

# Genetic relationships between production traits and reproductive performance in Holstein dairy cows

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## Abstract

In order to estimate genetic parameters for production traits and reproductive performance, 115 465 records of production traits and 90 942 records of reproductive performance from Iranian Holstein cows that were collected during 1980 to 2004 at Animal Breeding Center of Iran, were used. The estimations were performed using Restricted Maximum Likelihood method (REML) under an animal model by DF-REML and MATVEC software. Estimates of heritabilities for production traits were moderate, from 0.149 for fat yield to 0.26 for milk yield. Heritabilities for reproductive performance were low, and ranged from 0.04 for interval from calving to first service to 0.0743 for gestation length. Genetic correlations between production traits were from  $-0.505$  for milk yield and protein percentage to 0.81 between milk yield with fat yield. Most genetic correlations between reproductive performances were found close to zero. Genetic correlation estimates of production traits with reproductive performance were from  $-0.513$  for open days and protein yield to 0.96 for protein yield and calving interval.

**Keywords:** genetic parameter, production traits, reproductive performance, Holstein dairy cows

## Introduction

The primary selection objective in dairy cattle breeding has been milk production. Milk, fat, and protein yields and fat and protein percentages are the main economic traits for selection in dairy cattle. Precise estimates of genetic parameters are required for prediction of breeding values using mixed models or selection indices (Chauhan & Hayes 1991). Recently, functional traits such as reproduction and health traits have received increased focus because of biological, economical, and ethical reasons, and also animal welfare concerns. Profitability of dairy cattle does not only depend on milk production but also on nonproduction characteristics such as fertility and health traits.

Many secondary traits, such as reproduction traits (Kragelund *et al.* 1979, Pelissier 1982, Strandberg & Oltenacu 1989) and health traits (Jones *et al.* 1994) are important in minimising cost and maximising the net return of the dairy enterprise. Reproductive performance has also been found to deteriorate as milk yield increased (Berger *et al.* 1981, Hansen *et al.* 1983). Reduction in reproductive performance could affect culling rates and herd life and reduce the genetic gain from primary traits (Pelissier 1982).

Ignoring the genetic component of poor fertility masks the severity of the problem, and a failure to tackle the genetic component of the problem is expected to lead to a continuing downward genetic trend. However, the genetic variation for fertility measures is substantial, indicating potential to select for improved fertility (Philippson 1981). To improve the reproductive performance of herds, dairy producers must understand the complex interactions of milk production, reproduction, nutrition, genetics, and management. Foster *et al.* (1988) recommend improvements in management, such as detection of oestrus, insemination technique, herd health programs, and nutrition, to improve reproductive performance at higher production.

Breeding for increased production in dairy cattle has negative side effects on health and fertility traits (Pryce *et al.* 1997, Roxström *et al.* 2001). Selection for an increase in production under one management system may lead to more health risks than under other management systems. Thus, management and genetics have to be integrated to develop an effective program for improvement of health and fertility (Windig *et al.* 2006).

In dairy cattle, female reproduction problems lead to prolonged calving intervals, increased insemination and veterinary costs, higher culling rates, and thus increased replacement costs. Several studies using field data (Janson & Andreasson 1981, Hansen *et al.* 1983, Roxström *et al.* 2001) found unfavourable genetic correlations between milk yield and female fertility traits. High milk production per cow is one of the most important factors contributing to profitability of a dairy farm, and genetic selection for increased milk production has been the most consistent way to increase production per cow (Hansen *et al.* 1983). It has now been recognized that selection in dairy cattle solely for high milk production is generally accompanied by reduced fertility (Royal *et al.* 2000, Roxström *et al.* 2001) and reduced health (Pryce *et al.* 1998).

Most studies of the association between milk yield and reproductive measures in dairy cattle showed an unfavourable relationship between them. High milk yield per lactation has been associated with longer postpartum intervals to first service (Berger *et al.* 1981, Janson & Andreasson 1981), longer service period (Berger *et al.* 1981, Hansen *et al.* 1983), more open days (Berger *et al.* 1981, Hansen *et al.* 1983), and longer calving intervals. Most estimates of heritability of reproductive traits are less than 0.10 (Berger *et al.* 1981, Janson & Andreasson 1981, Hansen *et al.* 1983). Thus indicating that relatively slow improvement in fertility would result from selection. Even though most reproductive traits have low heritabilities, monitoring reproductive performance has merit because, after low milk yield, poor fertility is the leading reason for culling. Importance of fertility in dairy cattle is well known, both in functionality and farm economy (González-Recio *et al.* 2004, Pryce *et al.* 2004). Objectives of this study were to determine genetic (co)variances and correlations between production traits (milk yield, fat yield, protein yield, fat percent and protein percent) and fertility traits (days open, calving interval, days from calving to first insemination and gestation length) to account for selection of dairy cows.

## Material and methods

### *Data*

The data were collected by the Animal Breeding Center of Iran and consisted of production records with reproductive information for Iranian Holstein cows that were included 115 465 dairy cows distributed in 15 herds from 1980 to 2004. Five production traits and four fertility traits were considered. The production traits were 305-days milk yield (MILK), fat yield (FAT), protein yield (PRO), milk fat percent (FAT%) and milk protein percent (PRO%) in first lactation. The fertility traits were days open (DO), calving interval (CL), days from calving to first insemination (DFS) and gestation length (GL) which were used up to eight lactations.

Only cows with both production and reproductive records were considered. Records of cows with no report for first lactation were not used. Original files were edited to obtain appropriate data sets for the statistical analyses. Restrictions and rules for validation were applied to ensure the quality of production and reproductive data. Records meeting the following criteria were retained:

- 305-days milk yield ranged from 2 700 to 10 500 kg
- fat yield between 60 and 340 kg
- protein yield between 95 and 340 kg
- milk fat percent ranged from 1.5 to 4.6%
- milk protein percent between 2.5 and 4.5%
- Days from calving to first insemination were recorded as DFS. Lactations were omitted if DFS was lower than 30 days, higher than 300 days, or unknown.
- Days from calving to successful artificial insemination date were recorded as DO. Records with DO longer than 350 and shorter than 45 days were eliminated.
- Gestation length was considered to be ranged from 240 to 290 days to consider oestrus period around these days.
- Successive calving dates had to range from 300 to 600 days. If the following calving date was not available, CI was considered a missing value. Otherwise, lactation and insemination records were not considered.

Limits were required for DFS, GL, DO, and CI to not include in the analysis records or cows with serious problems other than fertility, such as diseases that could affect reproductive ability. A total of 27 766 first lactation records remained after editing and merging the both production and productive traits file together. Over 93% of cows had a fat yield, over 93% of cows had a milk fat percent, over 35% of cows had a protein yield, and over 33% of cows had a milk protein percent after editing the production file. In addition, for reproductive traits, after editing the fertility data in this study, over 57% of cows had a DO. Over 42% of cows had a CI; over 28% of cows had a DFS, and over 94% of cows had a GL. Structure of edited data sets and descriptive statistics for production and reproductive traits is presented in Table 1.

Table 1

Summary of data structure, mean±SD and coefficient of variance for production and reproductive traits

	MILK	FAT	FAT%	PRO	PRO%	CI	DO	DFS	GL
Number of records	27 766	26 072	26 021	9 908	9 278	11 674	15 895	7 949	26 147
Number of total animals in pedigree	35 447	34 001	33 960	14 370	13 718	9 238	10 250	8 847	20 503
Number of sires	672	660	658	478	471	385	407	395	580
Number of RYSC subclasses	452	452	452	145	145	ns	ns	ns	ns
Number of RYSB subclasses	ns	ns	ns	ns	ns	ns	293	289	384
Number of ApMp subclasses	ns	ns	ns	ns	ns	1 352	ns	1 071	1 777
Number of parities	1	1	1	1	1	8	8	8	8
Mean±SD,	6 564.65±	198.79±	3.072±	208.86±	3.086±	395±64	124±66	97±57	279±6
	1 256.64 kg	46.79 kg	0.591%	36.03 kg	0.28 %	days	days	days	days
Coefficient of variance, %	19.14	23.54	19.24	17.25	9.07	16.13	53.31	58.18	2.16

MILK: 305-days milk yield, FAT: fat yield, PRO: protein yield, FAT%: milk fat percent, PRO%: milk protein percent, CI: calving interval, DFS: days from calving to first insemination, DO: days open, GL: gestation length, RYSC: fixed effect of region by year of birth by season of calving, RYSB: fixed effect of region by year of birth by season of birth, ApMp: fixed effect of age at previous calving by month of previous calving by parity, ns: The effects of RYSC, RYSB and ApMp were statistically non significant ( $P>0.05$ ).

### Models (statistical analysis)

The estimates of genetic parameters have been observed to vary for different models of analysis, number of relationships accounted for (Dong *et al.* 1988), size of the data set, and nature of editing of the data. The estimates of genetic parameters have been reported to vary for the number of traits analysed (Lin & Lee 1986). The models were developed based on data availability, literature evidence, genetic evaluation models that are used in other countries, and available computing facilities. The data were first analysed by the least squares techniques using the general linear model procedure to determine the effects of the various factors on production and reproductive traits. Single-trait models for production and reproductive traits are listed below in a simplified scalar notation.

Models for production traits were:

$$y_{ijkl} = \mu + Rys_i + H(Rys)_{j(i)} + b.AFC_k + A_l + e_{ijkl} \quad (1)$$

where  $y_{ijkl}$  denoted production traits (MILK, FAT, PRO, FAT% and PRO%),  $Rys_i$  was fixed effect of region by year of birth by season of calving,  $H(Rys)_{j(i)}$  was the fixed effect of herd within  $Rys_i$ ,  $b$  was linear regression coefficients of Age of first calving,  $AFC_k$  was continuous variable representing age of animal at calving,  $A_l$  was a random animal genetic effect and  $e_{ijkl}$  was a random error term.

Models for reproductive traits were consisting of two models. The first one is belonging to DFS, GL and CI and the second one is belonging to DO.

$$y_{ijklm} = \mu + Rys_i + H(Rys)_{j(i)} + ApMp_k + A_l + PE_l + e_{ijklm} \quad (2)$$

where  $Y$  denoted CI, DFS, or GL,  $Rys_i$  was fixed effect of region by year of birth by season of

birth,  $H(Rys)_{j(i)}$  was the fixed effect of herd within RYS,  $ApMp_k$  was the fixed effect of age at previous calving by month of previous calving by parity,  $A_i$  was a random animal genetic effect,  $PE_i$  was a random permanent environmental effect and  $e_{ijklm}$  was a random error term.

$$y_{ijklm} = \mu + Rys_i + H(Rys)_{j(i)} + ApMf_k + A_i + PE_i + e_{ijklm} \quad (3)$$

where  $Y$  denoted  $DO$ ,  $Rys_i$  was fixed effect of region by year of birth by season of birth,  $H(Rys)_{j(i)}$  was the fixed effect of herd within RYS,  $ApMf_k$  was the fixed effect of age at previous calving by month of first insemination by parity,  $A_i$  was a random animal genetic effect,  $PE_i$  was a random permanent environmental effect and  $e_{ijklm}$  was a random error term.

Variance and covariance components were estimated by restricted maximum likelihood method using MATVEC program (Wang *et al.* 2001) and DFREML program (Meyer 1997) respectively. In addition, it should mention that the heritabilities of production traits are calculated by using MATVEC program based on univariate analyses and the heritabilities of fertility traits are calculated by using DFREML program based on repeatability analyses for parities up to 8th parities. Bivariate analyses were performed to obtain estimates for genetic and environmental correlations between production and fertility traits. Convergence criterion was defined as the error sum of squares between successive iterations and was set to 10-6.

## Results and discussion

### Production traits heritability estimation

Heritability of MILK, FAT, FAT%, PRO and PRO% are shown in Table 2. Heritability of production traits were moderate and ranged from 0.149 (FAT) to 0.26 (MILK). Among yield traits, the heritabilities of fat percent and protein percent were similar (0.228), but these heritabilities of percentage traits were in disagreement with most studies (DeJager & Kennedy 1987, Meinert *et al.* 1989, Van der Werf & deBoer 1989) and lower than these studies. Misztal *et al.* (1992) obtained much higher heritability estimates than those in the present study of 0.26, 0.149, and 0.238, respectively, for yields of milk, fat, and protein. The high estimates were thought to have been due to use of only registered cows or inclusion of genetic levels of unknown parents in the analysis. Visscher & Thompson (1992), with British cows, also reported higher heritability estimates for yields of milk and fat of 0.39 and 0.36, respectively. The heritability estimates for yield traits (Table 2) are slightly lower than those in the current literature (Miglior *et al.* 1995, Short & Lawlor 1992), possibly as a result of comparatively higher phenotypic variance.

Table 2

Additive genetic variances, residual variances, heritability, genetic correlation (above diagonal) environmental correlation (below diagonal) among production traits were calculated.

	Additive genetic variance	Residual variance	Heritability $\pm$ SE	MILK	FAT	FAT, %	PRO	PRO, %
MILK	291 728	827 485	0.26 $\pm$ 0.044		0.81	0.006	0.70	-0.505
FAT	153.2	874.4	0.149 $\pm$ 0.073	0.44		0.20	0.705	-0.0715
FAT%	0.0304	0.1062	0.228 $\pm$ 0.078	-0.39	0.30		-0.36	0.16
PRO	230.52	735.115	0.238 $\pm$ 0.078	0.76	0.68	-0.24		-0.11
PRO%	0.008	0.0267	0.228 $\pm$ 0.0006	-0.203	-0.10	0.13	-0.10	

MILK: 305-days milk yield, FAT: fat yield, PRO: protein yield, FAT%: milk fat percent, PRO%: milk protein percent

*Reproductive traits heritability estimation*

Table 3 provides a summary of variance components, ratios with respect to phenotypic variance for permanent environmental factors, heritability and repeatability for fertility traits. Heritability of reproductive traits in this study was low.

Table 3

Phenotypic variance, ratios with respect to phenotypic variance for permanent environmental factors, heritability, repeatability for fertility traits and estimates of genetic correlation (above diagonal) and environmental correlation (below diagonal) between fertility traits were calculated

	$\sigma_p^2$	$c^2$	$h^2 \pm SE$	$r$	CI	DFS	DO	GL
CI	3909.69	0.03	0.07 $\pm$ 0.013	0.09		0.0005	0.111	0.02
DFS	2921.38	0.02	0.04 $\pm$ 0.01	0.06	0.0001		0.0004	0.008
DO	4245.09	0.04	0.06 $\pm$ 0.008	0.10	0.0005	0.0002		0.008
GL	34.83	0.05	0.07 $\pm$ 0.002	0.12	0.0022	0.0012	0.003	

$\sigma_p^2$ : phenotypic variance,  $c^2$ : ratios with respect to phenotypic variance for permanent environmental factors,  $h^2$ : heritability,  $r$ : repeatability, CI: calving interval, DFS: days from calving to first insemination, DO: days open, GL: gestation length

Many researchers (Berger *et al.* 1981, Hansen *et al.* 1983) have reported heritabilities close to zero for reproductive traits and concluded that additive genetic variation is very small in proportion to phenotypic variation and that selection for improved fertility would not be worthwhile. Others (Janson & Andreasson 1981, Kragelund *et al.* 1979) have suggested that the deterioration of fertility may be possible to prevent through consideration of various indexes of fertility in selection decisions. Others (Berger *et al.* 1981, Hansen *et al.* 1983) have reported that heritabilities decrease as parity increases and that lactation length (60 to 305 days) increases with the measure of milk yield. Heritability of CI was low (0.07), which was consistent with previous estimates (Pryce *et al.* 1997, Veerkamp *et al.* 2001, Kadarmideen *et al.* 2003). This trait can be highly influenced by the length of the voluntary waiting period and if synchronization products have been used, which would inflate environmental variance. Estimated heritability for DO was small (0.06). Generally, heritability for DO is estimated to be  $\leq 0.09$  (Berger *et al.* 1981, Hansen *et al.* 1983); hence, these results are in good agreement with the previous literature despite the differences in data, models, and estimation procedures. The heritability for DFS in this research was estimated at 0.04 (Table 3) which was slightly higher than 3.01% obtained by Andersen-Ranberg *et al.* (2005) for Norwegian dairy cattle, and considerably lower than 6.1 and 5.8% reported by Weigel & Rekaya (2000) for Minnesota and California Holstein populations, respectively. The corresponding estimate by Roxström *et al.* (2001) was 3.37%. Other published heritability estimates for DFS range from 3.0 to 4.0% (Berger *et al.* 1981, Pryce *et al.* 1998, Wall *et al.* 2003). DFS is highly affected by the length of the voluntary waiting period, which differs among herds and among management groups within a herd. Nevertheless, selection for this trait would favour cows that demonstrate visible oestrus early in lactation. Repeatability estimates for fertility traits were low and ranged from 0.06 to 0.12. Low estimates of repeatability indicate that reproductive performance on any occasion is of little use in predicting later performance. The low repeatability estimates obtained in this study suggest that fertility traits are strongly influenced by temporary environmental factors. It is, perhaps, not surprising that repeatabilities of reproductive measures are low,

because all previously reported heritability estimates were low and because of the complex nature of reproductive traits, in particular, which are very much subject to decision policies of dairy producers with regard to when to rebreed a cow, difficulties in detection of oestrus, and various other managerial and nutritional factors.

#### *Genetic correlations between production traits*

The estimated of genetic (upper diagonal) and environmental correlations (lower diagonal) between production traits are shown in Table 2. Genetic Correlations among yield traits were high and positive. Genetic correlations were largest between MILK and FAT (0.81), followed by correlations for MILK and PRO (0.70). Estimates between pairs of yield traits in this study are slightly smaller or higher than other studies (DeJager & Kennedy 1987, Meinert *et al.* 1989), but all of these genetic correlations were high and positive. However, estimates from different studies are not directly comparable, mainly because of differences in data sets, models, and the number of traits analysed. Genetic correlations of FAT% with FAT and with PRO% were 0.20 and -0.071 respectively, and were smaller than those found by DeJager & Kennedy (1987) and Meinert *et al.* (1989). Van der Werf and de Boer (1989) reported a smaller genetic correlation for Pro and FAT%, but the correlation for MILK and Pro% was similar to the one found in this study. Genetic and environmental correlations between PRO% and PRO were slightly similar (-0.11, -0.10 respectively). Genetic correlations between PRO% and FAT were also low (-0.071).

#### *Genetic correlations between reproductive performance traits*

Table 3 shows genetic and environmental correlations among fertility traits. Estimated genetic correlations between reproductive performance traits were variable and lower (range =0.0005 to 0.111), indicating that cow fertilities seem to be genetically independent. Janson (1980) and Distl (1982) found high genetic correlations between heifer and cow fertility. In other studies, low or zero correlations have been reported (Hansen *et al.* 1983, Raheja *et al.* 1989). Most reproductive performance traits are mainly influenced by management practices and other environmental factors, but recent work suggests that there is significant genetic variation in measures of female fertility (Weigel & Rekaya 2000). Normally cause and effect may not be deduced from estimates of correlation, but these relationships may justify the inference that increased yield may be favourably related to improved fertility as heifer results suggest, but stress of increased yield may cause deterioration of genetic potential for improved fertility. Parturition and lactation could certainly influence the fertility level of first calf heifers. In addition, housing and management conditions may be different for heifers and cows. All these factors would cause correlations to be small. In general, these results disagree with strong genetic correlations estimated by other researchers. Recent studies, such as those of Kadarmideen *et al.* (2003) and Veerkamp *et al.* (2001) reported strong (positive and negative) correlations, ranging from  $\pm 0.70$  to  $\pm 0.98$  for fertility traits (except for DFS, which were moderate). In view of these results, DFS demonstrated as an indicator of the time that a cow needs to get ready to be inseminated. The last traits are composite measures of time to first insemination, such as CI and DO. CI and DO cannot distinguish between infertility due to a delay in reproductive performance or due to low success rate of AI events. Moreover, these traits are influenced by management practices and voluntary extension of lactations.

*Genetic correlations between reproductive performance and production traits*

Table 4 contains the genetic and environmental correlations between reproductive performance and production traits. Controversy has long existed over how or if reproductive performance is affected by milk yield. Milk production and reproductive performance are major factors affecting profitability of a dairy herd. Inadequate herd reproductive performance, manifested in prolonged calving intervals, increased forced culling, or both, can result in less milk and fewer calves per cow per year, less directional culling and therefore increased replacement cost, and, ultimately, lower net returns. Genetic antagonism of high milk production and measures of reproduction have been reported (Berger *et al.* 1981, Janson & Andreasson 1981, Pryce *et al.* 1998, Dematawewa & Berger 1998, Kadarmideen *et al.* 2000, Pryce & Veerkamp 2001).

Table 4

Estimates of genetic and environmental correlation between production and reproductive traits

Genetic correlation	MILK	FAT	FAT, %	PRO	PRO, %
CI	0.593	0.556	-0.19	0.96	-0.002
DO	0.355	0.62	0.385	-0.513	0.741
DFS	0.022	0.70	0.02	0.95	-0.003
GL	-0.24	-0.18	0.068	-0.168	0.21
Environmental correlation					
CI	0.011	0.041	0.25	-0.07	-0.003
DO	0.054	0.04	0.01	0.21	-0.003
DFS	0.045	0.002	0.009	-0.037	-0.01
GL	0.007	0.021	0.022	-0.022	-0.042

MILK: 305-days milk yield, FAT: fat yield, PRO: protein yield, FAT%: milk fat percent, PRO%: milk protein percent, CI: calving interval, DFS: days from calving to first insemination, DO: days open, GL: gestation length

Estimated genetic correlations between reproductive performance and MILK ranged from -0.24 to 0.593 (Table 4). The correlation of MILK with CI was strongly unfavourable (0.593), suggesting that increased milk production is associated with longer CI. Increasing the distance between two calving intervals can lead to reduce the number of calves born during the economic period of cows in the herds. Similar genetic correlations have been reported between CI and MILK in the literature, ranging from 0.23 to 0.67 (Veerkamp *et al.* 2001, Kadarmideen *et al.* 2003). Genetic correlation estimates between MILK and DO were unfavourable (0.355), with higher yield being associated with increased days to successful conception. Considering the positive relationship between MILK and CI, it seems that the increased DO is the main reason of increasing CI. Whereas genetic correlations between MILK and DFS were not significantly different from zero (0.022) which meaning days to the first services in higher milk yield cows are depending on environmental management. The genetic correlation existed between MILK and GL (-0.24) indicated that a shorter GL was associated with greater MILK in first lactation. Perhaps, herd management for both production and reproduction is of higher quality and is more consistent among cows in the higher producing herds.

Estimated genetic correlations between reproductive performance and FAT were different in magnitude and in sign. The estimated genetic correlation between CI and FAT was strong (0.556) and indicated that possibly heifers or dairy cows that were longer CI would seem to be more amounts of fat yield. Fat yield in first lactation was positively genetically correlated



with DO (0.62) and with DFS (0.70). These results have the same conclusion of the relationship between CI and FAT. However, the estimated genetic relationship between FAT and GL was moderately negative ( $-0.18$ ). This result suggested that the shorter into gestation length, the more production of fat yield in the first lactation.

Estimated genetic correlations between reproductive performance and FAT% were different in magnitude and in sign. The genetic correlation between CI and FAT% was estimated to be  $-0.19$ . Longer CI is generally viewed as undesirable; therefore, genetically a favourable relationship existed between CI and FAT% in first lactation. This correlation shows that a shorter CI was associated with greater FAT% in first lactation. The genetic correlation existed between FAT% and DO (0.385) and indicated that a longer DO was associated with greater FAT% in first lactation. However, FAT% in first lactation was not significantly different from zero genetically correlated with DFS (0.02) and with GL (0.068).

Estimated genetic correlations between reproductive performance and PRO were different in magnitude and in sign. The largest genetic correlation between reproductive performance and production traits is belonging to CI and PRO (0.96). This result demonstrates that focusing on protein yield lead to increasing the calving interval, which causes increased insemination and veterinary costs, higher culling rates, and thus increased replacement costs. A negative estimated genetic correlation was shown between DO and PRO in first lactation ( $-0.513$ ). Possibly, first-lactation cows that were emphasis to have more protein yields would seem to be shorter days open. According to the genetic correlations between reproductive traits in this study that showed DO and CI have no genetic relationship between together, the genetic correlation between CI and PRO have more efficiency than genetic correlation between DO and PRO. A genetic correlation of 0.95 (Table 4) was found between DFS and PRO. This is more highly than other studies reporting genetic correlations of 0.3 to 0.5 between the interval from calving to first insemination and protein yield (Pryce *et al.* 1998, Kadarmideen *et al.* 2000, Roxström *et al.* 2001). The correlation between DFS and PRO may be influenced by individual farmer decisions if high-yielding cows are inseminated later than cows with low or moderate yields. The estimated genetic correlation between GL and PRO was negatively moderate ( $-0.16$ ). This result indicated that by increasing protein yield in the genetic program solely, the gestation length occurred sooner. Consequently, shorter gestation length causes more calf per cows' lifetime.

Estimated genetic correlations between reproductive performance and Pro% were different in magnitude and in sign. genetic correlations between (CI and PRO%) and (DFS and PRO%) were not significantly different from zero ( $-0.002$  and  $-0.003$  respectively) which meaning days to the first services and calving intervals in cows which have produce more protein percent have controlled by environmental management because these traits have not a significant genetic correlation. Milk protein percent was positively genetically correlated with DFS (0.741) and with GL (0.21). Therefore, selecting cows in the first lactation that have more milk protein percent could increase DFS and GL in later lactations.

In conclusion, milk yield and reproductive performance play major roles in determining the profitability of a dairy herd. This study demonstrates the relationship of genetic variation for production traits and fertility traits in the Iranian dairy cattle population. This research indicates an undesirable relationship between production and fertility traits. However, fertility trait, particularly GL, had negatively genetic correlation with MILK, FAT and PRO that shows selecting for MILK, FAT and PRO would decrease GL. Selection for production traits

seems to have merit for genetically improving reproductive performance. Selection for an increase in production under one management system may lead to more health risks than under other management systems. Thus, management and genetic policy must integrate to develop an effective program for improvement of fertility.

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