Genetic Evaluation and Calculating Daughter Yield Deviation of Bulls in Iranian Holstein Cattle for Milk and Fat Yields

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ABSTRACT : This study was aimed at a genetic evaluation of Iranian Holstein cattle for milk and fat yields and calculating daughter yield deviation (DYD) of bulls. The data file that was used in this research included 367,943 first three lactation records of 186,064 Holstein cows which calved between 1983 and 2006 in 11,806 herd-year-season groups. The model included herd-year-season of calving and age at calving as fixed effects and animal and permanent environment as random effects. Mean breeding values of cows for each year were regressed on birth year to estimate genetic trends. Genetic trends in milk and fat yields were greater for cows born after 1997 (59.38 kg/yr and 1.11 kg/yr for milk yield and fat yield, respectively). Animal evaluations were partitioned into contribution from parent average, yield deviation (YD) and progeny. DYD of bulls was calculated as described by VanRaden and Wiggans (1991). DYD provides an indication of the performance of the daughters of a bull without consideration of his parents or sons. Variance of bull DYD was greater than variance of their predicted transmitting ability (PTA). Correlation of bull DYD and PTA was dependent on the number of daughters and when this increased, the correlation of DYD and PTA was increased. Also as lactation number of daughters increased, the correlation of bull DYD and PTA was increased. (**Key Words** : Daughter Yield Deviation, Genetic Evaluation, Genetic Trend, Holstein Cows)

INTRODUCTION

Since 1983 official milk recording schemes have been run by the Animal Breeding Center of the Ministry of Agriculture in Iran. Data for milk production and its components are recorded within 30±5 days for individual cows. Genetic evaluation of animals is done biannually using an animal model and results are sent to covered herds. The main object of genetic evaluation of animals is selection of sires and elite cows for the next generation. Results from animal model evaluations can be used in a post-evaluation step for calculating other measures, such as yield deviation (YD) of cows and daughter yield deviation (DYD) of bulls, that have not been calculated until now in Iran. The YD is a weighted average of the cow's yields adjusted for all effects of the model other than genetic merit and error. The DYD of bulls are average performance of their daughters that are adjusted for fixed and non-genetic random effects of the daughters and genetic effect of their mates (VanRaden and Wiggans, 1991; Liu et al., 2004).

DYD are not regressed on breeding values of bulls and are the most independent and accurate measure of phenotypic performance of a bull's daughters (VanRaden and Wiggans, 1991; Mrode and Swanson, 2001; Liu et al., 2004). DYD can be used as a dependent variable in quantitative trait loci (QTL) detection based on grand-daughter design (Weller, 2001; Freyer et al., 2002; Kim and Georges, 2002; Syzda et al., 2002; Kim, 2008), validating national genetic trends (Boichard et al., 1995) and international bull comparison (Schaeffer, 1994; Weigel et al., 2001, Docrocq et al., 2003). VanRaden and Wiggans (1991) showed calculations of YD for cows and DYD of bulls from results of a repeatability animal model. Mrode and Swanson (2002) presented how these measures can be calculated for a random regression model (RRM). Liu et al. (2004) developed a method for calculating DYD under general multiple trait models. Hence the objectives of this study were genetic evaluation of animals for milk and fat yields and calculating DYD of bulls, as well as their PTA, in Iranian Holstein cattle.

MATERIALS AND METHODS

Data

The database of the Animal Breeding Center of the

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Table 1. Characteristics of analyzed data

Description	Number
Records in data	367,943
Animals in pedigree	285,645
Sires	4,904
Herds	738
Years	24
Seasons	4
Herd-Year-Season groups	11,806

Ministry of Agriculture at Karadj, Iran was used in the analysis. Data consisted of individual lactation records for milk and fat yields of Holstein cows over 24 freshening years from 1983 to 2006. Milk and fat yields had been standardized for twice-daily milking and 305-d lactation length. Each record with at least 90 days lactation length and first calving age between 20 and 40 months was included in the analysis. The first three lactation records were considered in this analysis. Lactation records for cows with a missing first lactation record were excluded from evaluation to reduce selection bias. Records with unknown parents and obvious errors in calving or birth dates were also excluded. Herd-year-season classes were grouped using the four conventional seasons used in Iran: April to June, July to September, October to December and January to March. All herd-year-season classes were required to have at least 5 records to include in the analysis. The final data set included 367,943 records for 186,064 Holstein

cows which was distributed across 11,806 herd-year-season groups. Pedigrees were traced back as far as possible. Data structure is shown in Table 1 and 2.

Variance components estimation and BLUP analysis

Data were analyzed using a single-trait repeatability animal model. The AI-REML method was used for estimating variance components (Johnson and Thompson, 1995; Lee, 2000). Both variance components estimation and predicting of breeding values were carried out simultaneously using production records and full pedigree information by WOMBAT 1.0 software (Meyer, 2007).

The statistical model in matrix notation was:

$$y = Xb+Za+Wp+e \tag{1}$$

Where:

y = vector of observations for yields of milk and fat.

X = design matrix for the fixed effects.

b = vector of fixed effects of herd-year-season, linear and quadratic regression coefficient for age at calving.

Z = design matrix for the random effect of animal.

a = vector of random animal effects.

W = design matrix for the random effect of animal permanent environment.

p = vector of random animal permanent environmental effects.

e = vector of random residual effects.

Table 2. Data structure by year of freshening

Freshening year	Number of herds	Number of cws		
		1st Lac	2nd Lac	3rd Lac
1983	6	284	-	-
1984	10	130	153	-
1985	9	18	154	80
1986	11	114	27	137
1987	12	211	82	25
1988	13	221	140	47
1989	18	428	177	90
1990	28	572	296	135
1991	43	996	400	198
1992	58	1,796	653	253
1993	75	3,359	1,189	402
1994	102	5,352	2,378	843
1995	128	7,034	4,187	1,680
1996	174	8,491	5,147	2,797
1997	227	11,149	6,438	3,601
1998	283	11,854	8,189	4,396
1999	314	14,270	8,756	5,544
2000	354	15,718	10,385	5,689
2001	370	16,028	10,876	6,656
2002	388	16,446	10,842	6,613
2003	399	17,224	11,094	6,794
2004	401	17,203	11,735	6,870
2005	407	18,293	11,574	7,214
2006	411	18,596	10,430	6,344

The distributional properties were assumed to be as follows:

$$E \begin{bmatrix} y \\ a \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \end{bmatrix}, \quad var \begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_p^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

The matrix A is the additive relationship matrix among all animals in a, I is the identity matrix and σ_a^2, σ_p^2 and σ_e^2 are the additive genetic, permanent environmental and residual variances, respectively. The inverse of the additive numerator relationship matrix among animals (A^{-1}) was computed with inbreeding ignored.

Convergence was assumed when the change in log-likelihood values reached $<10^{-5}$.

Calculating DYD of bulls

An animal's PTA can be partitioned into three source of information which are parent average, half of its yield deviation and progeny contribution (VanRaden and Wiggans, 1991). This partitioning provides better understanding of calculating PTA for an animal.

$$PTA_{anim} = W_1 PA + W_2 (YD/2) + W_3 PC \qquad (2)$$

Where

W_1, W_2, and W_3 are weights assigned to each source of information and sum to 1. The numerator of W_1 is $2K_a q_{par}$; the numerator of W_2 is number of records for the cow; and the numerator of W_3 is $0.5 K_a \Sigma q_{prog}$.

Where q_{par} equals 1 if both parents are known, 2/3 if one is known, and 1/2 if neither is known, and q_{prog} equals 1 if progeny's other parent is known and 2/3 if unknown and $K_a = \sigma_e^2 / \sigma_a^2$. The denominator of all three W is the diagonal of $\acute{Z}Z + A^{-1}K_a$ from mixed model equation, which equals the sum of the three numerators (VanRaden and Wiggans, 1991).

For calculating YD of cows, their production records were adjusted for all effects of the model other than genetic effect and error and then averaged over lactation. In calculating sire proofs, the second part of the equation, i.e. YD, was not accounted for because bulls do not have their own production records. Parent average was calculated as

the average of parents PTA. Progeny Contribution (PC) was calculated as the weighted average of twice PTA_{prog} minus PTA_{mate}.

$$PC = \Sigma q_{prog} (2PTA_{prog} - PTA_{mate}) / \Sigma q_{prog} \qquad (3)$$

PC was regressed on bull PTA because in calculating PTA_{prog} (via equation 2), PTA of bull appeared in the parent average part and information from progeny's progeny (Granddaughter of bull) are included in the equation. Thus PC could not be an independent measure of progeny performance. A more accurate and independent measure of progeny performance is DYD. Equation for calculating DYD of bull is:

$$DYD = \Sigma q_{prog} W_{2prog} (YD_{prog} - PTA_{mate}) / \Sigma q_{prog} W_{2prog} \qquad (4)$$

$$\text{Where, } W_{2prog} = n/(n + 2K_a q_{prog}) \qquad (5)$$

and n is equal to the number of lactation records for each daughter (VanRaden and Wiggans, 1991; Mrode, 2005).

In other words, DYD of bulls are average yield deviations of a bull's daughters that are adjusted for the dams PTA. In calculating DYD for bulls, only production records of their own daughters were considered and information from granddaughters and sons were excluded. This is the other difference between procedures that were used in PC and DYD calculations, because information from both sons and daughters of bulls are included in the PC calculation.

RESULTS AND DISCUSSION

Descriptive statistics

Mean, standard deviation and coefficient of variation for milk and fat yields in different parities are shown in Table 3.

The overall means for milk and fat yields in this study were 7,200 kg and 228 kg respectively. Farhangfar and Naeimipoor (2005) reported a mean of 6,440 kg and 195 kg for milk and fat yields of Iranian Holstein cattle. Earlier estimates by Jahanshahi et al. (2003) reported a mean of 6,272 kg and 173 kg for these traits, respectively. This improvement in mean of milk and fat yields indicates a positive trend in the interval between these studies. This progress in milk and fat yields represents improvement in

Table 3. Descriptive statistics of the data

Parity	n	Milk (kg)			Fat (kg)		
		Mean	SD	CV (%)	Mean	SD	CV (%)
1	186,044	6,817	1,429	20.9	215	51.6	23.9
2	115,436	7,536	1,715	22.7	238	62.3	26.1
3	66,463	7,822	1,824	23.3	250	66.3	26.4
Total	367,943	7,200	1,643	22.8	228	59.4	26.0

Table 4. Estimated variance components and genetic parameters for milk and fat yields

Trait	Variance components[1]				Parameters[2]	
	σ_a^2	σ_p^2	σ_e^2	σ_T^2	h[2]±SE	R
Milk 305 d	367,397	370,753	894,070	1,632,220	0.225±0.005	0.45
Fat 305 d	300.90	283.06	956.39	1,540.36	0.195±0.004	0.38

[1] σ_a^2: additive genetic variance, σ_p^2: Animal permanent environmental variance, σ_e^2: Error variance, σ_T^2: total variance.

[2] h[2]: heritability, R: repeatability.
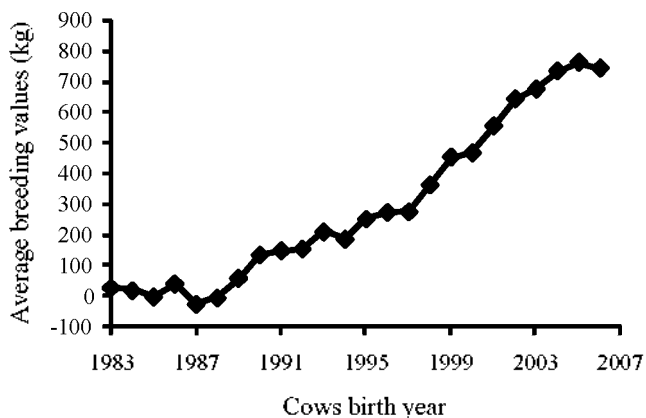
Figure 1. Breeding values for milk yield averaged by birth year of cows.
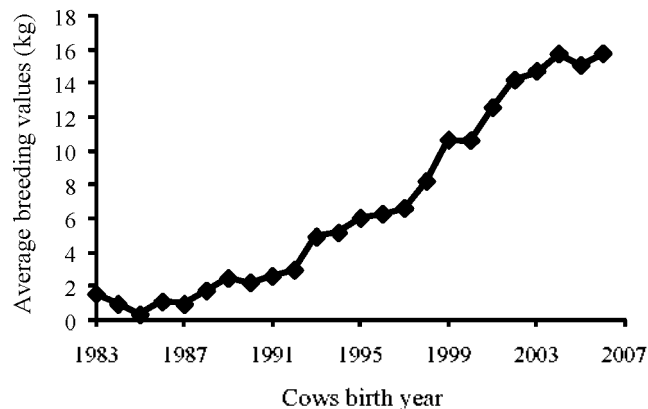
Figure 2. Beding values for fat yield averaged by birth year of cows.

many areas including management, feeding and genetic potential. This study reveals one part of the improvement which was caused by genetic progress.

Variance components

Estimates of variance components and genetic parameter are presented in Table 4.

Heritabilities for milk and fat yields were 0.22 and 0.19, respectively. The corresponding repeatabilities were 0.45 and 0.38, respectively. These estimates are close to those obtained by Jahanshahi et al. (2003) and Nazari et al. (2003) for 305 d milk and fat yields of Iranian Holsteins using a repeated records model. However, our estimates are lower than other estimates from an animal model that used first lactation records of Iranian Holstein cattle (Farhangfar and Naeimipoor, 2005; Shadparvar and Yazdanshenas, 2005). The heritability estimates decreased with the order of

lactation mainly as a result of increased environmental variance, and estimates from repeated records model are generally lower than those estimated with first lactation (Visscher and Thompson, 1992).

Estimated variance components are useful in national genetic evaluation because estimates are obtained from complete records and pedigree data (Jorjani et al., 2001).

Breeding values

Average estimated breeding values of milk yield for cows born in 1983 through 2006 are shown in Figure 1.

Breeding values changed with a negative trend for cows born from 1983 to 1987 with an annual change of -9.7 kg/yr (Table 5). This genetic decrease was not significant (p>0.05). Average breeding values for milk yield increased from 1987 to 1997 (30 kg/yr). A rapid increase in breeding values was observed for cows born after 1997(59.38 kg/yr).

Table 5. Annual genetic change in breeding values for milk and fat yields by period of birth year of cows

Trait and period	Annual genetic change	SE	Period average (kg)
Milk yield (kg)			
1983-1987	-9.7	8.26	13.24
1987-1997	30.00**	2.65	152.36
1997-2006	59.38**	3.31	567.20
Fat yield (kg)			
1983-1987	-0.163	0.119	0.930
1987-1997	0.581**	0.046	3.769
1997-2006	1.116**	0.089	12.356

* p<0.05. ** p<0.01.

The average genetic merit of cows for milk yield in the period of 1983 to 1987, 1987 to 1997 and 1997 to 2006 was 13.24, 152.36 and 567.20, respectively. The average genetic merit of cows born in 2006 was about 748 kg more than for cows born in 1983.

The mean of breeding values for fat yield of cows born in 1983 through 2006 are shown in Figure 2. Breeding values changed little for cows born from 1983 to 1987 with an annual change of -0.163 kg/yr. Breeding values increased from 1987 to 1997 (0.581 kg/yr). A rapid increase in breeding values was observed from 1997 to 2006 (1.116 kg/yr). The average genetic merit of cows for fat yield in the period of 1983 to 1987, 1987 to 1997 and 1997 to 2006 was 0.930, 3.769, and 12.356 respectively. The average genetic merit of fat yield for cows born in 2006 was about 14.7 kg more than for cows born in 1983.

Other studies in different regions of the country also reported a positive genetic trend for yield traits of Iranian Holsteins. Kolbehdari et al. (1993) reported a genetic trend of 81 kg/yr for milk yield of a Holstein herd in Tehran province. Naeimipoor (2004) reported a genetic trend of 9.27 kg/yr for milk yield of Holstein cows in Khorasan province. Dadpasand (2002) reported a genetic trend of 12.4 kg/yr and 0.13 kg/yr for milk and fat yields, respectively, of Iranian Holsteins.

During the last few years an increase in consumption of dairy products per head was the most recommendation of health organizations in Iran. In this direction, semen of high-ranking bulls on the basis of PTA for milk and fat yields has been imported from foreign countries. Furthermore, preliminary selection of young bulls on the basis of pedigree index (Bhatti et al., 2007) and running a national progeny test program for sire selection and giving an appropriate weight for milk and fat yields in the selection index of bulls accelerated the genetic improvement of these traits.

DYD of bulls

In Table 6, milk PTA of some bulls with a different number of daughters was partitioned into two source of information, namely parent average and progeny contribution.

This partitioning is valuable in providing a better understanding of procedures used to calculate sire proofs. It can be seen that in prediction of bull PTA, as number of bull progeny increased the weight assigned to progeny was increased. In fact the number of progeny has a direct relationship with W_3 and when the number of progeny increases, the numerator of W_3 ($0.5K_a\Sigma q_{prog}$) increases. This is one of the properties of the animal model so that each source of information takes optimal weight in respect of data structure.

The correlation between milk PTA and DYD for bulls with different numbers of daughters are shown in Table 7.

Table 6. Partitioning PTA of some bulls for milk yield in the data

Bulls	No of daughters	PTA	Partitioning PTA of bulls[1] $PTA = W_1(PA)+W_3(PC)$			
			W_1	PA	W_3	PC
A	10	-284.31	0.2857	-42.56	0.7143	-381.01
B	20	428.45	0.1666	432.33	0.8334	427.68
C	50	202.64	0.0740	273.86	0.9260	196.95
D	101	-152.19	0.0380	283.68	0.9620	-169.41
E	200	443.89	0.0196	580.67	0.9804	441.16
F	497	472.38	0.0079	409.7	0.9921	472.88
G	987	388.66	0.0040	49.45	0.9960	390.03
H	1,897	449.93	0.0021	190.26	0.9979	450.48

[1] PTA = Predicted transmitting ability, PA = Parent average, PC = Progeny contribution, W_1 and W_2 = Weighting factor.

Table 7. Correlation of milk PTA and DYD for bulls with different number of daughters

No of daughters	No of bulls	SD of PTA[1]	SD of DYD[2]	Correlation of PTA and DYD
10-19	1,442	225.02	341.20	0.839
20-29	651	237.62	308.01	0.929
30-39	556	230.01	283.13	0.967
40-59	533	263.18	307.32	0.987
60-100	520	254.58	284.42	0.994
100-199	534	280.85	301.27	0.997
200-499	460	293.15	303.89	0.998
>500	208	232.96	241.48	0.999

[1] PTA = Predicted transmitting ability. [2] DYD = Daughter yield deviation.

Table 8. Correlation of Bulls PTA and DYD with increasing lactation number of their daughters

No of daughters lactation	Correlation of PTA[1] and DYD[2]
1	0.501
2	0.583
3	0.689

[1] PTA = Predicted transmitting ability. [2] DYD = Daughter yield deviation.

As number of daughters increased, correlation of DYD and PTA was increased. This is in agreement with results obtained by Liu et al. (2004) in a simulation study. Expectation of DYD is $\frac{1}{2}\hat{a}_{bull} + \sum_m \frac{\hat{e}}{m}$ where m is the number of daughters. Thus, as m increases, $\sum_m \frac{\hat{e}}{m}$ tends towards zero and correlation of DYD and PTA increases (Mrode and Swanson, 2002). Variance of bulls DYD was greater than variance of bulls PTA and as number of daughters increased, the difference between these variances became less, but variance of DYD was still high. In the DYD calculation, DYD of one bull does not affect DYD of other bulls i.e. DYD calculation is done on a within-bull basis and parental contribution to bull is irrelevant. However, in predicting bulls PTA, parent average of bulls and also relationships of bulls (via A^{-1} in the denominator of W_1 and W_3) are considered; thus PTA of bulls became closer together rather than DYD of bulls. However, as a sire accumulates more daughter information and reliability increases, more weight is given to progeny in calculating PTA and less emphasis is placed on pedigree, and the difference between variance of PTA and DYD decreased. In the mixed model equations, the coefficient matrix is multiplied by the inverse of the residual variance matrix and therefore as the number of daughters increases, variance of DYD decreases while variance of PTA increases (Weller, 2001).

The correlation between PTA and DYD with increasing lactation number of bull's daughters is shown in Table 8. Correlation increased as lactation number of daughters increased. This may reflect a better correction for environmental factors in prediction of PTA for cows with more repeated records i.e. due to the model of analysis (repeated record model) estimates of environmental effect, especially permanent environmental effect, are more precise for cows that have three lactation records. Thus PTA of these cows was estimated accurately and since this PTA appeared in the PC section for estimation of their sires' proofs, PTA of their sires was estimated accurately and was more correlated with DYD.

Calculated DYDs can be used to characterize progeny test programs in the genetic evaluation of young sires (Vierhout et al., 1998), and also as a dependent variable in quantitative trait loci detection based on grand-daughter design (Weller, 2001; Freyer et al., 2002; Syzda et al., 2002), validating national genetic trends (Boichard et al., 1995) and international bull comparison (Schaeffer, 1994; Weigel et al., 2001; Docrocq et al., 2003).

CONCLUSION

Heritability and repeatability estimates were lower than those commonly found in the literature but were consistent with the estimates found for Iranian Holstein cattles. Approximately the same patterns of genetic trends in milk and fat yields of Holstein cows were observed and genetic trends were higher for cows born after 1997. Daughter Yield Deviation of bulls were calculated as well as their PTA. Variance of bull DYD was greater than variance of bull PTA and as number of daughters increased, correlation of DYD and PTA was increased. DYD of bulls provides preliminary information for international evaluation of foreign bulls that have been used in Iran and are the most used variable in quantitative trait loci detection designs.

REFERENCES

Bhatti, A. A., M. S. Khan, Z. Rehman, A. U. Heyder and F. Hassan. 2007. Selection of Sahiwal cattle bulls on pedigree and progeny. Asian-Aust. J. Anim. Sci. 20(1):12-18.

Boichard, D., B. Bonaiti, A. Barbat and S. Mattalia. 1995. Three methods to validate the estimation of genetic trend for dairy cattle. J. Dairy Sci. 78:431-437.

Dadpasand, M. 2002. Estimation of genetic trend for yield traits of Iranian Holstein cattle. MSc Thesis, University of Tehran, Iran.

Ducrocq, V., I. Delaunay, D. Boichard and S. Mattalia. 2003. A general approach for international genetic evaluations robust to inconsistencies of genetic trends in national evaluations. Interbull Bulletin 30:101-111.

Farhangfar, H. and H. Naeimipoor. 2005. Estimation of genetic and phenotypic parameters for 305-day yield and reproductive traits in Iranian Holsteins. J. Sci. Technol. Agric. Nat. Resour. 11:431-440.

Freyer, G., C. Stricker and C. Kuhn. 2002. Comparison of estimated breeding values and daughter yield deviations used in segregation and linkage analyses. Czech J. Anim. Sci. 47: 247-252.

Johnson, D. L. and R. Thompson. 1995. Restricted maximum likelihood estimation of variance components for univariate animal models using sparse matrix techniques and average information. J. Dairy Sci. 78:449-456.

Jorjani, H., J. Philipsson and J. Mocquot. 2001. Interbull guidelines for national and international genetic evaluation systems in dairy cattle with focus on production traits. Interbull Centre.

Kim, J. J. and M. Georges. 2002. Evaluation of a new fine-mapping method exploiting linkage disequilibrium: a case study analysing a QTL with major Effect on milk composition on bovine chromosome 14. Asian-Aust. J. Anim. Sci. 15

(9):1250-1256.

Kim, J. J. 2008. Detection of QTL on bovine X chromosome by exploiting linkage disequilibrium. Asian-Aust. J. Anim. Sci. 21(5):617-623.

Kolbehdari, D. 1993. Estimation of genetic trend for milk yield in a herd of Holstein cattle. MSc Thesis, University of Tehran, Iran.

Lee, C. 2000. Methods and techniques for variance component estimation in animal breeding. Asian-Aust. J. Anim. Sci. 13 (3):413-422.

Liu, Z., F. Reinhardt, A. Bunger and R. Reents. 2004. Derivation and calculation of approximate reliabilities and daughter yield-deviations of a random regression test-day model for genetic evaluation of dairy cattle. J. Dairy Sci. 87:1896-1907.

Meyer, K. 2006. WOMBAT - Digging deep for quantitative genetic analysis by restricted maximum likelihood. 8th WCGALP, Belo Horizonte, August 13-18, Communication 27.

Meyer, K. 2007. WOMBAT, version1.0. UserNotes. Available http://agbu.une.edu.au /~kmeyer/wombat.html

Mrode, R. A. and G. J. T. Swanson. 2002. The calculation of cow and daughter yield deviations and partitioning of genetic evaluations when using a random regression model. in Proc. 7 WCGALP, Communication #01-04, Montpellier, France. pp. 51-54.

Mrode, R. A. 2005. Linear models for the prediction of animal breeding values. CAB International.

Naeimipoor, H. 2004. Estimates of phenotypic and genetic trend for milk yield of Holstein cattles in Khorasan province of Iran. MSc Thesis, University of Zabol, Iran.

Nazari, B. M., R. Vaez-Torshizi, M. Moradi-Shahrebabak and M. B. Sayadnejad. 2003. Estimation of genetic parameters of milk production and reproduction traits in Iranian Holsteins. Proceedings of The First Seminar on Genetic and Breeding Applied to Livestock, Poultry and Aquatics, University of Tehran, Iran, pp. 99-105.

Safi-Jahanshahi, A., R. Vaez-Torshizi, N. Emam-Jomeh-Kashan and M. B. Sayadnejad. 2003. Estimates of genetic parameters of milk production traits for Iranian Holsteins, Using Different animal models. Proceedings of The First Seminar on Genetic and Breeding Applied to Livestock, Poultry and Aquatics, University of Tehran, Iran, pp. 40-46.

Schaeffer, L. R. 1994. Multiple-Country comparison of dairy sires. J. Dairy Sci. 77:2671-2678.

Shadparvar, A. A. and M. S. Yazdanshenas. 2005. Genetic parameters of milk yield and milk fat percentage test day records of Iranian Holstein cows. Asian-Aust. J. Anim. Sci. 18 (9):1231-1236.

Szyda, J., Z. Liu, R. Maschka, F. Reinhardt and R. Reents. 2002. Computer system for routine QTL detection and genetic evaluation under a mixed inheritance model in dairy cattle. in Proc. 7 WCGALP, Communication #28-10, Montpellier, France. pp. 749-750.

VanRaden, P. M. and G. R. Wiggans. 1991. Derivation, calculation, and use of national animal model Information. J. Dairy Sci. 74: 2737-2746.

Vierhout, C. N., B. G. Cassell and R. E. Pearson. 1998. Influences of progeny test programs on genetic evaluations of young sires. J. Dairy Sci. 81:2524-2532.

Visscher, P. M. and R. Thompson. 1992. Univariate and multivariate parameter estimates for milk production traits using an animal model. I. Description and results of REML analyses. Genet. Sel. Evol. 24:415-430.

Weigel, K. A., R. Rekaya, N. R. Zwald and W. F. Fikse. 2001. International genetic evaluation of dairy sires using a multiple-trait model with individual animal performance records. J. Dairy Sci. 84:2789-2795.

Weller, J. I., Y. Kashi and M. Soller. 1990. Power of daughter and granddaughter designs for determining linkage between marker loci and quantitative trait loci in dairy cattle. J. Dairy Sci. 73:2525-2537.

Weller, J. I. 2001. Quantitative trait loci analysis in animals. CAB International, UK.