

Genetic parameters for lactose percentage and urea concentration in milk of Polish Holstein-Friesian cows*

Alicja Satola**, Ewa Ptak, Agnieszka Otwinowska-Mindur,
Wojciech Jagusiak

Department of Genetics and Animal Breeding, University of Agriculture,
Al. Mickiewicza 24/28, 30-059 Krakow, Poland

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The objective of the study was to estimate genetic parameters for lactose percentage and urea concentration in milk of Polish Holstein-Friesian cows. Data consisted of 104,875 test-day records from the first three lactations of 6,299 cows. Genetic parameters were estimated using the Bayesian method via Gibbs sampling and the multitrait animal model. The linear model for lactose percentage, milk urea content and production traits (milk yield, fat percentage, protein percentage) included the fixed herd-test-day effect, fixed regressions within age at calving by season of calving subclasses, and random regressions for additive genetic and permanent environmental effects. All regressions were modeled using fourth-order Legendre polynomials. The average daily heritability of lactose percentage was on an intermediate level and ranged from 0.24 to 0.35. Average daily heritability of milk urea concentration was lower (0.16 to 0.24). Lactose percentage was positively genetically correlated with milk yield (0.29, 0.29 and 0.34 in first, second and third lactations, respectively) and negatively genetically correlated with protein percentage (-0.21, -0.19, -0.13 in lactations 1, 2 and 3), and fat percentage in the first lactation (-0.24). Genetic correlations of milk urea concentration and other milk traits (fat, protein and lactose percentages) were rather low or close to zero (-0.16 to 0.19), except for the genetic correlation with milk yield (0.19 to 0.35). The results show that selection for lactose percentage and milk urea content is possible, although more research on the relationship with other traits, mainly conformation, fertility and health, is needed.

KEY WORDS: dairy cattle / genetic parameters / lactose / milk urea

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**Corresponding author: a.satola@ur.krakow.pl

Lactose is a disaccharide synthesised in the milk gland from glucose and galactose. Average lactose content in cow's milk ranges from 4.42 to 4.97% [Welper and Freeman 1992, Miglior *et al.* 2006, Miglior *et al.* 2007, Samore *et al.* 2007, Stoop *et al.* 2007, Jesiołkiewicz *et al.* 2011, Ptak *et al.* 2012]. Lactose is a major component of whey, which is a by-product of cheese production. Lactose is widely used in different branches of industry (feed, food and pharmaceutical industries).

Urea is an organic molecule composed of carbon, nitrogen, oxygen and hydrogen. It is produced in the liver from unused ammonia. It diffuses to body fluids (blood, milk). Urea is a milk component, comprising part of the non-protein nitrogen (NPN) found in milk. The average herd milk urea concentration should be in the range of 250-270 mg/l. Milk urea content (MU) may be affected by many factors. The amount of crude protein and energy in the diet are the main factors influencing urea concentration in milk [Hof *et al.* 1997]. MU depends not only on nutrition. Parity group, stage of lactation, calendar month in which the milk samples are collected, sample types (morning or evening milking) and milk production level also influence MU [Godden *et al.* 2001, Arunvipas *et al.* 2003, Rajala-Schultz and Saville 2003, Wood *et al.* 2003, Hojman *et al.* 2004, Jilek *et al.* 2006, Fatehi *et al.* 2012, Rzewuska and Strabel 2013a]. The variability of milk urea concentration is also affected by genetic factors [Wood *et al.* 2003, Mitchell *et al.* 2005, Miglior *et al.* 2007, Stoop *et al.* 2007, Bastin *et al.* 2009, Hossein-Zadeh and Ardalan 2011, Loker *et al.* 2012, Rzewuska and Strabel 2013b].

In Poland the lactose content of cows' milk has been recorded since 1998 and milk urea concentration since 2000. These periods of time are sufficiently long for research aimed at examining whether these traits could be included in a breeding programme. The first step is to estimate the genetic parameters for these traits. In literature the reported heritability of lactose percentage ranges from 0.17 to 0.64 [Welper and Freeman 1992, Miglior *et al.* 2007, Samore *et al.* 2007, Stoop *et al.* 2007, Ptak *et al.* 2012], while that of MU – from 0.09 to 0.59 [Wood *et al.* 2003, Mitchell *et al.* 2005, Miglior *et al.* 2007, Stoop *et al.* 2007, Bastin *et al.* 2009, Hossein-Zadeh and Ardalan 2011, Loker *et al.* 2012, Rzewuska and Strabel 2013b]. This means that these traits might be genetically improved. The economic importance of lactose percentage and milk urea content is unclear, but their association with fertility and health traits, which are economically important but low-heritable, opens an opportunity for them to be used in selection programmes.

The relationship of lactose percentage with production traits has been the subject of many studies [Miglior *et al.* 2007, Welper and Freeman 1992, Samore *et al.* 2007, Stoop *et al.* 2007, Ptak *et al.* 2012]. For example, Miglior *et al.* [2007] found that lactose percentage was negatively genetically correlated with somatic cell score (-0.20); this suggests that lactose percentage can be used as an auxiliary trait in genetic evaluation of mastitis, together with somatic cell score. Miglior *et al.* [2006] investigated the relationship between lactose percentage and longevity and found that cows with a low lactose percentage were more likely to be culled. Buckley *et al.* [2003] and Francisco *et al.* [2003] studied the relationship of lactose percentage with reproduction traits.

Buckley *et al.* [2003] observed that a higher lactose percentage was connected with an increased pregnancy rate. Francisco *et al.* [2003] concluded that the percentage of lactose in milk was the greatest contributor to a model predicting days to second postpartum ovulation.

The relationship between milk urea content and fertility traits has also been studied. Melendez *et al.* [2000], Rajala-Schultz *et al.* [2001], Guo *et al.* [2004] and Hojman *et al.* [2004] showed that high values of MU might indicate problems with reproduction. König *et al.* [2008] obtained negative genetic correlations between MU and non-return rates (-0.13 for 56-days non-return rate, -0.12 for 90-days non-return rate). This suggests that selection for lower MU would slightly improve reproduction performance.

The potential use of lactose percentage and milk urea content in a selection programme requires insight into their relationship with other traits (production, conformation, fertility). The objective of this study was to estimate genetic parameters for lactose percentage or milk urea content and production traits (milk yield, fat percentage, protein percentage) in Polish Holstein-Friesians.

Material and methods

Data were made available by the Osowa Sien dairy farm. The data file consisted of 104,875 test-day (TD) records from the first three lactations of 6,299 Holstein-Friesian (HF) cows (50,344; 34,323 and 20,208 TD records from parities 1, 2 and 3, respectively). Records included 5 traits: TD milk yield, fat, protein and lactose percentages, and milk urea content. Urea concentration in milk was measured by infrared spectroscopy. Only records between 5 and 305 days in milk (DIM) were used in calculations. Cows with records in the second lactation were required to have records in the first one, and cows with records in the third lactation were required to have records in the two previous lactations. Cows calved between 2000 and 2012. They were daughters of 637 sires and 4,556 dams. There were 2,711 dams with their own records in the data file. The pedigree file contained 8,781 animals in total (cows with records and their parents).

Analysing all the 15 traits (milk yield, fat percentage, protein percentage, lactose percentage and milk urea content in the first three lactations) in one model was computationally unfeasible, so several analyses using fewer traits were conducted. Three 5-trait (milk yield, fat percentage, protein percentage, lactose percentage, MU) analyses were performed for each of the first three lactations separately to estimate genetic parameters within each lactation. Fifteen 2-trait analyses were also done to estimate genetic correlations between parities (1 and 2, 1 and 3, 2 and 3) within traits (milk yield, fat percentage, protein percentage, lactose percentage, MU).

In matrix notation the model for i -th trait was:

$$y_i = H_i h_i + X_i b_i + Z_i a_i + W_i p_i + e_i$$

where:

- y_i – vector of observations;
 h_i – vector of fixed herd-test-day effects;
 b_i – vector of fixed regression coefficients for season of calving by age at calving effects;
 a_i – vector of random regression coefficients for additive genetic effects;
 p_i – vector of random regression coefficients for permanent environmental effects;
 e_i – vector of residuals;

H_i, X_i, Z_i, W_i – incidence matrices assigning observations to effects.

Both fixed and random regressions were modeled using fourth-order Legendre polynomials [Kirkpatrick *et al.* 1994].

Two seasons of calving were created: April to September and October to March. The calving age classes (in months) were 20-24, 25-26, 27-28, 29-30 and 31-45 for primiparous cows, 31-38, 39-41, 42-44, 45-65 for cows in second lactation, and 43-51, 52-55, 56-74 for cows in third lactation. There were 1,410 herd-test-day classes (HTD) in the first lactation, 1,129 HTD in the second lactation, and 830 HTD in the third lactation.

The multiple trait model for t traits was as follows:

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

where: y – vector of observations, $y = [y_1' \dots y_t']'$;

h – vector of fixed herd-test-day effects, $h = [h_1' \dots h_t']'$;

b – vector of fixed regression coefficients for season of calving by age at calving effects, $b = [b_1' \dots b_t']'$;

a – vector of random regression coefficients for additive genetic effects, $a = [a_1' \dots a_t']'$;

p – vector of random regression coefficients for permanent environmental effects, $p = [p_1' \dots p_t']'$;

e – vector of residuals, $e = [e_1' \dots e_t']'$;

and H, X, Z, W are direct sums of matrices, that is,

$$H = \sum H_i, X = \sum X_i, Z = \sum Z_i, W = \sum W_i$$

Expectations and covariance structure for random effects can be described as:

$$E(y) = Hh + Xb, \quad E(a) = 0, \quad E(p) = 0, \quad E(e) = 0$$

$$V(a) = A \otimes G_0, \quad V(p) = I \otimes P_0, \quad V(e) = R$$

where: I is the identity matrix, A is the additive genetic relationship matrix, G_0 and P_0 are covariance matrices for additive genetic and permanent environmental regression

coefficients, R is a diagonal residual matrix with elements on the diagonal equal to residual variances for each trait, \otimes denotes the Kronecker product.

A Bayesian method via Gibbs sampling was used to estimate (co)variance components [Misztal 2008]. There were 100,000 samples of (co)variance components generated and the first 10,000 samples were discarded as the burn-in period. Estimates of (co)variance components were calculated as averages of the remaining 90,000 samples; they were used to estimate heritabilities and genetic correlations [Jamrozik and Schaeffer 1997].

Results and discussion

Variances

Genetic variances of lactose percentage and milk urea content were estimated for each day of the first three lactations. The changes of genetic variances for lactose percentage throughout the first lactation are presented in Figure 1. In the second and third lactations the changes of genetic variance were similar. The values were highest at the beginning and at the end of the lactations, and almost constant in the middle (0.015 in first lactation and 0.010 in second and third). On average, genetic variances for lactose percentage were quite similar in the first three lactations (0.017, 0.019 and 0.022 in first, second and third, respectively). In studies by Miglior *et al.* [2007], Ptak *et al.* [2012] and Jesiołkiewicz *et al.* [2011] the genetic variance of lactose percentage changed in a way similar to that shown in Figure 1, with higher values at the peripheries and almost constant values in the remaining part of the lactation. Miglior *et al.* [2007] and Jesiołkiewicz *et al.* [2011] obtained similar values of genetic variance for lactose percentage in the middle stage of the first lactation (0.010 and

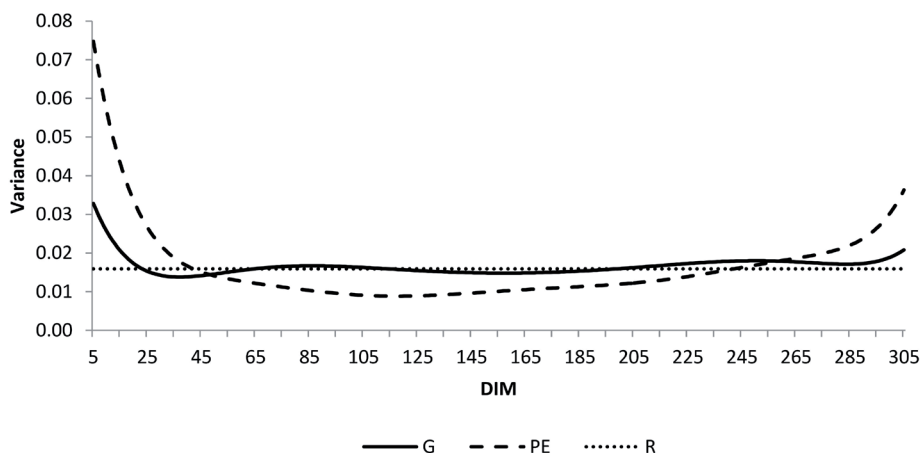


Fig. 1. Genetic (G), permanent environmental (PE) and residual (R) variances for lactose percentage in the first lactation.

0.015, respectively), whereas genetic variance estimated by Ptak *et al.* [2012] was higher (0.040). Permanent environmental (PE) variances for lactose percentage in the first three lactations were also higher at the peripheries than in the middle of lactation. Figure 1 presents changes of PE variance in the first lactation. Compared with genetic variances, PE variances were lower in the middle of lactation and higher at the peripheries. In the second and third lactations PE variance was higher than genetic variance for all DIM (figures not presented in the study). In contrast, Miglior *et al.* [2007] showed that PE variance was lower than genetic variance in each DIM within the first, second and third lactations.

It was assumed that residual variance for lactose percentage was constant throughout lactation, and estimated values were 0.016, 0.026 and 0.021 in lactations 1, 2 and 3, respectively.

Figure 2 shows daily genetic, permanent environmental and residual variances for MU in the first lactation. Average genetic variance was similar in the first (954) and second (921) lactations, and lower in the third lactation (607). In the case of MU, residual variance (2,066, 2,219, 2,127 in the first, second and third lactations) was higher than both genetic and permanent environmental variances in almost every DIM of the first three lactations. This is in agreement with results reported by Rzewuska and Strabel [2013b], who suggested that high residual variances might result from not including some effects which could influence MU (e.g. effect of feeding group) in the model. Also, measurement errors related to the use of infrared spectroscopy to determine MU may cause residual variance to be high.

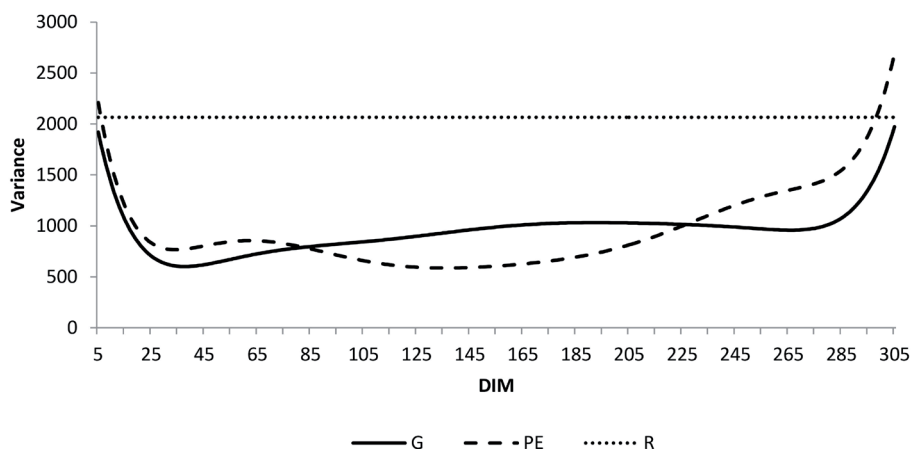


Fig. 2. Genetic (G), permanent environmental (PE) and residual (R) variances for milk urea content in the first lactation.

Heritabilities

Heritabilities of lactose percentage in subsequent DIM of the first three lactations are presented in Figure 3. They ranged from 0.26 to 0.40 in the first lactation, 0.16 to

0.37 in the second lactation, and 0.21 to 0.40 in the third lactation. Lower values of heritability for lactose percentage (0.17-0.31) in the first lactation were obtained by Ptak *et al.* [2012], while estimates reported by Jesiołkiewicz *et al.* [2011] were higher (0.37-0.57).

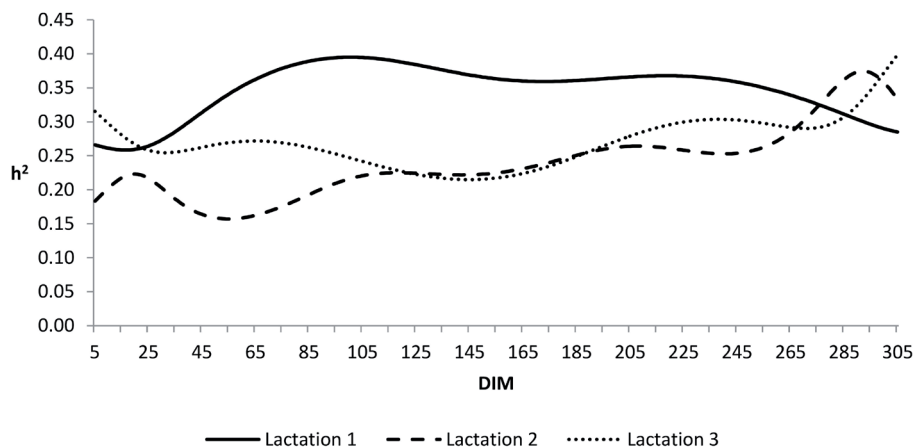


Fig. 3. Heritabilities (h^2) of daily lactose percentage throughout the first three lactations.

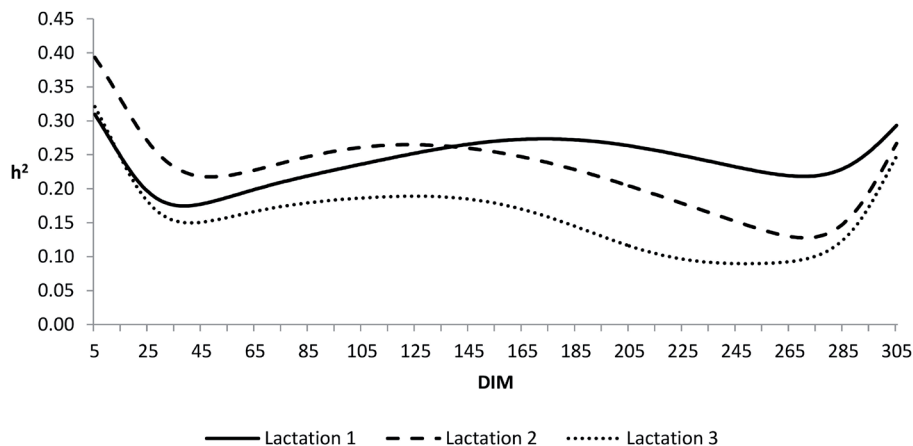


Fig. 4. Heritabilities (h^2) of daily milk urea content (MU) throughout the first three lactations.

Figure 4 shows heritabilities for milk urea content in successive DIM of the first three lactations, which ranged from 0.17 to 0.31 in the first lactation, 0.13 to 0.39 in the second lactation, and 0.09 to 0.32 in the third lactation, with the highest values observed at the beginning. Rzewuska and Strabel [2013b] estimated the highest values of daily heritability at the end of all three lactations and the lowest at 6-7 months of lactation, which is the opposite of our results. Hossein-Zadeh and Ardalan [2011] confirmed that

daily heritabilities of MU were the lowest at mid-lactation (5th month) and higher at the peripheries. Mucha and Strandberg [2011] reported that daily heritabilities of MU were practically constant during the first lactation, with values close to 0.20.

The heritabilities for both lactose percentage and milk urea concentration were higher than heritability for milk yield, and lower than the heritabilities for fat and protein percentages for almost all DIM (plots for milk yield, fat and protein percentage not presented in the study).

Average daily heritabilities for lactose percentage were 0.35, 0.24 and 0.27 for lactations 1, 2 and 3, respectively (Tab. 1). They were within the range of heritabilities reported in the literature [Welper and Freeman 1992, Miglior *et al.* 2007, Stoop *et al.* 2007, Hosseini-Zadeh and Ardalani 2011, Loker *et al.* 2012]. Stoop *et al.* [2007] obtained larger values of heritability for lactose percentage in the first lactation (0.64). They used an animal model and the REML method to estimate (co)variance components. Loker *et al.* [2012] and Miglior *et al.* [2007] used a random regression model and Bayesian Gibbs sampling; they also obtained high estimates for heritability of daily lactose percentage (0.48-0.52). The heritabilities of lactose percentage obtained by Welper and Freeman [1992] ranged from 0.43 to 0.53 depending on the type of model used (single-trait or multiple-trait, and with or without information on sire relationships and somatic cell score). They obtained higher values of heritability when somatic cell score was included in the model as a covariate. Lower values of heritability for lactose percentage than those presented in our study were reported only by Samore *et al.* [2007] for the Italian Brown Swiss population (0.17).

Table 1. Average daily heritabilities (on diagonal), genetic correlations (above diagonal) and permanent environmental correlations (below diagonal) with standard deviations (in parentheses) for all analysed traits, by lactation

Lactation Trait	Milk	Fat	Protein	Lactose	MU
1					
Milk (kg)	0.20 (0.02)	-0.64 (0.08)	-0.62 (0.13)	0.29 (0.08)	0.24 (0.07)
Fat (%)	-0.56 (0.09)	0.42 (0.07)	0.70 (0.11)	-0.24 (0.12)	-0.01 (0.05)
Protein (%)	-0.43 (0.07)	0.63 (0.18)	0.46 (0.12)	-0.21 (0.17)	-0.16 (0.09)
Lactose (%)	0.49 (0.07)	-0.44 (0.09)	-0.31 (0.07)	0.35 (0.04)	-0.03 (0.04)
MU (mg/l)	0.34 (0.13)	-0.04 (0.14)	-0.13 (0.30)	0.15 (0.13)	0.24 (0.03)
2					
Milk (kg)	0.20 (0.04)	-0.43 (0.14)	-0.54 (0.15)	0.29 (0.18)	0.19 (0.06)
Fat (%)	-0.57 (0.11)	0.40 (0.09)	0.65 (0.17)	-0.05 (0.05)	0.08 (0.07)
Protein (%)	-0.47 (0.10)	0.57 (0.15)	0.44 (0.12)	-0.19 (0.14)	-0.15 (0.06)
Lactose (%)	0.52 (0.07)	-0.30 (0.14)	-0.20 (0.07)	0.24 (0.05)	0.12 (0.08)
MU (mg/l)	0.41 (0.12)	-0.18 (0.10)	-0.18 (0.12)	0.26 (0.11)	0.22 (0.05)
3					
Milk (kg)	0.14 (0.02)	-0.40 (0.13)	-0.42 (0.16)	0.34 (0.12)	0.35 (0.18)
Fat (%)	-0.57 (0.09)	0.33 (0.03)	0.63 (0.20)	0.02 (0.17)	0.05 (0.09)
Protein (%)	-0.52 (0.07)	0.64 (0.17)	0.41 (0.06)	-0.13 (0.05)	-0.04 (0.19)
Lactose (%)	0.65 (0.04)	-0.37 (0.18)	-0.38 (0.09)	0.27 (0.04)	0.19 (0.13)
MU (mg/l)	0.44 (0.08)	0.00 (0.08)	-0.22 (0.10)	0.37 (0.05)	0.16 (0.05)

As mentioned above, this study showed that lactose percentage was more highly heritable in the first than in later lactations. An opposite trend was reported by Miglior *et al.* [2007] and Hossein-Zadeh and Ardalan [2011]. Miglior *et al.* [2007] estimated heritability equal to 0.48 in the first lactation and 0.51 in both the second and third lactations. Hossein-Zadeh and Ardalan [2011] also obtained increasing heritability values in subsequent lactations (0.29, 0.33 and 0.35 in lactations 1, 2 and 3, respectively).

According to the literature, heritability for MU ranges from 0.09 to 0.59 [Wood *et al.* 2003, Mitchell *et al.* 2005, Miglior *et al.* 2007, Stoop *et al.* 2007, Bastin *et al.* 2009, Hossein-Zadeh and Ardalan 2011, Loker *et al.* 2012, Rzewuska and Strabel 2013b]. Average heritability of daily milk urea content was highest in the first lactation (0.24) and lower in second (0.22) and third (0.16) (Tab. 1). Similar findings for the first three lactations were reported by Mitchell *et al.* [2005] (0.22-0.23), Hossein-Zadeh and Ardalan [2011] (0.18-0.20) and Rzewuska and Strabel [2013b] (0.21-0.22). Higher heritability of MU (0.36-0.41) was found by Canadian researchers, who used multiple-trait models with random regressions and Bayesian Gibbs sampling [Loker *et al.* 2012, Miglior *et al.* 2007]. Wood *et al.* [2003] presented even higher heritabilities of MU content for the Canadian population (0.44-0.59); they used a simpler model, without random regressions. Lower heritability of MU than in our study was estimated by Stoop *et al.* [2007] for Dutch Holstein-Friesians (0.14). Mitchell *et al.* [2005] obtained heritability of MU similar to that in our study, but only when MU was measured by the infrared method (IR), i.e. the same method as used in the Polish population. When MU was measured by the wet chemistry method (WC) the heritabilities were lower (0.09-0.15). The WC method is a direct measure of urea in milk, whereas in the IR method the milk urea value is calculated based on prediction equations employing spectrum analysis. The genetic correlation between MU measured with those two methods was low, only 0.38 in the first and 0.23 in the second lactation.

For each of the first three lactations the heritabilities for lactose percentage and milk urea concentration were higher than the heritability for milk yield and lower than the heritabilities for fat and protein percentages (Tab. 1).

Genetic correlations

Genetic correlations between lactose percentage and milk yield, fat and protein percentage in the first lactation are shown in Figure 5. Patterns of changes in the second and third lactations were similar to those from the first lactation (figures not shown).

Genetic correlations between lactose percentage and milk yield changed from 0.14 to 0.48 in the first, -0.02 to 0.66 in the second, and 0.14 to 0.59 in the third lactation, with means of 0.29, 0.29 and 0.34, respectively. Genetic correlations between lactose percentage and milk yield for individual DIM of the first three lactations estimated by Miglior *et al.* [2007] were lower, but the shapes of the curves were similar to those in Figure 5. Positive genetic correlation (0.55) between lactose percentage and milk yield was also estimated by Hossein-Zadeh and Ardalan [2011], who used a random

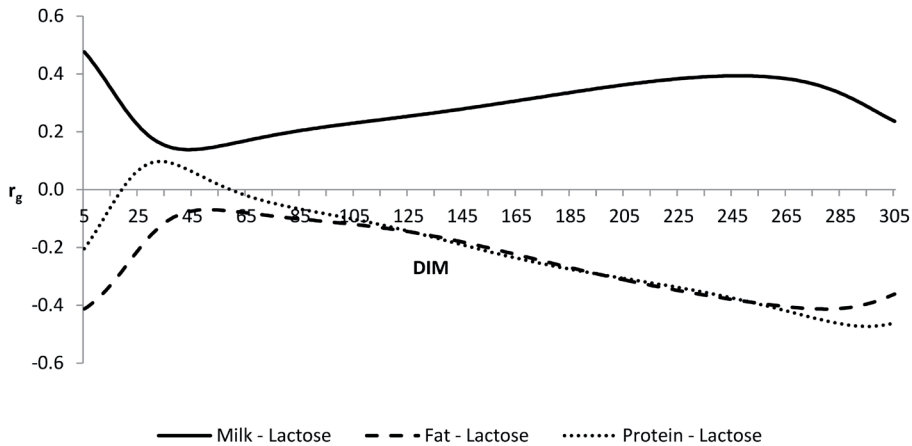


Fig. 5. Genetic correlations (r_g) between lactose percentage and milk yield, fat percentage and protein percentage in the first lactation.

regression model and Legendre polynomials to model lactation curves. However, negative or near-zero genetic correlations (-0.3 to 0.096) between lactose percentage and milk yield were reported by Welper and Freeman [1992], Miglior *et al.* [2007], Samore *et al.* [2007] and Jesiołkiewicz *et al.* [2011].

As shown in Table 1, lactose percentage and protein percentage were on average weakly genetically correlated in the first three lactations (-0.21, -0.19 and -0.13 in first, second and third, respectively). The average genetic correlation between lactose percentage and fat percentage in the first lactation was negative and moderate (-0.24); there were no genetic relationships between those two traits in the second and third lactations (-0.05 and 0.02, respectively). Miglior *et al.* [2007], Stoop *et al.* [2007] and Samore *et al.* [2007] confirmed no or a very weak genetic relationship between lactose percentage and fat or protein percentage. Our results show that selection for a higher lactose percentage in milk might increase the milk yield and protein percentage and should have no effect on fat percentage.

Moderate positive genetic correlations between MU and milk yield (0.19 to 0.35) were observed for all first three lactations (Tab. 1). Similar values of average genetic correlations between those traits were obtained by Rzewuska and Strabel [2013b], Stoop *et al.* [2007] and Hossein-Zadeh and Ardalán [2011] (0.20 to 0.42). It might be concluded that selection for a higher milk yield could cause higher MU. Wood *et al.* [2003] noted slightly lower genetic correlations between MU and milk yield in the first and second lactations (0.11 and 0.17, respectively) and no genetic correlation in the third lactation (-0.05). Miglior *et al.* [2007] also showed no genetic relationship between those two traits. Only Samore *et al.* [2007] estimated a negative genetic correlation between MU and milk yield for the Italian Brown Swiss population (-0.17).

Our results show that in the Polish HF population there was no or a weak genetic correlation between MU and fat percentage (-0.01 to 0.08), between MU and protein

percentage (-0.16 to -0.04), and between MU and lactose percentage (-0.03 to 0.19) (Tab. 1). This means that selection for a lower milk urea concentration should have no effect on other milk traits (fat, protein and lactose percentage). Samore *et al.* [2007], Stoop *et al.* [2007], Hossein-Zadeh and Ardalan [2011] and Rzewuska and Strabel [2013b] also reported no or a weak genetic correlation between MU and fat percentage (-0.09 to 0.21). A positive genetic correlation between those two traits (0.43) was estimated only by Miglior *et al.* [2007] for the Canadian population. The genetic correlations between MU and protein content in the first three lactations of Polish Holstein-Friesians, estimated by Rzewuska and Strabel [2013b] (-0.24, -0.19, -0.11), were negative and low to moderate, in agreement with our results. Miglior *et al.* [2007], Stoop *et al.* [2007] and Hossein-Zadeh and Ardalan [2011] found a positive genetic relationship between MU and protein content (0.20 to 0.30). Miglior *et al.* [2007], Samore *et al.* [2007], Stoop *et al.* [2007], Hossein-Zadeh and Ardalan [2011] and Rzewuska and Strabel [2013b] showed no genetic relationship between MU and lactose percentage (from -0.09 to 0.01). Similar results are presented in our study (0.03), but only for the first lactation. In the second and third lactations the genetic correlations between MU and lactose percentage were positive: 0.12 and 0.19, respectively. Changes of the genetic correlations between MU content and other milk traits (milk yield, fat, protein and lactose percentage) in the first lactation are presented in Figure 6.

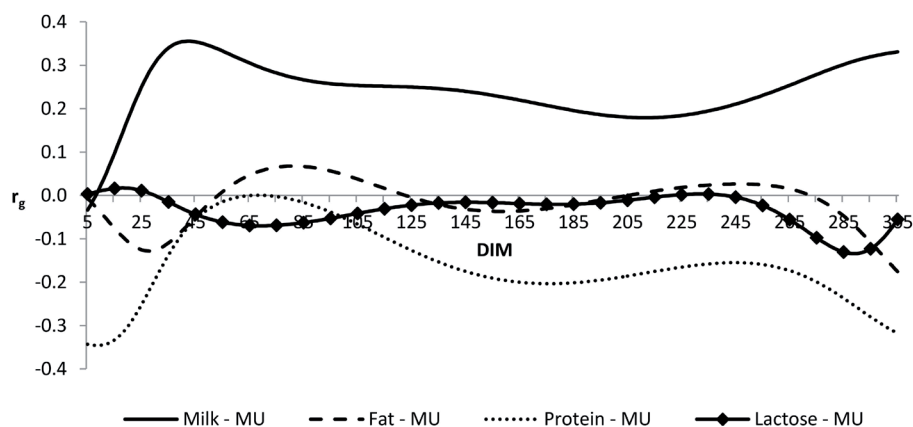


Fig. 6. Genetic correlations (r_g) between milk urea content (MU) and milk yield, fat percentage, protein percentage and lactose percentage in the first lactation.

The average genetic correlation between lactose percentage at the same DIM of adjacent lactations (first and second, second and third) was 0.72 and 0.76; between the first and third lactations it was slightly lower at 0.70 (Tab. 2). In the case of MU the highest genetic correlation was also found between the second and third lactations (0.70), while between the first and second or first and third lactations the correlations were much lower (0.54 on average in both cases). Miglior *et al.* [2007] obtained higher genetic correlations between lactations for the analysed milk traits. They reported

Table 2. Average genetic correlations, with standard deviations (in parentheses), among lactations within traits

Trait	Lactations		
	1 and 2	1 and 3	2 and 3
Milk (kg)	0.71 (0.10)	0.56 (0.18)	0.69 (0.11)
Fat (%)	0.81 (0.16)	0.76 (0.17)	0.82 (0.11)
Protein (%)	0.76 (0.14)	0.71 (0.21)	0.85 (0.10)
Lactose (%)	0.72 (0.13)	0.70 (0.14)	0.76 (0.08)
MU (mg/l)	0.54 (0.12)	0.54 (0.17)	0.70 (0.11)

the strongest genetic correlation for both lactose percentage (0.85) and MU (0.87) between the second and third lactations, as it was observed in the Polish population. Rzewuska and Strabel [2013b] confirmed the results of Miglior *et al.* [2007]. They obtained high genetic correlations between lactations for MU (0.81-0.83).

Our results show that heritabilities of lactose percentage (0.24-0.35) and urea content (0.16–0.24) in milk of Polish Holstein-Friesian cows in the first three lactations were moderate. The ranges of heritabilities for lactose percentage and milk urea content suggest that it is possible to use these two traits in breeding programmes, but further research on relationships with other traits (conformation, fertility and health) is needed. Lactose percentage was positively genetically correlated with milk yield, negatively genetically correlated with protein percentage, and not genetically correlated with fat percentage. Genetic correlations between milk urea content and milk production traits (fat, protein and lactose percentage) were low or close to zero. These results indicate that selection for milk urea content should have no effect on other milk traits (except for milk yield), unlike selection for lactose percentage, which could influence milk yield and protein percentage.

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