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GENETIC RELATIONSHIPS AMONG LINEAR TYPE TRAITS AND MILK PRODUCTION TRAITS OF HOLSTEIN DAIRY CATTLE

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Abstract

The aim of this study was to estimate genetic relationships among milk production and linear type traits of Holstein dairy cattle from seven herds in Isfahan province of Iran. Phenotypic data was collected from 2004 to 2012 and included milk yield (MY), fat yield (FY) and protein yield (PY) for first three lactations, six body traits (stature, ST; chest width, CW; body depth, BD; angularity, AN; rump angle, RA; rump width, RW), three feet and legs traits (rear legs side view, RLSV; rear legs rear view, RLRV; foot angle, FA) and eight udder traits (fore udder attachment, FUA; rear udder height, RUH; rear udder width, RUW; central ligament, CL; udder depth, UD; fore teat placement, FTP; rear teat placement, RTP; teat length, TL). The number of animals for each linear type trait was 3505. Multi-trait animal models were used to estimate the (co)variance components based on restricted maximum likelihood method (REML) using WOMBAT software. Heritability estimates of first, second and third lactations for MY were 0.28, 0.41 and 0.36; for FY were 0.22, 0.23 and 0.36 and for PY were 0.31, 0.33 and 0.25, respectively. The heritability estimates ranged from 0.17±0.04 to 0.24±0.04 for body traits, 0.06±0.03 to 0.15±0.04 for feet and leg traits and from 0.12±0.04 to 0.25±0.05 for udder traits. Genetic correlations among the recorded type traits ranged from –0.76±0.01 (between AN and RLRV) to 0.65±0.02 (between AN and RW). The low to moderate positive genetic correlations between AN and FUA with milk production traits indicate that cows with high AN and good FUA have higher milk, fat and protein yields. The results of this study indicated that considerable genetic variation exists for different type traits within this sample of the Iranian Holstein population and additive genetic variability of type traits can provide moderate genetic gains through selection.

Key words: dairy cattle, genetic parameters, production traits, type traits

The breeding goal in dairy cattle is to increase lifetime profit per animal. Profit is a function of production and the time that a cow remains in herd. Thus, profit can only be recorded when a cow is culled, and breeding value of more profitable ani-

mals should be able to be predicted by indexes from measurements at an early age of the cow (Pérez-Cabal and Alenda, 2002).

In the past, the most dairy cattle breeding objectives around the world have focused exclusively on production traits. Selection only on yield traits could decrease merit for traits with antagonistic genetic correlations with yield. There is a general consensus that only genetic selection toward increased milk production has reduced the genetic merit for health (Pryce et al., 1998) and fertility (Berry et al., 2003). Several studies have shown that the emphasis of selection for increasing milk production may result in a decrease in the merit of some type traits and influence the health of cows. Therefore, productive life decreases because of udder, reproductive, structural and locomotive disorders (Campos et al., 2012; Pérez-Cabal et al., 2006). Recently, type traits have been associated with production traits; and via selection indexes, they have been used as selection criteria in various countries (Miglior et al., 2005). Like production traits, type traits are an important component of breeding and have definitive importance for breeders in selection of sires (Costa et al., 2005). The most of type traits revealed moderate heritability estimates (Meyer et al., 1987) and can often be recorded in a single scoring, which makes them reliable and relatively inexpensive traits that can be included in selection indices for overall merit (Wiggans et al., 2004). Various studies have been conducted to quantify the importance and the impact of type traits on production traits in dairy cattle (Larroque and Ducrocq, 2001). Therefore, knowing the estimates of (co)variances of type traits is important for the implementation of selection programs. There is a potential to improve type traits of Holstein cattle under Iranian herd environments by selection. Therefore, the objective of this study was to estimate the genetic parameters of type traits in Holstein dairy cattle and relationship among type traits and milk production traits using multi-trait animal model.

Material and methods

The data originated from seven herds of Holstein dairy cows in Esfahan province of Iran and was collected from 2003 to 2012. The data set included milk yield (MY), fat yield (FY) and protein yield (PY) for the first three lactations, six body traits (stature (ST), chest width (CW), body depth (BD), angularity (AN), rump angle (RA), rump width (RW)), three feet and legs traits (Rear legs side view (RLSV), rear legs rear view (RLRV), foot angle (FA) and eight udder traits (fore udder attachment (FUA), rear udder height (RUH), rear udder width (RUW), central ligament (CL), udder depth (UD), fore teat placement (FTP), rear teat placement (RTP), teat length (TL). Based on visual assessment of the morphology of cows, the phenotypic data of linear type traits was classified on a scale of 1–9. All classifications were carried out by the Arian Delta Gene Company classifiers once during the first lactation; and each herd was classified by only one classifier. MY, FY and PY had been standardized for twice-daily milking and 305-d lactation length (Sheikhloo et al., 2009).

We selected common sires that had progeny in more than three herds to create genetic connectedness among herds (Bohlouli et al., 2013). Finally, each sire had at last 10 daughters in data file. Age at calving was from 18 to 30 months for the first lactation; from 32 to 44 months for the second lactation and from 45 to 56 months for the third lactation.

Table 1. Characteristics of pedigree used in computations

No. of total animals pedigree	4219
No. of animals with progeny	3117
No. of animals without progeny	1048
No. of animals with known parent	774
No. of sires with progeny	779
No. of dams with progeny	4219

Table 2. Descriptive statistics of data set for milk production traits

Parameter	First lactation	Second lactation	Third lactation	Total
Milk yield (305-d)				
no. of records	2423	2317	1539	6279
means (kg)	10280.0	11586.70	11965.80	
SD	1570.18	1993.69	1908.92	
minimum	4614.92	4251.07	4564.66	
maximum	15414.0	17370.60	17371.40	
Fat yield (305-d)				
no. of records	2420	2315	1539	6274
means (kg)	356.55	415.77	440.07	
SD	73.83	91.90	91.10	
minimum	22.42	49.97	46.21	
maximum	537.88	675.15	607.19	
Protein yield (305-d)				
no. of records	2142	1773	1309	5224
means (kg)	303.09	357.72	401.85	
SD	62.82	74.47	74.97	
minimum	39.21	95.29	109.47	
maximum	502.96	501.81	480.26	

After applying restrictions, the data file included 2423, 2420 and 2142 records of the first lactation, 2317, 2315 and 1773 records of second lactation and 1539, 1539 and 1309 records of third lactation for milk, fat and protein yields, respectively. For type traits, the data set included 3505 cows of 269 sires and pedigree included 4219 animals. Pedigree and the data are summarized in Tables 1 and 2, respectively. The choice of fixed effects to be considered was made after testing whether the effects were statistically significant with GLM procedure of SAS (Statistical Analysis System, 2003). For type traits, the fixed effects were herd (7 herds), age at recording (17 to 31 months, 15 classes) and year of recording (10 classes). For milk production

traits in the first three lactations, the fixed effects were herd (7 herds), age at calving (13, 13 and 12 classes, respectively for first, second and third lactations) and year–season at calving (40 classes).

Table 3. Descriptive statistics of data set for type traits

Type traits		Score		Optimum	Mean	SD
		1	9			
Body						
stature	ST	short	tall	9	6.18	1.54
chest width	CW	narrow	wide	9	4.46	2.36
body depth	BD	shallow	deep	7	7.27	1.25
angularity	AN	coarse	angular	9	6.24	1.57
rump angle	RA	high pins	low pins	5	4.04	2.00
rump width	RW	narrow	wide	9	4.76	1.93
Feet and Legs						
rear legs side view	RLSV	straight	sickle	5	5.20	1.18
rear legs rear view	RLRV	toe-out	parallel	9	4.76	2.52
foot angle	FA	low	steep	7	4.42	1.61
Udder						
fore udder attachment	FUA	loose	tight	9	4.51	2.79
rear udder height	RUH	low	high	9	4.87	2.39
rear udder width	RUW	narrow	wide	9	4.94	2.38
central ligament	CL	weak	strong	9	4.98	2.25
udder depth	UD	below	shallow	5	5.30	1.56
fore teat placement	FTP	outside of quarter	inside of quarter	5	3.58	1.76
rear teat placement	RTP	outside of quarter	inside of quarter	5	5.67	2.20
teat length	TL	short	long	5	5.20	1.35

Descriptive statistics of milk production traits and type traits are summarized in Tables 2 and 3, respectively. In notation matrix, the following multi-trait animal model was used to estimate variance components:

$$\begin{bmatrix} y_1 \\ \vdots \\ y_{20} \end{bmatrix} = \begin{bmatrix} X_1 & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & X_{20} \end{bmatrix} \begin{bmatrix} b_1 \\ \vdots \\ b_{20} \end{bmatrix} + \begin{bmatrix} Z_1 & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & Z_{20} \end{bmatrix} \begin{bmatrix} a_1 \\ \vdots \\ a_{20} \end{bmatrix} + \begin{bmatrix} e_1 \\ \vdots \\ e_{20} \end{bmatrix}$$

where y_i is observation for i^{th} trait (i=1 to 17 for type traits and 18 to 20 for milk production traits of first lactation), b is the a vector of fixed effects, a is the vector of additive genetic effects for i^{th} trait, e is the vector of random residual effects and X, and Z are incidence matrices relating the observations to the fixed and random effects, respectively.

Same model was used to estimate the genetic parameters of milk production traits for the first three lactations (i=1 to 9 for three traits in the first three lactations).

The following (co)variance structure was assumed for random effects of model:

$$Var \begin{bmatrix} a_1 \\ \vdots \\ a_{20} \\ e_1 \\ \vdots \\ e_{20} \end{bmatrix} = \begin{bmatrix} g_{1,1}A & \cdots & g_{1,20}A & 0 & \cdots & 0 \\ \vdots & \ddots & \vdots & \vdots & \ddots & \vdots \\ g_{20,1}A & \cdots & g_{20,20}A & 0 & \cdots & 0 \\ 0 & \cdots & 0 & r_{1,1}I & \cdots & r_{1,20}I \\ \vdots & \ddots & \vdots & \vdots & \ddots & \vdots \\ 0 & \cdots & 0 & r_{20,1}I & \cdots & r_{20,20}I \end{bmatrix}$$

where $g_{i,i}$ is the additive genetic variance for the direct genetic effect of ith trait (i=1 to 20); $g_{i,j}$ ($i \neq j$) is the additive genetic covariance between i^{th} and j^{th} traits; $r_{i,i}$ is the residual variance for i^{th} trait; $g_{i,j}$ ($i \neq j$) is the residual covariance between i^{th} and j^{th} traits. *A* is the additive genetic relationship matrix and I is an identity matrix for the residual. Heritability estimate for each trait (h^2) was calculated as:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$$

where σ_a^2 and σ_e^2 are additive genetic and residual variances, respectively. Additive genetic correlation between i^{th} and j^{th} trait ($r_{g(i,j)}$) was calculated as:

$$r_{g(i,j)} = \frac{Cov_{g(i,j)}}{\sqrt{Var_{g(i,i)} \times Var_{g(j,j)}}}$$

where $Cov_{g(i,j)}$, is genetic covariance between i^{th} and j^{th} trait; $Var_{g(i,i)}$ and $Var_{g(i,j)}$ are additive genetic variance for i^{th} and j^{th} trait, respectively. The variance components and standard error were estimated using REML method by WOMBAT software (Meyer, 2007).

Results

In the third lactation, average yields of MY, FY and PY (11965.80 kg, 440.07 kg and 401.85 kg, respectively) were higher than the other lactation productions. Phenotypic, genetic and residual variances and heritability estimates for milk production traits (the first three lactations) and for 17 type traits are shown in Table 4 and Table 5, respectively. Generally, estimated variances increased from the first to the third

lactation for all traits. Estimated heritability for MY was the lowest in the first lactation period (0.28) and was the highest in the second lactation (0.41); whereas for FY, the highest heritability was 0.36 in the third lactation; and for PY was 0.33 in the second lactation.

The heritability estimates for body traits varied from 0.17 for RW to 0.24 for RA. Heritability estimates for foot and leg traits were 0.06, 0.15 and 0.15 for RLRV, RLSV and FA, respectively; and for udder traits ranged from 0.12 (RUW) to 0.25 (FUA and RTP).

Table 4. Phenotypic (σ_P^2), genetic (σ_a^2) and residual (σ_e^2) variances and heritability (h²) for milk production traits

Lactation	Trait	σ_P^2 ±SE	σ_a^2 ±SE	σ_e^2 ±SE	h²±SE
First	MY	2178271.43±377842.60	610140.00±114325.30	1568131.43±316337.24	0.28±0.05
	FY	10585.45±1361.31	2326.60±321.36	8258.85±683.57	0.22±0.03
	PY	4727.42±682.81	1474.80±254.30	3252.62±671.36	0.31±0.07
Second	MY	3555446.34±715661.82	1457200.00±393431.27	2098246.34±463442.50	0.41±0.09
	FY	14498.26±1534.36	3341.50±760.87	11156.76±1542.24	0.23±0.04
	PY	4838.48±682.55	1593.40±297.08	3245.08±891.65	0.33±0.07
Third	MY	6821257.14±1020380.50	2387300.00±414321.65	4433957.14±705945.62	0.35±0.06
	FY	14618.61±1698.94	5269.90±1688.28	9348.71±2156.48	0.36±0.03
	PY	14702.40±3284.60	3683.10±728.90	11019.30±2769.33	0.25±0.02

Table 5. Phenotypic (σ_P^2), genetic (σ_P^2) and residual (σ_e^2) variances and heritability (h²) for type traits

Type traits	σ_P^2 ±SE	σ_a^2 ±SE	σ_e^2 ±SE	h²±SE
Body				
ST	1.94±0.05	0.45±0.07	1.49±0.07	0.23±0.04
CW	2.28±0.06	0.49±0.10	1.78±0.09	0.22±0.04
BD	1.46±0.04	0.26±0.06	1.21±0.06	0.18±0.04
AN	2.00±0.05	0.37±0.09	1.63±0.08	0.18±0.04
RA	1.92±0.05	0.54±0.09	1.47±0.09	0.24±0.05
RW	3.28±0.08	0.55±0.13	2.73±0.13	0.17±0.04
Feet and Legs				
RLSV	0.55±0.14	0.08±0.02	0.46±0.02	0.15±0.04
RLRV	3.88±0.21	0.24±0.12	3.63±0.14	0.06±0.03
FA	2.26±0.21	0.35±0.09	1.91±0.09	0.15±0.04
Udder				
FUA	5.21±0.21	1.28±0.25	3.93±0.23	0.25±0.05
RUH	5.37±0.13	0.86±0.21	4.51±0.21	0.16±0.04
RUW	5.25±0.13	0.62±0.19	4.63±0.20	0.12±0.04
CL	3.88±0.10	0.53±0.15	3.35±0.15	0.14±0.04
UD	1.32±0.03	0.30±0.06	1.02±0.06	0.23±0.04
FTP	2.95±0.07	0.65±0.13	2.30±0.12	0.22±0.04
RTP	4.27±0.01	1.07±0.21	3.21±0.16	0.25±0.05
TL	1.54±0.04	0.34±0.07	1.21±0.07	0.22±0.04

Table 6. Genetic (above diagonal) and phenotypic (below diagonal) correlations (±SE) among milk production traits of the first three lactations

Lactation	trait	First			Second			Third		
		MY	FY	PY	MY	FY	PY	MY	FY	PY
First	MY		0.34±0.11	0.25±0.19	0.7±0.13	0.22±0.14	0.25±0.10	0.27±0.09	0.18±0.08	0.16±0.11
	FY	0.48±0.03		0.88±0.12	0.32±0.09	0.21±0.12	0.19±0.15	0.22±0.12	0.20±0.14	0.14±0.15
	PY	0.54±0.04	0.86±0.01		0.20±0.07	0.19±0.11	0.24±0.14	0.28±0.16	0.16±0.05	0.28±0.20
Second	MY	0.50±0.08	0.25±0.05	0.24±0.01		0.42±0.09	0.46±0.19	0.35±0.15	0.17±0.10	0.14±0.09
	FY	0.24±0.01	0.11±0.07	0.06±0.08	0.57±0.04		0.93±0.04	0.17±0.10	0.26±0.09	0.22±0.07
	PY	0.28±0.09	0.10±0.01	0.11±0.07	0.62±0.04	0.88±0.05		0.14±0.11	0.12±0.10	0.53±0.17
Third	MY	0.43±0.08	0.27±0.05	0.30±0.05	0.46±0.01	0.22±0.01	0.26±0.04		0.67±0.25	0.71±0.21
	FY	0.29±0.08	0.18±0.07	0.13±0.04	0.30±0.01	0.21±0.04	0.18±0.03	0.58±0.08		0.77±0.27
	PY	0.28±0.04	0.13±0.04	0.20±0.07	0.33±0.04	0.16±0.07	0.21±0.08	0.62±0.04	0.68±0.06	

Table 7. Genetic (above diagonal) and phenotypic correlations (below diagonal) among type traits

No	Type trait	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	ST		0.05	−0.02	0.10	−0.10	0.26	−0.05	0.19	0.16	0.18	0.10	0.08	0.08	0.09	0.12	0.11	0.14
2	CW	−0.01		0.45	−0.03	−0.15	0.41	−0.55	0.17	0.04	0.34	0.15	−0.06	0.09	0.11	0.11	0.05	0.12
3	BD	0.06	0.35		0.63	−0.07	0.27	−0.05	−0.15	0.11	0.36	0.15	0.15	0.11	0.23	−0.05	−0.08	0.08
4	AN	0.06	−0.11	0.16		−0.09	0.65	0.07	−0.76	−0.15	0.49	0.21	−0.15	0.21	−0.05	0.09	−0.06	0.09
5	RA	0.06	−0.12	−0.10	−0.09		−0.04	0.05	−0.13	−0.12	−0.40	0.05	0.17	0.14	−0.12	−0.18	0.09	0.21
6	RW	0.29	−0.21	−0.06	0.10	0.06		0.43	−0.38	−0.31	−0.23	0.08	0.06	0.06	0.17	0.14	0.11	−0.09
7	RLSV	0.00	−0.12	0.04	0.03	0.06	0.04		−0.11	−0.62	−0.44	0.05	−0.10	0.02	0.12	−0.07	0.12	−0.07
8	RLRV	0.04	0.14	0.06	0.01	−0.07	0.01	−0.23		0.41	−0.25	0.05	−0.15	−0.02	0.23	−0.07	0.18	0.11
9	FA	0.03	0.08	0.01	−0.05	0.02	−0.03	−0.16	0.13		0.39	0.06	−0.05	0.09	0.14	0.14	0.16	0.08
10	FUA	0.05	0.03	−0.05	0.13	−0.08	−0.08	−0.11	−0.02	0.08		0.18	0.08	0.07	0.03	0.15	−0.08	0.09
11	RUH	0.04	0.06	−0.03	0.12	0.12	−0.05	0.08	0.02	−0.13	0.08		0.34	0.21	0.33	0.29	0.30	0.23
12	RUWH	0.03	0.03	0.05	0.14	−0.23	0.06	−0.14	−0.08	0.12	−0.01	0.11		−0.16	0.14	0.13	−0.13	0.10
13	CL	0.08	0.07	0.07	−0.07	0.25	0.05	−0.11	0.14	−0.08	−0.06	−0.04	−0.02		−0.09	0.03	0.31	0.41
14	UD	−0.04	0.07	0.02	0.08	0.20	0.13	0.08	0.21	0.09	0.00	0.01	−0.05	0.23		0.47	−0.04	−0.34
15	FTP	−0.08	0.01	0.06	0.12	0.14	0.04	0.08	−0.05	0.09	0.09	−0.04	−0.06	0.19	0.23		0.60	0.04
16	RTP	0.03	0.02	0.04	−0.06	0.06	−0.09	−0.06	−0.06	−0.07	0.11	−0.02	0.08	0.13	0.02	0.06		0.25
17	TL	0.11	0.03	0.07	−0.08	0.24	0.11	0.09	0.09	0.08	−0.03	0.01	0.05	0.37	0.14	0.05	−0.02	

Standard errors for parameters were in the range from 0.01 to 0.19.

The genetic and phenotypic correlations among the milk production traits are shown in Table 6. All genetic and phenotypic correlations among milk production traits for different lactations were positive.

Among all traits, Genetic correlations between the first and the second lactations ranged from 0.19 to 0.76 and between the first and the third lactations ranged from 0.14 to 0.28. For the first lactation, genetic correlations between MY and FY, between MY and PY and between FY and PY were 0.34, 0.25 and 0.88, respectively; and phenotypic correlations were 0.48, 0.54 and 0.86, respectively. Genetic correlations among production traits within lactations were high; and within lactation, genetic correlations obtained between FY and PY were the largest among all genetic correlation estimates. Genetic correlations obtained between second lactation for FY and PY (0.93) were the largest among all genetic correlation estimates.

Genetic and phenotypic correlations among type traits are shown in Table 7. There are low genetic and phenotypic correlations among several type traits. Generally, phenotypic correlations among the type traits were lower than the genetic correlations. The highest negative phenotypic correlation was observed between RLSV and RLRV (–0.23), while phenotypic correlation between RTP and TL was positive (0.61).

The highest phenotypic correlation for body traits and feet and legs traits was estimated between CW and RLRV (0.14), and for body and udder traits was estimated between CL and RA (0.25). Genetic correlations ranged from –0.76 (between AN and RLRV) to 0.65 (between AN and RW).

Table 8. Phenotypic and genetic correlations (±SE) among milk production traits of the first lactation and type traits

Genetic			Phenotypic			Correlation trait
PY	FY	MY	PY	FY	MY	
0.16±0.08	0.15±0.07	0.10±0.11	0.13±0.02	0.01±0.02	0.10±0.02	ST
0.12±0.14	0.10±0.19	0.12±0.09	0.02±0.02	0.08±0.02	0.13±0.02	CW
0.18±0.19	0.15±0.10	0.14±0.17	0.15±0.02	0.16±0.02	0.10±0.02	BD
0.21±0.17	0.19±0.14	0.26±0.08	0.14±0.02	0.13±0.02	0.10±0.02	AN
0.09±0.13	0.13±0.19	0.08±0.14	0.03±0.03	0.13±0.02	0.01±0.02	RA
0.10±0.14	0.09±0.07	0.05±0.12	0.07±0.02	0.07±0.02	0.05±0.02	RW
0.11±0.11	0.07±0.11	0.06±0.09	0.07±0.02	0.07±0.01	0.06±0.02	RLSV
–0.02±0.12	–0.05±0.15	0.04±0.09	0.02±0.02	–0.05±0.02	0.01±0.02	RLRV
–0.06±0.10	–0.08±0.13	–0.06±0.11	0.04±0.01	0.08±0.03	–0.08±0.02	FA
0.12±0.05	0.15±0.08	0.11±0.14	0.10±0.02	0.15±0.02	0.07±0.02	FUA
0.09±0.08	0.08±0.04	0.08±0.05	0.08±0.02	0.11±0.02	0.11±0.02	RUH
0.09±0.07	0.08±0.07	0.04±0.14	0.09±0.03	0.06±0.02	–0.03±0.02	RUW
0.06±0.11	0.10±0.04	0.15±0.06	0.04±0.02	0.10±0.02	0.07±0.02	CL
0.14±0.10	0.12±0.03	0.12±0.09	0.10±0.02	0.09±0.02	0.04±0.02	UD
–0.05±0.14	–0.03±0.08	0.02±0.11	0.00±0.02	–0.03±0.03	–0.01±0.02	FTP
–0.03±0.07	0.05±0.14	0.03±0.08	0.01±0.02	0.11±0.02	0.03±0.02	RTP
0.07±0.14	0.07±0.15	0.06±0.12	–0.09±0.02	0.13±0.02	–0.04±0.02	TL

Genetic correlations of RW with ST, CW, BD and AN were medium to high and ranged from 0.26 to 0.65 (Table 7). But genetic correlation of RW and RA was close to null. The highest positive genetic correlation for body traits and feet and legs traits was obtained between RW and RLSV (0.43), and for body and udder traits was obtained between AN and FUA (0.49). Among udder traits, FTP and RTP have the highest positive genetic correlation (0.6).

Phenotypic and genetic correlations among milk production traits of the first lactation and type traits are shown in Table 8. The phenotypic correlations among MY and type traits ranged from –0.08 (FA) to 0.13 (CW); for FY ranged from –0.05 (RLRV) to 0.16 (BD) and for PY ranged from –0.09 (TL) to 0.15 (BD). The highest genetic correlations were estimated among AN and milk production traits and the lowest genetic correlations were estimated between FTP and MY (0.02), between FTP and FY (–0.03) and between RLRV and PY (–0.02). Weak correlations were estimated among udder related traits with MY, FY, and PY. Higher but still low genetic correlations were estimated between FUA and UD with MY, FY, and PY.

Discussion

Heritability
Milk production traits

In the current study, the heritability estimations of MY, FY, and PY were similar to those reported by Liu et al. (2014) and Sheikhloo et al. (2009). Although lower heritabilities were reported by DeGroot et al. (2002), similar estimations were reported in the most studies (Zavadilova et al., 2005; Muir et al., 2007). Heritability estimates for MY in the first three lactations (0.28, 0.41, and 0.35) were similar to the results reported in previously implemented studies on Iranian Holstein cows by Shadparvar and Yazdanshenas (2005), Bohlouli et al. (2013), Mohammadi and Alijani (2014) and Abdullahpour et al. (2013). Estimated heritabilities were higher in comparison with other studies in Tunisian Holsteins (Hammami et al., 2008) and in Polish black and white cattle (Strabel and Jamrozik, 2006). In addition, the heritability estimates were lower in comparison with the results of De Roos et al. (2004). Heritability estimates were reported to be 0.51, 0.49, and 0.47 for MY in the first three lactations by De Roos et al. (2004). These differences may be due to the difference of used models and/or studied cattle population. Heritabilities obtained from the milk production traits of one herd were significantly higher compared to estimated heritabilities of a great number of herds within several provinces (Abdullahpour et al., 2013). For this reason, in circumstances of high diversity of climates, environmental changes and feeding systems, the model might result in greater residual variance and therefore lower heritability (Abdullahpour et al., 2013; Bohlouli et al., 2013).

Type traits

The heritability estimates of type traits were within the range of most recent studies (Campos et al., 2012; Pérez-Cabal et al., 2006; Zink et al., 2011). Schaeffer et al. (1985) reported heritability estimates between 0.14 and 0.40 for linear type

traits. They found smaller heritabilities for udder traits than for non-udder traits. The heritability estimates for the type traits varied from 0.24 to 0.43 for UK and Irish data sets (Pérez-Cabal and Alenda, 2002) and these estimations were higher than this study reports.

The high heritability estimated for RA and low heritability for RLRV were similar to those described by Zink et al. (2011). In general, heritability estimates for feet and leg traits (0.06 to 0.15) were lower than other type traits. These estimates confirm those reported by Berry et al. (2004) and Zink et al. (2011). The heritability estimate for the udder-related type traits (0.12 to 0.25) agree with other estimates for udder type traits (Short et al., 1991; Berry et al., 2004). In the same study by Berry et al. (2003), the heritabilities for the udder-related type traits were from 0.13 to 0.33. The results indicated that some of traits showed high heritabilities and therefore would show greater responses to selection such as FUA and RTP; and also the heritability of ST and RA were medium (0.23 and 0.24, respectively) and would show medium responses to selection. Campos et al. (2012) reported that greater responses to selection can be achieved for ST and FTP in Holstein cows of Brazil.

For type traits, estimates of heritability can vary significantly according to breed, the classification system, statistical model definitions, number of records per animal and data editing procedures. So comparisons between studies should be done cautiously (Nemcova et al., 2011).

Genetic and phenotypic correlations
Among milk production traits
For same lactation, phenotypic correlations among milk production traits were the largest among all phenotypic correlations. These trends were similar to those observed in Tunisian (Hammami et al., 2008) and Iranian (Mohammadi and Alijani, 2014; Mohammadi et al., 2014) Holstein dairy cattle.

The largest genetic correlations occurred between the first and the second lactation, and the lowest were observed between the first and the third lactation. Similar correlations were estimated for the same traits in Holstein dairy cows by Hammami et al. (2008) and Jakobsen et al. (2002). With increasing distance between lactations, genes controlling milk productions vary different effects and genetic correlation between traits of two lactations decreased (Zavadilova et al., 2005; Hammami et al., 2008). Accordingly, genetic correlation between MY of the first lactation and FY of the third lactation was lowest (0.16).

Among type traits
The results of genetic and phenotypic correlations were similar to those observed in previously published studies (Bakhtiarizadeh and Moradi Shahrbabak, 2010; Berry et al., 2004; Nemcova et al., 2011). For some traits, the correlations were close to zero and assert that apparently no important correlation exists among those traits and were in agreement with those obtained by Pérez-Cabal and Alenda (2002). The moderate to high and positive values for genetic correlations between RW and ST (0.26), CW (0.41), BD (0.17) and AN (0.65) indicate that selection for rump width leads to a good genetic improvement in the mentioned traits (ST, CW, BD and AN). Similar results were found by Campos et al. (2012). High genetic correlation between rump

width and rear legs side view indicated that breeding programs could be successful without one of these traits. This point is possible for all traits that have moderate to high genetic correlations (Campos et al., 2012) such as for AN and FUA traits. For udder traits, low to moderate genetic correlations agree with other estimates for udder-related type traits (Short et al., 1991; Veerkamp and Brotherstone, 1997; Berry et al., 2004; Campos et al., 2012). Estimates among pairs of type traits in this study were slightly smaller than in some studies (e.g. Campos et al., 2012). The strong genetic (0.60) correlation between FTP and RTP indicates the possibility of reducing the number of udder traits assessed on each animal with the loss of very little information. This estimation is slightly stronger than previous reports (DeGroot et al., 2002; Berry et al., 2004). However, estimates from different studies are not directly comparable, mainly because of differences in data sets, models, and the number of traits analyzed.

Among milk production and type traits

The magnitude and direction of the phenotypic correlations among milk production and type traits in this study were similar to those reported in the other studies (Tapki and Ziya Guzey, 2013; Pahlevan and Moghimi Esfandabadi, 2010). The low to moderate positive genetic correlations among AN and milk production traits indicate that cows with high AN have higher milk and protein yield per lactation than those with lower AN. Other body traits (ST, CW, BD, RA and RW) showed low but positive correlations with milk production traits. In a study on Czech Holstein cows, genetic correlations among MY, FY, and PY with body traits were mostly close to zero; and moderate genetic correlations of those traits with AN were 0.32, 0.42, 0.34, respectively (Zink et al., 2014). For the Italian Brown Swiss cattle, Samore et al., (2010) also estimated moderate to low genetic correlations for angularity with MY, FY, and PY (0.36, 0.39, and 0.23, respectively).

Results of relationship among udder type traits and milk production traits were in agreement with previous reports (Campos et al., 2012; Zink et al., 2014). High--yielding cows have deeper udders (Norman et al., 1988). Generally, the genetic correlations showed that higher yielding cows were more AN, have relatively deeper body, deeper udders, good UD and good FUA.

Positive genetic correlations among milk production traits and the body type traits may reflect past emphasis on milk production traits simultaneously with increased cow AN, ST, CW, BD, RA and RW in Holstein breeding programs (Campos et al., 2012; Liu et al., 2014; Zink et al., 2014). Genetic correlations among the udder type traits and milk production traits indicate that genetic selection for increased milk production alone will result in cows with better FUA, RUH, RUW, CL and UD. These results are in agreement with those obtained by Berry et al. (2004). Although more studies reported positive genetic correlations among udder traits and milk production traits, negative genetic correlations were observed by Brotherstone (1994). Based on results of Berry et al. (2004), a combined selection objective including FUA and RA may be warranted to alleviate the deleterious effects of selection on milk production traits.

Lund et al. (1994) reported a positive genetic correlation between angularity and somatic cell count. In this study, due to the moderate correlation between angularity

and milk production (0.26), more angular cows with low body condition score may be indicative of cows in negative energy balance and may be under greater metabolic stress. This may have deleterious consequences for their immune system making them more susceptible to mammary infections (Berry et al., 2004). Berry et al. (2004) reported that less–angular cows with more body condition and lower pins had lower somatic cell count; and similarly, cows with tighter FUA and stronger udders with shorter, closer teats had lower SCC levels.

Finally, type traits have a direct influence on the management of cows (for example the quality or type of bed) and are related to the profitability of the herd. Although there are unfavorable genetic correlations between angularity and fertility traits (based on previous studies), with management improvements, improvement of milk production traits may be achieved through selection of cows with more angularity (Campos et al., 2012).

On the other hand, reproduction traits are usually unfavorably genetically correlated with milk production traits; and for fertility traits, due to low heritability, direct selection may be inefficient. An alternative way to improve fertility could be through selection for linear type traits that are favorably correlated with reproductive traits (Zink et al., 2011).

Conclusions

The results from this study indicate that the additive genetic variability of type traits can provide moderate genetic gains through selection. Genetic correlations among some type traits were strong and indicate the opportunity of reducing the number of traits in selection program. The results suggested that emphasis on selection for angularity and udder attachment (with management improvements) would bring benefits to improve milk production. However, there are low and unfavorable genetic relationships among some of type traits. The achieved results suggest that in addition to milk production traits, it may be feasible and economically desirable to include some of type traits in breeding goals of dairy cattle industry; and finally, genetic parameters estimated in this study can be used for genetic evaluation of dairy cattle in Iran; and future research needs to investigate the relationship between reproductive and linear type traits.

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