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Genetic Parameters Estimation for Some Functional Milk Traits of Brown Swiss Dairy Cattle

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Abstract

The objective of this study was to estimate heritabilities and to investigate the genetic relationship between some functional milk traits such as milk yield (**MY**), dry matter (**DM**), fat (**F**) and milking duration (**MD**) on Brown Swiss dairy cattle breeding in Turkey with random regression model using heterogeneous residual error variance interval. Variance components were estimated with 4 multiple-trait (4 traits at a time) random regression model via restricted maximum likelihood (REML) with AI-REML algorithm. Data were obtained from an experimental farm and comprised 636 test day (TD) records for each trait. Average heritability for MY, DM, F and MD were 0.29, 0.10, 0.16 and 0.05, respectively. The largest genetic correlation interval were found between F and MD and ranged from -0.34 to 0.72 throughout lactation. The shape of genetic correlation curve of DM-MD was similar to F-MD and genetic correlation between DM-MD ranged from -0.24 to 0.61. Genetic correlations of other traits changed from 0.08 to 0.65 for MY-DM, -0.16 to 0.28 for MY-MD and 0.04 to 0.59 for MY-F throughout lactation. Results from this study implied that increasing fat percentage in milk and other milk components may have led to decrease the flow of milk and consequently, affected the milking duration.

Key words: Random regression model, functional milk traits, genetic parameter

Esmer Irkı Süt Sığırlarında Bazı İşlevsel Süt Verim Özelliklerine İlişkin Genetik Parametre Tahminleri

Özet

Bu çalışmanın amacı Türkiye de yetiştiriciliği yapılan Esmer ırkı süt sığırlarında süt verimi **(MY)**, kuru madde **(DM)**, süt yağı **(F)** ve sağım süresi **(MD)** gibi bazı işlevsel süt verim özelliklerinin kalıtım derecelerini hesaplamak ve bu özelliklerin aralarındaki genetik ilişkiyi araştırmaktır. Araştırma da şansa bağlı regresyon modeli kullanılmış ve denetim günleri aralıklarında hata varyansının farklı olduğu kabul edilmiştir. Varyans bileşenleri şansa bağlı regresyon modelinde dört özelliğin aynı anda modele dahil edilmesi ile kısıtlanmış en yüksek olabilirlik (REML) metodu ile AI-REML algoritması kullanarak tahminlenmiştir. Araştırma da deneysel bir çiftlikten elde edilen ve her bir süt verim özelliğinin dahil olduğu 636 denetim günü kaydı kullanılmıştır. MY, DM, F and MD için kalıtım dereceleri ortalamaları sırasıyla 0.29, 0.10, 0.16 ve 0.05 olarak hesaplanmıştır. Özellikler içinde laktasyon boyunca en geniş genetik korelasyon aralığı F - MD arasında saptanmış olup -0.34 ile 0.72 aralığında değişmiştir. DM-MD arasındaki genetik korelasyon eğrisinin şekli F-MD arasındaki genetik korelasyon eğrisi ile benzerlik göstermiş ve değerler -0.24 ile 0.61 aralığında saptanmıştır. laktasyon boyunca diğer özelliklere ilişkin genetik korelasyonlar MY-DM için 0.08 ile 0.65, MY-MD için -0.16 ile 0.28 ve MY-F için ise 0.04 ile 0.59 aralığında değişmiştir. Bu sonuçlar süt bileşenleri içinde yağ yüzdesindeki artışın süt akıcılığını azaltarak süt sağım hızını etkilediğini göstermektedir.

Anahtar kelimeler: Şansa bağlı regresyon modeli, işlevsel süt verim özellikleri, genetik parametre

Introduction

Literature regarding genetic parameters especially genetic correlations between milk production traits such as fat, protein, lactose and milk urea nitrogen for dairy cattle populations breeding in Turkey is very scarce. In dairy cattle, random regression model methodology is commonly used for regular genetic evaluation of milk production traits (Interbull, 2007; Bohmanova et al., 2008), such as F, protein and lactose (i.e.). Considering literature for genetic parameters for dry matter is fairly rare. Yield of DM components (fat protein, lactose) is advantageous for the needs of milk processing and could be the reason for an increasing interest in the analysis of DM in milk. Considering the chemical analysis, dry matter is relatively easy to carry out, it seems to be worthwhile to estimate genetic parameters for that trait and to use the results in breeding practice (Yazgan et al., 2010).

Milking speed is a functional trait that relates to the incidence of clinical mastitis, labor time, and electrical power (Boettcher et al., 1998; Ilahi and Kadarmideen, 2004; Karacaören et al., 2006). And also, long milking duration results with more electricity consumption. A single milking speed observation per animal may be insufficient, because genetic and environmental factors that affect the milking speed of individual cows may vary during a lactation or between subsequent lactations and milking duration may have optimum because most producers prefer cows with relatively uniform milking duration that do not decrease the flow of cows through the milking parlor (Zwald et al., 2005).

When aimed to estimating (co)variance component, to reduce the number of parameters and the dimension of likelihood searchers and some computing problems, error variances may be assumed constant throughout lactation. In practice error variance can be highly variable not only monthly interval but also day to day. So, when use random regression model in genetic analysis if defining classes of residual variances by test days records, estimation of genetic parameters can be more accurate. When the models applied in pair-wise analyses obtaining genetic parameters such as heritability and genetic correlation could not be same as those fitted for each of the traits in the univariate analyses. Furthermore, considering a trait, could be different for this trait between two pair-wise analyses. If additive genetic correlation is low between traits, order of estimated breeding values can be different by univariate and multivariate analyses (Kumlu, 2003). Using with four traits at a time, obtained genetic parameters can be more accurate. Especially, more than two traits with large data set, multivariate random regression analyses needs to large computer memory (RAM) and processor (CPU). However, owing to development of computer and software technology, computing problems such as long CPU time, has begun to decrease and made possible the multivariate (four or more trait) analyses.

Various REML algorithms were developed to compute variance and covariance components. The relatively simpler algorithm is derivative-free methods. Because of no derivate are used in this method and potentially unreliable for complicated model such as multiple traits. On the other hand average information (AI-REML) algorithm is the most popular algorithm involving the second derivate (Misztal ,2008).

In Turkey there are only very few studies on genetic correlation between milk yield, fat and milking duration traits that we chose to analyze in this research. Especially fat ratio in milk may be an important factor affecting milk flow rate or milking duration. Therefore, there is a need to research and detect the correlations with other traits. Additionally, obtained parameters via such calculations i.e. breeding values and other genetic parameters can be used for selection of animals.

Therefore objective of this study was to estimate heritabilities and genetic relationships between some functional milk traits such as milk yield (MY), milk dry matter (DM), milk fat (F) and milking duration (MD) on Brown Swiss dairy cattle breeding in Turkey with random regression model using heterogeneous residual error variance interval.

Materials and Methods

Data

Data set were the first, second and third lactation records of 59 healthy Brown Swiss dairy cows raised at experimental research farm of the Atatürk University, Agriculture Faculty in Erzurum province of Turkey over the period from 2006 to 2007. Traits (MY, DM, F and MD) were recorded fortnightly. Because animals used for another research, MY were recorded until 196*th* days in milk (DIM). MY and MD were measured twice (morning and evening) with milk-o meter unit that have the traditional type (Sharaby et al., 1977). A milk-o tester device was used to analyses for F and for the analysis of milk dry matter was used drying method in oven. The animals sheltered in compartments having open and closed section. Dimensions of the panes were; 25.0m x 8.0m for the open pail and 5.0m x 9.50m x 8.0m for the closed pail. Roughage was supplied in the open division at the feeders which has of 1.0 m width and 8.0 m length. In the research is not implementing a special feed or feeding program. Cows in the barn were supplied with ad-libitum roughage twice a day (09:00 pm and 14:00 am). The cows had no limitation for water supply. According to actual milk yield, the concentrate feed was supplied during the milking for each cow, separately. Components of the concentrate feed consisted of 18% crude protein, 2.80% crude fat, crude fiber 9.90%, crude ash 8.40%, macro elements, micro elements, vitamins. Concentrate feed that had 2700 mcal/ kg energy. Total number of animals in pedigree file was 115 (59 cows, 15 sires and 41 dam). There were 13 cows with unknown sire and 10 cows with unknown dam.

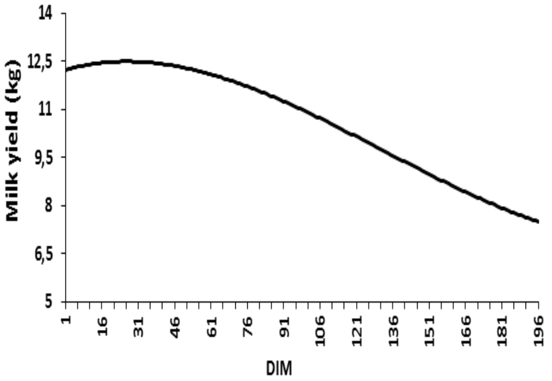

Figure 1. Lactation curve fitted by second order Legendre polnomiyal

Statistical analysis and models

Variance components, covariances and genetic parameters for MY, MD, F and MD were estimated with 4 multiple-trait (4 traits at a time) random regression model via restricted maximum likelihood (REML) with AI-REML algorithm, using WOMBAT software (Meyer, 2007). The multiple traits random regression model for the genetic analysis can be written as:

$$y_{ijklmo} = CY_{ij} + P_{ik} + \sum_{n=1}^{3} \beta_{iln}\, x_n(t) + \sum_{n=1}^{3} \alpha_{imn}\, x_n(t) + \sum_{n=1}^{3} \rho_{imn} x_n(t) + e_{ijklmo}$$

Where;

y_{ijklmo} : is the *o*th test-day record of the *m*th cow for a trait *i* (TD milk, milk dry matter, fat percentage or milking time).

CY_{ij} : is the *j*th year effect for a trait *i.*

P_{ik} : is the *k*th parity effect for a trait *i.*

β_{iln} : is the *n*th fixed regression coefficient for a trait *i* and specific to the *l*th TD class.

α_{imn} : is the *n*th random regression coefficients for the additive genetic effect of cow m separate for trait *i.*

ρ_{imn} : is the *n*th random regression coefficient for the permanent environmental effect of cow *m* for trait *i.*

$x(t)$: is a vector of covariates of size 3 (because of second order Legendre polynomial has 3 parameters) describing the shape of lactation curve of fixed and random regressions evaluated at *t* DIM.

e : is the residual (different value in each DIM interval for different traits).

There were 2 calving years (2006-2007) and 3 class of lactation parity (1-3). In matrix notation the model can be written as:

$$y = Xb + Za + Wp + e$$

Where; **y** is a vector of observations, **b** is a vector of fixed effects, **a** and **p** are vectors of random regression coefficients for additive genetic and permanent environmental effects, respectively, **e** is a vector of residuals. Matrices **X**, **Z** and **W** are incidence matrices which relate observations to effects. The (co)variance matrix for random effects in the model can be written as:

$$var\begin{pmatrix}\mathbf{a}\\ \mathbf{p}\\ \mathbf{e}\end{pmatrix} \sim N\left[0;\begin{pmatrix}\mathbf{G}\otimes\mathbf{A} & 0 & 0\\ 0 & \mathbf{P}\otimes\mathbf{I} & 0\\ 0 & 0 & \mathbf{R}\end{pmatrix}\right]$$

Where **G** and **P** are (co)variance matrices for additive genetic and permanent environmental random regression coefficients, respectively. **A** is additive genetic relationship matrix, **I** is the identity matrix, and **R=I** σ_e^2. Residuals variances σ_e^2, were assumed as heterogeneous between DIM intervals for different traits. DIM intervals were arranged as 1-16, 17-31, 32-46, 47-61, 62-76, 77-91, 92-106, 107-121, 122-136, 137-151, 152-166, 167-182 and 183-196. To obtain covariance and full genetic correlations between all traits throughout DIM, following expression was used;

$$\hat{G} = \Phi x G x \Phi'$$

where $\hat{G}$ (56×56) is the matrix includes all (co)variance at t^{th} DIM for all traits. The matrix G (12×12) of order k contains the variance components for the random regression coefficients in the model. The matrix Φ of order t × k contains second order Legendre polynomial coefficients. Genetic correlations between all traits at the t^{th} time were calculated using following expression;

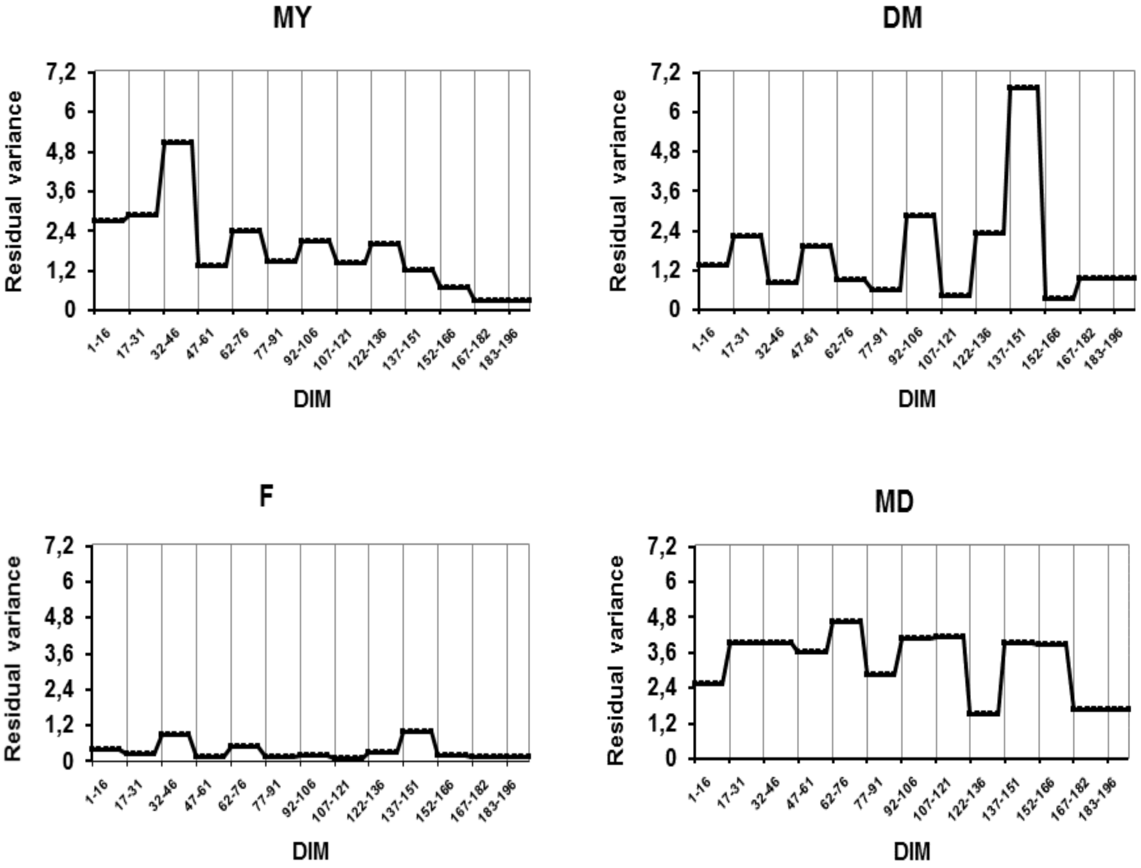

Figure 2. Residual variance by DIM interval for milk yield (MY), dry matter (DM), fat (F) and milking duration (MD)

$$r_g(t) = \frac{COV_t(\text{trait}(n), \text{trait}(n'))}{\sqrt{V_t(n) * V_t(n')}}$$

Where $r_g(t)$: Genetic correlations between two traits at *t*th DIM time, $COV_t(\text{trait}(n), \text{trait}(n'))$: covariance between two traits n and n', $V_t(n)$ and $V_t(n')$ are the respective variances for the two traits at t^{th} DIM.

Results

Descriptive statistics for MY, DM, F and MD were given in Table 1. The means of MY, DM, F and MD were 10.62 kg, 11.22%, 3.90% and 6.70 min respectively. At result of the analysis Log L was detected as -1680. Lactation curve consisting with estimation daily milk yields was given in Figure 1. Considering the shape of the curve it could be said that second order Legendre polynomial function defined the lactation curve as typical (Macciotta et al., 2005).

Variances

Residual variances for MY, DM, F and MD by interval were given in Figure 2. Considering all traits, fat was the lowest residual error variances for all intervals and ranged from 0.082 – 1.007. At the 137-151 DIM interval, residual variance of DM reached to 6.737 and it was the highest value between all traits and all intervals. Residual error variance for MY fallowed this and reached 5.080 at the 32-46 DIM interval. Except from F, residual error variances of traits were undulating form throughout DIM.

Estimates of genetic and permanent environment variances for MY, DM, F and MD were given in Figure 3. Genetic and permanent environmental variances of MY were the highest in all traits and ranged from 0.32 - 7.68 and 2.13-3.22 respectively. Alteration of DM and F variance components were similar. Except MY, especially genetic variance have typical ''U'' form for all traits. However, for MY, genetic variance values were continuously decreasing form. On the other hand, permanent environmental variances of MD decreased to 0.05 from 0.37 over 1-136 DIM.

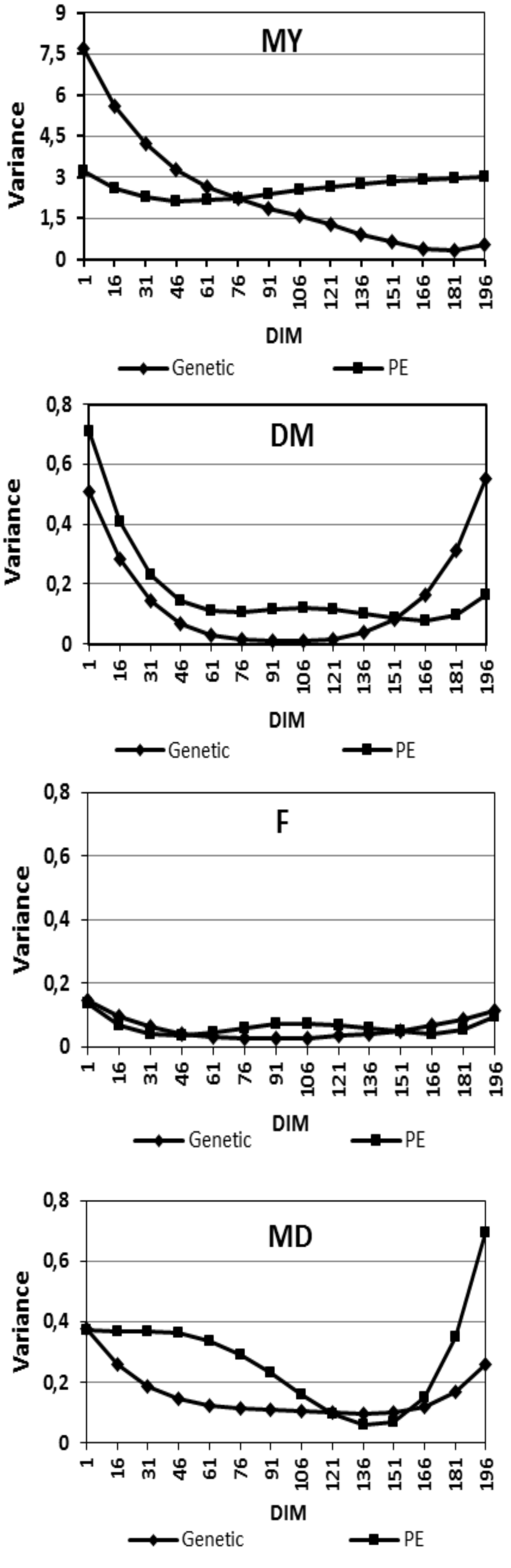

Figure 3. Additive genetic and permanent environment variances for milk yield (MY), dry matter (DM), fat (F) and milking duration (MD)

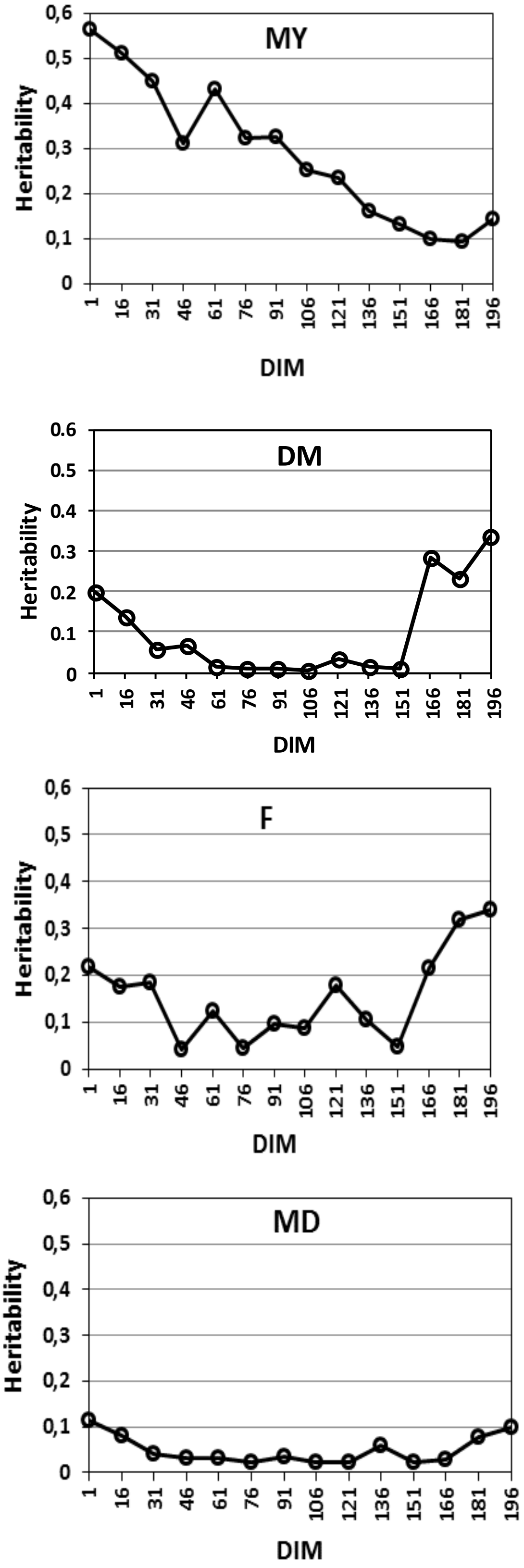

Figure 4. Heritability estimations for milk yield (MY), dry matter (DM), fat (F) and milking duration (MD)

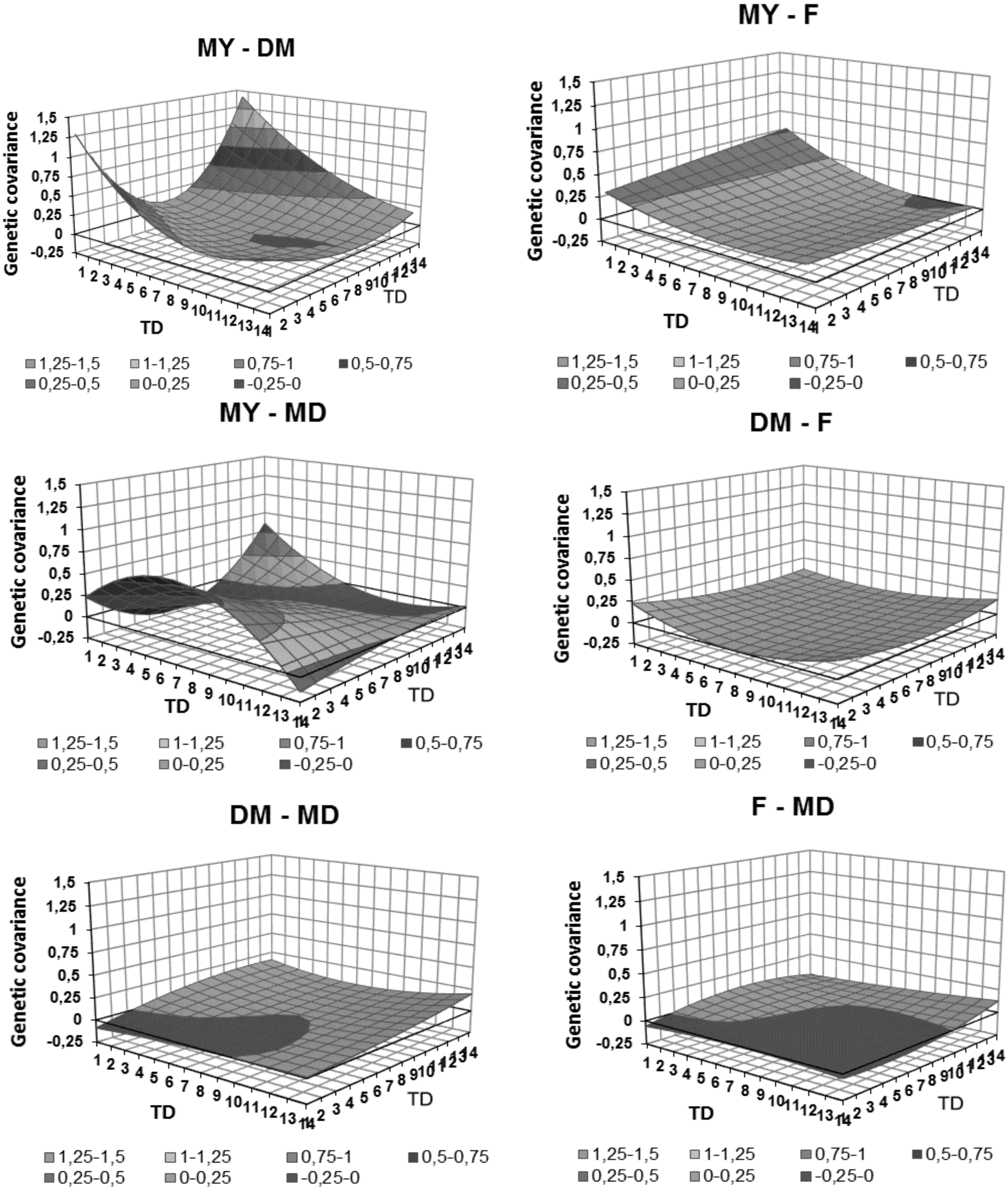

Figure 5. Genetic covariances between milk yield - dry matter (MY-DM), milk yield – fat (MY-F), milk yield – milking duration (MY-MD), dry matter – fat (DM – F), dry matter – milking duration (DM – MD) and fat – milking duration (F – MD)

After this point, it accented sharply and reached to 0.69 at DIM 196. In addition, after 76 DIM, genetic variances were less than permanent environmental variances for MY. Similarly, genetic variances were less than permanent environmental variances before 151 DIM for DM. Considering F, between 61-151 DIM, and for MD between 1-121 and 166-196 DIM, genetic variances were less than permanent environmental variances.

Heritabilities

Heritability estimations of all traits over DIM were given in Figure 4 and calculated average heritabilities from this by traits were given in Table 2. The highest values of heritability (0.56) were

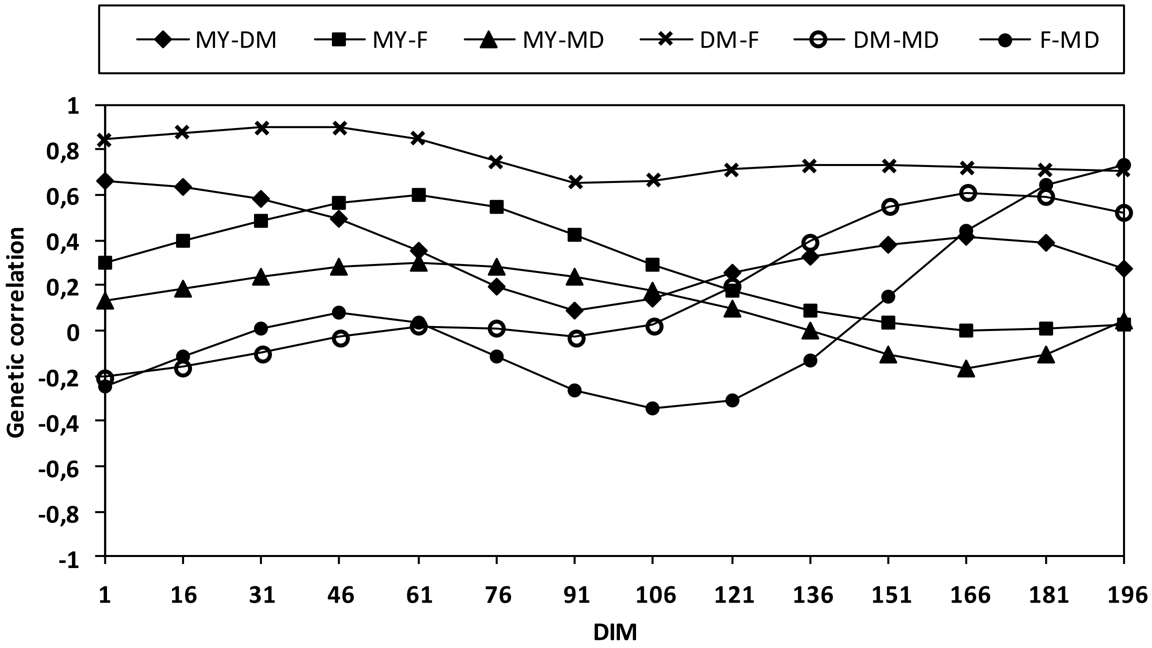

Figure 6. Genetic correlations between milk yield - dry matter (MY-DM), milk yield – fat (MY-F), milk yield – milking duration (MY-MD), dry matter – fat (DM – F), dry matter – milking duration (DM – MD) and fat – milking duration (F – MD)

found for MY at the beginning of lactation. After this point, values decreased throughout DIM. At 181 DIM found lowest heritability value for MY and it was 0.10. Considering all traits, the lowest heritability values were found for MD during 1- 196 DIM and vary from 0.023 to 0.115. For DM, heritability values were 0.20 at the beginning of lactation, however, very low values found between 61 and 151DIM. After this point heritability values upraised sharply and reached to 0.33 at 196 DIM. Considering F, heritability values were in fluctuating form and they ranged from 0.042 to 0.33.

Covariances and genetic correlations

Genetic correlations and covariances between MY-DM, MY-F, MY-MD, DM – F, DM – MD and F – MD were given in Figure 5 and 6.

Table 1. Number of records (n), means ($\bar{X}$), and standard errors (SE) for milk yield (MY), dry matter (DM), fat (F) and milking duration (MD) by test day (TD) records.

			MY (kg)		DM (%)		Fat (%)		MD (min)	
TD	DIM[1]	n	$\bar{X}$	SE	$\bar{X}$	SE	$\bar{X}$	SE	$\bar{X}$	SE
1	1	59	11.82	0.532	10.27	0.244	3.98	0.107	6.98	0.222
2	16	59	12.15	0.557	10.56	0.137	3.58	0.077	7.08	0.244
3	31	59	12.76	0.502	11.32	0.158	3.69	0.066	6.96	0.290
4	46	59	13.04	0.446	11.14	0.142	3.78	0.130	6.73	0.255
5	61	56	11.86	0.375	10.59	0.173	3.64	0.069	6.72	0.281
6	76	54	10.77	0.437	11.30	0.145	3.87	0.091	6.96	0.290
7	91	49	10.83	0.434	11.35	0.124	3.69	0.064	6.46	0.252
8	106	44	10.21	0.471	10.59	0.203	3.79	0.078	6.78	0.319
9	121	41	9.34	0.421	11.76	0.127	3.86	0.059	7.32	0.284
10	136	35	9.14	0.408	10.91	0.213	4.03	0.091	6.17	0.216
11	151	33	8.04	0.405	12.71	0.242	4.84	0.156	6.15	0.327
12	166	31	7.96	0.362	12.41	0.114	4.10	0.080	4.78	0.196
13	181	30	7.28	0.334	12.28	0.184	4.18	0.070	6.99	0.284
14	196	27	6.11	0.267	11.90	0.239	4.70	0.092	6.86	0.327

[1] Days in milk

Throughout DIM, highest genetic correlations were found between DM – F and ranged from 0.65- 089. At the middle of the TD periods covariance between DM and F showed a downward trend. However, at the beginning of lactation and towards the end of TD covariance between DM and F were tending to up rise, as shown in Figure 6. Although, covariance between especially MY-F, DM-F and DM-MD have smooth surface, MY-MD covariance surface was in fluctuating form (Figure 5). The largest correlation interval were found for F-MD and ranged from -0.34 (middle of the DIM) to 0.72 (end of DIM). The shape of genetic correlation curve of DM-MD was similar to F-MD and genetic correlation for DM-MD ranged from -0.24 to 0.61. Genetic correlations of other traits were varying from 0.08 to 0.65 for MY-DM, -0.16 to 0.28 for MY-MD and 0.04 to 0.59 for MY-F. As in shown in Figure 6, except F-MD, genetic correlations were positive between all traits, generally.

Discussion

Variances

In this research the estimates residual error variances for MY were generally lower when compared to the results obtained in previous researches (e.g. Karacaören et al., 2006 and Bohmanova et al., 2008) that error variance were assumed to be heterogeneous during lactation. Similarly, residual error variances obtained from this study for MD throughout DIM (Figure 1), were generally lower when compared with findings reported by Karacaören et al. (2006) for milking speed trait. On the other hand residual error variances for MD were higher when compared with findings reported by Zwald et al. (2005). They calculated residual error variance for MD as 1 min^2.

Considering error variance for DM very low when compared results with previous study by Yazgan et al. (2010). As in shown Figure 2, except F, residual error variances were in fluctuating form for all traits. Unknown environmental factors could have caused these fluctuations throughout DIM. As shown in Figure 2, residual error variances for MY reached to maximum value during at 32-46 DIM. As shown in Figure 1, most of dairy cows reaches to the peak yield at this time interval (Macciotta et al., 2011) and coincide with estrous cycles. This can explain that why error variance reached to peak level in this interval. Similarly, DM ratio in milk begins to increase at the end of lactation when compared with middle of lactation and this might cause to increase of error variance for DM during at 137-151 DIM (Figure 2).

As given in Figure 3, estimated additive genetic variances for MY were high at the beginning of lactation and low towards to end of DIM. Inother words, curve of variances was in decreasing shape and not typical ‘’U’’ form as mentioned earlier. Similar results were obtained from studies used second order Legendre polynomial by Takma and Akbaş (2009). Different from this study, Cobuci et al. (2005), Miglior et al. (2007) and Galiç and Kumlu (2012) were found high additive genetic variance at the beginning and end of lactation when compared with the middle of lactation. Also, estimated additive genetic variances for MY in this study were high when compared the result of research conducted by Hammami et al. (2008). Estimated additive genetic variances values for DM throughout DIM were very close to results from previous study (Yazgan et al., 2010). Additionally, estimated additive genetic variances for MD in this study were low when compared result of research conducted by Zwald et al. (2005). It could be explained by the fact that they used different methods of measuring traits and they analyzed much larger population with Gibbs sampling.

The estimation of permanent environmental variance for MY were close to stable and about 3kg^2 throughout DIM (Figure 3). Different from this study Takma and Akbaş (2009) reported that permanent environmental variances for test day milk yields were higher (near to 9 kg^2) at early lactation and lower (near to 3 kg^2) for the rest of lactation. In addition, permanent environmental variances for MY were estimated over 25 kg^2 by Hammami et al. (2008) and very high when compared with our study. Using different number of animals and breeds and also experimental data set used in this research, may cause to obtain different permanent environmental variances.

Heritabilities

In this research estimates of heritability values for MY were in continuously decreasing form throughout DIM. It could be explained by; while permanent environmental variances were relatively stable throughout DIM, additive genetic and residual variances were continuously decreasing parallel to each other. For this data set were small and obtained from a non-commercial experimental farm, permanent environmental variances for MY can be stable. Results from our research were opposite to the findings reported by Takma and Akbaş (2009). They found low heritability value at the beginning of lactation relative to end of lactation. It could be explained by the fact that they assumed to be constant residual error throughout lactation. Whereas in this research were heterogeneous throughout

DIM. Also they analyzed a much larger population of cows and used DF-REML. These could be other reason for different results between two researches.

In this research, estimates of heritability for MY generally were similar when compared to estimates of Hossein-Zadeh and Ardalan (2011) and Karacaören et al. (2006). On the other hand, heritability estimates were lower than the values obtained from studies conducted by Stoop et al. (2007), Miglior et al. (2007), Bohmanova et al. (2008). Conversely, our values were higher than reported by Haile-Mariam, et al. (2001), Silvestre, et al. (2005), Hammami, et al. (2008), Yazgan et al. (2010) and Galiç and Kumlu (2012).

Results from this study for average MY heritability values were same when compered another researches which findings obtained by REML - BLUP procedures but nonrandom regression methods fulfilled by Ünalan and Cebeci (2004) and Duru, et al. (2012). However, Ertuğrul, et. al. (2002) and Tilki, et. al. (2008) were estimated lower heritability values for MY.

Estimates of heritability values for DM were slightly lower, when compared to values obtained from previous research (Yazgan et al., 2010). However, trend of values throughout DIM were similar between two researches. While heritability values at the beginning and end of lactation high, at the middle of lactation were low for this two researches. In this research, the highest heritability values for milk yield while the near to lowest for DM yield.

Similar with DM, in this research, the highest heritability values for MY while the lowest for F yield. Similar results obtained from previous study by Yazgan et al. (2010). On the other hand estimates of heritability values for F generally were similar with the findings from studies conducted by Hammami et al. (2008) and Yazgan et al. (2010). However, heritability values for F were lower than the findings obtained from studies conducted by Silvestre et al. (2005), Stoop et al. (2007), Miglior et al. (2007), Bohmanova et al. (2008) and Hossein-Zadeh and Ardalan (2011).

Considering MD, estimates of heritability values were very low than results reported by Zwald et al. (2005). They reported the heritability value for MD as 0.17. These differences could be explained by the fact that they used a different model and method (Sire model and Bayesian method) of data analyzing and they analyzed a much larger population of cows. On the other hand heritability values for MD obtained from our study were high when compared to heritability values for milking speed reported by Karacaören et al. (2006).

Table 2. Average heritability for milk yield (MY), dry matter (DM), fat (F) and milking duration (MD).

Trait	h^2
MY (kg)	0.29
DM (%)	0.10
F (%)	0.16
MD (min)	0.05

Genetic relation between traits

In this research genetic (co)variances and correlations between traits were estimated using multiple trait (4 traits at a time) random regression model. Hence, results can be useful to change genetic patterns through selection using multiple trait selection indexes.

Genetic covariance between MY and DM were low at the middle of the DIM but were high in the beginning and end of DIM (Figure 6). Accordingly, genetic correlations between for these two traits were close to 0 around at 91 DIM (Figure 5). Considering genetic correlation between MY and DM different results were obtained from previous study (Yazgan et al., 2010). While low genetic correlations were found at the beginning, it was high in the rest of lactation. Using different cattle breeds between two researches may cause thise differences.

In this research estimated genetic correlation between MY and F were moderate and vary from 0.30 – 0.59 until 61 DIM. After this point it was tend to fall and very close to 0 at 196 DIM. Results from this study generally lower when compared with results of studies conducted by Silvestre et al. (2005), Stoop et al. (2007), Miglior et al. (2007), Hammami et al. (2008) and Hossein-Zadeh and Ardalan (2011). They found genetic correlation between MY- F and vary from 0.43 to 0.93. It could be explained by fact that they used Holstein dairy cows whereas; in this research Brown Swiss cows were used different from other studies.

As in shown Table 1, while MY was decreasing after 46 *th* to end of DIM, DM and F percentage disposed to increase as typical. Contrary to expectations, decreased milk yield, milking time remained constant. It could be explained by the fact that increasing F percentage in the milk towards end of TD. Because genetic correlations between DM - F were very high almost at all DIM (Figure 6). In other words, this implied that F percentage more increased in MY than other components (protein and lactose or other solids). Additionally, as in shown in Figure 5, genetic correlation trend MY-F and MY-MD were similar. Increased percentage of F in milk and other milk components could have reduced milk flow and because of this, MD may have been fixed.

In this research estimated genetic correlations between MY-MD were vary from -0.16 to 0.30 and generally lower when compared with the correlation between milk yield and milking speed estimated by Karacaören et al. (2006).

Eventually, for this data set were small and obtained from a non-commercial experimental farm, results could not be directly compared with the results of field research. Nevertheless, suggest about how could be variance components estimates with 4 multiple-trait (4 traits at a time) random regression model via restricted maximum likelihood (REML) with AI-REML algorithm using heterogeneous residual error interval. As mentioned earlier, In Turkey there are only very few studies on genetic correlation between milk yield, fat and milking duration traits we chose to analyze in this research. So, further study should be focused on such research with large data sets in Turkey.

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