

Genetic relationship of conformation traits with lactose percentage and urea concentration in milk of Polish Holstein-Friesian cows*

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The objective of this study was to estimate genetic correlations of lactose percentage and urea concentration in milk with conformation traits related to udder and legs of Polish Holstein-Friesian cows. Data consisted of 5,813 test-day records and type scores of 791 primiparous cows. The analysis involved two descriptive traits (udder, feet and legs, scored from 50 to 100) and 11 linearly scored traits (describing udder: fore udder height, rear udder height, central ligament, udder depth, udder width, fore teat placement, teat length, rear teat placement; describing legs: rear legs – side view, foot angle, rear legs – rear view; on a scale of 1 to 9). Genetic correlations were calculated based on (co)variances estimated using the Bayesian method via Gibbs sampling and the multitrait animal model. Genetic correlations between lactose content and conformation traits ranged from -0.18 to 0.23, while those between milk urea concentration and conformation traits ranged between -0.02 and 0.43, respectively. Absolute values of average genetic correlations with daily lactose percentage exceeded 0.15 only for udder (descriptive trait) and several linearly scored traits, i.e. central ligament, udder depth, rear teat placement, and rear legs – rear view. Milk urea content was weakly or moderately genetically correlated with six type traits: udder, and five linearly scored traits: fore udder height, central ligament, udder width, teat length, and rear legs – side view. Absolute values of genetic correlations between these traits exceeded 0.15. Our results showed that type traits connected with udder were more highly genetically correlated with both lactose and milk urea contents than type traits describing legs. It meant that an increase in both lactose percentage and urea concentration in milk might be expected as an indirect response to selection for better udder, whereas selection for improvement of legs would not affect lactose percentage and milk urea content.

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In Poland lactose content of cows' milk has been routinely recorded since 1998, while milk urea concentration (MU) – since 2000. These two traits could be potentially included into the selection index for Polish Holstein-Friesians. Lactose percentage and MU may be used in indirect selection for health and fertility traits, which are economically important, but of low heritability. Miglior *et al.* [2007] reported that lactose percentage was negatively genetically correlated with somatic cell score (-0.20) and may be used in selection for resistance for mastitis together with somatic cell score. Some authors investigated the relationships between lactose percentage and fertility traits. Buckley *et al.* [2003] concluded that a higher lactose percentage was connected with an increased pregnancy rate and Francisco *et al.* [2003] showed that lactose percentage in milk was the greatest contributor to a model predicting days to second postpartum ovulation. Miglior *et al.* [2006] while investigating the relationship between lactose percentage and longevity found that cows with a low lactose percentage were more likely to be culled. That result suggested that lactose percentage may be used as an auxiliary trait for genetic evaluation for longevity. The relationships between milk urea content and fertility traits have also been studied. Melendez *et al.* [2000], Rajala-Schultz *et al.* [2001], Guo *et al.* [2004], Hojman *et al.* [2004] and Konig *et al.* [2008] showed that high values of milk urea might indicate problems with reproduction and selection for lower milk urea would slightly improve reproduction performance. The results obtained by Rzewuska and Strabel [2015] for the Polish Holstein-Friesian population were not so promising. Those authors mentioned that better fertility was genetically related with higher MU, whereas an increase of milk urea concentration is undesirable. Rzewuska and Strabel [2013] suggested that the effect of direct selection on MU would cause a reduction of nitrogen emission from dairy farms, but now there is no legal obligation motivating farmers to reduce greenhouse gas emissions.

In Poland the period of collecting data on lactose content and urea concentration in milk is sufficiently long to estimate heritabilities and genetic correlations with other traits, especially those included in the selection index. In the literature 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, Rzewuska and Strabel 2013]. Ptak *et al.* [2012] reported heritability of lactose percentage for Polish Holstein-Friesians on the medium level (0.17-0.36) and average heritability of milk urea concentration in the first three lactations obtained by Rzewuska and Strabel [2013] for the Polish Holstein-Friesian population was also on the medium level (0.21-0.22). The ranges of heritabilities imply that lactose percentage and MU may be used in the genetic evaluation of Polish Holstein-Friesians. However, before including these traits into the selection index it would be advisable to know relationships of lactose percentage and MU with the traits under selection.

Conformation traits form an important part of the selection index for Polish Holstein-Friesians due to their huge impact on cows' health and longevity. Many authors

have investigated relationships between conformation traits and milk production traits (i.e. milk, fat and protein yield), and between conformation traits and somatic cell score [Meyer *et al.* 1987, Harris and Freeman 1991, Misztal 1992, Short and Lawlor 1992, Brotherstone 1994, DeGroot *et al.* 2002, Ptak *et al.* 2011]. In the cited papers the relationship between conformation traits and yield traits was investigated based on lactation milk, fat and protein yields. To our knowledge, no research has addressed the relationships of conformation traits with lactose percentage and milk urea content.

The objective of this study was to estimate genetic correlations of conformation traits with lactose percentage and urea concentration in milk of Polish Holstein-Friesian cows throughout the course of lactation. The application of random regression models to estimate genetic parameters provides genetic relationships between conformation traits and milk yield traits in each day of lactation.

Material and methods

Data consisted of 5,813 test-day records and type scores of 791 primiparous Polish Holstein-Friesian cows, made available by the Osowa Sien dairy farm. Samples of milk were analyzed with a MilkoScan™CombiFoss 6000 analyser by a certified milk evaluation laboratory. Milk urea concentration was measured by infrared spectrophotometry. Phenotypic information about MU (mg/l) rather than MU converted to milk urea nitrogen (MUN) was used by Polish farmers. Two descriptive traits (udder, feet and legs) and eleven linearly scored traits describing udder and legs were included in the analysis. The udder traits included fore udder height, rear udder height, central ligament, udder depth, udder width, fore teat placement, teat length, and rear teat placement; leg traits included rear legs – side view, foot angle, and rear legs – rear view. The descriptive traits were scored on a scale from 50 to 100, while linear traits were scored on a scale from 1 to 9. One classifier evaluated all cows. Each cow was scored only once between 15 and 180 days in milk of the first lactation. Cows were daughters of 30 sires and 752 dams and calved for the first time between 2000 and 2011 in 8 herds. The following restrictions were imposed: minimum 10 cows in each subclass of herd-year of calving-season of calving, minimum of 10 daughters per sire, and test-day records between 5 and 305 days in milk with information on lactose percentage and milk urea content in each record.

Four multitrait analyses were performed. Lactose percentage and milk urea content were included in each of them. Additionally, two descriptive traits (udder, feet and legs) were included in the first analysis, three linearly scored leg traits (rear legs – side view, foot angle, rear legs – rear view) in the second analysis, four linearly scored udder traits (fore udder height, rear udder height, central ligament, udder depth) in the third and the other linearly scored udder traits (udder width, fore teat placement, teat length, rear teat placement) in the fourth.

Days in milk were divided into 11 classes of lactation stage as 15-day intervals (15-30, 31-45, 46-60, 61-75, 76-90, 91-105, 106-120, 121-135, 136-150, 151-165,

166-180). Two seasons of calving were created (April to September, October to March), and 5 classes of age at calving (in months): 20-24, 25-26, 27-28, 29-30, and 31-45. There were 33 classes of herd-year of calving-season of calving. The pedigree file included 1,522 animals in total (cows and their parents).

There were two linear models used in each multitrait analysis: one for milk urea content and lactose percentage and the other for type traits. The model for lactose percentage ($m=1$) and milk urea content ($m=2$) was:

$$\mathbf{y}_m = \mathbf{H}_m \mathbf{h}_m + \mathbf{X}_m \mathbf{b}_m + \mathbf{Z}_m \mathbf{a}_m + \mathbf{W}_m \mathbf{p}_m + \mathbf{e}_m$$

where:

\mathbf{y}_m – vector of observations for trait m ($m = 1, 2$);

\mathbf{h}_m – vector of fixed herd-test-day effects;

\mathbf{b}_m – vector of fixed regression coefficients for season of calving-age at calving effects;

\mathbf{a}_m – vector of random regression coefficients for additive genetic effects;

\mathbf{p}_m – vector of random regression coefficients for permanent environmental effects;

\mathbf{e}_m – vector of residuals;

$\mathbf{H}_m, \mathbf{X}_m, \mathbf{Z}_m, \mathbf{W}_m$ – incidence matrices assigning observations to effects.

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

For each of n conformation traits the linear model was:

$$\mathbf{y}_m = \mathbf{Z}_m \mathbf{a}_m + \mathbf{T}_m \mathbf{t}_m + \mathbf{F}_m \mathbf{f}_m + \mathbf{U}_m \mathbf{u}_m + \mathbf{e}_m$$

where:

\mathbf{y}_m – vector of observations for conformation trait m ($m = 3, \dots, n + 2$);

\mathbf{a}_m – vector of random additive genetic effects;

\mathbf{t}_m – vector of fixed effects of herd-year of calving-season of calving;

\mathbf{f}_m – vector of fixed effects of stage of lactation;

\mathbf{u}_m – vector of fixed linear regression coefficients on age at calving;

\mathbf{e}_m – vector of residuals;

$\mathbf{Z}_m, \mathbf{T}_m, \mathbf{F}_m, \mathbf{U}_m$ – incidence matrices assigning observations to respective effects.

Two models described above could be presented as one multiple trait model as follows:

$$\mathbf{y} = \mathbf{Hh} + \mathbf{Xb} + \mathbf{Za} + \mathbf{Wp} + \mathbf{Tt} + \mathbf{Ff} + \mathbf{Uu} + \mathbf{e}$$

where:

$$\mathbf{y} = [\mathbf{y}_1' \dots \mathbf{y}_{n+2}']', \mathbf{h} = [\mathbf{h}_1' \mathbf{h}_2']', \mathbf{b} = [\mathbf{b}_1' \mathbf{b}_2']', \mathbf{a} = [\mathbf{a}_1' \dots \mathbf{a}_{n+2}']', \mathbf{p} = [\mathbf{p}_1' \mathbf{p}_2']'$$

$$\mathbf{t} = [\mathbf{t}_3' \dots \mathbf{t}_{n+2}']', \mathbf{f} = [\mathbf{f}_3' \dots \mathbf{f}_{n+2}']', \mathbf{u} = [\mathbf{u}_3' \dots \mathbf{u}_{n+2}']', \mathbf{e} = [\mathbf{e}_1' \dots \mathbf{e}_{n+2}']'$$

and

$$\mathbf{H} = \begin{bmatrix} \mathbf{H}_1 \oplus \mathbf{H}_2 \\ \mathbf{0} \end{bmatrix}, \mathbf{X} = \begin{bmatrix} \mathbf{X}_1 \oplus \mathbf{X}_2 \\ \mathbf{0} \end{bmatrix}, \mathbf{Z} = \oplus \mathbf{Z}_m, \mathbf{W} = \begin{bmatrix} \mathbf{W}_1 \oplus \mathbf{W}_2 \\ \mathbf{0} \end{bmatrix}$$

$$\mathbf{T} = \begin{bmatrix} \mathbf{0} \\ \oplus \mathbf{T}_m \end{bmatrix}, \mathbf{F} = \begin{bmatrix} \mathbf{0} \\ \oplus \mathbf{F}_m \end{bmatrix}, \mathbf{U} = \begin{bmatrix} \mathbf{0} \\ \oplus \mathbf{U}_m \end{bmatrix}$$

where $\mathbf{0}$ represents zero matrices and $\mathbf{T}_m, \mathbf{F}_m, \mathbf{U}_m$ are incidence matrices for m -th conformation trait ($m = 3, \dots, n + 2$). The symbols \oplus is the direct sum of matrices.

Expectations and (co)variance structure may be described as:

$$\mathbf{E}(\mathbf{y}) = \mathbf{H}\mathbf{h} + \mathbf{X}\mathbf{b} + \mathbf{T}\mathbf{t} + \mathbf{F}\mathbf{f} + \mathbf{U}\mathbf{u}, \quad \mathbf{E}(\mathbf{a}) = \mathbf{0}, \quad \mathbf{E}(\mathbf{p}) = \mathbf{0}, \quad \mathbf{E}(\mathbf{e}) = \mathbf{0},$$

$$\mathbf{V}(\mathbf{a}) = \mathbf{A} \otimes \mathbf{G}_0, \quad \mathbf{V}(\mathbf{p}) = \mathbf{I} \otimes \mathbf{P}_0, \quad \mathbf{V}(\mathbf{e}) = \mathbf{R}$$

where: \mathbf{I} is an identity matrix, \mathbf{A} is an additive genetic relationship matrix, and \mathbf{G}_0 and \mathbf{P}_0 are covariance matrices of random regression coefficients for additive genetic and permanent environmental effects, respectively. \mathbf{R} is a diagonal residual matrix with elements on the diagonal equal to residual variances for each trait. In the case of lactose percentage and milk urea content, homogenous variances were assumed. The symbol \otimes denotes the Kronecker product.

$$\tilde{\mathbf{G}} = \begin{bmatrix} \hat{\mathbf{G}}_1 & \hat{\mathbf{G}}_{1,2} & \hat{\mathbf{g}}_{1,3} & \hat{\mathbf{g}}_{1,4} & \dots & \hat{\mathbf{g}}_{1,n+1} & \hat{\mathbf{g}}_{1,n+2} \\ & \hat{\mathbf{G}}_2 & \hat{\mathbf{g}}_{2,3} & \hat{\mathbf{g}}_{2,4} & \dots & \hat{\mathbf{g}}_{2,n+1} & \hat{\mathbf{g}}_{2,n+2} \\ & & \hat{\sigma}_{\mathbf{g}3}^2 & \text{cov}_{\mathbf{g}3,4} & \dots & \text{cov}_{\mathbf{g}3,n+1} & \text{cov}_{\mathbf{g}3,n+2} \\ & & & \hat{\sigma}_{\mathbf{g}4}^2 & \dots & \text{cov}_{\mathbf{g}4,n+1} & \text{cov}_{\mathbf{g}4,n+2} \\ & & & & \ddots & \vdots & \vdots \\ & & & & & \hat{\sigma}_{\mathbf{g}n+1}^2 & \text{cov}_{\mathbf{g}n+1,n+2} \\ & & & & & & \hat{\sigma}_{\mathbf{g}n+2}^2 \end{bmatrix}$$

The Bayesian method via Gibbs sampling was used to estimate (co)variance components [Misztal 2008]. There were 100,000 samples of (co)variance components generated, with the first 10,000 samples discarded as the burn-in period. Estimates

$$\hat{\sigma}_{\mathbf{g}j}^2 \text{ — additive genetic variance of conformation trait } j \text{ (} j = 3, \dots, n + 2 \text{);}$$

of (co)variances were calculated as averages of the remaining 90,000 samples. The (co)variance matrix for the additive genetic effect was as follows:

where:

$\hat{\mathbf{g}}_{1,j}$ and $\hat{\mathbf{g}}_{2,j}$ — vectors of covariances of additive genetic effect for conformation trait j ($j = 3, \dots, n + 2$) and additive genetic regression coefficients for lactose percentage or for milk urea content, respectively;

$\text{cov}_{\epsilon_{ij}}$ – additive genetic covariance between conformation traits i and j ($i, j = 3, \dots, n + 2, i \neq j$).

\hat{G}_1 and \hat{G}_2 – (co)variance matrices of the additive genetic regression coefficients for lactose percentage (\hat{G}_1) and milk urea content (\hat{G}_2);

$\hat{G}_{1,2}$ – covariance matrix of additive genetic regression coefficients for lactose percentage and milk urea content;

The (co)variance matrix was used to calculate genetic correlations of conformation traits with lactose percentage and milk urea content in each DIM [Jamrozik and Schaeffer 1997]. Those correlations were averaged within two periods of lactation: when type traits were evaluated (i.e. between 15 and 180 DIM) and for the whole 305-day lactation (i.e. between 5 and 305 DIM).

Results and discussion

Table 1 shows the means (with SD) and ranges for all analyzed traits: lactose percentage, milk urea content, two descriptive traits and eleven linearly scored traits which describe udder and legs. The optima for linearly scored type traits are also presented in Table 1. The means for descriptive traits (udder and feet and legs) were

Table 1. Means (with SD) and ranges for lactose percentage, milk urea content (MU) and conformation traits, with optimum values for linearly scored traits

Trait	Mean	SD	Minimum	Maximum	Optimum
Lactose (%)	4.97	0.19	3.28	5.67	–
MU (mg/l)	226	92	20	569	–
Descriptive					
feet and legs	80.0	3.0	52	87	–
udder	79.2	3.9	50	86	–
Linear					
rear legs – side view	5.4	0.9	1	9	5
foot angle	5.4	1.1	2	9	7
rear legs – rear view	5.3	1.1	2	9	9
fore udder height	5.8	1.2	2	9	7
rear udder height	5.5	1.0	2	8	9
central ligament	5.9	1.5	1	9	9
udder depth	5.5	1.1	1	9	7
udder width	5.6	1.1	1	9	9
fore teat placement	6.4	1.6	1	9	5
rear teat placement	4.5	1.0	1	9	4
teat length	5.4	1.3	1	9	5

high (79.2 and 80.0, respectively), with standard deviations representing only about 4-5% of the means. The average scores for a majority of linear conformation traits were close to 5.0, the value in the middle of the nine-point scale, which in most cases was lower than the optimum. Only teats scored slightly higher than the assumed optimum (Tab. 1).

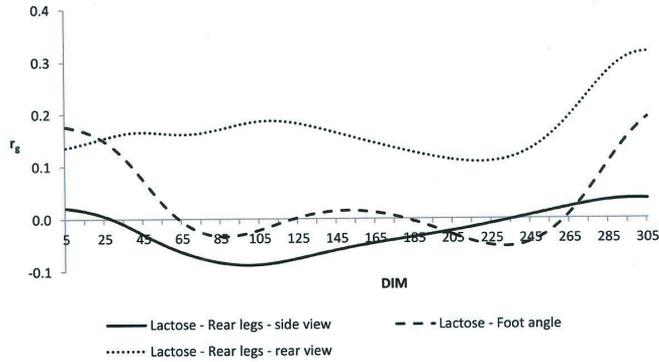


Fig. 1. Genetic correlations (r_g) between lactose percentage in each DIM of the first lactation and three linearly scored leg traits: rear legs – side view, foot angle, rear legs – rear view.

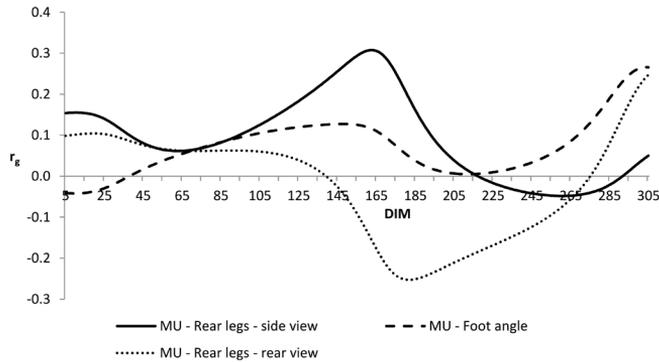


Fig. 2. Genetic correlations (r_g) between milk urea content (MU) in each DIM of the first lactation and three linearly scored leg traits: rear legs – side view, foot angle, rear legs – rear view.

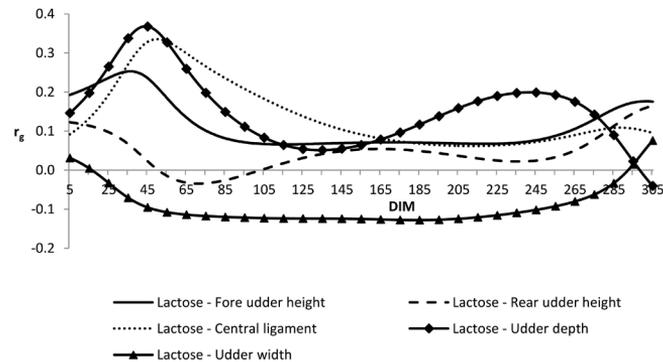


Fig. 3. Genetic correlations (r_g) between lactose percentage in each DIM of the first lactation and five linearly scored udder traits: fore udder height, rear udder height, central ligament, udder depth, udder width.

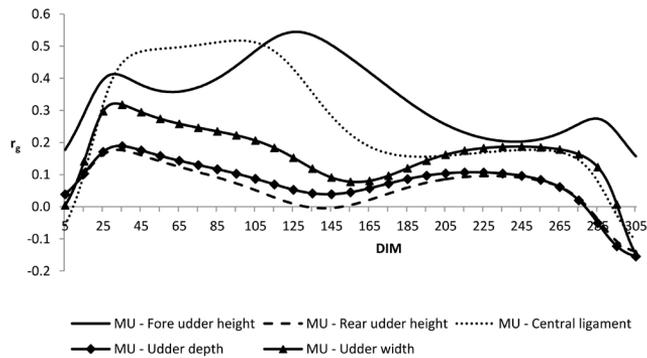


Fig. 4. Genetic correlations (r_g) between milk urea content (MU) in each DIM of the first lactation and five linearly scored udder traits: fore udder height, rear udder height, central ligament, udder depth, udder width.

Genetic correlations of each conformation trait with daily lactose percentage and milk urea concentration are shown in Figures 1-4 and Table 2. In most cases the values of the genetic correlation of conformation traits with lactose percentage and milk urea content were positive, although some type traits were negatively correlated with lactose percentage and milk urea content throughout the lactation. For example, lactose percentage was weakly negatively correlated with udder width in almost every DIM (Fig. 3), and with rear legs – side view between 30 and 235 DIM (Fig. 1). In the case of milk urea content negative daily correlations with rear legs – rear view were also observed, but within a shorter period of lactation (between 140 and 275 DIM) (Fig. 2). In general we observed no clear regularity in changes of daily genetic correlations for different combinations of type traits and lactose percentage or milk urea concentration; thus only the average genetic correlations of conformation traits with lactose percentage and milk urea content were interpreted.

Average genetic correlations of conformation traits with lactose percentage in the period of type evaluation, between 15 and 180 DIM, ranged from -0.18 to 0.23 (Tab. 2). They were similar to or slightly higher than the mean correlations calculated for DIM between 5 and 305 (-0.18 to 0.20). Absolute values of average genetic correlations with daily lactose percentage were higher than 0.15 for udder as a descriptive trait ($r_{180} = 0.23$, $r_{305} = 0.20$) and several linearly scored traits: udder depth ($r_{180} = 0.16$, $r_{305} = 0.15$), rear teat placement ($r_{180} = -0.18$, $r_{305} = -0.18$), and rear legs – rear view ($r_{180} = 0.17$, $r_{305} = 0.17$). Favourable genetic correlations with lactose percentage were also obtained for central ligament ($r_{180} = 0.19$, $r_{305} = 0.14$). These results indicate that good characteristics for udder are associated with a greater genetic merit for lactose content in milk. Ptak *et al.* [2011] obtained favourable genetic correlations of central ligament and udder depth with daily somatic cell score (-0.16 and -0.17, respectively). All those results suggested that selection for stronger central ligament and shallow udder would reduce the somatic cell score and increase the lactose percentage in milk. The negative genetic correlation between lactose percentage and rear teat placement (-0.18) was difficult to interpret, as

Table 2. Genetic correlations (r with SD) of conformation traits with daily lactose percentage and milk urea content, averaged for 15-180 DIM (r_{180}), and for 5-305 DIM (r_{305})

Trait	Lactose (%)		MU (mg/l)	
	r_{180}	r_{305}	r_{180}	r_{305}
Descriptive				
feet and legs	0.14 _(0.04)	0.15 _(0.05)	0.10 _(0.02)	0.08 _(0.07)
udder	0.23 _(0.07)	0.20 _(0.09)	0.27 _(0.08)	0.17 _(0.13)
Linear				
rear legs – side view	-0.05 _(0.03)	-0.03 _(0.04)	0.16 _(0.08)	0.09 _(0.10)
foot angle	0.02 _(0.06)	0.02 _(0.07)	0.07 _(0.05)	0.07 _(0.07)
rear legs – rear view	0.17 _(0.01)	0.17 _(0.05)	0.02 _(0.10)	-0.02 _(0.13)
fore udder height	0.12 _(0.07)	0.11 _(0.06)	0.43 _(0.07)	0.34 _(0.11)
rear udder height	0.03 _(0.04)	0.04 _(0.05)	0.08 _(0.06)	0.06 _(0.07)
central ligament	0.19 _(0.08)	0.14 _(0.08)	0.39 _(0.13)	0.27 _(0.17)
udder depth	0.16 _(0.11)	0.15 _(0.09)	0.10 _(0.05)	0.08 _(0.07)
udder width	-0.11 _(0.03)	-0.09 _(0.05)	0.20 _(0.08)	0.17 _(0.08)
fore teat placement	0.00 _(0.05)	-0.01 _(0.04)	0.07 _(0.09)	0.05 _(0.07)
rear teat placement	-0.18 _(0.02)	-0.18 _(0.03)	0.03 _(0.16)	0.07 _(0.17)
teat length	0.07 _(0.06)	0.03 _(0.08)	0.29 _(0.07)	0.29 _(0.06)

the optimum for rear teat placement was 4 points, i.e. in the middle of the scale. We might only suggest that selection for wider rear teat placement could cause an increase in lactose percentage, whereas selection in the opposite direction might decrease it.

Leg conformation traits were more weakly genetically correlated with lactose percentage in comparison to udder conformation traits (Tab. 2). Only one descriptive trait (feet and legs; $r_{180} = 0.14$, $r_{305} = 0.15$) and one linearly scored trait (rear legs – rear view; $r_{180} = 0.17$, $r_{305} = 0.17$) were favourably genetically correlated with lactose percentage; higher lactose percentage was associated with better-built legs.

Average genetic correlations between milk urea concentration and conformation traits ranged from 0.02 to 0.43 for 15 to 180 DIM (Tab. 2). When all daily genetic correlations throughout the 305-day lactation were averaged, the genetic correlations were slightly lower (-0.02 to 0.34). Only six conformation traits (one descriptive trait: udder; five linearly scored traits: fore udder height, central ligament, udder width, teat length, rear teat placement, rear legs – side view) were weakly or moderately genetically correlated with milk urea content. All these correlations exceeded 0.15. Udder traits were generally unfavourably genetically correlated with milk urea content. The genetic correlations of the udder descriptive trait ($r_{180} = 0.27$, $r_{305} = 0.17$) with milk urea content indicated that selection for udder improvement would increase it. Milk urea content was moderately genetically correlated with four linearly scored udder traits: fore udder height ($r_{180} = 0.43$, $r_{305} = 0.34$), central ligament ($r_{180} = 0.39$, $r_{305} = 0.27$), udder width ($r_{180} = 0.20$, $r_{305} = 0.17$), and teat length ($r_{180} = 0.29$, $r_{305} = 0.29$). These results show that selection for stronger fore udder height and central ligament and for wider udder might raise the milk urea concentration, which is not desirable. The relationship between teat length and milk urea content indicates that selection towards shorter teats might lead to a decreased milk urea content, but for cows having teats of optimal or shorter than optimal length such a selection is not reasonable. The

genetic correlation of milk urea concentration with rear legs – side view ($r_{180} = 0.16$, $r_{305} = 0.09$) is difficult to interpret, because the optimum for this type trait was in the middle of the scale (5 points). Straight legs seemed to be genetically associated with lower milk urea content, whereas sickled legs were apparently associated with a higher milk urea concentration. Selection towards the optimum might be favourable in the case of bulls whose daughters had sickled legs (high score).

Our results show that type traits describing udder were more strongly genetically correlated with both lactose and milk urea contents than traits describing legs. Genetic correlations of the udder descriptive trait with lactose percentage and milk urea content ranged from 0.17 to 0.27, while genetic correlations of the leg descriptive trait with lactose percentage and milk urea content were lower (0.08 to 0.15). Among the linearly scored traits for legs, only rear legs – rear view was genetically correlated with lactose percentage (0.17) and rear legs – side view with milk urea concentration (0.16). Generally, linearly scored udder traits were weakly or moderately genetically correlated with lactose percentage and milk urea content. The exceptions were rear udder height and fore teat placement, which were not genetically correlated with lactose percentage or with milk urea content. Selection for better legs will not affect lactose percentage and milk urea content, but increases in both lactose percentage and milk urea concentration may be expected as an indirect response to selection for better udder.

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