Genetic Analysis of Daily Milk, Fat Percentage and Protein Percentage of Iranian First Lactation Holstein Cattle

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Abstract: The main objective of this study was to investigate the use of daily tests of milk yield, fat and protein percentages for genetic analysis and evaluations of Iranian Holstein cattle. Test-day records of 103462 first lactation Holstein cows in Iran were analysed for milk yield, fat and protein percentages. The model of analysis applied Legendre polynomials to fit traits curves. Additive genetic and permanent environmental effects and heterogeneous residual along days in milk were fitted as random effects and their variance components were estimated by REML methodology. Heritabilities and repeatabilities were estimated and illustrated along lactation for the traits. Heritability ranges were 0.13 - 0.21, 0.07 - 0.11 and 0.11 - 0.18 for milk, fat and protein percentages respectively. Residual variances for the traits were higher at the early and the end of lactation. Genetic trend of milk yield has increased during the past years, while the genetic trend for fat and protein percentages declined as a result of correlated response to genetic selection for milk.

Key words: Test-day Model · Legendre polynomials · Fat percent · Protein percent

INTRODUCTION

Dairy production is one of major agricultural sectors in Iran's economy and the Iranian dairy herd includes an approximate number of one million Holstein cows on commercial dairy farms. Genetic improvement of dairy cattle would increase benefits of dairy industry. The aim of selection in animal breeding is the choice of parents whose progeny will retrieve the highest economic profit under the given production circumstances [1]. Genetic evaluation for identifying superior animals for selection is done using performance data. In diary farms, milk traits performance are recorded at various times along with lactation and each cow is expected to have about 10 daily records per lactation. Hence, these records are known as longitudinal data. In traditional methods of genetic evaluations the daily tests would be transformed to a measure for the whole lactation and there will be one record for each animal per lactation. This will decrease the amount of data and cause computational parsimony, but nowadays, thanks to the progress in computer hardware technology, the analysis of large amounts of data has become feasible [2] and then test-day models has been developed which can use test day data directly.

Some advantages of test day models are greater flexibility about milk recording programs [3], accounting more accurately for environmental factors that affect cows at different stages of lactation at the time of test [3 - 6], modeling the shape of the lactation curve [3, 7], increasing the accuracy of genetic evaluations, accounting for the number of records per cow and the interval between records [8], decreasing the costs of milk recording by making fewer measurements [9], flexibility and the potential to slightly reduce the generation interval by frequent genetic evaluations [5].

The main objective of this paper was to study the use of daily tests of milk yield, fat percentage and protein percentage for genetic analysis and evaluations of Iranian Holstein cattle.

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MATERIALS AND METHODS

Daily records of Holstein cattle were obtained from Animal Breeding Center of Iran. First lactation records of animals in 5 to 330 days in milk, having at least one known parent, calved at ages 20 to 36 months during 1997 to 2009 were extracted. Finally, 1002251 milk test day records from 103462 cows distributed in 265 herds were used for genetic analysis. The pedigree included 5986 sires and totally 239926 animals.

Single-trait animal models with Legendre polynomials for describing traits curves in population were used to fit data. Legendre polynomials are defined for the range of -1 to +1, thus the days in milk values transformed as below to be in this range,

$$d^*_t = -1 + 2\,(d_t - d_{min})/(d_{max} - d_{min})$$

Where d_{min} and d_{max} are the minimum and maximum values for the days in milk variable in data.

For the t-th standardized days in milk (d^*_t), the k-th polynomials is given as

$$\phi(d^*_t)_k = \frac{1}{2^k}\sqrt{\frac{2k+1}{2}}\sum_{m=0}^{k/2}(-1)^m \binom{k}{m}\binom{2k+1}{r}(d^*_t)^{r-2m}$$

Where $k/2 = (k-1)/2$ if k is odd and m is an index number needed to determine the k-th polynomial [10].

The model equation for the analysis of data can be expressed as:

$$y_{tij} = F_i + \sum_{k=0}^{n}\phi_{tk}\beta_k + u_j + pe_j + e_{tij},$$

Where y_{tijk} is the test day milk yield or fat percentage or protein percentage record, F_i represent fixed effects in the model including herd-test date, year-month of calving, milking frequency and age of calving as covariate, β_k are fixed regression coefficients to describe the curve of traits for the whole population, u_j and pe_j refer to the j-th animal additive genetic and permanent environmental effects, respectively, ϕ_{jtk} is the k-th Legendre polynomial for the standardized time t of milking (days in milk), n is the order of Legendre polynomials for fitting traits curve for the population which was 8 for milk and 9 for fat and protein percentage and e_{tij} is the random residual effects describing the unknown effects on traits. To account for heterogeneity in residual effect along the lactation trajectory, days in milk were partitioned into 11 equal segments of about 30 days each and an independent residual variance structure was assumed. In matrix notation, the model may be written as:

$$y = Xb + Qu + Zp + e$$

Where y is the vector of test day yields, b is a vector of solutions for fixed effects and regression coefficients on days in milk, u and p are vectors of animal additive genetic and permanent environmental effects, respectively. The matrices X, Q and Z are incidence matrices relating effects to observations. The (co) variance structure was assumed as:

$$var\begin{bmatrix} u \\ p \\ e \end{bmatrix} = \begin{bmatrix} G & 0 & 0 \\ 0 & P & 0 \\ 0 & 0 & R \end{bmatrix}$$

Where $G = A\sigma_a^2$, $P = I\sigma_p^2$ and R is a diagonal matrix containing the 11 constant variances of residuals and A is the numerator relationship matrix among animals, σ_a^2 and σ_p^2 are the variances for additive genetic and permanent environmental effects respectively and I denotes an Identity matrix. Genetic parameters were estimated using the estimated variance components; heritability as ratio of additive genetic variance to phenotypic variance and repeatability as the ratio of additive genetic and permanent environmental variance components to phenotypic variance. Standard errors for the parameters were calculated using Delta method [11]. Genetic analyses were done using ASREML software [12] with REML procedure for estimation of covariance components.

RESULTS AND DISCUSSION

Statistical Descriptions of the Traits: A summary statistics for the traits along days in milk are shown in Table 1. They revealed the variation of fat percentage is about twice of that for protein percentage. Also the variation for milk increased during first half of lactation and then declined whereas variation in percentages declined first and then increased.

Figure 1 shows changes of the traits along days in milk and indicates that the amount of fat and protein percentages decreased when the milk yield increased and *vice versa*. The estimated regression coefficients for Legendre polynomials of days in milk to describe the curves of milk, fat and protein percentages are shown in Table 2 which the intercepts were constrained to zero due to estimation method.

Table 1: Number (N), mean and standard deviation (SD) for milk, fat percentage (Fat %) and protein percentage (pro %) records along days in milk (DIM)

		Milk			Fat %			Pro %		
Test	DIM	N	Mean	SD	N	Mean	SD	N	Mean	SD
1	5-30	93819	26.35	6.67	85486	3.49	0.96	55172	3.09	0.47
2	31-60	101733	30.18	6.93	93425	3.09	0.82	60340	2.91	0.40
3	61-90	101804	30.40	7.00	93481	3.04	0.80	60688	2.95	0.40
4	91-120	101741	29.88	7.06	93627	3.05	0.80	60921	3.02	0.40
5	121-150	101622	29.07	7.13	93579	3.10	0.80	61173	3.08	0.40
6	151-180	101713	28.19	7.21	93570	3.16	0.80	61275	3.12	0.41
7	181-210	99387	27.31	7.12	91335	3.22	0.81	60025	3.17	0.41
8	211-240	95713	26.35	7.05	87863	3.28	0.81	57693	3.21	0.42
9	241-270	87622	25.23	6.98	80470	3.37	0.83	53106	3.25	0.42
10	271-300	68463	24.36	6.97	62766	3.43	0.84	41603	3.29	0.43
11	301-330	48634	23.62	6.97	44545	3.47	0.85	29778	3.33	0.44
Total	5-330	1002251	27.70	7.33	920147	3.22	0.84	601774	3.11	0.43

Table 2: Legendre polynomial regression coefficients and their standard errors to fit population curves for milk, fat percentage (Fat%) and protein percentage (Pro%)

	Order									
Trait	1	2	3	4	5	6	7	8	9	10
Milk	0	-2.616 ±0.2017	-1.619 ±0.0066	1.104 ±0.0063	-0.692 ±0.0061	0.523 ±0.0061	-0.263 ±0.0061	0.095 ±0.0059	-0.074 ±0.0058	.
Fat%	0	0.101 ±0.0164	0.154 ±0.0012	-0.119 ±0.0011	0.073 ±0.0011	-0.051 ±0.0011	0.034 ±0.0011	-0.018 ±0.0011	0.016 ±0.0010	-0.004 ±0.0010
Pro%	0	0.161 ±0.0093	0.033 ±0.0006	-0.051 ±0.0006	0.053 ±0.0006	-0.041 ±0.0006	0.027 ±0.0006	-0.018 ±0.0006	0.011 ±0.0005	-0.009 ±0.0005

Table 3: Residual variance (σ_e^2), phenotypic variance (σ_p^2), heritability (h^2) and repeatability (r) estimates with their standard errors below them for milk, fat percentage (Fat%) and protein percentage (Pro%) in months along lactation

|		Month										
Parameters		1	2	3	4	5	6	7	8	9	10	11
Milk	σ_e^2	25.07 ±0.13	17.63 ±0.09	13.18 ±0.07	11.19 ±0.06	10.04 ±0.05	10.02 ±0.05	10.00 ±0.05	10.58 ±0.06	12.37 ±0.07	14.72 ±0.09	17.24 ±0.12
	σ_p^2	43.79 ±0.29	36.35 ±0.28	31.9 ±0.27	29.91 ±0.27	28.76 ±0.27	28.74 ±0.27	28.72 ±0.27	29.29 ±0.27	31.09 ±0.27	33.43 ±0.28	35.96 ±0.17
	h^2	0.136 ±0.005	0.164 ±0.0059	0.187 ±0.0067	0.199 ±0.0071	0.207 ±0.0074	0.208 ±0.0074	0.208 ±0.0074	0.204 ±0.0073	0.192 ±0.0069	0.178 ±0.0064	0.166 ±0.0059
	r	0.427 ±0.005	0.515 ±0.0065	0.587 ±0.0073	0.626 ±0.0078	0.651 ±0.008	0.651 ±0.008	0.652 ±0.008	0.639 ±0.0079	0.602 ±0.0075	0.56 ±0.007	0.521 ±0.0077
Fat%	σ_e^2	0.627 ±0.003	0.424 ±0.002	0.379 ±0.002	0.366 ±0.002	0.362 ±0.002	0.365 ±0.002	0.379 ±0.002	0.381 ±0.002	0.404 ±0.002	0.429 ±0.003	0.445 ±0.003
	σ_p^2	0.714 ±0.004	0.511 ±0.003	0.466 ±0.003	0.452 ±0.003	0.449 ±0.003	0.452 ±0.003	0.466 ±0.003	0.468 ±0.003	0.491 ±0.003	0.516 ±0.003	0.531 ±0.003
	h^2	0.07 ±0.0021	0.098 ±0.003	0.107 ±0.0033	0.11 ±0.0034	0.111 ±0.0034	0.11 ±0.0034	0.107 ±0.0033	0.106 ±0.0033	0.102 ±0.0031	0.096 ±0.003	0.094 ±0.0029
	r	0.122 ±0.0026	0.17 ±0.0036	0.186 ±0.0039	0.192 ±0.004	0.193 ±0.0041	0.192 ±0.004	0.186 ±0.0039	0.185 ±0.0039	0.177 ±0.0037	0.168 ±0.0036	0.163 ±0.0035
Pro%	σ_e^2	0.109 ±0.0007	0.076 ±0.0005	0.063 ±0.0004	0.058 ±0.0004	0.059 ±0.0004	0.059 ±0.0004	0.061 ±0.0004	0.064 ±0.0004	0.071 ±0.0005	0.082 ±0.0006	0.09 ±0.0008
	σ_p^2	0.132 ±0.0009	0.099 ±0.0007	0.085 ±0.0007	0.08 ±0.0006	0.081 ±0.0007	0.082 ±0.0007	0.083 ±0.0007	0.087 ±0.0007	0.094 ±0.0007	0.104 ±0.0008	0.113 ±0.0008
	h^2	0.11 ±0.0034	0.147 ±0.0045	0.171 ±0.0052	0.182 ±0.0055	0.179 ±0.0055	0.178 ±0.0054	0.175 ±0.0053	0.168 ±0.0051	0.155 ±0.0047	0.14 ±0.0043	0.129 ±0.0039
	r	0.171 ±0.004	0.227 ±0.0053	0.264 ±0.0061	0.281 ±0.0065	0.277 ±0.0064	0.275 ±0.0064	0.271 ±0.0063	0.259 ±0.006	0.24 ±0.0056	0.216 ±0.005	0.199 ±0.0048
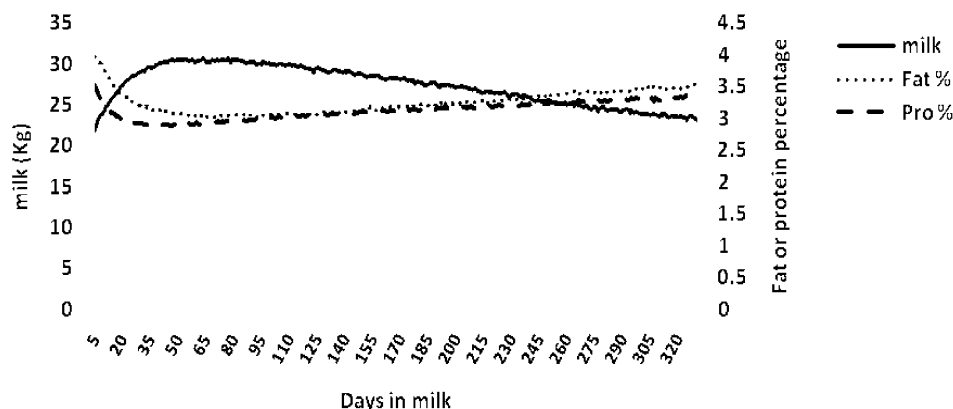
Fig. 1: Average of milk, fat percentage (Fat%) and protein percentage (Pro%) along days in milk
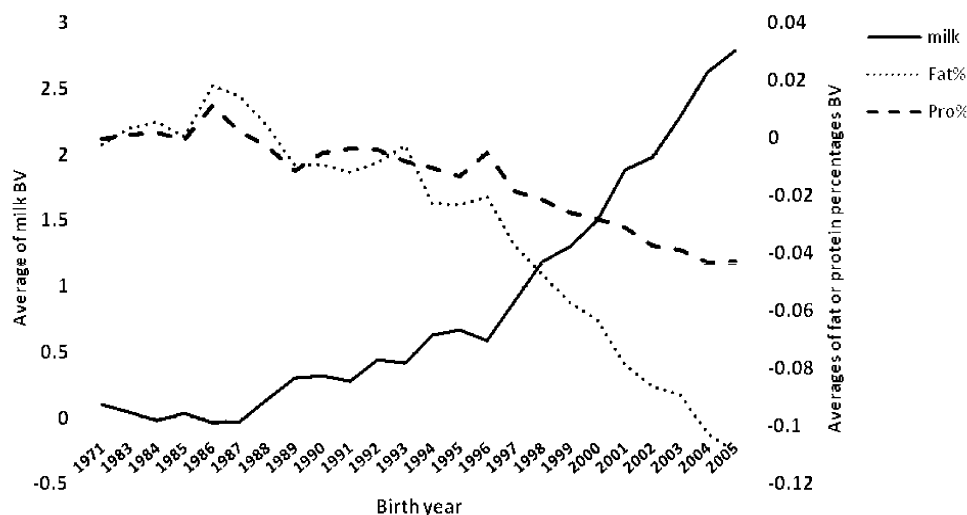
Fig. 2: Trends of average breeding values (BV) for milk yield, fat percentage (Fat%) and protein percentage (Pro%) across birth years

Parameter Estimation: Estimates of additive genetic variance were 5.96 ± 0.21, 0.05 ± 0.002 and 0.015 ± 0.0004 for milk, fat percentage and protein percentage, respectively. For permanent environmental effect, the estimated variances for milk, fat percentage and protein percentage were 12.75 ± 0.16, 0.037 ± 0.001 and 0.008 ± 0.0003 respectively. Residual and phenotypic variances, heritability and repeatability for traits in months along lactation are shown in Table 3.

Residual variances of traits had changes along months of lactation for traits; they first decreased toward mid lactation and then increased for the second part of lactation. Similar trends for residual variances were reported by authors [14 - 16]. This pattern of changes mainly comes from difference in farm management for a lactating cow regarding to the stages of lactation. Heritability estimates for fat percentage were lower than those for milk and protein percentage. Similarly, Silvestre *et al.* [17], DeGroot *et al.* [18] and Hammami *et al.* [19] estimated lower heritabilities along lactation for fat than those for milk and protein. The characteristics of fat percentage in the way of being much influenced by temporary environmental effects may be the main reason for its lower heritabilities.

Genetic Trend: Regression coefficients for estimated animal breeding value on animal birth year as the indicator of genetic trend were estimated as 0.10 ± 0.0004, -0.004 ± 0.00003 and -0.002 ± 0.00002 for milk yield, fat percentage and protein percentage, respectively. Figure 2 shows these positive genetic trend for milk

yield and negative genetic trends for fat and protein percentages during previous years. Similar trends were reported by Sahebhonar [20] using the 305 day measures of the traits. They indicated that Iranian Holstein cattle population genetically improved for milk yield. The interest of farmers to use sperms from genetically superior bulls could be the main factor which caused these changes.

Negative trends for fat and protein percentages are the result of major emphasis on milk yield and neglecting fat and protein percentages in sire selection at the level of the farms during past years. This condition could cause a correlated response for fat and protein percentages as a result of selection for milk because of the negative correlation between milk yield and fat and protein percentages. Strong negative genetic correlations between 305 day measure of milk and fat and protein percentages have been reported for Iranian Holstein population [20]. Hashemi and Nayebpour [21] also reported a moderate negative genetic correlation between milk yield and fat percentage in Iranian Holstein population.

CONCLUSION

Genetic analyses of milk production traits by means of a test-day model provided more complete and accurate information from the data especially along lactation trajectory, so resulted parameters are more suitable for genetic evaluations. Negative estimates of genetic trends for fat and protein percentages demonstrate the

conditions where some economic important traits are genetically negatively correlated with other important traits. The results obtained in this study provided population specific parameters with a higher accuracy that could be used in order to develop the national selection index of Holstein dairy cows.

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