A Study on the Association of Days Open with the Genetic Ranking of Iranian Holstein Bulls for the Trait of Milk Yield

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ABSTRACT

The genetic evaluation of dairy bulls is based on their daughters' production, type traits, and fertility. It is unknown how the different number of days open of the daughters of a bull influences its Estimated Breeding Values (EBVs) and ranking in the population. The present study aimed to examine the effect of days open on milk production of Holstein dairy cows and the ranking of the bulls according to their predicted breeding values. A total number of 706,653 test day records of the first parity of 78,517 Iranian Holstein cows in 448 herds during 1991 to 2016 were used. The daughters of the same bulls were allocated into nine groups of days open, the differences of which were 21 days. Data were analyzed using a random regression model and predicted the breeding values of bulls. The effect of herd-year-season on milk yield were significant ($P \leq 0.001$). The heritability of 270 days milk for the first to ninth groups were estimated to be 0.24(±0.04), 0.26(±0.02), 0.23(±0.02), 0.21(±0.03), 0.18(±0.03), 0.19(±0.04), 0.16(±0.05), 0.17(±0.05) and 0.11(±0.04), respectively. The Spearman rank correlation coefficient of predicted breeding value of the same sires in different groups were 0.60-0.75 ($P \leq 0.01$). The results showed a negative relation between the number of days open and the predicted breeding value of bulls. It can be concluded that the number of days open affects the prediction of breeding value and ranking of the sires and it should be corrected for, while predicting the breeding value of sires.

Keywords: Breeding value, Random Regression, Reproductive performance, Test day.

INTRODUCTION

Reproductive performance is an important factor affecting profitability in dairy cattle industry. Poor fertility results in an increase in calving interval, number of services per conception, fewer calves per cow per year, involuntary culling rate and herd replacement cost, as well as a decrease in milk production, and a reduction in the herd income. A research reported that 36 % of cow culling reasons were related to reproductive problems (Boujenane, 2017). For several years, the selection objectives of breeding companies for dairy cattle improvement has been for milk production. This objective has affected the reproductive traits in a negative way, especially in high producing cows. This is because of the antagonistic genetic relationship between milk production and fertility (Pryce *et al*., 2004). Therefore, to control the decline of fertility and even to improve it, the genetic improvement programs of different countries incorporate the reproductive traits as selection objectives.

The dairy bulls are genetically evaluated for several traits, including production,

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health, fertility, and type traits. A number of different statistical models and techniques are presented for estimating the breeding value of the bulls. The use of a well-fitted model can increase the accuracy of the assessment (Weigel *et al*., 2017). The concepts of Predicted Transmitting Ability (PTA), reliability and percentile rank are the criteria that are used to make proper sire selection decisions. Percentile ranks are tables or graphs of PTA distributions that provide helpful information regarding the rank or position of a given bull within the population evaluated for a given trait of interest.

The specific definitions of various measures of milk production and reproductive performance need to be carefully considered to better interpret the sire ranking. A general belief across the dairy community, both scientific and commercial, is that of an antagonistic association between milk production and reproductive performance of dairy cows (Royal *et al*., 2000). Although perceived as production–reproduction antagonism, there are relevant issues that seem to have been previously misrepresented or overlooked (Bello *et al*., 2012). Studies in Holstein Friesian cows in 16 countries have shown that fertility rates declined between 2000 and 2007, but this trend improved afterwards (Pryce *et al*., 2014). In general, the appropriate and economic period of the birth interval is discussed and considered by producers and breeding specialists. At the same time, the general view is that the birth interval should be reduced as much as possible (Huirne *et al*., 2002). Nutrition, genetics, energy balance, diseases, reproductive health, moment of insemination, insemination technique, sperm quality, and housing status are effective factors in reducing the number of days open and calving intervals (Stephen, 2013).

Days open, which is the interval from calving to conception, affects the amount of milk yield, calving interval and the number of calves per cow (Makuza and Mc Daniel, 1996). A common economic measure of

reproductive performance is the cost of extended days open, referring to how much money is lost for every extra day a cow is not pregnant. Generally, dairy farmers and industry professionals estimate this cost at $3 to $5 per day open. However, this estimate may not account for variation in expenses and revenues over time or between herds, meaning that cost per day open is likely overestimated in some conditions while underestimated on others (Boujenane, 2017). Also, the value of daughter pregnancy rate in the USA, which is a genetic measure of fertility, assumes a $1.50 cost per extra day open excluding the cost of increased culling (De Vries, 2006). In Holstein dairy cattle, the decrease of 2.40 kg of milk and 0.112 kg of fat for each additional days open is reported (Louca and Legates, 1967). In a research the differences of milk production between the 20 open day periods from the 20 to 220 days open compared. The results showed a significant difference in milk production in different groups. Therefore, adjustment of 305-day records for days open was proposed (Schaeffer and Henderson, 1971). The heritability of fertility-related traits such as days open and calving interval is low and reported to be 0.02-0.12, which means the effect of environmental factors on variation of these traits is high (Liu *et al*., 2008; Aghajari *et al*., 2015). The genetic correlation of predicted breeding values of days open and milk production in Holstein cows is 0.41 (Liu *et al*., 2008).

In Canadian dairy cattle herds, 26 percent of successful pregnancies occur during 85 days after parturition, which means the lactation period is less than 305 days (Van Doormaal and Beavers, 2016). The cows that get pregnant earlier in the herd are dried out sooner than other cows. Therefore, the number of days in milking is less, affecting the total milk yield. These animals have different recorded amounts of total milk, fat and protein than their herd mates. This research aimed to assess the impact of the number of days open on milk yield and the rank of bulls according to their genetic

evaluations for milk production of their daughters in Iranian Holstein dairy cattle.

MATERIALS AND METHODS

The Iranian Animal Breeding Center supplied the data. The original data file for reproduction traits consisted of test day records that were matched to pedigree and calving information to calculate the traits of interest. The days open was defined as the number of days between calving and conception. Data file was edited using SPSS software (ver. 24) and cows without pedigree information were excluded. In order to prevent the effect of bias due to culling dairy cows according to yield or other factors, only the data of the first parity cows were used for analysis. Meanwhile, the effects of parity on days open was reported to be non-significant (Boujenane and Draga, 2021).

Herds with more than 1,000 test day records and the sires each with more than 100 daughters in the herd were selected. A completed 305 days lactation period would have 7 to 10 test days' yields such that the factors affecting test day yields would be averaged (Jamrozik and Schaeffer, 1997). The records were selected with at least 270 days and twice milking per day. The animals were then divided into nine groups based on the duration of the estrous cycle (21 days) and days open. Usually, due to some special conditions of delivery and placental abruption and the need to improve the uterus and eliminate infectious and non-infectious problems, the first estrus after parturition might be delayed. Therefore, in this study, the period up to 45 days after calving was called the first, and the period for the other eight groups was considered to be 21 days. Therefore, for the first group of cows, a time interval of 45 days after calving was considered and the period for the other eight groups was considered to be 21 days. The grouping was done in such a way that the sires were the same for all 9 groups. In other words, each of the sires in each of the 9

groups had their daughters' records. The final data set comprised of 706,653 milk test day records of the first calving of 78,517 cows from 448 herds born during 1991 to 2016. More details of the data are presented in Table 1. According to the number of days open, the daughters of 793 sires were attributed to nine different groups (Table 2). Due to the limited data, the number of sires for the eighth and ninth groups were 721 and 714, respectively. The use of 305 days lactation records is the international standard for expressing lactation records. It is based on a targeted calving interval of 12 months (365 days) and 60 days dry period. Therefore, if a cow gets pregnant prior to 45 days in milk would usually be dried off before a lactation length of 270 days or 9 test day records. In models used for genetic evaluation of dairy cattle, the animal performances are compared within groups of assumed similar environment. Such environmental groups are commonly formed by fitting factors such as herd, year, and season of calving and are usually treated as fixed effects. These factors, as well as the two- and three-way interactions between them, are the main environmental effects, accounting for about 40 percent of the total variance in milk and fat yields (McGill *et al.*, 2014). In this study, the herd, year and season effects on days open in different groups were significant (P≤ 0.001) and, therefore, used in the model for breeding value prediction.

The test day records were analyzed using a random regression model (Jamrozik and Schaeffer, 1997; Mrode, 2014) and the DMU software (Jensen and Madsen, 1994) was used for data analysis.

Model;

$$Y_{tijk} = F_i + \sum_{k=1}^{nf=2} \emptyset_{jtk}\, \beta_k$$

$$+ \sum_{k=1}^{nr=3} \emptyset_{jtk} U_{jk}$$

$$+ \sum_{k=1}^{nr=3} \emptyset_{jtk} PEe_{jk} + \varepsilon_{tijk}$$

Table 1. Summary of information of data used for analysis.

No of animals	No of sires	No of dams	No of herds	No of provincs	No of test-day	270 days milk yield ($\bar{x} \pm SD$)	Days open ($\bar{x} \pm SD$)
78517	793	71851	448	20	706653	8659.3 ±1582	109 ±53

Table 2. Average of milk production in 270 days and the heritability of milk yield in different groups. [a]

Group	No of animals	Percent	Days open (Days)	270 Days milk yield ($\bar{x} \pm SD$)	h^2
1	6073	7.7	≤45	8315 ±1223[ab]	0.24 ±0.04
2	15417	19.6	46-67	8430 ±1256[a]	0.26 ±0.02
3	14179	18.1	68-89	8507 ±1231[abc]	0.23 ±0.02
4	11437	14.6	90-111	8510 ±1215[bcd]	0.21 ±0.03
5	8371	10.7	112-133	8558 ±1206[abcd]	0.18 ±0.03
6	6881	8.8	134-155	8551 ±1200[d]	0.19 ±0.04
7	5473	7.0	156-177	8582 ±1198[cd]	0.16 ±0.05
8	4469	5.7	178-199	8629 ±1199[bcd]	0.17 ±0.05
9	6217	7.8	≥200	8629 ±1211[d]	0.11 ±0.04

[a] a-d The difference in the average milk production of groups with different letters is significant (P≤ 0.05); Turkey's.

Where, Y_{tijk} is the test day record k of cow j made on day t within F subclass i; F_i is the Fixed effect of herd-year-season i; β_k are the fixed regression coefficients specific to subclass k. U_{jk} and PEe_{jk} are the vector of the k_{th} random regression for animal and Permanent Environmental effects, respectively, for animal j; $\emptyset_{jtk}$ is the vector of the k_{th} Legendre polynomials for the test day record of cow j made on day t; nf is the order of polynomials fitted as fixed regressions; nr is the order of polynomials for animal and PEe effects; and ε_{tijk} is the random residual. The model in matrix notation is:

y = Xb + Qu + Zpe + e

Where, y is the vector of test day yields, b is a vector of solutions for herd –year– season and fixed regressions; the matrix X is the incidence matrix; u and pe are vectors of random regressions for animal additive genetic and pe effects. The matrices Q and Z are covariable matrices and, if only animals with records are considered, the i_{th} row of these matrices contains the orthogonal polynomials (covariables) corresponding to

the days in milk of the i_{th} test day yield and the order of fit is the same for animal and pe effects, i.e. Q=Z. This would not be the case if the order of fit is different for animal and pe effects. In general, considering animals with records, the order of either Q or Z is number of test day (TD) records by nk, where nk equals nr times the number of animals with records. It is assumed that Var(u)= A*G, Var(pe)= I*P and Var(e)= $I\sigma_e^2$= R, where A is the numerator relationship matrix, * is the Kronecker product, and G and P are of the order of polynomial fitted for animal and pe effects.

The mixed model equation (MME) is as follows:

$$\begin{pmatrix} X'R^{-1}X & X'R^{-1}Q & X'R^{-1}Z \\ Q'R^{-1}X & Q'R^{-1}Q + A^{-1} \otimes G & Q'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Q & Z'R^{-1}Z + P \end{pmatrix}$$

$$\begin{pmatrix} \hat{b} \\ \hat{u} \\ \hat{pe} \end{pmatrix} = \begin{pmatrix} X'R^{-1}y \\ Q'R^{-1}y \\ Z'R^{-1}y \end{pmatrix}$$

Meanwhile, it was assumed the days open in nine groups to be different traits. Therefore, their genetic correlations was estimated with a linear multiple trait animal

model, using the BLUPF90 software (Misztal *et al.,* 2014).

RESULTS AND DISCUSSION

The milk yield of cows in groups with more days open was higher (Table 2). These findings show the 270 days milk yield of cows thst have longer calving interval (longer days open) is more than the cows with shorter calving interval. The genetics and management improvement are the main factors affecting the pregnancy of cows in the first 100 days of calving, which can increase reproductive efficiency in the herd. The results of this study showed that 45.4 % of days open were less than 90, (7.7% of which are up to 45 days) and 40 % were more than 90 days after calving (Table 2). These results are from 448 dairy herds in 20 different provinces, consistent with studies in other countries (Van Doormaal and Beavers, 2016). The differences of average 270 days milk production between the groups were significant (P≤ 0.05) and the lowest and highest milk yield was estimated for groups 1 and 9, respectively (Table 2). The total milk production in the first parity cows is reported to be 1.16 kg more per day of more days open (Louca and Legates, 1967). It is clear that cows that become pregnant earlier in lactation are less likely to have a lactation period of 305 days and a lower average milk production. In the similar study in Canada, it was reported that 5 and 26% of successful pregnancies occur before 50 days and up to 85 days after parturition, respectively (Van Doormaal and Beavers, 2016). In a research, it was found that the milk production of the first parity cows with the longest calving interval was more than others (Riecka and Candrak, 2011). The range of heritability of milk yield of 9 groups of days open was 0.1 0.26 and was lower with increasing days open (Table 2). It seems that with the increase in the number of lactation days, the impact of environmental facto`rs on variation of milk production increases and, therefore, the

genetic variance decreases. One study reported that the additive genetic variance decreased with increasing lactation period (Ashrafian *et al*., 2018). The heritability of 305 days of milk production and days open of Iranian Holstein cows is reported to be 0.30 and 0.07, respectively (Aghajari *et al*., 2015) and the genetic correlation of two traits in the first calving cows were reported to be 0.23 (Bitaraf Sani *et al*., 2013). In this study, the grouping is based on the number of days open. Therefore, the number of lactation days increases with the grouping number (Table 2).

The estimates of genetic correlation between the nine days open were low (-0.01 to 0.26) and the estimates of their heritability were low, too (0.02 to 0.15), (Table 3). These estimates reveal that most of the variation of days open in the population is influenced by non-genetic factors such as management and other environmental factors. The heritability of days open of Holstein cows in Germany is reported to be 0.03 (Liu *et al*., 2008).

The breeding value of the same sires in different groups was predicted according to the test day records of milk production in each group (Table 4). The average breeding value of the sires in each group was predicted. The average breeding values of the same sires in nine groups were 504.5±14.65, 770.4±17.15, 601.7±15.92, 518.7±14.09, 514.6±12.67, 294.7±13.29, 310.5±10.73, 196.3±13.01 and 100.8±7.6, respectively. The average breeding value of sires in the second group was highest (770.4 kg). However, the average breeding value of the same sires in groups of longer days open was lower, and for group 9 was 100.8 kg. However, the total milk production was higher for groups with more days open, similar to the results of other studies (Faid Allah, 2015; Schaeffer and Henderson, 1971). In a German study, the genetic correlation of estimated breeding value of milk production and the days open was 0.41 (Liu *et al*., 2008). Data analysis showed a negative relationship between the estimated breeding value of sires and the number of

Table 3. Correlation (above diagonal) and heritabilities (on diagonal), of nine groups of days open.

Group	≤ 45	46-67	68-89	90-111	112-133	134-155	156-177	178-199	≥ 200
≤ 45	0.06 ±0.005	-0.11	-0.04	-0.05	-0.08	0.01	0.08	-0.04	0.14
46-67		0.02 ±0.002	0.09	0	-0.18	0.26	-0.15	0.08	-0.24
68-89			0.02 ±0.002	0.12	0.15	0.01	0	0.25	-0.1
90-111				0.04 ±0.003	0.09	-0.16	-0.12	0	-0.16
112-133					0.06 ±0.005	-0.07	0.07	0.17	0.1
134-155						0.11 ±0.008	-0.04	0.16	-0.08
156-177							0.07 ±0.006	-0.01	0.15
178-199								0.15 ±0.012	-0.12
≥ 200									0.05 ±0.004

Table 4. Average Breeding Value (BV) of sires for different groups.

Group	≤45	46-67	68-89	90-111	112-133	134-155	156-177	178-199	≥ 200
No of sires	793	793	793	793	793	793	793	721	714
Mean	504.5	770.4	601.7	518.7	514.6	294.7	310.5	196.3	100.8
SE	14.65	17.15	15.92	14.09	12.67	13.29	10.73	13.01	7.60

Table 5. Correlation of breeding values of the same sires in different groups.

group	1	2	3	4	5	6	7	8	9
1		0.73**	0.71**	0.67**	0.70**	0.68**	0.65**	0.64**	0.63**
2			0.75**	0.72**	0.71**	0.70**	0.68**	0.64**	0.67**
3				0.70**	0.69**	0.70**	0.68**	0.66**	0.69**
4					0.66**	0.65**	0.66**	0.63**	0.66**
5						0.70**	0.62**	0.60**	0.64**
6							0.60**	0.61**	0.61**
7								0.66**	0.62**
8									0.61**
9									

** P≤ 0.01.

days open. It should be noticed that, in the present study, the same sires were allocated to nine open day groups and the breeding values of milk production was compared. In other studies (Bitaraf Sani *et al*., 2013; Makuza and McDaniel., 1996), the number of days open for different cows was fitted as a single variable, and the breeding value of sires was estimated for this variable, which is a different approach from the present study.

Due to Genotype×Environment interaction (G×E), the genetic correlation in two environments are lower than unity (Falconer and Mackay, 1996). The range of genetic correlation of breeding values of the same sires between nine groups were 0.60-0.75 (Table 5). It is suggested that genetic

correlation of milk production traits of the same sires in two different environments should be between 0.80 and 1.00, and if it is less than 0.85, the reason is the G×E interaction (Hayes *et al*., 2003; Kearney *et al*., 2004). The genetic correlations in two environments are lower for functional traits than for milk production traits. For example, the average genetic correlation of longevity in different countries is 0.59 (Mark, 2004).

In this study, the genetic correlation of the same sires in different groups were less than 0.85, which shows that the number of days open of the daughters affects ranking of the same sires.

CONCLUSIONS

The correlation between the Estimated Breeding Value (EBV) of all 793 sires having daughter records was less than 0.85 and shows the effect of G×E on predictions. It can be concluded that the number of days open affects the rank of the sires and variation of this effect should be accounted or corrected for when the breeding value of sires is predicted.

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بررسی تاثیر تعداد روز غیرآبستن بر رتبه بندی ژنتیکی گاوهای نر هلشتاین ایران برای تولید شیر

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چکیده

ارزیابی ژنتیکی گاوهای نر مولد بر مبنای رکورد تولید دختران آنها، صفات تیپ و صفات مرتبط با باروری انجام می شود. در ارتباط با تاثیر تعداد روز غیرآبستن دختران گاوهای نر بر پیش بینی ارزش ارثی و رتبه بندی ژنتیکی ان ها مطالعه ای نشده است. لذا در این تحقیق نحوه تاثیر تعداد روز غیرآبستن بر مقدار تولید شیر گاوهای نژاد هلشتاین و پیش بینی ارزش ارثی مولدهای نر و رتبه بندی آن ها بررسی شد. برای این منظور از تعداد ۷۰۶۶۵۳ رکورد روز آزمون زایش اول ۷۸۵۱۷ گاو هلشتاین در ۴۴۸ گله در سال های ۱۳۷۰ تا ۱۳۹۴ استفاده شد. دختران مولدهای نر بر اساس تعداد روز غیرآبستن با فواصل ۲۱ روز در ۹ گروه به نحوی تقسیم بندی شدند که از هر مولد نر در کلیه گروه ها دختر وجود داشت. داده ها با یک مدل رگرسیون تصادفی آنالیز و ارزش ارثی مولدهای نر پیش بینی شد. اثر ثابت گله-فصل-سال بر تغییرات تولید شیر معنی دار بود (P 0.001≥). وراثت پذیری تولید شیر ۲۷۰ روز برای ۹ گروه به ترتیب (۰/۰۴±)۰/۲۴، (۰/۰۲±)۰/۲۶، (۰/۰۲±)۰/۲۳، (۰/۰۳±)۰/۲۱، (۰/۰۳±)۰/۱۸، (۰/۰۴±)۰/۱۹، (۰/۰۵±)۰/۱۶، (۰/۰۵±)۰/۱۷ و (۰/۰۴±)۰/۱۱ بود. همبستگی میانگین ارزش ارثی مولدهای نر مشابه در گروه های مختلف ۰/۷۵-۰/۶۰ بود. رابطه تعداد روز غیرآبستن و مقدار پیش بینی ارزش ارثی مولدهای نر منفی بود. این امر نشان می دهد که تعداد روز غیرآبستن می تواند بر مقدار پیش بینی ارزش ارثی مولدهای نر و رتبه بندی آنها تاثیر داشته باشد. لذا تعداد روز غیرآبستن باید به عنوان یک عامل در مدل های مربوط به محاسبه ارزش ارثی مولدهای نر منظور گردد.