

Estimation of genetic parameters for udder type traits in the first lactation of Iranian dairy Holstein cattle

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Abstract

The objective of this study was to estimate genetic parameters of 8 udder type traits in the first lactation of Holstein dairy cows. The data set consisted of records of 2325 Holstein cows from 1998 to 2011. This data was obtained from Agricultural-Jihad Organization in Khorasan Razavi Province (Northeast of Iran). Traits, all scored on 1 to 9 point scale, were fore udder attachment, udder depth, suspensory ligament, teat length, front teat placement, rear teat position. Genetic parameters were estimated using univariate and bivariate analysis by Wombat software. The models included fixed effects of herd, year, season of calving and the random effect of animal. Heritability estimates obtained from univariate analysis were similar to those obtained from bivariate analysis. Heritability ranged from (0.03) to (0.32) for suspensory ligament and udder depth respectively. Genetic correlations among the udder type traits ranged from (-0.54) to (0.99) for (udder depth and teat length) and (suspensory ligament and udder depth) respectively. Corresponding phenotypic correlations for most pairs of traits were similar in direction but smaller in magnitude than the genetic correlations. Estimated parameters for udder type traits will be used to update the selection index of Holstein dairy cattle.

Keywords: Genetic correlations, Heritability, Iranian Holstein dairy cattle, Udder type traits

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Introduction

The concept of linear analysis of type traits was introduced in 1976 and the first programs for linear type trait evaluation were implemented and tested (Lucas et al. 1984; Vinson et al. 1982; Toghiani, 2011). The Holstein Association began routinely scoring cows with a linear system as part of its herd appraisal program on January 1, 1983. Linear type traits are scored from one biological extreme to another using a continuous scale from 1 to 50 points (Funk et al. 1991). Selection on yield traits alone could decrease merit for traits with antagonistic genetic correlations with yield. Selection emphasis on type traits associated with increased herd life may be beneficial to decrease involuntary culling and increase profitability (Rogers et al. 1988). Conformation traits are recorded in many

dairy cattle breeds (Foster et al. 1988; Harris et al. 1992; De Haas, et al. 2007; Toghiani, 2011). These traits have medium to high heritability (Meyer et al. 1987) and can often be recorded in a single assessment, which makes them reliable and relatively inexpensive traits that can be included in selection indices for overall merit (Schaeffer et al. 1985; Wiggans et al. 2004). The relationships of these traits to herd life and profitability, survival and workability, udder health and somatic cell score, and genetic defects have been investigated (Gengler et al. 1997; Toghiani, 2011). Among the linear type traits, udder traits have strongest effect on the survival of cows. Udder traits have the strongest relationships with functional herd life compared to other structural body traits (Schneider et al. 2003). Udder traits have an important influence on involuntary culling decisions, mainly because of their

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influence on susceptibility to injuries and mastitis infections. Improvement of udder health management has been accompanied by an increase in clinical mastitis cases caused by environmental bacteria in well-managed herds (Bramley et al. 1990; Gonzalez et al. 1990; DeGraves et al. 1993). This may be due to developments in health care that allow immunologically inferior animals to reproduce (Dunklee et al. 1994). Although improvement of health standards is welcome, breeding principles that have long-lasting, cumulative and permanent effects should be developed and implemented. Improvements of health traits in dairy cows can be achieved by environmental means as well as through genetic improvement. The purpose of this study was to estimate the genetic parameters and genetic correlations between some selected udder type traits in the first lactation of Iranian Holstein cows.

Materials and Methods

Type classification records were extracted from the ten herds in Mashhad suburb in Khorasan Razavi Province, which is one of the most important centres of dairy product manufacturing located in Northeast of Iran, close to the borders of Afghanistan and Turkmenistan. This area includes more than one tenth of total commercial dairy cattle population of Iran. The data set consisted of udder type traits records from 2325 Holstein cows between years 1998 to 2011. All cows were scored for conformation traits between 30 and 210 days in milk (DIM) of the first lactation. The following type traits scored on 1 to 9 scale except rear udder height and rear udder width as in the Iranian classification system were analysed: 8 udder traits – fore udder attachment, rear udder height, udder depth, rear udder width, suspensory ligament, teat length, front teat placement and rear teat position. Structure of edited data sets and descriptive statistics for type traits are presented in (Table 1). Further information in the data set included, season of calving, year of calving, herd, date of classification, identification of the classifier and 3-generation pedigree. Age at first calving ranged from 660 to 960 days. Estimation of genetic parameters was performed by Wombat software version 1.0 (Meyer, K. 2008) with univariate and bivariate procedures for udder type traits. Data were also analysed by uni- and bivariate models, which consisted of the fixed and random effects as those included in bivariate settings. All statistical analysis was performed using the statistical software SAS 9.1. The models included fixed effect of herd-year-season of calving (HYS) and the random effect of animal. The following model was applied to all traits for estimation of genetic parameters:

$$Y_{ij} = \mu_p + A_i + HYS_j + e_{ij} \text{ where:}$$

Y_{ij} = observation for trait p on animal i, μ_p = overall mean for trait p, HYS = fixed effect of herd-year-season

of calving, A_i = random additive genetic effect, e_{ij} = random residual effects.

Results and Discussion

Descriptive statistics for the udder type traits are given in (Table 1). Linear udder type traits values varied from 1 to 9. The means of the udder type traits of fore udder attachment and front teat placement varied between 6.67 and 4.35 respectively. The means for teat length, rear udder width, suspensory ligament, rear teat position, udder depth, and rear udder height were 4.9, 18.7, 6.3, 5.1, 5.5, and 27.8, respectively. Fore udder attachment, udder depth, rear udder width and rear udder height were lower than the ideal score. Front teat placement was more than 2 points below the ideal score of 7, indicating on average a wider, more undesirable front teat placement. Scores for suspensory ligament and teat length were close to the ideal scores of 6 and 5, respectively. The means for front teat placement obtained in this study are well within the scope of results reported in the literature (Meyer et al. 1987; Short et al. 1992), but are higher than those reported by Klassen et al. (1992). Comparing of linear type traits scores with results obtained in similar studies is rather difficult because of differences in scoring systems, different traits that are being evaluated, as well as variation in breeds (Pantelić et al. 2011). Taking into consideration the fact that linear type score is based on assumption that traits being scored have normal distribution through the population, i.e. that there is small number of animals with extremely bad or good characteristics; it is possible to treat these traits as quantitative properties. Therefore, it is possible to apply certain methodological procedures to determine the degree of transmission of these properties or traits to their progeny Pantelić et al. (2011). Heritability estimates are shown in Table 2. Only those estimates from univariate analyses are presented on diagonal of table; because parameters obtained in the set of bivariate analyses (table 2) averaged over 8 estimates for each of the analyzed traits, gave similar values based only on the univariate analyses. In this study, heritability estimates for udder type traits were low to moderate. Heritability estimates ranged from (0.03) to (0.32) for suspensory ligament and udder depth, respectively. The lowest heritability (0.03) estimated for suspensory ligament trait were similar to those described by Pantelić et al. (2011), indicating that little response to selection could be expected in these trait. This result shows the importance of environmental effects and non-additive genetic effects in the total variation of these traits. Heritability was estimated 0.23 for front teat placement that was in accordance with the findings of (Short et al. 1991; Spehar et al. 2012). Heritability was estimated 0.31 for rear udder height. Our findings are similar to (Degroot et al. 2002; Mazza et al. 2012). The results of the present study showed heritability of (0.27)

Table 1: Means and standard deviations (SD) of Udder type traits

Trait	Mean (SD)	No.of records	Type traits	score	Ideal score
			1	9	
FTP	4.32(1.03)	2325	Loosely attached	Tightly attached	8
RTP	5.17(1.13)	2325	Very low	Very high	30
RUH	27.8(2.53)	2325	Narrow	Wide	25
RUW	18.0(2.19)	2325	Absent	Deep	6
FUA	6.67(1.73)	2325	Wide	Close	7
SL	6.03(1.04)	2325	External	Internal	5
TL	4.98(1.01)	2325	Below hock	Under-developed	7
UD	5.55(1.05)	2325	Very short	Very long	5

FTP - fore teat placement; RTP - rear teat placement; RUH - rear udder height; RUW - rear udder width; FUA - fore udder attachment; SL- suspensory ligament ;TL - teat length; UD - udder depth

Table 2: Heritabilities (on diagonal) and genetic (above diagonal) and phenotypic (below diagonal) correlations among udder traits

Parameter	FTP	RTP	RUH	RUW	FUA	SL	TL	UD
FTP	0.23(0.01)	0.94(0.1)	0.06(0.02)	0.12(0.03)	0.76(0.03)	0.99(0.6)	-0.64(0.02)	0.25(0.05)
RTP	0.66(0.02)	0.26(0.09)	-0.15(0.02)	0.89(0.05)	0.59(0.02)	0.99(0.4)	0.44(0.2)	0.77(0.17)
RUH	-0.06(0.02)	0.06(0.03)	0.26(0.01)	-0.25(0.02)	0.2(0.02)	0.6(0.08)	-0.11(0.02)	0.05(0.01)
RUW	-0.04(0.03)	-0.04(0.03)	-0.28(0.03)	0.31(0.09)	0.18(0.02)	0.16(0.08)	0.36(0.02)	-0.14(0.02)
FUA	0.27(0.03)	0.28(0.03)	-0.1(0.03)	0.02(0.03)	0.27(0.09)	0.87(0.94)	-0.23(0.03)	0.56(0.18)
SL	0.4(0.03)	0.45(0.03)	-0.09(0.03)	-0.08(0.03)	0.31(0.03)	0.03(0.01)	-0.23(0.79)	0.99(0.53)
TL	-0.06(0.03)	-0.09(0.03)	0.01(0.03)	0.09(0.03)	0.04(0.03)	0.08(0.03)	0.22(0.09)	-0.54(0.27)
UD	0.4(0.03)	0.43(0.03)	-0.06(0.03)	-0.13(0.03)	0.44(0.03)	0.33(0.03)	-0.03(0.01)	0.32(0.01)

FTP - fore teat placement; RTP - rear teat placement; RUH - rear udder height; RUW - rear udder width; FUA - fore udder attachment; SL- suspensory ligament ;TL - teat length; UD - udder depth

for fore udder attachment. Němcová et al. (2011) published a heritability of 0.24 for fore udder attachment, similar to our results. (Schaeffer et al.1985; Spehar et al. 2012) reported heritability of (0.14) for fore udder attachment. They found smaller heritabilities for udder traits than for non-udder traits. The heritabilities of linear type traits estimated in this study were similar to values reported by Short et al. (1991) for the Holstein breed and Wiggans et al. (2006) for Guernsey and Brown Swiss. The traits that showed the highest heritability and therefore would show greater responses to selection in breeding programs are rear udder width (0.31) and udder depth (0.32). The lowest heritability (0.03) estimated for the suspensory ligament trait were similar to those described by Short et al.(1991), indicating that little response to selection could be expected for these trait. Most estimates of heritability were higher than 0.21, (table 2) except suspensory ligament trait. The magnitudes of these values indicate that a considerable proportion of the phenotypic variation occurs due to differences in genes with additive effects and that there may be genetic gains in response to selection procedures. This result shows the importance of environmental effects and non-additive genetic effects in the total variation of udder type traits. Discrepancies among reports may be due to differences across studies in scales used for scoring, statistical model definitions, breed involved, number of records per animal, accuracy and consistency of classifiers and data editing procedures. Heritability values of udder type traits in the studies by numerous authors show great variability depending on the breed, housing system and scoring system (Smith et al.

1998; Van Dorp et al. 1998). Genetic and phenotypic correlations among the currently recorded udder type traits are shown in Table 2. The genetic correlations were generally higher than the phenotypic correlations. The values obtained for the phenotypic correlations between most udder type traits, were of low magnitude (Table 2). Larger phenotypic associations can be observed between front teat placement and rear teat position (0.66), rear teat position and suspensory ligament (0.45) traits. Genetic correlations ranged from (-0.54) between udder depth and teat length to (0.99) between suspensory ligament and udder depth. It means that cows with deep udder depth had short teat length and strong suspensory ligament. Correlations were generally higher than those reported in most previous studies (Rogers et al 1996; Sorensen et al. 2000). Genetic correlations were estimated (0.56) between fore udder attachment and udder depth. It means that cows with genetic predisposition to strong fore udder attachment incline to deeper udders and strong phenotypic (0.44) correlations between fore-udder attachment and udder depth indicate the possibility of reducing the number of type traits assessed on each animal with the loss of very little information. The strength of the correlation between fore udder attachment and udder depth are slightly stronger than previous reports (Lund et al. 1994; DeGroot et al. 2002). strong genetic associations were found also for the following pairs of traits: rear udder height and rear udder width (-0.25), rear udder width and teat length (0.36), front teat placement and rear teat position (0.94), fore udder attachment and rear udder width (0.18), and suspensory ligament and rear udder

height (0.06). Because of the high genetic correlation between front teat placement and rear teat position, cows have close front teat placement they have close rear teat position. Jagtenberg et al. (1994) reported that cows with poor teat placement are unlikely to be compatible with robotic milking systems. Thus, a combined selection objective including teat placement may be warranted to alleviate the deleterious effects of selection on milk yield. (Buenger et al. 2001; Schneider et al. 2003) reported that cows with extremely close rear teats were more likely to be culled compared with cows with extremely wide rear teats. Positive genetic correlations indicate that selection for increased scores in one trait will be accompanied by increased scores in the correlated trait, regardless of the direction of the score that improves the trait (Toghiani. 2011). Traits in this study are similar to those reported in the literature (Schaeffer et al., 1985; Lawstuen et al. 1987; Foster et al. 1988; Wiggans et al. 2004; Némecova et al. 2011). In agreement with our findings, Schaeffer et al. (1985), Lawstuen et al. (1987), and Foster et al. (1988) reported high positive genetic correlations between the following udder traits: between fore udder attachment and udder depth. In addition, Foster et al. (1988) reported a genetic correlation of (0.35) between suspensory ligament and udder depth and genetic correlations of (0.44) and (0.43) between fore udder attachment and rear udder height and width, respectively. Similar results were found by Lawstuen et al. (1987). High positive front teat placement and rear teat position was reported by Perez-Cabal et al. (2006). Foster et al. (1988) reported high positive genetic correlations between the following udder traits: between fore udder attachment and udder depth and/or rear udder height and rear udder width. In addition, Foster et al. (1988) reported a genetic correlation of 0.35 between central ligament and udder depth and genetic correlations of 0.44 and 0.43 between fore udder attachment and rear udder height and width, respectively. DeGroot et al. (2002) reported that the highest genetic correlations between traits of the conformation section, and questioned the need to evaluate the two traits in the same animal, which would result in greater flexibility at the time of collecting in the field and therefore save financial resources. The estimated Genetic correlations showed favorable and high genetic correlation between mammary system traits. These genetic correlations indicate that Udder type traits are the most useful indicators of functional herd life. The trends of some traits may have resulted from selection for higher milk production. Harris et al. (1992) pointed out that selection to improve milk production is likely to increase udder dimension and weaken fore udder attachment and depth.

Conclusion

Genetic trends for Udder type traits followed clearly discernible trends over the years, showing how responsive they are to selection. This suggests that changes can be

expected if selection is carried out on some of these traits, which may also bring about correlated improvement in susceptibility to mastitis (Dube et al. 2008). Selection on one trait is expected to result in genetic change in another with which it is highly correlated. Thus, the number of traits in the selection criteria for mastitis resistance can be optimized, using these correlations, to achieve maximum genetic progress. The trends of some traits may have resulted from selection for higher milk production. Genetic parameters were estimated in order to update genetic evaluation system of type traits and to analyze the genetic correlations. Estimated parameters for udder type traits will be used to update the selection index of Holstein dairy cattle. Practically, by selection the genetic basis of individual animal, populations and breeds is changed, with goal to obtain new genotypes which would enable maximum production performance and economic effects. We can conclude that the new sets of genetic parameters can be used to update the national genetic evaluation for conformation. Information provided in this study could be used to create specific selection indices that would reflect the optimal conformation of dairy cows in each region.

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