Genetic relationship between milk dry matter and other milk traits in extended lactations of Polish Holstein cows

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ABSTRACT: The objective of this research was to examine heritabilities and genetic, phenotypic and permanent environmental relationships between milk dry matter (DM) and milk traits such as milk, fat, protein and lactose yields, milk urea nitrogen (MUN) and somatic cell score (SCS) in extended (to 395 days) lactations of Holstein cows from a big farm in Poland. The data set consisted of 78 059 test day records from the first, second and third lactations of 3 792 cows, daughters of 210 sires and 1 677 dams. Single- or two-trait random regression models were used with fixed effects of calving year, calving month, dry period and calving interval and random additive genetic and permanent environmental effects. The last two fixed effects were not included in the analysis of first lactation data. The highest values of heritabilities for all traits, except DM, were observed in the second lactation. First lactation heritabilities for all traits – except milk yield and SCS – were smaller than those in the third lactation. Lactose yield was highly heritable, with average h^2 equal to 0.25, 0.29 and 0.28 in lactations 1, 2 and 3, respectively. Heritability for DM was slightly lower than that for lactose (0.22, 0.26 and 0.28 for lactations 1, 2 and 3, respectively). In all lactations heritabilities for SCS were below 0.1. Genetic correlations between DM and milk yield (0.64–0.74) were lower than those between MUN and milk yield (0.67–0.79) as well as between lactose and milk yield (0.72–0.82). In general, DM was much more closely correlated with fat or protein yield (0.55–0.79) than with MUN or lactose (0.38–0.76). Only in the third lactation the correlation between DM and protein (0.72) was lower than between lactose and protein (0.76). For all lactations there were very high genetic correlations between DM and lactose (0.96–0.98) and high correlations between DM and MUN (0.63–0.83) and between lactose and MUN (0.70–0.85). The results suggest that further research is needed, focused on DM and its relationship with other traits in larger populations.

Keywords: genetic parameters; milk dry matter; extended lactation; milk urea nitrogen; lactose

Random regression models (RRM) have recently been used not only in the analysis of milk traits such as milk, fat and protein yield, but also somatic cell score (SCS), lactose yield and milk urea nitrogen (MUN), and very seldom they have been applied to analyze milk dry matter (DM) yield. RRM have many advantages over lactation models: 1) they account more accurately for environmental factors affecting the performance of cows in each day in milk (DIM) throughout the lactation, 2) they allow

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to model the shape of the lactation curve specific to each cow and to some groups of cows, 3) they provide daily and lactation genetic evaluations of animals, 4) cows' breeding values are obtained earlier, 5) persistency within and across lactations can be genetically evaluated (Ptak and Schaeffer, 1993; Schaeffer et al., 2000). Schaeffer et al. (2000) reported that RRM used for the analysis of test-day records provided more accurate genetic evaluations of cows than those from 305-day lactation yields (4–8%).

Literature dealing with the application of RRM to the analysis of milk traits is relatively large (Jamrozik et al., 1997, Strabel and Misztal, 1999; Mrode and Swanson, 2003; Strabel et al., 2005; Zavadilová et al., 2005; Strabel and Jamrozik, 2006; Miglior et al., 2007; Stoop et al., 2007). For example, Strabel and Jamrozik (2006) used a random regression test day model to estimate genetic parameters for milk, fat, and protein yield in the first 3 lactations of Polish Black and White cattle. They had three data sets with slightly different edits on minimal number of days in milk and on the size of herd-year subclasses. Each data subset included more than 0.5 million test-day records of more than 58 000 cows. The authors reported higher heritabilities of 305-days milk yield (0.18, 0.16, 0.17 in lactations 1, 2 and 3, respectively) than those for fat yield (0.12, 0.11, 0.12) and protein yield (0.13, 0.14, 0.15).

Lactose as an important milk component is highly heritable with h^2 values ranging from 0.46 to 0.53 (Miglior et al., 2007; Stoop et al., 2007). Miglior et al. (2007) reported that milk and lactose yields were highly genetically correlated (r = 0.97). Welper and Freeman (1992) found lower heritability for lactose yield (0.26), but this trait was highly correlated with milk yield traits, and negatively correlated with milk content traits. Stoop et al. (2006) proved that lactose yield was highly correlated with fat and protein yield (0.58 and 0.86, respectively) and less correlated with MUN (0.22). Miglior et al. (2006) found a statistically significant association between lactose percentage and MUN in the first lactation with functional survival in Canadian Ayrshire and Holstein cows.

MUN is considered as a normal non-protein nitrogen milk component, the concentration of which in milk results from dietary protein level and protein metabolism (Moore and Varga, 1996; Zhai et al., 2006). The increase in MUN is associated with the increase of protein yield (Miglior et al., 2005; Stoop et al., 2007). Jílek et al. (2006) proved that milk urea (MU) concentration was positively related to milk yield and negatively to milk fat. They found that MU concentration should be evaluated in association with lactation, days in milk, milk yield, milk fat percentage and milk protein percentage. Higher concentrations of MU were determined in the first and second lactation compared to the third and fourth lactation. In the study of Řehák et al. (2009) a significant effect of MU concentration on calving to first service interval was estimated. Mitchell et al. (2005) reported that the evidence of phenotypic relationship between MUN concentration and reproductive performance suggested a possibility of using MUN concentration in indirect selection for improving reproductive performance. Heritabilities for MUN concentration, measured by infrared method, were between 0.22 and 0.59 for the first three lactations (Wood et al., 2003; Mitchell et al., 2005; Miglior et al., 2007). Stoop et al. (2007) examined milk samples by the infrared method and estimated heritability values for MUN concentration in the first lactation as 0.14. Mitchell et al. (2005) reported 0.15 and 0.22 as h^2 for MUN concentration, measured by wet chemistry and infrared methods, respectively.

The use of SCS as an indirect selection tool for reducing mastitis has been reported in many studies (Emanuelson, 1988; Mrode and Swanson, 1996, 2003). Němcová et al. (2007) found the highest SCS in the cows with deep udders, weak central ligaments and fore attachments and low rear udder height. Estimates of heritability for daily SCS ranged from 0.06 to 0.35 (Interbull, 2008). Haile-Mariam et al. (2001) found that genetic and environmental correlations between SCS and milk yield estimated by multi-trait RRM were negative and generally similar. Environmental correlations between milk traits and SCS were negative, particularly when two correlated traits were measured in the same test day or in days close to each other. The strength of negative correlation increased with lactation. The genetic correlations between SCS and milk, protein and fat yield were: –0.55 to 0.21, –0.46 to 0.25 and –0.56 to 0.43 in the first three lactations (Haile-Mariam et al., 2001).

On the contrary, literature regarding genetic parameters for DM is very scarce. High yield of basic DM components (fat, protein, lactose) is advantageous for the needs of milk processing. This could be the reason for an increasing interest in the analysis of DM in milk. Considering the fact that the

chemical analysis for DM 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.

Lactation length in high-producing cows has increased over the last decade in some populations (Gonzalez-Recio et al., 2004), and presently in many countries cows have lactations extended beyond 305 days (Vargas et al., 2000). It results from extending days open, mainly because of reproductive difficulties. So, extending lactations becomes a part of contemporary management strategy (Tarazon-Herrera et al., 2000; Gonzalez-Recio et al., 2006; Dematawewa et al., 2007).

The objective of this study was to estimate heritabilities as well as genetic, phenotypic and permanent environmental relationships between DM and milk traits: milk, fat, protein and lactose yield, MUN and SCS in extended lactations of Holstein cows from a big farm in Poland.

MATERIAL AND METHODS

Data

The data set was provided by one of the biggest commercial dairy farms in Poland. The farm – located in the Wielkopolska region, which is the leading area of milk supply – can be a good example of the best large-scale dairy enterprises. Many years of crossbreeding and improvement of animal feeding and management have resulted in a change in the structure of Polish cattle population towards almost pure Holstein breed and in a considerable increase of milk yield by about 200 kg per year during the last 10 years. In 2007 the average yield of cows enrolled in the national recording system was 6 688 kg (Polish Federation of Cattle Breeders and Dairy Farmers, 2008).

Cows from the studied herd were housed in free-stall barns and received three kinds of TMR (Total Mixed Ration) with the amount appropriate to milk yield. The rations were balanced according to INRA standards (IZ-INRA, 2001). The average milk production per lactation was above 9 000 kg. Cows yielding less than 25 kg of milk per day were milked twice a day and cows yielding at least 25 kg of milk per day were milked three times daily in a fish-bone parlour. According to ICAR (2007) methodology, the interval between the subsequent milk recordings was from 22 to 37 days.

Table 1. Descriptive statistics of test day records used for (co)variance components estimation

Lactation	Test-day		Milk (kg)		Fat (kg)		Protein (kg)		Lactose (kg)		MUN[1] (g)		SCS[2]		DM[3] (kg)	
	records	cows	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD
1	36 155	3 342	24.62	7.06	0.97	0.26	0.83	0.21	1.21	0.36	6.06	3.17	5.11	0.53	3.20	0.85
2	25 914	2 361	27.99	9.89	1.10	0.38	0.95	0.29	1.35	0.50	6.21	4.38	5.25	0.55	3.60	1.19
3	15 990	1 467	28.63	10.60	1.12	0.41	0.96	0.31	1.37	0.54	7.07	4.18	5.36	0.56	3.66	1.28
Total	78 059	3 792	26.56	9.05	1.05	0.34	0.90	0.27	1.29	0.45	6.31	3.87	5.21	0.55	3.43	1.09

[1]milk urea nitrogen; [2]somatic cell score (log-transformed somatic cell count); [3]dry matter

The data set consisted of 78 059 test-day records from the first three lactations of 3 342 Holstein cows, which calved between 1999 and 2007. Cows were daughters of 184 sires and 1 677 dams. Only records from extended lactations, i.e. that lasted at least 270 days and no longer than 395 days, were chosen for the estimation of (co)variance components for 7 traits: milk, fat, protein and lactose yields (kg), MUN (g), somatic cell count (SCC) (10^3/ml), DM (kg). Before analysis SCC was log-transformed to SCS according to the formula SCS = $\log_2$(SCC/100 000) + 3. The descriptive statistics of the data are shown in Table 1.

Chemical analysis of milk samples

Milk composition was examined by the Certified Laboratory for Milk Evaluation. All samples were analyzed with a MilkoScan^{TM} CombiFoss 6000 analyzer for milk fat, protein, lactose, MUN and DM by the spectrophotometric method in the infrared area of the spectrum (FT-MIR) and with a fluoro-opto-electronic counter for SCC. Calibration samples were analyzed for fat by Rose-Gottlieb (ISO 1211), for protein by Kjeldahl (ISO 8968), for MUN by pH difference (EN ISO 14637), for DM by drying (FIL 21B) and for SCC by a microscopy method (EN ISO 13366-1). The reference values for lactose were calculated indirectly as a difference between the values determined for DM and the total values for the remaining components of DM.

Statistical analysis and models

The following random regression animal model was used for analysis:

$$y_{tijklsm} = CY_{ti} + CM_{tj} + DP_{tk} + CI_{tl} + \sum_{n=0}^{5} b_{tn}X_{tsmn} + \sum_{n=0}^{2} a_{tsn}X_{tsmn} + \sum_{n=0}^{2} p_{tsn}X_{tsmn} + e_{tijklsm}$$

where:

$y_{tijklsm}$ = observation of the t^{th} trait (milk, fat, protein, lactose, MUN, DM or SCS) for the i^{th} calving year, j^{th} calving month, k^{th} class of dry period length and l^{th} class of the calving interval of the s^{th} animal on d_{sm} days in milk

CY_{ti} = fixed effect of calving year

CM_{tj} = fixed effect of j^{th} calving month

DP_{tk} = fixed effect of dry period length

CI_{tl} = fixed effect of calving interval

b_{tn} = fixed regression coefficient

a_{tsn}, p_{tsn} = random regression (RR) coefficients for additive genetic and permanent environmental effects, respectively

X_{tsmn} = Legendre polynomial of n^{th}-degree corresponding to d_{sm} days in milk of s^{th} cow

$e_{tijklsm}$ = the random residual

There were 9 calving years (1999 through 2007), 5 classes of dry period (DP) defined as: <30, 30–45, 46–60, 61–75, >75 days and 6 calving intervals (CI) created as: <365, 365–395, 396–425, 426–475, 476 to 505, >505 days. The fixed effects of DP and CI were not included in the model for analyses of the first lactation data. The total number of animals in the pedigree file was 5 966 (3 342 cows, 184 sires, 1 677 dams and 763 grandparents). There were 212 cows with unknown sires and 901 cows with unknown dams. Within each lactation single-trait and two-trait RRM was used to estimate (co)variance components. Having 3 lactations and 7 traits (DM, milk, fat, protein, lactose, MUN, SCS) 84 analyses were performed.

In matrix notation the model can be written as:

$$y = Xf + Za + Wp + e$$

where:

y = vector of observations

f = vector of fixed effects

a, p = vectors of random regression coefficients for additive genetic and permanent environmental effects, respectively

e = vector of residuals

matrices X, Z, W = incidence matrices which relate observations to effects

The (co)variance matrix for random effects in the model can be written as:

$$var\begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} A\otimes G & 0 & 0 \\ 0 & I\otimes P & 0 \\ 0 & 0 & R \end{bmatrix}$$

where:

G and **P** = the (co)variance matrices for additive genetic and permanent environmental random regression coefficients, respectively, each of order 3 × 3 for single-trait analyses and 6 × 6 for two-trait analyses

A = the additive genetic relationship matrix,

I = the identity matrix, and $\mathbf{R} = \mathbf{I}\sigma_e^2$

Residual variances σ_e^2 are assumed to have the same value in each DIM for one trait, with different values of σ_e^2 for different traits.

Heritabilities of daily yields were estimated using variance components from single-trait runs and correlations were calculated using (co)variance components from two-trait analyses. Estimates of (co)variance components were obtained by the REML method. The DXMRR program from DFREML package, using the AI-REML algorithm for multivariate analysis, was applied (Meyer, 1997).

RESULTS AND DISCUSSION

Means with standard deviations of all analyzed traits are given in Table 1. The number of cows decreased from 3 342 (lactation 1) to 1 467 (lactation 3) and the number of test day records decreased from 36 155 to 15 990. Overall means of milk, fat, protein and lactose yield, MUN, SCS and DM were 26.56 kg, 1.05 kg, 0.90 kg, 1.29 kg, 6.31 g, 5.21 and 3.43 kg, respectively. Variation of most traits was similar (coefficient of variation /*CV*/: 30% – 35%) with the exception of SCS (*CV* about 10%) and MUN (*CV* about 60%).

Heritabilities

Average daily heritabilities of all analyzed traits are given in Table 3. They ranged from 0.15 to 0.28 for milk, 0.11 to 0.21 for fat, 0.12 to 0.21 for protein, 0.25 to 0.29 for lactose, 0.14 to 0.25 for MUN, 0.03 to 0.07 for SCS, and 0.22 to 0.28 for DM. For all milk traits (except DM) the heritabilities reached the highest values in the second lactation; the heritabilities of DM were the highest in the third lactation. Samoré et al. (2008) observed a similar pattern of changes in daily heritabilities for protein (the lowest in 1, the highest in lactation 2) whereas daily heritabilities for SCS were increasing with the lactation number. Zavadilová et al. (2005) found that heritability estimates for milk, fat and protein were the lowest in the first lactation and the highest in the third lactation. The highest values were obtained for milk yield while the lowest for fat yield. Strabel and Jamrozik (2006) estimated heritabilities of daily milk, fat and protein yield in Polish Black-and-White cattle and obtained the values between 0.1 and 0.2 for all traits in the first three lactations. Their estimates of h^2 were higher for milk than for fat and protein, which generally agreed with our results. In the earlier study of the Polish Black-and-White population conducted by Strabel and Misztal (1999) the test-day heritabilities for milk yield in lactations 1 and 2 were from 0.14 to 0.19 and 0.10 to 0.16, respectively, and they were also higher than those for fat (0.11–0.16 in the first and 0.11–0.22 in the second lactation) and protein (0.10–0.15 in the first and 0.06–0.15 in the second lactation). Similar conclusions about heritabilities of milk traits of Polish Black-and-White cattle were reported by Strabel et al. (2005).

The lowest values of daily heritabilities were found for SCS. DeGroot et al. (2007) obtained the test-day

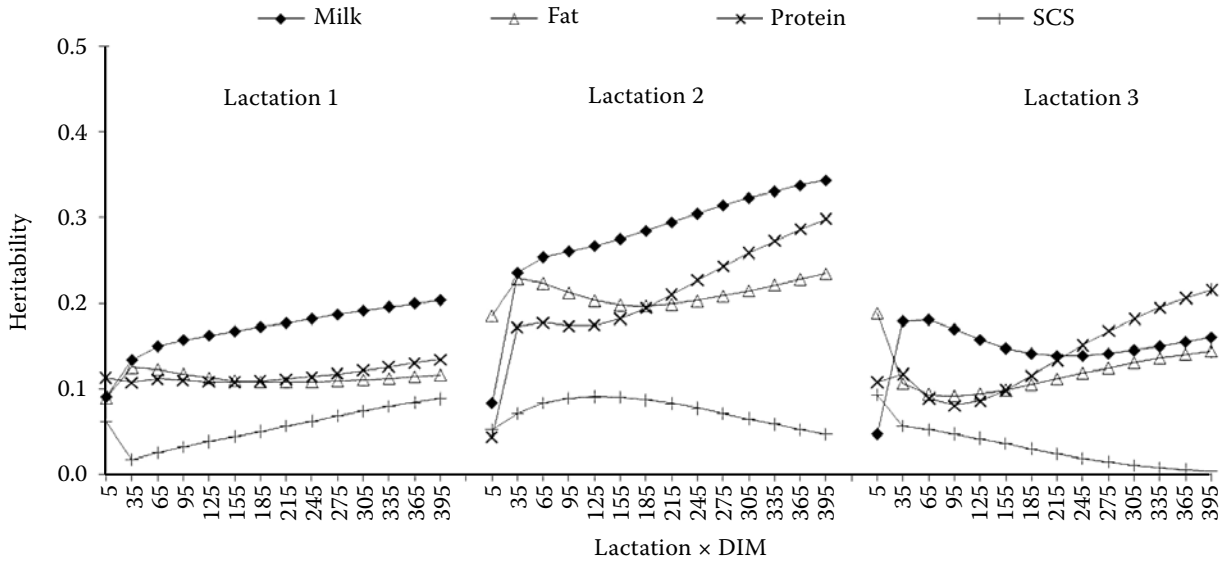

Figure 1. Heritability for milk, fat, protein and SCS over DIM by lactations 1, 2 and 3

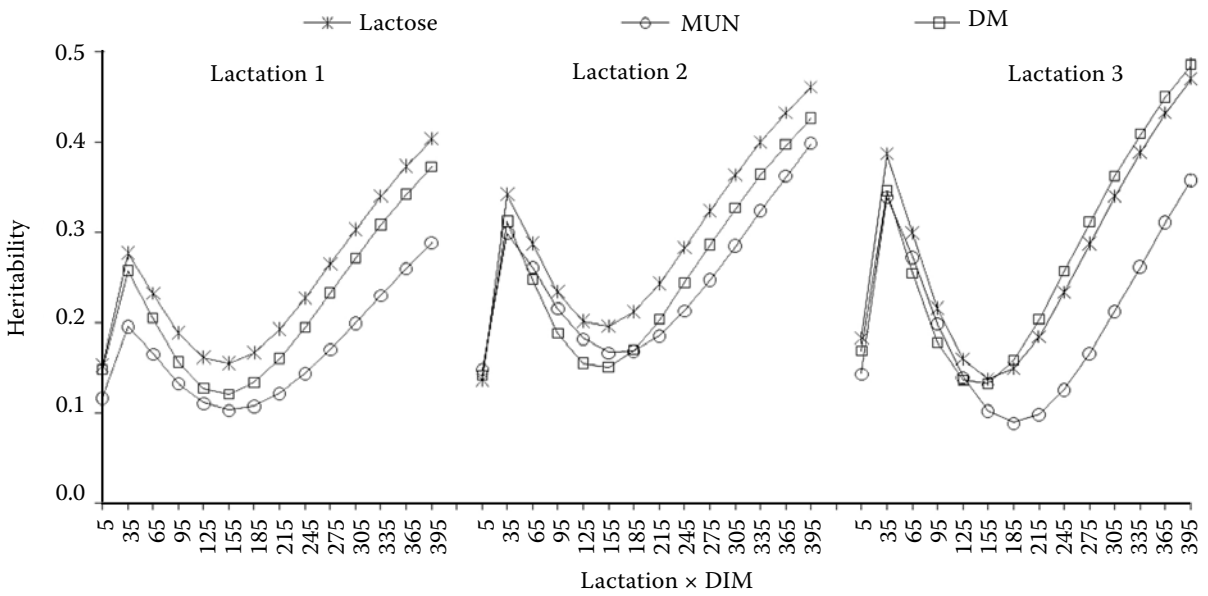

Figure 2. Heritability for lactose, MUN and DM over DIM by lactations 1, 2 and 3

SCS heritabilities which ranged from 0.02 to 0.06 in the first three lactations. Mrode and Swanson (2003) also estimated small values of SCS heritabilities, especially in the first lactation (0.04 to 0.09). On the other hand, Miglior et al. (2007) and Samoré et al. (2008) reported much higher h^2 for SCS with a tendency to increase distinctly with lactation (0.15–0.19, 0.19–0.27 and 0.25–0.34 on average in lactations 1, 2 and 3). In the present study heritability values were much lower than

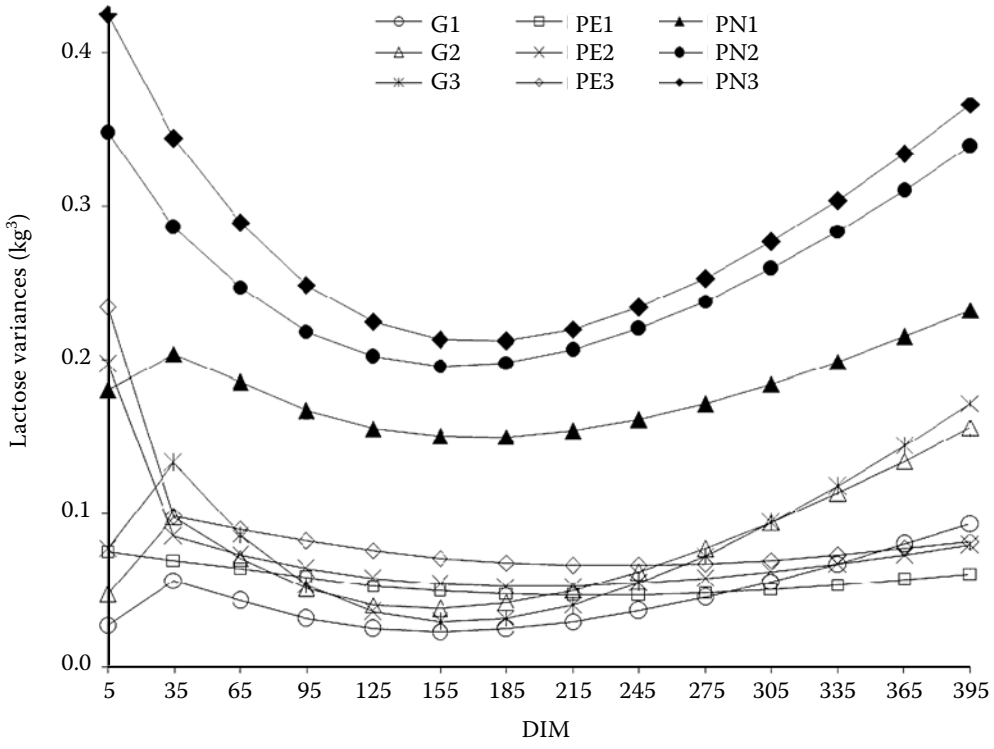

Figure 3. Genetic (G), permanent environmental (PE) and phenotypic (PN) variance for lactose over DIM by lactations 1, 2 and 3

in the study by Miglior et al. (2007), not only for SCS but also for other analyzed traits, mainly for milk and lactose. However, they used a larger data set of Canadian Holsteins and different RRM with different fixed effects. Heritabilities obtained by Samoré et al. (2008) were higher compared to ours, probably because they had a much deeper pedigree (3 generations back) and different functions to model regressions in RRM although their data set was smaller than ours.

Changes in daily heritabilities in the first three lactations are shown in Figures 1 and 2. Heritability curves for milk, fat, protein and SCS differed in their shape in consecutive lactations (Figure 1). Heritabilities of milk yield increased with DIM during the first two lactations whereas they were relatively constant during the third lactation. The changes in h^2 for milk in the second and third lactation were in agreement with the results presented by Strabel and Jamrozik (2006) while the first lactation graphs were different. Heritability curves for first-lactation fat and protein were rather flat and they both show an increasing tendency in the next two lactations, similarly like in the paper by Strabel and Jamrozik (2006). For SCS, the heritability curve increased with DIM in the first lactation and decreased in the third lactation. In the second lactation the increase of daily h^2 in the first months was followed by a continuous decrease until the end of lactation (Figure 1). The pattern of first-lactation heritabilities for SCS presented by Mrode and Swanson (2003) was similar to our results. Changes in heritabilities for lactose, MUN and DM showed the same pattern within each lactation (Figure 2). Heritability curves rose rapidly from 5 to 35 DIM, then went down to the minimum at about 155 DIM and rose again until the end of lactation.

Variances and covariances between traits

Figures 3–5 show the genetic, permanent environmental and phenotypic variances over DIM by lactation for lactose, MUN and DM, respectively. Changes in lactose and DM variance components were similar. In all lactations, genetic variances of lactose, MUN and DM increased up to 35 DIM, then they decreased until the middle of lactation, and

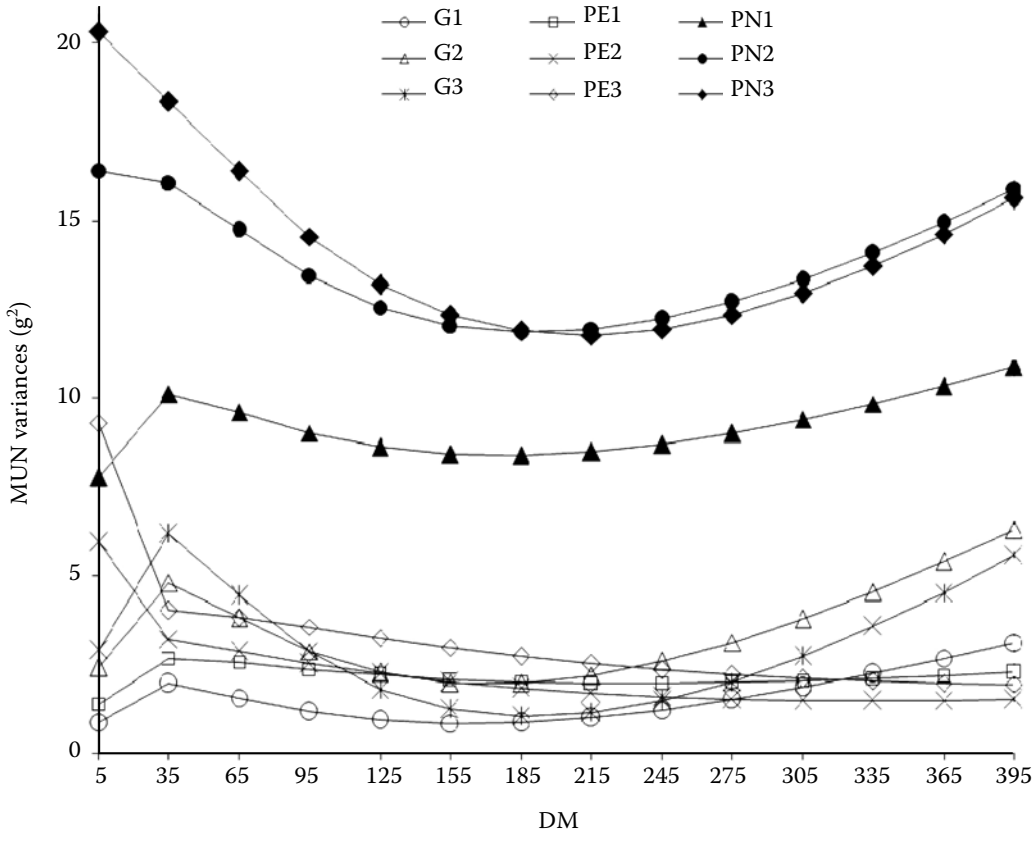

Figure 4. Genetic (G), permanent environmental (PE) and phenotypic (PN) variance for MUN over DIM by lactations 1, 2 and 3

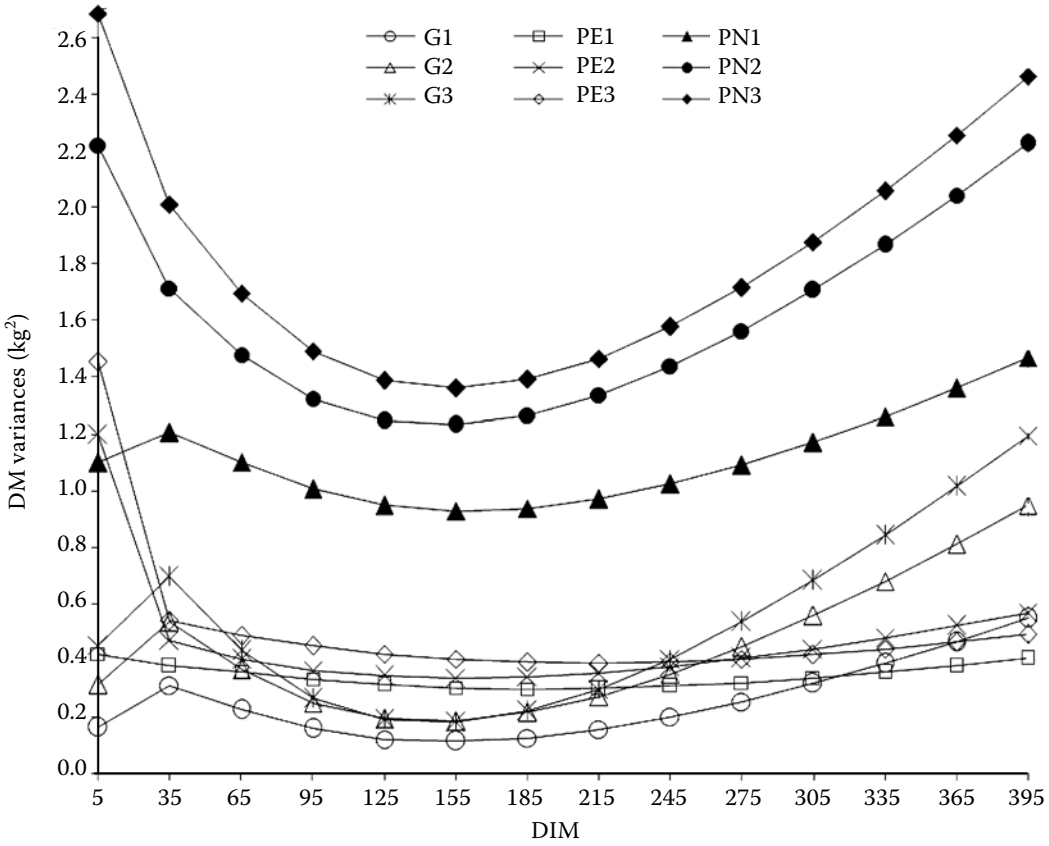

Figure 5. Genetic (G), permanent environmental (PE) and phenotypic (PN) variance for DM over DIM by lactations 1, 2 and 3

increased again till the end of lactation. Permanent environmental variances for lactose, MUN and DM were very high at the beginning of the second and third lactation, then they decreased during the first month, and tended to be quite constant during the rest of the lactation period. Generally they varied less than genetic variances, mainly in later lactations. In the first lactation permanent environmental variances were flattened over DIM. Phenotypic variances showed a similar tendency of changes like

Table 2. Residual variances (on diagonal) and covariances (above diagonal) among traits averaged across lactations and DIM

Trait	Milk		Fat		Protein		Lactose		MUN[1]		SCS[2]		DM[3]	
	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD
Milk	**15.17**	4.56	0.69	0.17	0.66	0.15	0.90	0.19	5.57	1.37	0.00	0.00	2.32	0.53
Fat			**0.05**	0.01	0.03	0.01	0.04	0.01	0.24	0.06	0.04	0.01	0.12	0.03
Protein					**0.03**	0.01	0.04	0.01	0.23	0.05	0.03	0.01	0.10	0.02
Lactose							**0.10**	0.02	0.48	0.10	0.04	0.01	0.25	0.05
MUN									**4.19**	1.50	0.16	0.03	1.23	0.26
SCS											**0.41**	0.07	0.12	0.03
DM													**0.67**	0.14

[1]milk urea nitrogen; [2]somatic cell score (log-transformed somatic cell count); [3]dry matter

Table 3. Average heritabilities (on diagonal), genetic correlations (below diagonal) and permanent environmental correlations (above diagonal) among traits within lactations 1, 2 and 3

Lactation	Milk		Fat		Protein		Lactose		MUN[1]		SCS[2]		DM[3]	
Trait	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD
1														
Milk	**0.17**	0.03	0.92	0.06	0.97	0.04	0.93	0.06	0.89	0.03	–0.12	0.09	0.90	0.06
Fat	0.44	0.14	**0.11**	0.01	0.94	0.04	0.88	0.04	0.78	0.04	–0.14	0.19	0.90	0.04
Protein	0.85	0.06	0.62	0.27	**0.12**	0.01	0.93	0.06	0.84	0.03	–0.08	0.17	0.79	0.34
Lactose	0.72	0.20	0.38	0.17	0.57	0.20	**0.25**	0.08	0.91	0.04	–0.13	0.17	0.99	0.01
MUN	0.67	0.11	0.40	0.17	0.54	0.10	0.70	0.05	**0.14**	0.06	–0.16	0.17	0.91	0.04
SCS	0.07	0.30	0.12	0.10	0.14	0.28	0.10	0.15	0.08	0.13	**0.05**	0.02	–0.16	0.23
DM	0.64	0.18	0.55	0.17	0.62	0.13	0.96	0.02	0.63	0.07	0.01	0.00	**0.22**	0.08
2														
Milk	**0.28**	0.07	0.92	0.10	0.97	0.07	0.94	0.07	0.88	0.10	–0.27	0.19	0.92	0.08
Fat	0.47	0.19	**0.21**	0.01	0.91	0.10	0.90	0.09	0.82	0.15	–0.23	0.22	0.92	0.09
Protein	0.87	0.10	0.83	0.09	**0.21**	0.06	0.96	0.03	0.86	0.11	–0.21	0.28	0.94	0.06
Lactose	0.82	0.18	0.39	0.41	0.75	0.19	**0.29**	0.09	0.91	0.08	–0.26	0.30	0.99	0.01
MUN	0.79	0.16	0.62	0.19	0.73	0.26	0.83	0.15	**0.25**	0.08	–0.28	0.26	0.90	0.09
SCS	–0.29	0.10	–0.28	0.11	–0.13	0.17	–0.05	0.18	–0.25	0.23	**0.07**	0.02	–0.27	0.26
DM	0.74	0.26	0.70	0.20	0.79	0.18	0.97	0.02	0.81	0.15	–0.11	0.33	**0.26**	0.10
3														
Milk	**0.15**	0.03	0.88	0.11	0.95	0.06	0.91	0.08	0.86	0.06	–0.25	0.12	0.92	0.09
Fat	0.67	0.15	**0.12**	0.03	0.93	0.09	0.84	0.11	0.79	0.15	–0.23	0.16	0.90	0.08
Protein	0.90	0.04	0.69	0.27	**0.14**	0.05	0.91	0.08	0.84	0.11	–0.24	0.27	0.92	0.07
Lactose	0.72	0.25	0.51	0.32	0.76	0.09	**0.28**	0.11	0.88	0.08	–0.29	0.23	0.98	0.01
MUN	0.74	0.09	0.51	0.18	0.69	0.08	0.85	0.06	**0.20**	0.09	–0.29	0.20	0.88	0.09
SCS	–0.42	0.38	–0.37	0.37	–0.09	0.30	–0.16	0.29	–0.16	0.11	**0.03**	0.03	–0.27	0.23
DM	0.65	0.32	0.57	0.36	0.72	0.20	0.98	0.02	0.83	0.09	–0.16	0.11	**0.28**	0.12

[1]milk urea nitrogen; [2]somatic cell score (log-transformed somatic cell count); [3]dry matter

genetic variances only in the first lactation, whereas in the second and third lactation the curves had a typical "U" shape. Miglior et al. (2007) reported a similar genetic variance trend for lactose and MUN during the whole lactation period (except the first month). Changes in permanent environmental variances over DIM for both traits were unlike the results of our study. It could be explained by the fact that they used a different method of measuring traits (lactose and MUN) and they analyzed a much larger population of cows.

In Table 2 residual variance-covariance matrices in lactations 1, 2 and 3 for milk traits are presented. As expected, milk yield had the highest residual variance (15.17). Residual variance of MUN was much lower (4.19). For fat, protein, lactose, SCS and DM these variances were 0.05, 0.03, 0.10, 0.41 and 0.67, respectively. The covariances between traits ranged from 0.00 to 5.57 and they were generally low. Average error covariances between DM and other milk traits were lower than those between milk yield and other milk traits.

Correlations between traits

Genetic and permanent environmental correlations between milk traits in lactations 1–3 are given

Table 4. Average phenotypic correlations among traits within lactations 1, 2 and 3

Lactation	Fat		Protein		Lactose		MUN[1]		SCS[2]		DM[3]	
Trait	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD	mean	SD
1												
Milk	0.73	0.09	0.88	0.10	0.74	0.08	0.60	0.06	–0.04	0.05	0.71	0.08
Fat			0.81	0.11	0.62	0.09	0.49	0.07	0.11	0.08	0.71	0.10
Protein					0.73	0.09	0.58	0.07	0.12	0.09	0.74	0.09
Lactose							0.66	0.09	0.07	0.07	0.94	0.14
MUN									0.03	0.05	0.64	0.09
SCS											0.10	0.08
2												
Milk	0.75	0.10	0.88	0.10	0.79	0.09	0.63	0.08	–0.11	0.08	0.75	0.10
Fat			0.80	0.12	0.65	0.12	0.53	0.09	0.03	0.08	0.74	0.12
Protein					0.77	0.10	0.61	0.09	0.08	0.15	0.78	0.11
Lactose							0.69	0.10	0.03	0.12	0.94	0.14
MUN									–0.02	0.09	0.67	0.11
SCS											0.05	0.13
3												
Milk	0.74	0.11	0.88	0.10	0.76	0.10	0.61	0.07	–0.10	0.06	0.72	0.11
Fat			0.79	0.12	0.62	0.13	0.49	0.08	0.07	0.08	0.70	0.13
Protein					0.75	0.10	0.60	0.08	0.10	0.13	0.76	0.11
Lactose							0.69	0.10	0.04	0.10	0.94	0.14
MUN									0.00	0.07	0.68	0.11
SCS											0.07	0.11

[1]milk urea nitrogen; [2]somatic cell score (log-transformed somatic cell count); [3]dry matter**s**

in Table 3. For all lactations genetic correlations between DM and lactose were very high (0.96 to 0.98). Correlations between milk and protein (0.85 to 0.90), milk and lactose (0.72 to 0.82), and lactose and MUN (0.70 to 0.85) were also relatively high. Stoop et al. (2007) found high genetic correlations between MUN and lactose (0.82) and MUN and protein (0.86) whereas the genetic relationship between lactose and fat was moderate (0.58). In our study the latter was slightly lower (0.38 in the first to 0.51 in the third lactation). Genetic correlations of milk with fat (0.56) and with protein (0.89) estimated by Miglior et al. (2007) were similar like in the present study. However, those authors found a very high (close to 1) genetic correlation between lactose and milk yield, which exceeded the values obtained in our study (0.72–0.82). A high genetic correlation of lactose with milk yield (0.92) was also estimated by Welper and Freeman (1992). We estimated the genetic correlation very close to 1 only between lactose and DM. While the genetic relationship between DM and MUN (0.63) was similar to that between milk and MUN (0.67) in the first lactation, in later lactations these correlations (0.81 and 0.83) were much higher than correlations between milk and MUN (0.79 and 0.74). Haile-Mariam et al. (2001) pointed out that most literature estimates of genetic relationships between milk traits and SCS calculated on lactation basis are positive in the first lactation and negative in later lactations. Similarly to that study, our genetic correlations between milk yield and other milk traits, including SCS, were quite low in the first lactation and negative in the second and third lactation. In general, the relationships between SCS, protein and lactose obtained in the present study were in agreement with the results of Miglior et al. (2007), who found genetic correla-

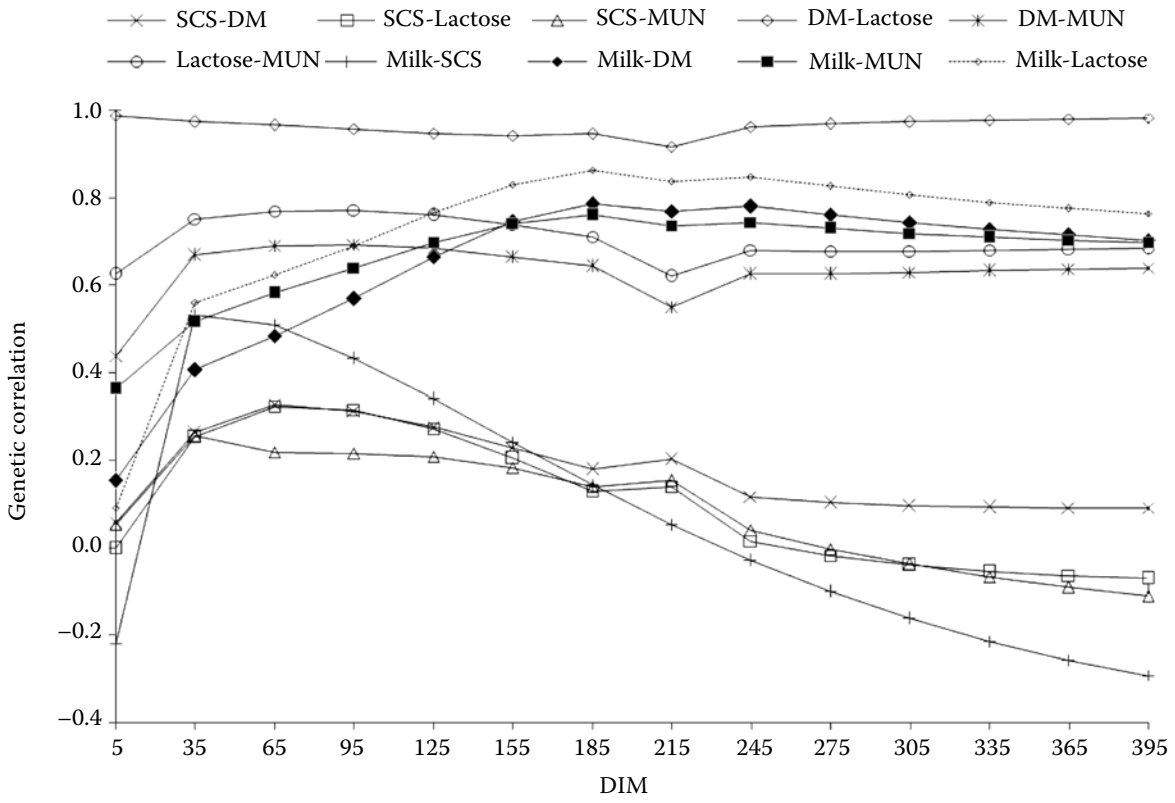

Figure 6. Genetic correlations between milk, SCS, MUN, DM and lactose over DIM for lactation 1

tions of SCS with protein and with lactose equal to 0.014 and –0.024, respectively.

Genetic correlations between milk, lactose, MUN, SCS, and DM over DIM in subsequent lactations (1, 2 and 3) are shown in Figures 6–8. In all lactations, genetic correlations between DM and lactose were close to 1 throughout the whole lactation. In the first lactation other correlations increased during the first month, and they showed different trends of changes afterwards. Genetic relationships between SCS and other traits decreased to values close to 0, while correlations of milk with DM, MUN and lactose increased, reaching values 0.6–0.8 from 125 DIM to the end of 395-day lactation. Correlations between DM and MUN as well as between lactose and MUN remained approximately constant from 35 DIM to the end of lactation with one small temporary decline at 215 DIM (Figure 6). In the second and third lactation genetic correlations between milk and DM, MUN and lactose increased gradually to values greater than 0.7 at DIM = 185 and remained quite constant later on. Correlations between DM and MUN, and lactose and MUN, were over 0.8 (Figures 7 and 8). In the second lactation, all correlations between SCS and other traits were falling down with DIM, except the correlation of SCS with lactose, which was decreasing only to 65 DIM, and correlations of SCS with milk and MUN, which were increasing during the first month. In the third lactation all genetic correlations between SCS and other traits decreased with DIM. The values of correlation coefficients between SCS and other traits were negative in a major part of lactations 2 and 3, and (except the correlation of SCS with DM) during the last five months of lactation 1.

Permanent environmental correlations between traits were quite high – from 0.78 to 0.99 (Table 3) – with one exception: between SCS and other milk traits they ranged from –0.29 to –0.08. Miglior et al. (2007) also found high permanent environmental correlations between yield traits (milk-fat, protein-fat, milk-protein and milk-lactose) ranging from 0.857 to 0.979. Similarly like in our study, permanent environmental relationships between SCS and milk, fat, and protein were negative amounting to –0.233, –0.244 and –0.216, respectively.

Average phenotypic correlations between milk traits in lactations 1–3 are shown in Table 4. In each lactation these correlations were almost the same between such traits as milk and fat (0.73 to 0.75), and exactly the same between milk and pro-

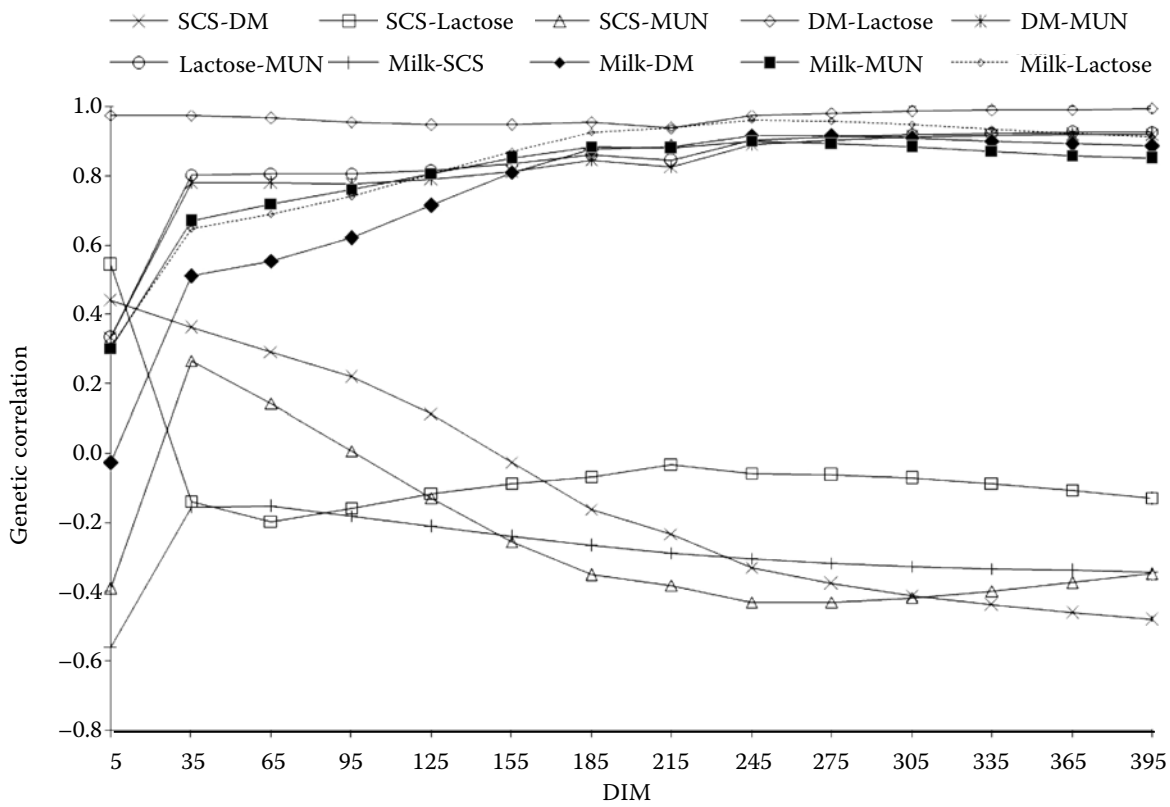

Figure 7. Genetic correlations between milk, SCS, MUN, DM and lactose over DIM for lactation 2

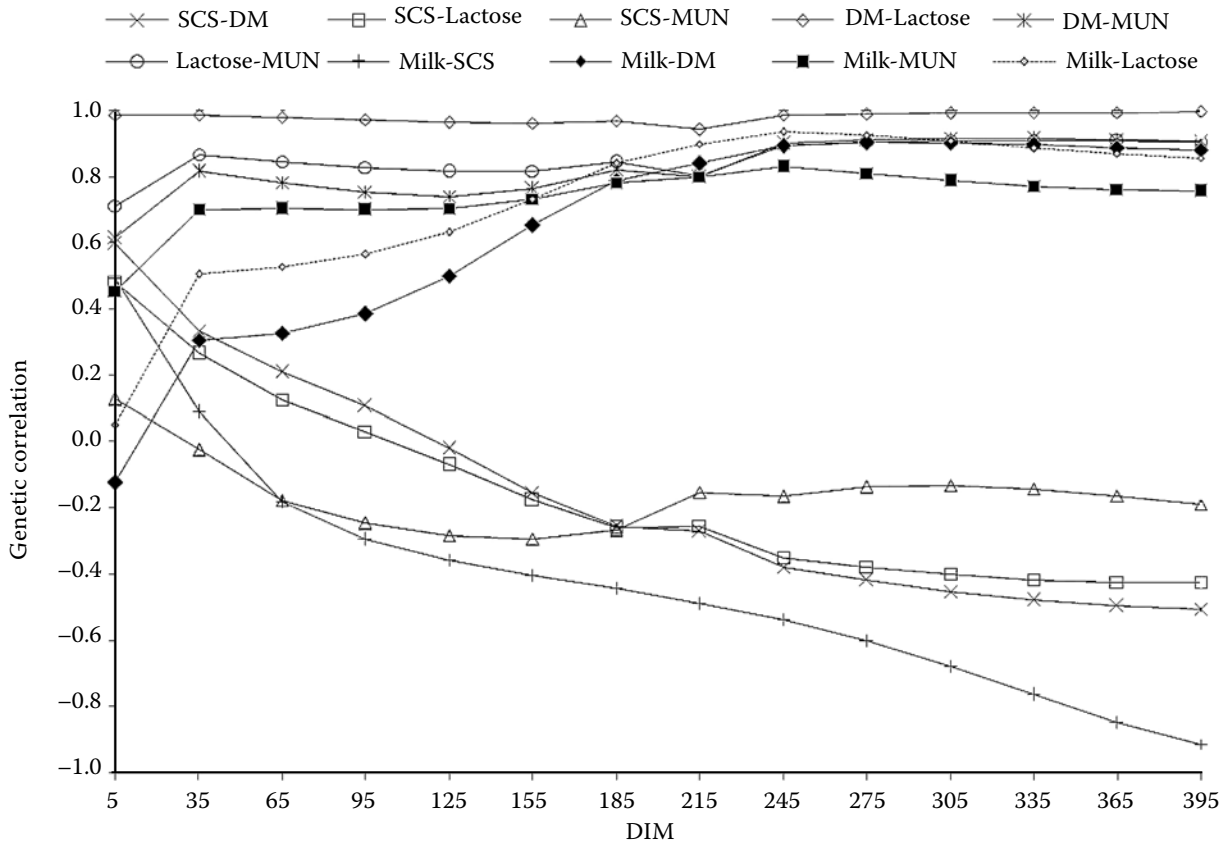

Figure 8. Genetic correlations between milk, SCS, MUN, DM and lactose over DIM for lactation 3

tein (0.88). These results were similar to those of Miglior et al. (2007) and Stoop et al. (2007). In their studies correlations between milk and fat ranged from 0.66 to 0.78, and between milk and protein from 0.92 to 0.93. In all lactations SCS was lowly phenotypically correlated with other traits (values ranged from –0.11 to 0.12). Phenotypic correlations between SCS and milk yield were low and negative (–0.04, –0.11 and –0.10 in the first three lactations, respectively). Similar phenotypic relationships were reported by Miglior et al. (2007). Phenotypic correlations of MUN with other traits were moderate: the lowest between MUN and fat (0.49–0.53) and the highest between MUN and lactose (0.66–0.69). These results were very close to those obtained by Stoop et al. (2007). They found phenotypic correlations between MUN and milk, fat, protein and lactose as 0.46, 0.64, 0.60 and 0.68, respectively. We estimated very high phenotypic correlations between DM and lactose in all lactations (0.94). They were higher than correlations between DM and milk, fat and protein (0.70 to 0.78) and between milk and lactose (0.74 to 0.79).

CONCLUSIONS

Most of the estimated genetic parameters (heritabilities and genetic correlations) are similar to the results of other studies dealing with data from larger populations and a higher number of herds. We found a high genetic correlation between DM and lactose (close to 1) in all lactations, and a little lower genetic correlation between DM and MUN (0.81 and 0.83) in the second and third lactation. As DM in milk is relatively easy to measure, its favourable genetic relationships with other traits can be utilized in selection, especially towards increasing yields of some milk components. The results of the present study indicate the need of further research on larger populations.

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