
We used data collected on 48,739 cows from 1982 to 2013 from Foka farm in the Isfahan province of Iran to assess the reasons for culling in Iranian Holstein dairy cattle in the context of breeding values of economic traits, and also to study the relationship between longevity and production traits. Estimation of (co)variance components and genetic parameters for studied traits including MY, FY, herd life (HL) and length of production life (LPL) was by AI-REML algorithm in WOMBAT software. The results showed that 27.11% of cows were culled voluntarily under the farmers’ command. The number and reasons for culling animals varied considerably over the years. Also, the results showed that involuntarily culled animals were valuable with significantly higher breeding values for MY and FY (P < .0001) than those of voluntarily culled individuals. The estimates of heritability for longevity traits (HL and LPL) were low (0.11 and 0.09), but their genetic correlation with production traits were high and positive (0.63–0.70). Our results suggest that some opportunity may exist for genetic improvements in fat and milk yield in Iranian Holsteins.

Introduction
Annually a number of female cows in dairy cattle farms are culled and replaced by heifers. In constant conditions of herd size, replacement rates are reduced and higher profitability of heifers is obtained by increasing longevity of female cows which would lead to profitability of the dairy cattle enterprise (Berry et al. 2005). On the other hand, since milk production is higher in older animals, the change in the age pyramid of cows increases milk production (Shahmoradi et al. 2008). So, longevity, or lifespan of dairy cattle, is an economically important trait for dairy farmers because increased longevity helps to increase profitability (Van Pelt et al. 2015). According to Ducrocq (1992) two types of longevity could be distinguished: real and functional longevity. The real longevity is strongly dependent on the milk yield and the functional longevity is the ability of the cow to avoid culling for other reasons than low performance. Culling can be voluntary or involuntary. In the voluntary culling scenario of dairy cows, the farmer has complete freedom to choose or cull the cows that would lead to growth of farmer profit (Mohammadi & Sedighi, 2009). There is a very narrow freedom in the involuntary culling scenario for breeders; however, most of the time, it is necessary to cull animals from the herd (e.g. due to infectious diseases) which could almost wipe off a breeder’s freedom of choice. Some studies have shown that the revenue of dairy farms may be increased by reducing involuntary culling (Rogers et al. 1988; Short & Lawlor 1992; Bonneville-Hébert et al. 2011; Chiiumia et al. 2013; Sanjabi & Javanmardi 2014). About 90% of lifetime variation of cows is due to management, environmental factors and diseases. Thus, changes in the environment, housing and management facilities could cause most of the involuntary culling (Shahmoradi et al. 2008). Statistics of culling in many dairy herds show that after low milk production, the main reasons for culling dairy cows are due to infertility and mastitis problems (Caraviello et al. 2004). Moraveji (2008) through evaluation of the dairy cow culling rates and their causes in a number of dairy farms in several provinces in Iran came up with three main reasons of culling dairy cows in Iran: reproductive disorders, nutritional-metabolic abnormalities and infectious diseases. Vergara et al. (2009) reported that in high-production herds, 16–32% of the culling is due to reproduction problems leading to excessive herd replacement costs. The objective of this study was to investigate the reasons of culling, compare the genetic capacity of cattle breeding value; AI-REML algorithm

Data
Data for this study were collected from 1982 to 2013 from Foka farm, one of the largest dairy farms in the Middle East, located in
the Isfahan province of Iran. Pedigree information was available for 67,210 cows. The structure of pedigree used is presented in Table 1. Due to its excellent management system, different types of records are measured monthly. For example, grouping causes of culling of cows in different biological classified categories is a routine Foka farm practice. To the best of our knowledge, these types of data are rarely collected in other dairy farms nationally or internationally. Storing, revising and editing the data were done with the use of the SQL database. The database included information of pedigree, insemination records, production records, reproduction records, culling records and veterinary, and management. There were nine culling categories identified and these are presented in Table 2. Those data elements that did not belong to the first category, for example, ‘voluntary culling’, were lumped with so-called ‘involuntary culling’. Therefore, we noticed that involuntary culling itself was divided into different categories. The production traits studied were milk yield (MY) and fat yield (FY). These traits was divided into different categories. The production traits analyzed in this study were milk yield (MY) and fat yield (FY). These traits were standardized to a 305-d and twice daily milking basis. Due to the low number of observations for the sixth lactation (93.55% of records) and onwards, only the first five lactations were used in the analysis. Also, the records of second parity and onwards were considered in the analysis, provided previous records were available. Data editing was done to include age of 20 years and onwards were considered in the analysis, provided previous records were used. Due to the low number of observations for the sixth lactation (93.55% of records) and onwards, only the first five lactations were used in the analysis. Also, the records of second parity and onwards were considered in the analysis, provided previous records were available. Data editing was done to include age of the first calving (20–36 months), open days (20–200 days), milk production (1000–16,000 kg) and calving interval (300–600 days) in the analysis (Farhangfar & Younesi 2007; Chookani et al. 2010). Longevity traits were herd life (HL) and length of productive life (LPL). Herd life was defined as the difference in days between the culling date and the date at birth. Length of productive life was considered as total number of days from first calving to culling date. Descriptive statistics of all traits are summarized in Table 3.

### Statistical analysis

Firstly, environmental effects were examined using generalized linear model (GLM) procedure in SAS (version 8) software. The effect of year-season of calving was considered as fixed effect and the age at first calving as covariate. Since these effects were significant for all traits, they were considered in the final model. Genetic parameters and components of (co)variance were estimated by fitting an animal model using the AI-REML algorithm. For production (MY and FY), HL and LPL traits, model [1], model [2] and model [3] were fitted, respectively. The statistical form of the models were:

**Model[1]:**

\[ y_{ijk} = \mu + YS_i + b(Age - \overline{Age}) + a_j + pe_k + e_{ijk}, \]

**Model[2]:**

\[ y_{ij} = \mu + YS_i + a_j + e_{ij}, \]

**Model[3]:**

\[ y_{ij} = \mu + YS_i + b(Age - \overline{Age}) + a_j + e_{ij}. \]

In these models, \( y \) is the trait value measured for each trait, \( \mu \) is the overall mean for the trait, \( YS_i \) is the fixed effect of ith year-season of calving for MY and FY, and year-season of birth for HL, \( b \) is the regression coefficients of age of the animal at calving in the relevant period(day) as co-variable, \( \overline{Age} \), the average age of the herd’s (day), \( a_i \) is direct genetic random effect, \( pe \) is the random effect of animal permanent environment and \( e \) is the random residual effect. The genetic and phenotypic correlation between production and longevity traits were estimated by fitting an animal model using a bivariate analysis. The fixed and random effects in these models were those of single trait analysis. In matrix form, bivariate animal models were set up as follows, in which case, the kind of fixed effects depending on traits were different.

\[
\begin{bmatrix}
  y_1 \\
  y_2 \\
\end{bmatrix}
= 
\begin{bmatrix}
  X_1 & 0 \\
  0 & X_2 \\
\end{bmatrix}
\begin{bmatrix}
  b_1 \\
  b_2 \\
\end{bmatrix}
+ 
\begin{bmatrix}
  Z_1 & 0 \\
  0 & Z_2 \\
\end{bmatrix}
\begin{bmatrix}
  a_1 \\
  a_2 \\
\end{bmatrix}
+ 
\begin{bmatrix}
  e_1 \\
  e_2 \\
\end{bmatrix}
\]

It was assumed that

\[
\text{var} \begin{bmatrix}
  y_1 \\
  y_2 \\
\end{bmatrix} = \begin{bmatrix}
  A a_1 & 0 & 0 & 0 \\
  0 & A a_2 & 0 & 0 \\
  0 & 0 & I e_1 & 0 \\
  0 & 0 & 0 & I e_2 \\
\end{bmatrix}
\]

where \( a_1 \) and \( e \) are the vector of additive genetic and residual effects, respectively. \( \sigma_a^2 \) and \( \sigma_e^2 \) are variances due to direct genetic and residual effects, respectively; \( \sigma_{a12} (=\sigma_{a1}) \) are covariance of direct genetic effects between traits; \( \sigma_{e11} (=\sigma_{e1}) \) are covariance of random residual effects between traits; A represents a numerator relationship matrix for direct genetic effects; I refers to an identity matrix.

To investigate the relationship between the reasons for culling and genetic merit of the cows, least square means of breeding values of individuals for MY and FY were compared among different reasons for culling. To this end, GLM procedure of the SAS programme was used. Breeding values of individual animals were predicted with Best Linear Unbiased Prediction methodology. The WOMBAT software (Meyer 2007) was used.

### Table 1. Structure of pedigree file.

| Item | Number |
|------|--------|
| Animal in pedigree | 67,210 |
| Base animals | 7956 |
| Sires | 2135 |
| Dams | 34,891 |
| Animals with both parents known | 51,701 |

### Table 2. Causes groups of culling of dairy cattle.

| Group | Descriptions |
|-------|--------------|
| Voluntary | Low milk production, low growth, sale of surplus and moderate values |
| Feet & leg problems | Joint infection, dislocation and fracture of the hands, legs and hip, lameness, crippling, hoof diseases and spinal cord injuries |
| Reproductive problems | Impregnability, ovarian cysts, recurrent abortions, freemartin, mummy (wax) abortion, uterus problems (rupturing, bleeding, infections and diseases) |
| Udder problems | Protracting and rupturing ligaments of the gland, complete teat-cistern obstruction, udder gangrene and bleeding |
| Infectious diseases | Leucosis, brucellosis, pneumonia, tuberculosis, black leg, pulpy kidney (enterotoxaemia), foot-and-mouth disease, lung and liver infections |
| Congenital defect | Genetic defects, immature, paralytic, congenital diseases |
| Metabolic and digestive problems | Bloating, fatty liver, ketosis, milk fever, displaced abomasum, obstruction and twisting of gut, omasum accumulation, abomasum and rumen |

### Table 3. Causes of culling of dairy cattle.

| Item | Description |
|------|-------------|
| Birth | First |
| Culling | Second |
| Culling | Third |
| Culling | Fourth |
| Culling | Fifth |
| Culling | Sixth |
| Culling | Seventh |
| Culling | Eighth |
| Culling | Ninth |
| Culling | Tenth |
| Culling | Eleventh |
to carry out all analyses. The model convergence criterion was fixed as $10^{-8}$.

**Results and discussion**

Distribution of different culling categories is provided in Table 4. The results showed that 27.11% of cows were under farmers’ control and culled voluntarily. The most important reason for voluntary culling from the results was low milk production. This is supported by Dadpasand-Taromsari et al. (2006) who studied culling strategies in Holstein dairy cows of Iran by using survival analysis and reported that risk of culling of the cows with milk production less than 1.5 standard deviations from the mean was about 4 times greater than the class of high-producing cows. In this study, 72.89% of cows were culled involuntarily; this has positive effects on the profitability; its increase will directly have a negative effect on net farm revenue. This result is consistent with findings of SahebHonar et al. (2010) and Teymuri et al. (2012) who reported 76% and 74.74%, respectively. Among the involuntary groups, the most frequent culling percent is related to infectious diseases (23.46%) and reproductive problems (21.27%) groups. In addition, the culled proportion of animals due to mastitis (udder) system problems (9.05%), metabolic and digestive problems (7.82%) as well as feet and leg problems (6.36%) was considerable. Among the culling groups, the minimum percent (0.68%) is due to congenital defects. Genetic resistance of animals to pathogens in a particular region usually develops as a result of natural selection for many years. Furthermore, it is expected that the Holstein breed will be sensitive to some native pathogens of Iran. Some other studies have reported that infectious diseases are the most important reason of culling of Holstein dairy cows in Iran (Moraveji 2008; Sanjabi & Javanmardi 2014). In addition to the direct effect of reproductive problems on farm profitability, they can affect profitability via decreasing lifetime and longevity mean of the herd. The remarkable percentage of culling resulting from reproductive problems in the current study may be partially explained by the difference in the climatic conditions of Iran and the origin of Holstein cows. Similar findings were reported by some other authors (Allaire et al. 1977; Bascom & Young 1998; Ruegg et al. 1998). Mohammadi and Sedighi (2009) and Shahmoradi et al. (2008) reported that infertility and reproductive problems are major factors in culling Holstein cattle in other regions of Iran. Mastitis and problems with the udder are the greatest reasons for culling and this study confirms that fact as well. Some researchers have reported that udder health problems such as mastitis are strongly associated with longevity and are the main reason for culling dairy cattle (Holtsmark et al. 2008; Ahlman et al. 2011). Improving the mastitis system has a significant role in preventing involuntary culling. If female cows are evaluated properly, improving udder-type traits also improves longevity traits. Seifi et al. (2010) stated that udder-type traits’ improvement through selection will lead to positive effects on longevity and the udder-type traits in the first lactation is appropriate to predict the productive lifetime. Sanjabi et al. (2010) reported that association of udder-type traits of dairy cattle and culling will be immediate through increase in somatic cells, mastitis and dystocia. Ahlman et al. (2011) declared that 24.7% dairy cows are culled due to a weak mastitis system.

Distribution of culled cows for various levels of animal ages, parities and the years are shown in the Supplementary Tables (Tables S1–S3). Frequency analysis of animals culled at different ages indicated that the most important factors of culling for yearling calves were infectious diseases (42.75%), mortality (26.66%) and metabolic problems (15.14%). Distribution of various reasons for culled cases showed that voluntary culling is downward up to the fourth parity, and then increases with parity so that by the sixth parity and older over 20% of cullings are voluntary. During the first four parities, most of the cows will be culled due to reproductive problems, infectious diseases and mastitis system problems. SahebHonar et al. (2010) reported that 59% of the six-year-olds (peak of production) and younger animals had been culled for involuntary causes. Also, in all parities a considerable number of animals were culled due to infectious disease, which agreed with the report of Teymuri et al. (2012). Metabolic and digestive problems cause culling of a considerable number of animals in the second to fifth parities. Since, milk production increases by parities, the negative energy balance can also be a most likely reason. Dadpasand-Taromsari et al. (2006) stated that most of the culling of the second to fourth lactation animals occurred in the early stages of lactation which may coincide with the peak of production and negative energy balance and subsequently metabolic diseases such as acidosis, mastitis and other diseases may exacerbate culling. In general, in all culling groups, the percentage of cow culling did not show regular fluctuation over the years. It may probably be due to differences in various factors like nutritional management and climatic conditions in different years. Tables 5 and 6 show means for breeding value of MY and FY traits in the culling reason groups (voluntary and involuntary) and various subgroups of involuntary culling. Voluntarily culled

| Table 3. Summary of the data structures for production and longevity traits. |
| --- |
| Trait | No of records | Mean | Standard | Minimum | Maximum | CV% |
| Milk yield | 76,920 | 9183.66 | 2047.16 | 1000.48 | 14,997.84 | 22.29 |
| Fat yield | 67,736 | 242.70 | 80.61 | 50.02 | 488.02 | 33.21 |
| Herd life | 18,342 | 1501.21 | 1078.47 | 1 | 6004 | 71.84 |
| Length of productive life | 10,670 | 1189.24 | 823.11 | 1 | 5249 | 69.38 |
| Death | 553 | 2.99 | 1 | 1 | 7.68 | 25.52 |
| Infectious diseases | 4332 | 23.46 | 15.07 | 0 | 130.99 | 100.00 |
| Reproductive problems | 3298 | 21.27 | 14.96 | 0 | 92.43 | 100.00 |
| Udder problems | 1672 | 9.05 | 6.23 | 0 | 31.08 | 100.00 |
| Feet & leg problems | 1175 | 6.36 | 4.07 | 0 | 22.88 | 100.00 |
| Congenital defect | 126 | 0.68 | 0.51 | 0 | 1.68 | 100.00 |
| Metabolic and digestive problems | 1444 | 7.82 | 5.30 | 0 | 31.08 | 100.00 |

| Table 4. Distribution of cows by the different culling reason groups. |
| --- |
| Group | Number | % |
| Voluntary | 5007 | 27.11 |
| Feet & leg problems | 1175 | 6.36 |
| Reproductive problems | 3298 | 21.27 |
| Udder problems | 1672 | 9.05 |
| Infectious diseases | 4332 | 23.46 |
| Congenital defect | 126 | 0.68 |
| Metabolic and digestive problems | 1444 | 7.82 |
| Death | 553 | 2.99 |
| Others | 230 | 1.25 |
animals by farmers had very low breeding values for milk and fat productions ($P < .0001$). These findings indicate that involuntarily culled animals were very valuable but for some reasons the farmers had to cull them; besides, there is higher risk of culling high-producing cows due to sensitivity to environmental conditions in cattle. This is supported by the findings of SahebHonar et al. (2010) who reported that most voluntarily culled cows include animals with low milk yield and economical values; in contrast, the involuntarily culled cows have high genetic merit for production traits. Therefore, it can be noted that involuntary culling has undesirable effects on genetic improvement of dairy cattle production traits. The dead culling group had the highest mean of breeding values for both traits. It is likely that genetic improvement of animals for production traits tend to undermine the immune system. In addition, animals culled because of reproductive problems, infectious diseases and congenital defects are valuable animals for milk production. Thus, this culling imposes a very high expense on the farmer, and similar results have been reported (Allaie et al. 1977; Weigel 2004; SahebHonar et al. 2010).

The estimates of variance components and corresponding genetic parameters are presented in Table 7. The estimated heritability for fat yield (0.16) was lower than that of milk yield (0.25). These results were in agreement with Abdallah and McDaniel (2000) and Makgahlela et al. (2008). The estimates of heritability for herd life and length of productive life were 0.11 and 0.09, respectively, which were similar to the reports of Strandberg and Solkner (1996). Generally, these results were in the range of results reported by Caravetto et al. (2004) (0.05–0.13) and Sewalem et al. (2005) (0.09–0.14).

Lower estimates of heritability for longevity traits have been reported by Páčová et al. (2005) for Holstein cattle in the Czech Republic (0.025–0.041), Zavadilová et al. (2009) for Czech Fleckvieh cows (0.04 and 0.05 for longevity corrected and uncorrected for milk, respectively) and Du Toit (2011) for South African Jersey cattle (0.01–0.03). Sasaki (2013) reviewed the genetic parameters for longevity traits of dairy cattle and stated that the variations among estimates of most of the estimates of heritability obtained by the linear model are <0.10. Our estimates were lower than those reported by Pfieffer et al. (2015) in Austrian Fleckvieh cattle and Irano et al. (2014) in Holstein cows under tropical conditions.

The strong effects of environmental factors, nonlinear dependency of herd life on these factors and evaluation of those animals available in the herd and were not culled were given as reasons why these traits show low heritability (Sefi et al. 2010). The estimated correlations among traits were positive and genetic correlations were higher than phenotypic estimates (Table 8). Genetic correlations of milk yield with HL (0.69) and LPL (0.70) were higher than the corresponding phenotypic correlations (0.15 and 0.38, respectively). Genetic (phenotypic) correlations of fat yield with two longevity traits were similar 0.63 (0.11). Similar results can be seen in Harris et al. (1992) and Vukašinović et al. (1995). However, Wasana et al. (2015) reported lower estimates of genetic correlation of productive life and production traits in three parities for Korean Holstein. Their estimates were in the range of 0.04–0.35 for milk yield and 0.02–0.18 for fat yield. In addition, positive and lower genetic correlation estimates of functional productive life and milk yield (0.33) and fat yield (0.23) have been reported in US dairy goats (Castañeda-Bustos et al. 2014). On the other hand, Fuerst-Waltl et al. (2013) reported unfavourable correlations between milk yield and LPL in both extensive (−0.159) and intensive (−0.192) management systems in Austrian Fleckvieh (dual-purpose Simmental). Pritchard et al. (2013) stated that lifespan score is negatively correlated with milk yield (−0.34) and fat yield (−0.18) in the Holstein–Friesian breed. Differences among estimates can be due to different study breed (dairy and dual-purpose), data size and fitted model. The results suggest that considering low heritability estimate for longevity traits, it is possible to improve the performance of these traits using correlated response and indirect selection for production traits (milk and fat yield).

### Table 7. Variance component and genetic parameter estimates for production and longevity traits obtained using a univariate animal model.

| Traits       | $\sigma^2_{\text{P}}$ | $\sigma^2_{\text{PE}}$ | $\sigma^2_{\text{E}}$ | $\sigma^2_{\text{G}}$ | $h^2 \pm \text{SE}$ | $c^2 \pm \text{SE}$ |
|--------------|------------------------|-------------------------|------------------------|------------------------|----------------------|----------------------|
| Milk yield   | 643,451                | 588,957                 | 1315,102               | 2547,510.90            | 0.25 ± 0.001         | 0.23 ± 0.001         |
| Fat yield    | 509.87                 | 514.22                  | 2169.4                 | 3193.21                | 0.16 ± 0.009         | 0.16 ± 0.008         |
| HL           | 86,854.4               | -                       | 737,645                | 824,497                | 0.105 ± 0.008        | -                    |
| HPL          | 50,447.9               | -                       | 535,543                | 585,991                | 0.086 ± 0.014        | -                    |

Notes: HL: herd life; LPL: length of production life. $\sigma^2_{\text{P}}$, $\sigma^2_{\text{PE}}$, $\sigma^2_{\text{E}}$ and $\sigma^2_{\text{G}}$ are additive genetic, permanent environment, error and phenotype variances, respectively.

### Table 8. Phenotype and genetic correlation among the production and longevity traits obtained from bivariate analysis.

| First trait | Second trait | Genotypic correlation | Phenotypic correlation |
|-------------|--------------|-----------------------|------------------------|
| Milk yield  | HPL          | 0.68                  | 0.15                   |
| Fat yield   | HPL          | 0.70                  | 0.38                   |
| HPL         | HPL          | 0.63                  | 0.11                   |
