Estimation of genetic parameters for production traits and somatic cell score in Iranian Holstein dairy cattle using random regression model

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Abstract In this study test-day records of milk (kg), fat (g), and protein (g) yields, somatic cell score (SCS, cells/ML) collected by Animal Breeding Center of Iran during 2007 and 2009 were used to estimate genetic parameters using random regression model. Models with different order of Legendre polynomials were compared using Bayesian information criterion (BIC).For milk, fat yield and SCS genetic and permanent environmental effects were modeled with 3th order of Legendre polynomials and for protein yield genetic and permanent environmental effects were modeled with 4th and 3rd order of Legendre polynomials, respectively. The mean heritability for milk, fat, protein yield and SCS were 0.24, 0.12, 0.23 and 0.07, respectively. For all the traits except for SCS, the estimated heritabilities were lowest at the beginning and higher at the end of the lactation period. Around peak yield (DIM 50 to 150), heritability was lowest for all traits and then increased to the end of lactation. Phenotypic correlations were high between adjacent yields and small between yields at the extremes of the lactation curve. Negative genetic correlations were observed between tests at the beginning and at the end of lactation in this research. The present study showed clear evidence for the benefits of using a random regression TD model for management decisions.

Keywords: genetic parameters, random regression, production traits, somatic cell score, Iranian Holstein dairy cattle.

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Introduction

Test-day (TD) yield records provide a great source of information for both breeding and management programs. Because increasing the sampling size for each individual increases the accuracy of parameter estimates (Karacaoren, 2001), it could be expected that using daily test day data may provide more accurate parameter estimations compared aggregated 305-d yields.

TD models are used in most countries to perform genetic evaluations for dairy cattle using TD observations instead of aggregated 305-days yield observations (Ptak and Schaeffer, 1993; Reents et al., 1995; Jamrozik and Schaeffer, 1997a; Schaeffer et al., 2000). The use of TD models to analyze milk, fat and protein yields and somatic cell score (SCS) has several advantages over the use of other models such as multivariate models.

TD models account for environmental factors that could affect the performance of cows throughout the lactation period (Ptak and Schaeffer, 1993; VanRaden, 1997). This model can be used for incomplete lactations. Also TD models are able to detect outliers (Mayeres et al., 2004).

TD models have been suggested for monitoring genetics and several management applications in dairy cattle. Mayeres et al. (2004), Pool and Meuwissen (1999) and (Schaeffer et al., 2000) scrutinized the capability of a TD model to predict yield from TD records and reported TD models provide 4 to 8% more accurate genetic evaluations of cows compared with evaluations from 305-d yields. The inclusion of herd TD (HTD) and herd curve (HCUR) effects is another important aspect of TD models and would be applicable for management. The HTD effect accounts for month-to-month variability and is especially informative with regard to short-term management changes that affect the whole herd at a particular TD. Koivula et al. (2007) described the use of monthly herd-management effect solutions from a TD model in Finland.

The quality of TD evaluation is somewhat dependent on the accuracy of (co)variance components that are used. More complicated models are potentially more accurate, but estimates of parameters for these models are more difficult (Strabel and Misztal, 1999)

In recent years, there has been increased emphasis on estimating genetic parameters for not only production traits but also health, fertility, feed efficiency, survival, and body condition traits for use in optimized selection indexes in dairy cattle (Kadarmideen, 2004).

Mastitis is the most costly disease affecting dairy cattle. Reducing the incidence of mastitis through genetic selection is of great importance both for economical and animal health reasons. Mastitis has an unfavorable genetic correlation with milk production (Madsen et al., 1987; Mrode and Swanson, 1996; Heringstad et al., 2000), and selection for increasing milk production is accompanied to increase the incidence of the disease. However, if selection against mastitis is included in a total merit index, the genetic level of mastitis may be kept constant or even improved (Heringstad et al., 2003).

Genetic parameters of TD milk traits using random regression (RR) models have been reported for several dairy cattle populations from fitting various functions to model additive genetic lactation curves (Strabel et al., 2005; Muir et al., 2007).

Estimates of genetic parameters for traits of economic importance in dairy cattle are necessary for implementing efficient breeding programs. Accurate heritability and correlation estimates are required to predict expected selection response and to obtain predicted breeding values using mixed model procedures. Traits related to milk, fat, and protein production and SCS, conformation, length of productive life, reproduction, workability, and health are included in breeding programs of dairy cattle in many countries (Mark, 2004; VanRaden, 2004) to maximize improvement of a breeding goal involving traits related to income and costs (Dekkers and Gibson, 1998).

The objective of this study was to estimate genetic parameters for TD milk, fat, and protein yield, and SCS in Iranian Holstein dairy cattle using random regression model.

Materials and methods

Data

Test-day milk (kg), fat (kg), and protein (kg) yield, and Somatic Cell Count (cells/ML) records collected by Animal Breeding Center of Iran during 2007 and 2009 were used. Cows were deleted if they had fewer than four test-day records and ages at first calving were restricted between 20 and 39 month. A complete lactation was considered to have a minimum of four milk recordings, an average test-day interval of a maximum 35 d, at least one test-day record at or before d 80, and one at or after d 280. Test-day observations before d 5 and after d 305 were deleted. SCC records outside the range 10000 to 800,000 cells/ml were discarded. The observations were transformed to SCS [$\log_2$ (SCC/100,000) + 3] (Neuenschwander et al., 2005), to achieve an approximate normal distribution of the test-day records. The simple statistics of the final data are presented in Table 1. The final dataset contained 175,267, 174,474, 175,033 and 159,300 records for test-day milk, fat, and protein yield and somatic cell score (SCS), respectively. These records were measured on 24,144 Iranian Holstein cows in 114 herds.

Model

Milk, fat, and protein yield, and SCS were analyzed using a multiple-lactation, single-trait random regression model. The random regression model was as follows:

$$Y_{iklmnps} = L_i + HTD_k + HB_l + \sum_{n=1}^{k} b_n \left(age_{iklmn}\right)^n + \sum_{n=1}^{k} c_n \left(\dim_{iklmn}\right)^n + \sum_{n=1}^{k_\alpha - 1} \alpha_{pn} \varphi_n \left(\dim_{iklmn}\right) + \sum_{n=1}^{k_{PE}-1} \gamma_{pn} \varphi_n \left(\dim_{iklmn}\right) + e_{iklmnps}$$

where, $Y_{iklmnps}$ is test-day records (milk, fat, protein yield or SCS) of cow *p* obtained at ith lactation, kth herd-test date, *l*th Herd-Birth date of cow, L_i fixed effect of ith

Table 1. Descriptive statistics of the test-day records for some selected days in milk (DIM)

	Milk (Kg)			Fat (Kg)			Protein (Kg)			SCC (number of cell per/mLit)		
DIM	N	Mean	SD	N	Mean	SD	N	Mean	SD	N	Mean	SD
5-35	20569	35.81	8.76	20396	1.28	0.40	20539	1.09	0.27	18880	201412	134200
36-65	22267	39.49	8.68	22050	1.27	0.39	22218	1.14	0.25	19983	193790	136780
66-95	22344	38.78	8.22	22181	1.26	0.39	22303	1.15	0.24	20137	199095	141890
96-125	23561	37.58	7.97	23463	1.25	0.37	23516	1.15	0.24	21371	206010	144560
126-155	21610	36.24	7.81	21536	1.23	0.36	21578	1.13	0.24	19594	212640	147250
156-185	19809	34.80	7.53	19777	1.22	0.34	19789	1.11	0.23	18066	222870	154320
186-225	16251	33.18	7.45	16229	1.18	0.33	16242	1.07	0.23	14834	230545	156900
216-245	13198	31.81	7.24	13192	1.15	0.33	13194	1.04	0.23	12109	233468	154070
246-275	9643	30.31	7.05	9637	1.12	0.31	9639	1	0.22	8822	239967	158270
276-305	6015	29.20	6.90	6013	1.09	0.31	6015	0.97	0.22	5504	243150	159500

lactation yield (i=1, . . . , 3), HTD_k fixed effect of k^{th} Herd-Test date, HB_l fixed effect of l^{th} Herd-Birth date of cow, b_n age at calving fixed effect coefficient, c_n days in milk fixed effect coefficient, age_{iklmn} fixed effect of age at calving, dim_{iklmn} fixed effect of days in milk, φ_n n^{th} Legender polynomial for days in milk, α_{pn} additive genetic random effect, γ_{pn} permanent environmental random effect, $e_{iklmnps}$ residual random effect.

Models with different order of Legendre polynomials for the additive genetic effects and the animal permanent environmental effects were compared using Bayesian information criterion (BIC).

Parameter estimation

Heterogeneous residual variance has been found in the course of lactation in several studies (Olori et al., 1999; Brotherstone et al., 2000; Rekaya et al., 2000). The heterogeneity of residual variance is related to the lactation stage and is larger at the extremes of the lactation. This is likely due to a set of non-specified factors in the model equation (days open, pregnancy status, characteristics of the dry period, body condition at calving, etc.) that make the temporary measurement errors larger and highly variable at the beginning and at the end of the lactation. The inclusion of all of these effects in the model might be difficult, mainly because of the lack of information (Lopez-Romero et al., 2003). Olori et al. (1999) show that the assumption of homogeneity of residual variance along the lactation leads to biases in the residual variance estimates in early lactation, but does not have a significant influence on the rest of the variance components. Rekaya et al. (2000) also stated that assuming a homogeneous residual variance would directly affect the genetic evaluation through the different weights assigned to the information depending on the stage of the lactation.

In this research to account for heterogeneity in residual variance along lactation trajectory, days in milk were partitioned into 10 equal segments of 30 days and independent residual variance structure was assumed.

Both the additive genetic and permanent environmental effects were modeled with Legendre polynomials of different orders of fit. Bayesian Information Criterion (BIC) (BIC) was used to compare the different order of fit.

Results and discussions

Statistical description of the traits

Figures 1, 2 and 3 show changes of the traits along days in milk and indicates that the amount of fat and protein increased but SCS decreased when the milk yield increased.

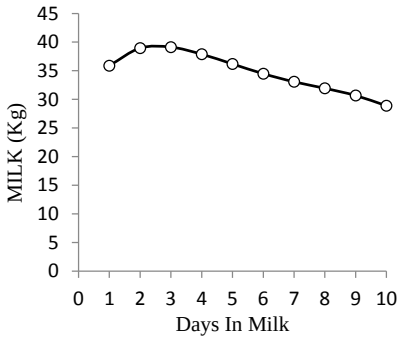

Fig. 1. changes of the milk yield along days in milk

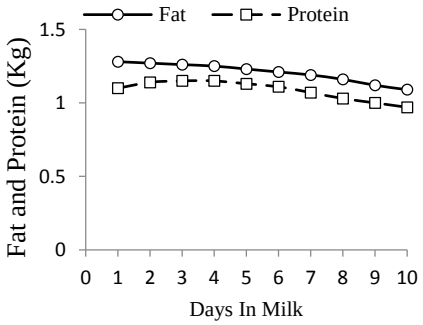

Fig. 2. changes of the fat and protein yield along days in milk

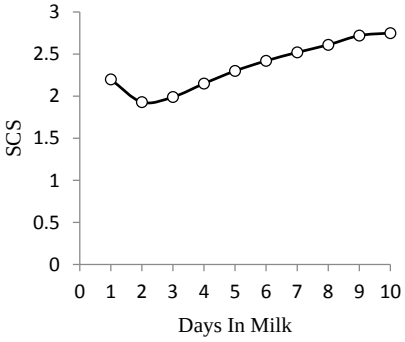

Fig. 3. changes of the SCS along days in milk

Table 2. Number of regression coefficients, log likelihood values and Bayesian Information Criterion (BIC) for test-day milk, fat and; protein yields and SCS

Trait	Ka[1]	Kpe[2]	Number of parameters	Log likelihood	BIC
Milk	3	3	28	-378160	756173
Fat	3	3	28	122420.5	-244694
Protein	4	3	31	213281.9	-426726
SCS	4	3	28	-124071	247996.1

[1] ka: order of fit for additive genetic effect; [2] ke: order of fit for permanent environmental effect.

Model

For milk, fat yields and SCS, genetic and permanent environmental effects were modeled with 3rd order of Legendre polynomials and for protein yield genetic and permanent environmental effects were modeled with 4th and 3rd order Legendre polynomials, respectively. The number of regression coefficients, log likelihood and Bayesian Information Criterion (BIC) for all the traits are given in Table 2.

Variance component

Variance components of TD milk, fat, and protein yields, and SCS were estimated by applying a random regression test day model. Estimates of phenotypic (*Vp*), additive genetic (*VA*), animal permanent environmental (*VEp*) and residual (*Ve*) variances (average)in the beginning (b), middle (m) and end (e) of lactation period for milk, fat, protein yields and SCS are given in Table 3. Phenotypic, additive genetic, permanent environmental and residual variances trend for milk, fat and protein yield and SCS over DIM are presented in Figures 4, 5, 6 and 7 respectively.

For all traits except SCS, additive genetic variances (V_A) increased slowly during the lactation trajectory. For milk yield, the residual variance was relatively small compared with the total phenotypic variance, indi-

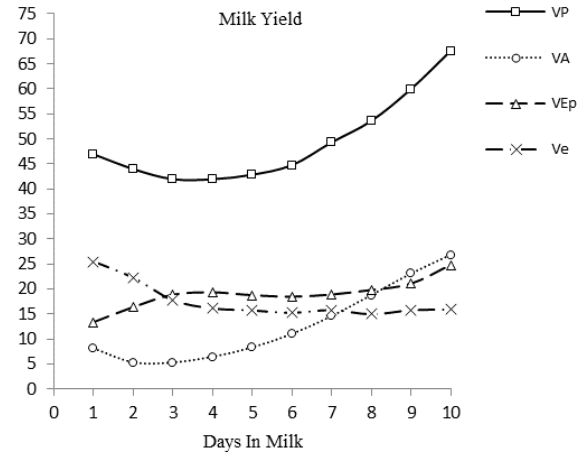

Fig. 4. phenotypic (*Vp*), additive genetic (*VA*), animal permanent environmental (*VEp*) and residual variances (*Ve*) for Milk yield

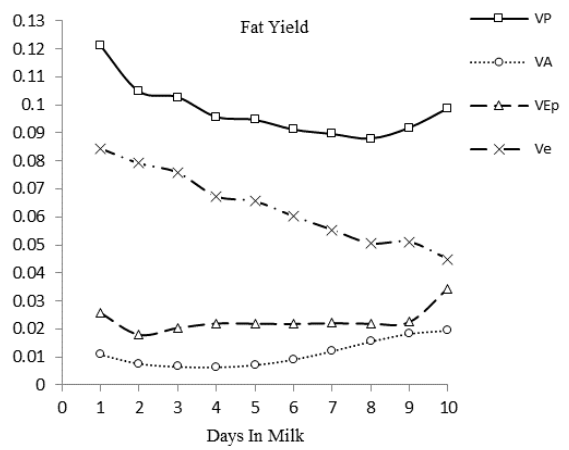

Fig. 5. phenotypic (*Vp*), additive genetic (*VA*), animal permanent environmental (*VEp*) and residual variances (*Ve*) for Fat yield

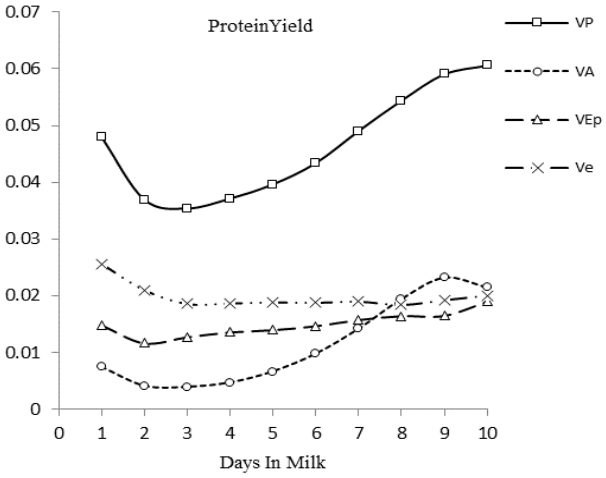

Fig. 6. phenotypic (*Vp*), additive genetic (*VA*), animal permanent environmental (*VEp*) and residual variances (*Ve*) for Protein yield

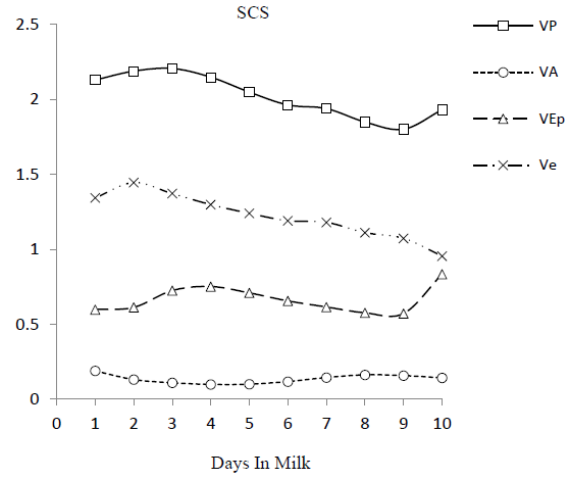

Fig. 7. phenotypic (*Vp*), additive genetic (*VA*), animal permanent environmental (*VEp*) and residual variances (*Ve*) for SCS

Table 3. Estimates of heritability (h^2), phenotypic (*Vp*), additive genetic (*VA*), animal permanent environmental (*VEp*), residual (*Ve*) variances, (r_p)phenotypic correlation and (r_g) genetic correlation (average) in the beginning (b), middle (m) and end (e) of lactation period for milk, fat, protein yields and SCS

	milk			fat			protein			SCS		
	b	m	e	b	m	e	b	m	e	b	m	e
VP	44.25	44.69	60.33	0.11	0.093	0.093	0.04	0.042	0.058	2.17	2.02	1.86
VA	6.24	10.09	22.87	0.008	0.009	0.018	0.005	0.009	0.021	0.14	0.12	0.15
VEp	16.20	18.86	21.89	0.021	0.022	0.026	0.013	0.014	0.017	0.64	0.68	0.66
Ve	21.81	15.75	15.57	0.08	0.06	0.05	0.022	0.019	0.019	1.37	1.23	1.05
h^2	0.14	0.22	0.38	0.09	0.1	0.19	0.13	0.2	0.37	0.07	0.06	0.08
r_g	0.28	0.66	0.52	0.37	0.68	0.52	0.3	067	0.57	0.47	0.71	0.56
r_p	0.32	0.49	0.46	0.16	0.24	0.24	0.26	0.41	0.38	0.21	0.29	0.25

cating a good fit of the model. The residual variance was larger for protein yield and SCS and largest for Fat yield, indicating that the model could be explain less variance and that observations for these traits might therefore be less predictable. Around of peak yield (DIM 50 to 150), additive genetic variances were lower for all traits. Estimated additive genetic, permanent environmental (VE_P), and residual variances (V_e) are in line with other studies (De Roos et al., 2004; Gengler et al., 2004).In general, the trends in the V_A and VE_P variance estimates throughout lactation obtained in this study are comparable to trends found by Olori et al. (1999), Druet et al. (2005), Strabel et al. (2005), and Zavadilova et al. (2005).

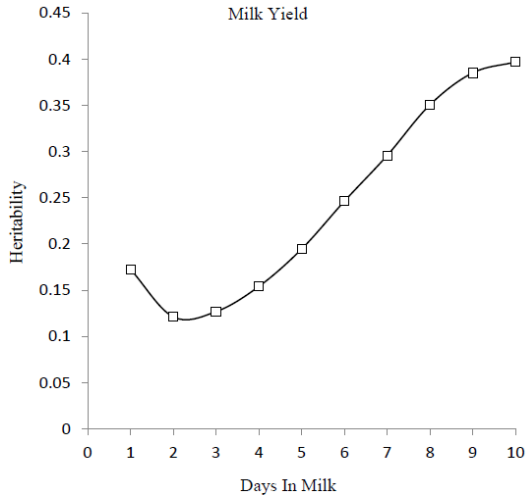

Fig. 8. heritability estimates for test-day Milk yield

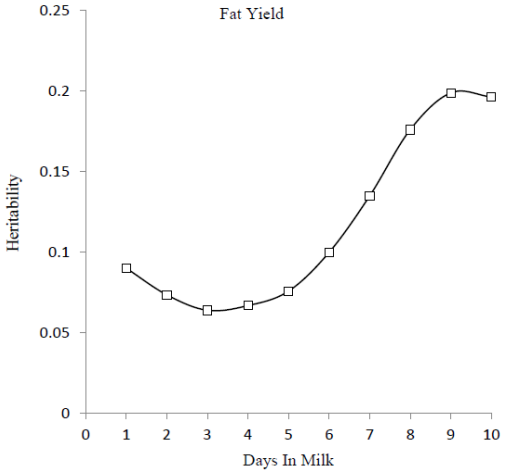

Fig. 9. heritability estimates for test-day Fat yield

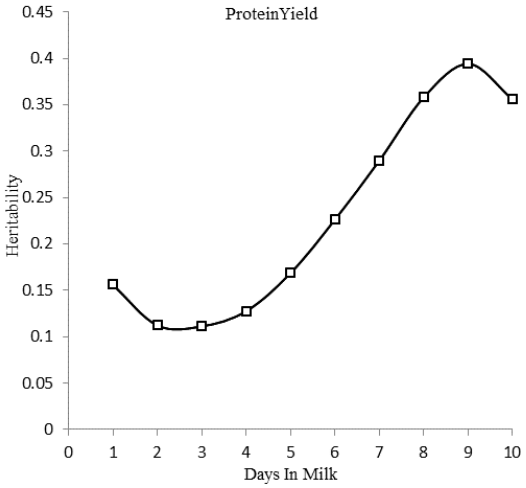

Fig. 10. heritability estimates for test-day Protein yield

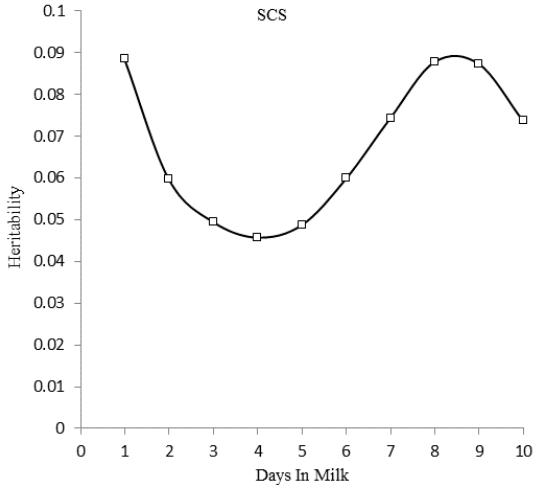

Fig. 11. heritability estimates for test-day SCS

Heritabilities

Range of estimated heritabilities for milk yield were based on daily records from 5 to 305 d varied from 0.17 to 0.40 with an overall of 0.24 (Figure 8), for fat yield from 0.06 to 0.20 (mean $h^2 = 0.12$)(figure 9), for protein yield from 0.11 to 0.39 (mean $h^2 = 0.23$)(figure 10) and for SCS from 0.05 to 0.09 (mean $h^2 = 0.07$)(figure 11). For all traits except SCS, heritability estimates were lowest at the beginning and higher at the end of lactation. Around of peak yield (DIM 50 to 150), heritability was lowest for all traits and then increased to the end of lactation. Druet et al. (2005) found the heritability for milk yield ranged from 0.16 to 0.39 using a random regression test day model from field data. Strabel and Misztal (1999) found a slightly lower heritability for milk yield, in the range of 0.13 to 0.17. Olori et al. (1999) found a heritability of 0.41 to 0.52. Jamrozik and Schaeffer (1997) found heritabilities ranging from 0.40 to 0.59, predicted the highest heritability during the first 10 d of lactation, and credited the result to properly accounting for DIM within test days in the random regression model Estimated heritabilities for yield traits were lower in this study compared with estimates reported by Samore et al. (2002) in Italy using a random regression test-day model with the Wilmink function as coefficients, and were much lower than estimates reported by Muir et al. (2004) in Canada using an identical model. Previous estimates of heritability of SCS in Italy were 0.06 to 0.09 in the first lactation (varying by region) with a test-day repeatability model (Samore et al., 2001) and 0.15 to 0.25 with a multiple-trait random regression test-day model with the Wilmink function (Samore et al., 2002). Miglior et al. (2009) found the average daily heritabilities ranged between 0.222 and 0.346 for the yield traits (milk, fat and protein yields) and between 0.092 and 0.187 for SCS.

Correlations

Phenotypic and genetic correlations for milk, fat and

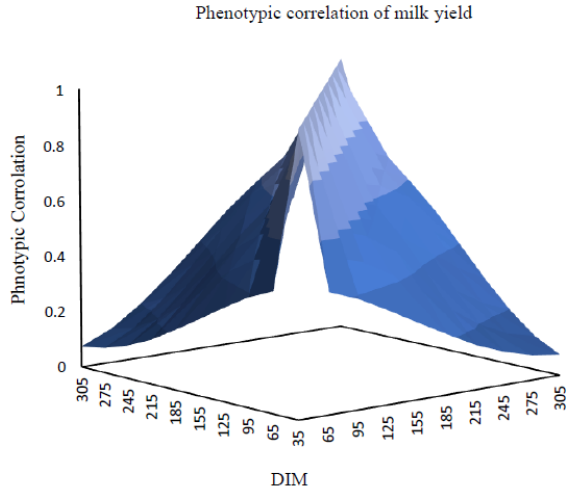

Fig. 12. Phenotypic correlation for test-day Milk yield

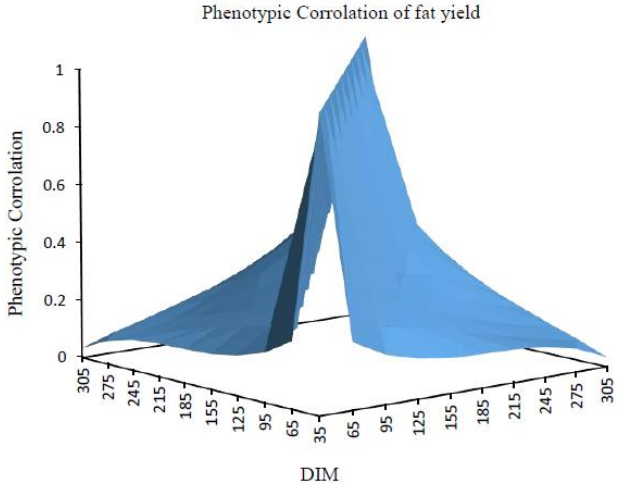

Fig. 13. Phenotypic correlation for test-day Fat yield

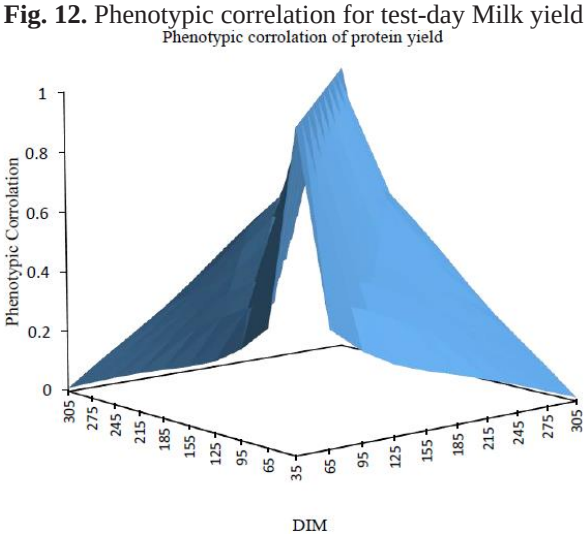

Fig. 14. Phenotypic correlation for test-day Protein yield

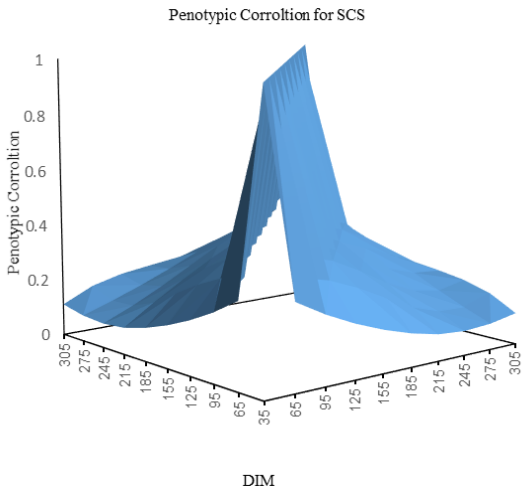

Fig. 15. Phenotypic correlation for test-day SCS

protein yields and SCC over DIM are presented in Figure12 to 19.

Phenotypic correlations estimated in this research, for the four traits, showed similar surfaces. Estimates were High (0.73, 0.45, 0.65 and 0.4 for milk, fat, protein yields and SCS respectively) between adjacent yields and small (0.07, 0.03, 0.01 and 0.09 for milk, fat, protein yields and SCS respectively) between yields at the extremes of the lactation curve. Same pattern was observed for genetic correlation estimates. The genetic correlation estimates between adjacent yields were nearly 0.99 for all the traits investigated. It was decreased up to 0.01 when the age distances were increased. These results agree with those from Herrera *et al.* (2008).Other authors have reported the same trend, with positive estimates that are higher between closer productions (Lidauer *et al.*, 2003; Mayeres *et al.*, 2004).negative genetic correlations were observed between tests at the beginning and at the end of lactation in this research. These estimates may suggest over-parameterization of these random regression model (RRM). Negative genetic correlations between yields during early and late lactation were also obtained by Brotherstone *et al.* (2000), using parametric functions to fit RRM, such as Wilmink and Ali and Schaeffer functions, for Holstein TDMY. López-omero and Carabano (2003) pointed out that these parametric functions tend to underestimate the genetic correlations between milk yield at the beginning and the end of lactations. Probably this is also truth for Legendre polynomials.

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References

Brotherstone, S., White, I.M.S., Meyer, K., 2000. Genetic modeling of daily milk yield using orthogonal polynomials and parametric curves. *Journal of Animal Science*. 70, 407–415.

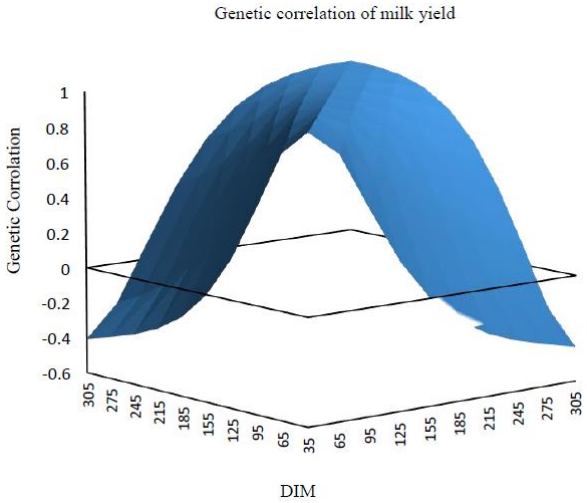

Fig. 16. Genetic correlation for test-day Milk yield

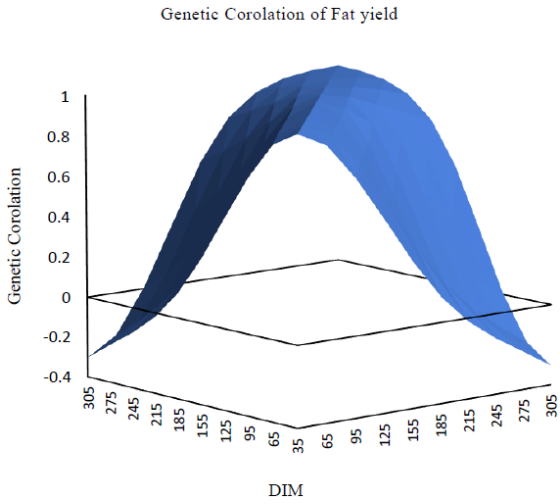

Fig. 17. Genetic correlation for test-day Fat yield

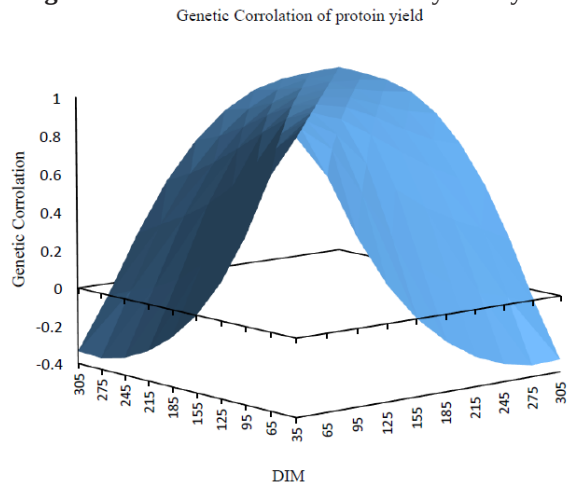

Fig. 18. Genetic correlation for test-day Protein yield

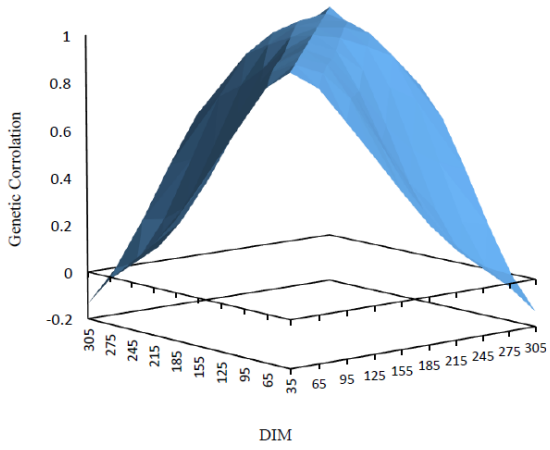

Fig. 19. Genetic correlation for test-day SCS

Caccamo, M., Veerkamp, R.F., Jong, G.D., Pool, M.H., Petriglieri, R., Licitra G., 2008. Variance components for test-day milk, fat, and protein yield, and somatic cell score for analyzing management information. *Journal of Dairy Science*. 91, 3268–3276.

De Roos, A.P.W., Harbers, A.G.F., de Jong, G., 2004. Random herd curves in a test-day model for milk, fat, and protein production of dairy cattle in the Netherlands. *Journal of Dairy Science*. 87, 2693–2701.

Dekkers, J.C.M., Gibson, J.P., 1998. Applying breeding objectives to dairy cattle improvement. *Journal of Dairy Science*. 81, 19–35.

Druet, T., Jaffrezic, F., Ducrocq, V., 2005. Estimation of genetic parameters for test-day records of dairy traits in the first three lactations. *Genetic Selection Evolution*. 37, 257–271.

Gengler, N., Tijani, A., Wiggans, I., 1999. Estimation of (co)variances function coefficient for test-day yield with expectation-maximization restricted maximum likelihood algorithm. *Journal of Dairy Science*. 82, 225.

Gengler, N., Wiggans, G.R., Gillon, 2004. Estimated heterogeneity of phenotypic variance of test-day yield with a structural variance model. *Journal of Dairy Science*. 87, 1908–1916.

Heringstad, B., Chang, Y.M., Gianola, D., Klemetsdal, G., 2003. Genetic analysis of longitudinal trajectory of clinical mastitis in first lactation Norwegian cattle. *Journal of Dairy Science*. 86, 2676–2683.

Heringstad, B., Klemetsdal, G., Ruane, J., 2000. Selection for mastitis resistance in dairy cattle a review with focus on the situation in the Nordic countries. *Livestock Production Science*. 64, 95–106.

Herrera, L.G.G., El Faro, L., Albuquerque, L.G., Tonhati, H., Machado, C.H.C., 2008. Estimates of genetic parameters for milk yield and persistency of lactation of Gyr cows applying random regression models. *Revista Brasileira de Zootecnia*. v.37, n.9, 1584-1594.

Jakobsen, J.H., Madsen, P., Jensen, J., Pedersen, J., Christensen, L.G., Sorensen, D.A., 2002. Genetic parameters for milk production and persistency for Danish Holsteins estimated in random regression models using REML. *Journal of Dairy Science*. 85, 1607–1616.

Jamrozik, J., Schaeffer. L.R., 1997. Estimates of genetic parameters for a test day model with random regressions for yield traits of first lactation Holsteins. *Journal of Dairy Science*. 80, 762–770.

Kadarmideen, H.N., 2004. Genetic correlations among body condition score, somatic cell count, production, reproduction and conformation traits in Swiss Holsteins. *Journal of Animal Science*. 79, 191–201.

Karacaoren, B., 2001. Analysis of univariate selection index using different statistical methods. *M. Sc. Thesis, Akdeniz University, Turkey*. (In Turkish)

Kirkpatrick, M., Lofsvold, D., Bulmer, M., 1990. Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics*. 124, 979–993.

Koivula, M., Nousiainen, J.I., Nousiainen, J., Mantysaari, E.A., 2007. Use of herd solutions from a random regression test-day model for diagnostic dairy herd management. *Journal of Dairy Science*. 90, 2563–2568.

Lidauer, M., Mantysaari, E.A., Stranden, I., 2003. Comparison of test-day models for genetic evaluation of production traits in dairy cattle. *Livestock Production Science*. 79, 73–86.

Lopez-Romero, P., Rekaya, R., Carabano, M.J., 2003. Assessment of homogeneity vs. heterogeneity of residual variance in random regression test-day models in a bayesian analysis. *Journal of Dairy Science*. 86, 3374–3385.

Madsen, P., S. M. Nielsen, M. D. Rasmussen, N. O. Klastrup, N. E. Jensen, P. T. Jensen, P. S.Madsen, B. Larsen, and J. Hyldgaard- Jensen. 1987. Investigations on genetic resistance to Bovine mastitis. *Report no. 621 from the National Institute of Animal Science, Denmark*.

Mark, T., 2004. Applied genetic evaluations for production and functional traits in dairy cattle. *Journal of Dairy Science*. 87, 2641–2652.

Mayeres, P., Stoll, J., Bormann, J., Reents, Gengler, N., 2004. Prediction of daily milk, fat, and protein production by a random regression model. *Journal of Dairy Science*. 87, 1925–1933.

Miglior, F., Gong, W., Wang, Y., Kistemaker, G.J., Sewalem, A., Jamrozik, J., 2009. Genetic parameters of production traits in Chinese Holsteins using a random regression test-day model. *Journal of Dairy Science*. 92, 4697–4706.

Mrode, R.A., Swanson, G.J.T., 1996. Genetic and statistical properties of somatic cell count and its suitability as an indirect means of reducing the incidence of mastitis in dairy cattle. *Animal Breeding*. Abstract. 64, 847–857.

Muir, B.L., Kistemaker, G., Jamrozik, J., Canavesci, F., 2007. Genetic parameters for a multiple-trait multiple-lactation random regression test-day model in Italian Holsteins. *Journal of Dairy Science*. 90, 1564–1574.

Muir, B.L., Kistemaker, G., Van Doormaal, B.J., 2004. Estimation of genetic parameters for the Canadian Test Day Model with Legendre polynomials for Holsteins based on more recent data. *Report to the Dairy Cattle Breeding and Genetics Committee and the Genetic Evaluation Board*. March 2004. http://www.cdn.ca/ ommittees /Apr2004 /GEB Legendre New for Holsteins April 2004. Pdf Accessed Oct. 19, 2004.

Neuenschwander, T., Kadarmideen, H.N., egmann, S., De Haas, Y., 2005. Genetics of calving-dependant production increase and its relationship with health, fertility, longevity, and conformation in Swiss Holsteins. *Journal of Dairy Science*. 88, 1540–1551.

Olori, V.E., Hill, W.G., McGuirk, B.J., Brotherstone, S., 1999. Estimating variance components for test-day milk records by restricted maximum likelihood with a random regression animal model. *Livestock Production Science*. 61, 53–63.

Pool, M.H., Janss, L.L.G., Meuwissen, T.H.E., 2000. Genetic parameters of Legendre polynomials for first-parity lactation curves. *Journal of Dairy Science*. 83, 2640–2649.

Pool, M.H., Meuwissen, T.H.E., 1999. Reduction of the number of parameters needed for a polynomial random regression test day model. *Livestock Production Science*. 64, 133–145.

Pool, M.H., Meuwissen, T.H.E., 2000. Prediction of daily milk yields from a limited number of test days using test day models. *Journal of Dairy Science*. 82, 1555–1564.

Ptak, E., Schaeffer. L.R., 1993. Use of test day yields for genetic evaluation of dairy sires and cows. *Livestock Production Science*. 34, 23–34.

Reents, R., Dekkers, J.C.M., Schaeffer, L.R., 1995. Genetic evaluation for somatic cell score with a test day model for multiple lactations. *Journal of Dairy Science*. 78, 2858–2870.

Rekaya, R., Carabano, M.J., Toro, M.A., 2000. Assessment of heterogeneity of residual variances using changepoint techniques. *Genetic Selection Evolution*. 32, 383–394.

Rekeya, R., Carabano, M.J., Toro, M.A., 1999. Use of test day yields for the genetic evaluation of production traits in Holstein-Friesian cattle. *Livestock Production Science*. 57, 203–217.

Samore, A.B., Boettcher, P., Jamrozik, J., Bagnato, A., Groen, A.F., 2002. Genetic parameters for production traits and somatic cell scores estimated with a multiple trait random regression model in Italian Holsteins. *Commun. No. 01-07. 7th World Congress on Genetics Applied to Livestock Production, Montpellier, France*.

Samore, A.B., Van Arendonk, J.A.M., Groen, A.F., 2001. Impact of area and sire by herd interaction on heritability estimates for somatic cell count in Italian Holstein Friesian cows. *Journal of Dairy Science*. 84, 2555–2559.

Schaeffer, L.R., Jamrozik, J., Kistemaker, G.J., Van Doormaal, B.J., 2000. Experience with a test-day model. *Journal of Dairy Science*. 83, 1135–1144.

Strabel, T., Misztal, I., 1999. Genetic parameters for first and second lactation milk yields of Polish Black and White cattle with random regression test-day models. *Journal of Dairy Science*. 82, 2805–2810.

Strabel, T., Szyda, J., Ptak, E., Jamrozik, J., 2005. Comparison of random regression test-day models for Polish black and white cattle. *Journal of Dairy Science*. 88, 3688– 699.

VanRaden, P.M., 1997. Lactation yields and accuracies computed from test-day yields and (co)variances by best prediction. *Journal of Dairy Science*. 80, 3015–3022.

VanRaden, P.M., 2004. Invited review: Selection on net merit to improve lifetime profit. *Journal of Dairy Science*. 87, 3125– 131.

Zavadilova, L., Jamrozik, J., Schaeffer. L.R., 2005. Genetic parameters for test-day model with random regressions for production traits of Czech Holstein cattle. *Czech Journal of Animal Science*. 50, 142–154.

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برآورد پارامترهای ژنتیکی صفات تولیدی و نمره سلول‌های بدنی در گاوهای هلشتاین ایران با استفاده از مدل رگرسیون تصادفی

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چکیده در این تحقیق رکوردهای روز آزمون تولید شیر، چربی، پروتئین (کیلوگرم) و نمره سلول‌های بدنی (SCS) که به وسیله مرکز اصلاح نژاد کشور بین سال‌های ۲۰۰۷ تا ۲۰۰۹ جمع‌آوری گردیده بود جهت برآورد پارامترهای ژنتیکی این صفات با استفاده از مدل رگرسیون تصادفی مورد استفاده قرار گرفت. مدل‌های مورد استفاده با درجات برازش مختلف توابع لژاندر با استفاده از شاخص BIC مورد مقایسه قرار گرفتند. در صفات تولید شیر، چربی و SCS درجات برازش توابع لژاندر برای اثرات ژنتیکی افزایشی و محیطی دائم به ترتیب برابر با ۳ و ۳ و برای صفت تولید پروتئین درجات برازش به ترتیب برابر با ۴ و ۳ بود. متوسط وراثت‌پذیری برای صفات تولید شیر، چربی، پروتئین و SCS به ترتیب ۰/۲۴، ۰/۱۲، ۰/۲۳ و ۰/۰۷ برآورد گردید. میزان وراثت‌پذیری برآورد شده در تمامی صفات به استثنای صفت SCS در شروع دوره شیردهی پایین و در پایان دوره شیردهی بالا بود. وراثت‌پذیری برآورد شده در تمامی صفات در ماه‌های نزدیک به پیک تولید (۵۰ تا ۱۵۰ روزگی شیردهی) پایین بود و سپس تا انتهای دوره شیردهی افزایش یافت. میزان همبستگی فنوتیپی بین رکوردهای نزدیک به هم بالا گزارش گردید همچنین نشان داده شد که با افزایش فاصله بین رکوردها میزان همبستگی فنوتیپی بین آن‌ها کاهش می‌یابد. در این تحقیق یک همبستگی ژنتیکی منفی بین رکوردهای ابتدا و انتهای دوره شیردهی مشاهده گردید. تحقیق حاضر شواهد واضحی از سودمندی استفاده از مدل رگرسیون تصادفی با استفاده از رکوردهای روزآزمون در تصمیمات مدیریتی نشان داد.