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Investigation of the Possibility of Using Predicted Herd Life Records in Genetic Evaluation of Iranian Holstein Cows

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Abstract: Many of cows still exist in the herd at the time of genetic evaluation for herd life and hence, their herd life records are incomplete. On the other hand, it is possible to predict herd life of a cow using its production and reproduction records. The main aim of this study was to investigate the possibility of using predicted records in place of incomplete records in genetic evaluation of Holstein cows. For this aim, 3 sort of files were constructed: file 1 was composed of totally 55596 records of herd life that were collected by Center for Animal Breeding from 163 herds during 1993-2007. There were 32432 complete records of herd life and the rest were incomplete records. File 2 included only complete records (i.e., 32432 records). File 3 was like the file 1 except predicted records were in place of incomplete records. The results showed use of predicted records instead of incomplete records resulted to reduce phenotypic variance and increased heritability for herd life. The lesser coefficient of variance and higher heritability in consequence of using predicted records revealed that these records are more reliable than incomplete records for genetic evaluation of herd life.

Key words: Herd life, genetic evaluation, incomplete records, Holstein cow, herd life, heritability

INTRODUCTION

Dairy cows herd life as an economic traits of breeding goal, regularly has a significant role in determining economic performance of the herd and lack of exact information regarding to this trait, encountered genetic evaluation of the other relative economic trait with many challenges; therefore, it would be necessary to reach new methods of herd life genetic evaluation of dairy cows (Caraviello *et al*., 2004).

Herd life could be described as the time interval between first calving ages to culling or the last replacement of herd (Sewalem *et al*., 2008). This description consisted of 2 voluntary and involuntary culling items. Culling based on low milk yield frequently describe as voluntary culling and culling based on disease or reproductive problems describe as involuntary one (Allaire and Gibson, 1992).

Various factors effect on herd life genetic evaluation but it could be refer as sir or animal models, selection of fixed or random effects, herd life evaluation procedure (direct or indirect), herd life description, correction or in-correction regarding to environmental factors and linear or non linear model witch have been used.

Whatever, identified heritability rate of herd life is low (<0.1). Larroque and Ducrocq (2001) believed that using indirect evaluation of herd life and non-linear statistic models, higher heritability estimated for this trait. In recent years, by using description of productive herd life in survival analysis models and applying all the existing records in data set and regarding abnormal data's distribution, higher heritability estimated for herd life.

Different methods existed for genetic evaluation of cows, which had incomplete records of herd life. In some cases, related data from cow's relationship have been used. Larroque and Ducrocq (2001) used incomplete time models for genetic evaluation of incomplete herd life records as survival analysis. Jairath *et al*. (1998) used a linear repeatability model for evaluation of survival within special lactation (Van Raden and Klaaskate, 1993). Predicted herd life records for cows witch lived during record keeping and used these records in a linear model for genetic evaluation of herd life. Innovation of appropriate methods for genetic evaluation of herd life paved the way for better developments.

Many factors such as age at 1st calving, milk yield and number of days open effects on the herd life. These factors might not being linearly and had many diversities

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in different times (Onyiro *et al.*, 2008). As herd life heritability was low (<0.1), genetic merit of herd life would be less than other economic traits. Different study showed that genetic correlation between milk yield at 1st lactation period and herd life was 0.3-0.9; but, these estimates were intensively biased due to voluntary culling based on milk yield and could not justify expected genetic response for the selection (Vollema *et al.*, 2000; Vollema and Groen, 1997). By means of existed relation between milk yield and some reproductive traits such as days open and age at 1st calving, it could predict herd life of a cow by traits, which were obtainable after the end of 1st lactation period.

In Iran, similar to the other countries, many of cows still exist in the herd at the time of genetic evaluation for herd life and prediction of herd life and investigation of the possibility of using predicted records in genetic evaluation considered as a necessary. So that the goal of this research, investigation of the possibility of using predicted and completed herd life records in genetic evaluation of Holstein cows in Iran and its comparison with applying manner of incomplete herd life records.

MATERIALS AND METHODS

The data set related to 55596 record of Iranian Holstein cows were provided by NABC (National Animal Breeding Center) from 163 herds. The data file consisted records on productive and reproductive traits. All animals were book-registered and were born during the years 1993 and 2007.

The variables in this study including effects of Herd-Year-Season (HYS) and State (ST) as discontinuous variables, 305 days Milk Yield (MY) corrected by 3.5% fat, Age at First Calving (AFC) Days In Milk (DIM) and Days Open at 1st lactation period (DO) as continuous variables and herd life are considered as dependent variable.

Length of herd life was defined as times (days) from one calving to the next calving, death, or culling. Age at 1st calving outside an 18-40 months range was excluded from the analysis. The number of 32432 records of cows from this data set related to cows had a culling date during record keeping and so that they had a completed herd life records, but rest of that still exist in the herd and have not been culled and their herd life record were incomplete. These records collection made file 1 in this study. Removing incomplete herd life records has made file 2. Except these 2 files; another file (file 3) existed similar to the file 1 but predicted herd life records used instead of incomplete records.

A general linear, quadratic and cubic model was used for estimating the predicted Eq. 1 for herd life of dairy cows. The model demonstrated as follows:

$$\begin{aligned} Y_{ijk} = {} & U + HYS_i + ST_j + b_1 MY_{ijk} + b_2 MY^2_{ijk} + b_3 MY^3_{ijk} \\ & + b_4\ AFC_{ijk} + b_5 AFC^2_{ijk} + b_6 AFC^3_{ijk} + b_7 DIM_{ijk} \\ & + b_8 DIM^2_{ijk} + b_9 DIM^3_{ijk} + b_{10} DO_{ijk} + b_{11} DO^2_{ijk} \\ & + b_{12} DO^3_{ijk} + e_{ijk} \end{aligned} \quad (1)$$

where:

Y_{ijk} = Predicted records of herd life for kth cow living in jth state within ith herd-by-year-by-season

μ = Overall mean

HYS_i = Fixed effect of ith herd-by-year-by-season

ST_j = Fixed effect of state i (i = 1, ..., 28)

$b_{1\text{-}3}$ = Linear, quadratic and cubic regression values of 305 days milk yield corrected by 3.5 fat percent of 1st lactation

MY_{ijk} = Random effect of 305 days milk yield corrected by 3.5 fat percent of 1st lactation

$b_{4\text{-}6}$ = Linear, quadratic and cubic regression values of 1st calving age

AFC_{ijk} = Random effect of calving age of 1st lactation (in day)

$b_{7\text{-}9}$ = Linear, quadratic and cubic regression values of days in milk

DIM_{ijk} = Random effect of days in milk

$b_{10\text{-}12}$ = Linear, quadratic and cubic regression values of days open

DO_{ijk} = Random effect of days open

e_{ijk} = Residual random error term

Estimation of type III means squares, F statistics and least squares means computed using PROC GLM of SAS statistical software package to select statistical model for each dependent variable in a way that all continuous and discontinuous variables existing in model being significant ($p<0.01$).

In this way, by having the regression values of continuous variables, the predicted equation of herd life was derived. In each files 1-3, genetic parameters of herd life was estimated by REML using DFREML algorithm.

RESULTS AND DISCUSSION

Average, minimum, maximum, standard deviation and coefficient of variance about 305 days milk yield corrected based on 3.5% fat, age at 1st calving, days in milk, days open at first calving and herd life by using file 1 have been shown in Table 1.

Table 1: Estimation of average, minimum, maximum, standard deviation and coefficient of variance about milk yield, age at first calving, days in milk, days open and herd life by using file 1

Trait	Average	Minimum	Maximum	SD	Coefficient of variance
Milk yield (kg)	8762.0	2012.8	12245.4	1819.3	20.7
Age at 1st calving (day)	1079.0	855.0	1110.0	41.5	3.8
Days in milk	487.0	73.0	305.0	57.6	11.8
Days open	83.9	50.0	139.0	13.1	15.6
Herd life (day)	1124.0	379.0	2418.0	382.0	33.9

Average age at first calving was 1079±41.5 days (36 months Aprox.) with low standard deviation. In many cases, it has been shown that genetic merit of age at first calving regarding to other reproductive traits was higher and positive genetic merit resulted from a breeding program (Caraviello *et al*., 2004). The average of days open was 83.9±13.1 days. Regularly, phenotypic correlation of days open and calving interval with age at first calving reported negatively that showed low age of young cows during first mating had undesired effects on days open and calving intervals in the next lactations (Setati *et al*., 2004). The average of herd life of dairy cows from file 1 was 1124±382 days (37 mounts Aprox.) that because of existing of incomplete records of herd life had a high standard deviation. In file 1, exist cows with herd life of 379 days, which probably culled after the 1st lactation period or at the end of 1st lactation period was coincident with record keeping that cows still exist in the herd and their herd life records were incomplete.

Predicted Eq. 2 of herd life was as follows:

$$Y = 1670.143310 + 0.018199\times MY - 0.000265\times AFC^2 + 0.003126\times DIM - 2.349854\times DO + 0.010053DO^2 \qquad (2)$$

For determination of predicted equation of herd life, it is clear the linear effect of milk yield, quadratic effect of age at 1st calving, linear effect of days in milk and linear and quadratic effects of days open at first lactation period were significant ($p<0.01$) (Eq. 2); but, the other effects were not significant ($p>0.01$). The true numerical data of milk yield at first lactation period, age at first calving, days in milk and days open at first lactation are taken in the Eq. 1 and herd life records of lived cows being predicted.

Estimations of herd life from file 1-3 have been shown in Table 2. The average of herd life in file 2 was more that 2 other files (1267 days against 1124, 1026 days about file 1 and 3, respectively) due to the absence of incomplete herd life records in file 2. Average herd life resulted from file 3 closer to the amount of file 1, which related to the presence of predicted herd life records in this file. Using predicted records, which had lower diversity toward completed herd life records, caused less coefficient of variance of herd life in file 3 toward 2 other files. Coefficient of variance of files 2 and 3 were closer to each other (26.8 and 25.6, respectively), which showed the effectiveness of predicted equation of herd life in this study. Residual variance of herd life was high (83061.9, 35102.0 and 31060.1 about files 1-3, respectively) which, showed the important role of environmental effects on herd life variability (Table 2). Culling of incomplete herd life records of lived cows resulted to the close of average of herd life records toward completed herd life records in file 2 and also reduced dispersion of observations around the average. So that phenotypic variance of herd life decreased severely in file 2 toward files 1 and 3 (1039396.2, 368087.3 and 310158.4 about files 1-3, respectively).

Table 2: Estimation of statistics and genetic parameters of herd life by using files 1-3

Statistics	File 1	File 2	File 3
No. records	55596	32432	55596
Average	1124	1267	1206
Minimum	379	744	719
Maximum	2418	2418	2418
SD	382.0	340.3	309.1
Phenotypic variance	1039396.2	368087.3	310158.4
Additive genetic variance	76915.3	32023.6	28224.4
Residual variance	83061.9	35102.0	31060.1
Heritability	0.07	0.08	0.09
Coefficient of variance (%)	33.9	26.8	25.6

File 1: Incomplete and complete herd life records; File 2: Complete herd life records; File 3: Complete and predicted herd life records

Estimations heritability of herd life from files 1-3 were <0.1 (0.07, 0.08 and 0.09 about files 1-3, respectively); but, estimation resulted from file 3 was more then two other ones. In this file (file 3) by using regression model for prediction of herd life records of lived cows and completed herd life records, the effects of different factors on numerical data's herd life were neutralized, therefore, the amount of variance components in this file (file 3) regarding to two other files (files 1 and 2) was lower which, resulted in higher heritability of this file.

This comparison showed that replacement of predicted records instead of incomplete records caused less variance and more heritability for this trait. According to the less coefficient of variance in file 3, showed that using predicted records instead of incomplete records had more reliability in genetic evaluation of herd life.

CONCLUSION

In order to study the possibility of using predicted herd life records instead of incomplete herd life records

(records belong the cows exist in the herd at the time of record keeping) in genetic evaluation of Iranian Holstein cows, determined a predicted equation of herd life to predict herd life records of lived cows by using productive and reproductive variables. The results showed use of predicted records instead of incomplete records resulted to reduce phenotypic variance and increased heritability for herd life. The lesser coefficient of variance and higher heritability in consequence of using predicted records revealed that these records are more reliable than incomplete records for genetic evaluation of herd life. Therefore, the predicted herd life records, which depended on productive and reproductive information of 1st lactation period of dairy cows could used instead of incomplete records in genetic evaluation of herd life and this led to more accuracy and efficiency of selection.

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