Genetic parameters for linear type traits in Czech Holstein cattle

E. Němcová, M. Štípková, L. Zavadilová

Institute of Animal Science Praha Uhříněves, Prague, Czech Republic

ABSTRACT: The objectives of this study were to estimate genetic parameters for 18 currently recorded linear conformation traits in Czech Holstein cattle. The data set consisted of 78 886 first-lactating Holstein cows. Traits, all scored on a 9-point scale, were fore udder attachment, rear udder height, udder depth, rear udder width, central ligament, teat length, front teat placement, rear teat position, stature, angularity, chest width, body depth, rump angle, rump width, rear legs rear view, rear leg set (side view), foot angle, and bone quality. Uni- and bivariate animal models were used. The models included fixed effects of herd-date of classification-classifier, classifier, and season of calving, quadratic regressions on age at calving and on days in milk and the random effect of animal. Heritability estimates obtained in univariate and in bivariate analyses were of similar magnitude. Heritabilities ranged from 0.17 to 0.32 for udder traits, 0.10 to 0.16 for foot and leg traits, and 0.18 to 0.45 for traits related to body size. Genetic correlations among the currently recorded linear traits ranged from –0.67 between foot angle and rear leg set (side view) to 0.75 between fore udder attachment and udder depth. Substantial genetic correlations were found for the following pairs of traits: rear udder height and rear udder width (0.70), chest width and body depth (0.69), front teat placement and rear teat position (0.68), angularity and bone quality (0.67). Corresponding phenotypic correlations for most pairs of traits were similar in direction but smaller in magnitude than the genetic correlations.

Keywords: linear type traits; genetic parameters; dairy cattle

A primary reason for collecting and utilizing information on type is to aid breeders in selecting profitable, functional cows in order that early culling for causes unrelated to yield (involuntary culling) can be avoided (Misztal et al., 1992). Selection on yield traits alone could decrease merit for traits with antagonistic genetic correlations with yield. Selection emphasis on type traits associated with increased herd life may be beneficial to decrease involuntary culling and increase profitability (Rogers and McDaniel, 1989). Conformation traits are recorded in many dairy cattle breeds (Foster et al., 1988; Harris et al., 1992; de Haas, et al., 2007). These traits have medium to high heritability (Meyer et al., 1987) and can often be recorded in a single assessment, which makes them reliable and relatively inexpensive traits that can be included in selection indices for overall merit (Schaeffer et al., 1985; Wiggans et al., 2004).

The objective of this study was to estimate genetic parameters for currently recorded type traits and to utilize them in the genetic evaluation system and eventually in selection indices. These new estimates should provide improved accuracy of type evaluations, particularly for traits whose (co)variances have changed over time.

MATERIAL AND METHODS

Data collection

Type classification records were extracted from the Czech-Moravian Breeder's Association official

---

Supported by Ministry of Agriculture of the Czech Republic (Project No. QH71275).

database. The data set consisted of records from 78 886 Holstein cows from 1018 herds and 1861 sires. Daughters of sire with fewer than 3 daughters were excluded from analysis. The minimal number of contemporaries in herd-date of classification-classifier was 2.

All cows used in the analysis were scored for conformation traits between 30 and 210 days in milk (DIM) of the first lactation during 2003 through 2007.

The following type traits scored on a 9-point scale were analysed: 8 udder traits – fore udder attachment, rear udder height, udder depth, rear udder width, central ligament, teat length, front teat placement and rear teat position; 6 body traits – stature, angularity, chest width, body depth, rump angle, and rump width; 4 foot and leg traits – rear legs rear view, rear leg set (side view), foot angle and bone quality (Table 1). All traits were scored on all cows, with the exceptions of rear udder width (65 384 records). In preliminary study, the normality of traits was tested. All the analysed traits were normally distributed.

Further information in the data set included cow age, season of calving, herd, date of classification, identification of the classifier and 4-generation pedigree. Age at first calving was in the range from 660 to 960 days. Pedigree included 321 817 animals, 237 600 dams, 11 114 sires, 3027 maternal grand sires.

Estimation of genetic parameters

(Co) variance components were estimated using REMLF90 (Misztal et al., 1999) and REML procedures based on multivariate animal models. To reduce computer memory requirements, estimation of variance components was performed in 210 bivariate analyses, each of which included 2 linear type traits. Data were also analysed by univariate models, which consisted of the same fixed and random effects as those included in bivariate settings. The convergence criterion was set to 10^{-11} for all analyses. Standard errors of genetic component estimations from REMLF90 were not available.

Table 1. Means and standard deviations of linear type traits

Trait	Mean	SD	Type traits score	
			1	9
Fore udder attachment	5.3	1.57	weak and loose	extremely strong and tight
Rear udder height	5.6	1.53	very low	high
Udder depth	5.8	1.48	below hock	shallow
Rear udder width	5.3	1.52	narrow	wide
Central ligament	5.7	1.61	weak	strong
Teat length	4.7	1.13	short	long
Front teat placement	4.9	1.25	outside of quarter	inside of quarter
Rear teat position	5.6	1.49	outside of quarter	inside of quarter
Stature	5.9	1.30	short	tall
Angularity	5.6	1.21	lacks angularity, coarse	very angular
Chest width	5.7	1.37	narrow	wide
Body depth	5.8	1.38	shallow	deep
Rump angle	4.9	1.27	high pins	extreme slope
Rump width	5.8	1.36	narrow	wide
Rear legs rear view	5.3	1.61	extreme toe out	parallel feet
Rear leg set (side view)	5.2	1.33	straight	sickle
Foot angle	4.9	1.20	very low angle	very steep
Bone quality	5.8	1.44	coarse	flat

However, they can be calculated using the following formulas (Falconer, 1981):

$$\sigma\,(h^2) = \sqrt{2/N}\,;\ \sigma(r_{xy}) = \frac{\dfrac{1 - r_{xy}^{2}}{\sqrt{2}}}{\sqrt{\dfrac{\sigma h_x^2\,\sigma h_y^2}{h_x^2\,h_y^2}}}$$

where:

$\sigma(h^2)$ = standard error of heritability

N = number of observations

$\sigma(r_{xy})$ = standard error of genetic correlations

The model equation can be described as follows:

$$Y_{ijklmn} = \mu + \mathrm{HDC}_i + \mathrm{C}_j + \mathrm{S}_k + a_l + \beta_1\mathrm{age}_m + \beta_2\mathrm{age}_m^2 + \gamma_1 s_n + \gamma_2 s_n^2 + e_{ijklmn}$$

where: dependent variables (y_{ijklmn}) were linear type trait scores and fixed effects were HDC_i (herd-date of classification-classifier, 6618 levels), C_j (classifier, 6 levels), and S_k (season of calving, 4 levels). The model included linear and quadratic regressions on age at calving $\beta_1\mathrm{age}_m + \beta_2\mathrm{age}_m^2$ and linear and quadratic regressions on DIM at scoring $\gamma_1 s_n + \gamma_2 s_n^2$. Random effects were animal (a_l) and the residual term (e_{ijklmn})

RESULTS AND DISCUSSION

Heritabilities of traits

Heritability estimates are shown in Table 2. Only those estimates from univariate analyses are presented; because parameters obtained in the set of bivariate analyses, averaged over 18 estimates for each of the analysed traits, gave similar values. Based only on the univariate analyses, heritability estimates ranged from 0.17 to 0.32 for udder traits, from 0.10 to 0.16 for foot and leg traits, and from 0.18 to 0.45 for traits related to body size.

The analyses confirmed our expectation of low values of heritability for foot and leg traits, intermediate heritabilities for udder traits and higher heritabilities for body traits. Pérez-Cabal et al. (2006) published a heritability of 0.12 for foot angle and 0.19 for rear leg set (side view), similar to our results. Schaeffer et al. (1985) reported heritabilities for linear type traits between 0.14 for fore udder attachment and 0.40 for stature. They

Table 2. Genetic and residual variances and heritability estimates of linear type traits resulting from univariate analyses

Trait	Genetic variance	Residual variance	h^2
Fore udder attachment	0.56	1.73	0.24
Rear udder height	0.49	1.46	0.25
Udder depth	0.64	1.38	0.32
Rear udder width	0.28	1.41	0.17
Central ligament	0.46	1.90	0.20
Teat length	0.34	0.87	0.28
Front teat placement	0.39	1.09	0.26
Rear teat position	0.55	1.40	0.28
Stature	0.66	0.81	0.45
Angularity	0.38	0.85	0.31
Chest width	0.30	1.37	0.18
Body depth	0.40	1.24	0.24
Rump angle	0.52	1.00	0.34
Rump width	0.67	0.98	0.40
Rear legs rear view	0.21	2.03	0.10
Rear leg set (side view)	0.25	1.33	0.16
Foot angle	0.12	1.12	0.10
Bone quality	0.45	1.18	0.28

Approximate standard errors of h^2 ranged from 0.0050 to 0.0122

Table 3. Genetic correlations (above diagonal) and phenotypic correlations (below diagonal) between linear type traits

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	Fore udder attachment		0.44	0.75	0.20	0.19	−0.02	0.33	0.24	0.17	0.07	0.11	0.02	−0.21	0.11	0.29	−0.16	0.17	0.05
2	Rear udder height	0.30		0.49	0.70	0.36	−0.06	0.22	0.33	0.18	0.51	−0.22	−0.11	−0.06	0.16	0.22	0.04	0.00	0.46
3	Udder depth	0.44	0.27		−0.04	0.35	−0.07	0.30	0.27	0.35	0.14	−0.17	−0.37	−0.15	0.09	0.15	−0.16	0.19	0.19
4	Rear udder width	0.16	0.46	−0.05		0.22	0.01	0.23	0.28	0.17	0.54	0.02	0.29	−0.15	0.33	0.33	0.12	0.05	0.42
5	Central ligament	0.16	0.23	0.27	0.14		0.10	0.14	0.48	0.15	0.21	−0.03	−0.01	−0.11	0.03	0.18	−0.05	0.08	0.27
6	Teat length	0.05	0.04	−0.01	0.11	0.09		−0.30	−0.21	0.08	−0.08	0.14	0.07	−0.04	−0.03	0.05	−0.05	0.03	−0.07
7	Front teat placement	0.17	0.05	0.15	0.05	0.12	−0.07		0.68	0.20	0.29	0.01	0.07	−0.09	0.15	0.07	−0.02	0.09	0.11
8	Rear teat position	0.13	0.11	0.18	−0.04	0.27	−0.06	0.40		0.24	0.36	−0.08	0.02	−0.08	0.19	0.04	0.09	0.04	0.23
9	Stature	0.04	0.03	0.11	0.16	0.04	0.08	0.05	0.00		0.47	0.13	0.17	0.08	0.41	0.08	−0.06	0.21	0.11
10	Angularity	0.00	0.23	0.08	0.23	0.13	0.01	0.04	0.09	0.19		−0.27	0.14	−0.21	0.33	0.01	0.35	−0.12	0.67
11	Chest width	0.08	−0.03	−0.13	0.17	−0.01	0.11	0.03	−0.01	0.16	−0.05		0.69	−0.15	0.24	0.25	−0.19	0.23	−0.52
12	Body depth	0.09	0.00	−0.23	0.25	0.03	0.14	0.05	0.03	0.15	0.12	0.55		−0.20	0.23	0.16	0.02	0.05	−0.18
13	Rump angle	−0.13	0.02	−0.08	−0.04	−0.09	−0.03	−0.04	−0.07	0.10	−0.07	−0.04	−0.10		−0.24	−0.14	−0.07	−0.04	−0.16
14	Rump width	0.02	0.04	−0.01	0.19	0.00	0.05	0.01	0.01	0.31	0.11	0.22	0.19	−0.06		0.11	0.03	0.11	0.04
15	Rear legs rear view	0.13	0.21	0.04	0.33	0.06	0.06	0.02	−0.04	0.11	0.04	0.10	0.14	−0.07	0.05		−0.40	0.39	0.16
16	Rear leg set (side view)	−0.13	−0.09	−0.10	−0.10	−0.01	−0.05	−0.01	−0.01	−0.15	0.07	−0.05	−0.06	0.00	−0.02	−0.31		−0.67	0.23
17	Foot angle	0.09	0.06	0.04	0.11	0.04	0.04	0.01	0.00	0.15	0.01	0.06	0.10	−0.06	0.06	0.24	−0.40		−0.19
18	Bone quality	0.02	0.21	0.10	0.19	0.12	−0.04	0.02	0.10	0.00	0.42	−0.18	−0.08	−0.07	−0.03	0.13	0.02	−0.06	

Approximate standard errors of r_g ranged from 0.0076 to 0.0336 found smaller heritabilities for udder traits than for non-udder traits. The heritabilities of linear type traits estimated in this study were similar to values reported by Short et al. (1991) for the Holstein breed, Harris et al. (1992) for Guernsey cows, and Wiggans et al. (2006) for Guernsey and Brown Swiss. Discrepancies among reports may be attributable to differences across studies in scales used for scoring, statistical model definitions, breed(s) involved, number of records per animal, accuracy and consistency of classifiers and data editing procedures.

Genetic and phenotypic correlations

Genetic and phenotypic correlations among the currently recorded linear type traits are shown in Table 3. Genetic correlations ranged from –0.67 between foot angle and rear leg set (side view) to 0.75 between fore udder attachment and udder depth. It means that cows with straight legs tend to have steeper foot angle and vice versa. Cows with genetic predisposition to weak fore udder attachment incline to deeper udders. Close genetic associations were found also for the following pairs of traits: rear udder height and rear udder width (0.70), chest width and body depth (0.69), front teat placement and rear teat position (0.68), angularity and bone quality (0.67), angularity and rear udder width (0.54), chest width and bone quality (–0.52) and angularity and rear udder height (0.51). Because of the high genetic correlation between rear udder height and rear udder width and angularity, cows have either high and wide udders and tend to be angular or they have narrow and very low udders and tend to lack angularity. Wide cows are characterized by deep body and are more coarse due to genetic correlations between chest width, body depth and bone quality.

The corresponding phenotypic correlations were similar in direction but smaller in magnitude: between foot angle and rear leg set (side view) (–0.40), fore udder attachment and udder depth (0.44), rear udder height and rear udder width (0.46), chest width and body depth (0.55), front teat placement and rear teat position (0.40), angularity and bone quality (0.42), angularity and rear udder width (0.23), chest width and bone quality (–0.18), and angularity and rear udder height (0.23).

The magnitude and direction of the genetic relationships among the currently recorded conformation traits in this study are similar to those reported in the literature (Schaeffer et al., 1985; Lawstuen et al., 1987; Foster et al., 1988; Misztal et al., 1992; Wiggans et al., 2004). In agreement with our findings, Schaeffer et al. (1985), Lawstuen et al. (1987), and Foster et al. (1988) reported high positive genetic correlations between the following udder traits: between fore udder attachment and udder depth and/or rear udder height and rear udder width. In addition, Foster et al. (1988) reported a genetic correlation of 0.35 between central ligament and udder depth and genetic correlations of 0.44 and 0.43 between fore udder attachment and rear udder height and width, respectively. Similar results were found by Lawstuen et al. (1987). De Haas et al. (2007) found the positive genetic correlation of 0.22 between rump width and body depth for Holstein.

High genetic correlations between dairy form and rear udder width (0.59) and dairy form and rear udder height (0.52) reported by Wiggans et al. (2004) for Brown Swiss, Jersey, Guernsey and Milking Shorthorn are in agreement with our results for angularity. However, Lawstuen et al. (1987) published lower genetic correlations than ours between angularity and rear udder width and with rear udder height for Swiss Holsteins. Low genetic correlations between these traits were also reported by Misztal et al. (1992) in Holsteins.

High positive front teat placement and rear teat position was reported by Pérez-Cabal et al. (2006), who found a positive genetic correlation (0.73) between foot angle and feet and legs. At the same time they found negative correlations (–0.39 and –0.44) between rear leg set and foot angle and feet and legs, respectively. In agreement with our findings, high negative genetic correlations (over –0.50) between foot angle and rear leg set (side view) were reported by Boelling and Pollot (1998) and by van der Waaij et al. (2005) for Holsteins. On the other hand, lower negative genetic correlations (between –0.30 and –0.50) were reported by Lawstuen et al. (1987), Foster et al. (1988), Misztal et al. (1992), and Pérez-Cabal et al. (2006) for Holsteins and by Wiggans et al. (2004) for Ayrshire, Brown Swiss, Jersey, Guernsey, and Milking Shorthorns.

The estimated heritabilities were compared with those used in national genetic evaluation (Interbull, 2010). Although the differences between them were small, we can conclude that the new sets of genetic parameters can be used to update the national genetic evaluation for conformation.

CONCLUSIONS

Genetic parameter estimates for type traits from our investigation will allow the updating of genetic evaluation procedures for exterior characteristics of Czech Holstein cattle. We recommend their inclusion in the classification system of Holstein cattle in the Czech Republic.

Acknowledgments

The authors thank I. Misztal, University of Georgia (Athens), for providing the computer program to estimate variance components and J. Wolf, Institute of Animal Science (Prague, Czech Republic) for helpful comments. Special thanks are extended to W. D. Hohenboken (Corvallis, Oregon) who edited the English of the paper.

REFERENCES

Boelling D., Pollott G.E. (1998): Locomotion, lameness, hoof and leg traits in cattle. II. Genetic relationships and breeding values. Livestock Production Science, 54, 205–215.

Falconer D.S. (1981): Introduction to Quantitative Genetics. Ed. 2. Longmans Green, London/New York.

Foster W.W., Freeman A.E., Berger P.J., Kuck A. (1988): Linear type trait analysis with genetic parameter estimation. Journal of Dairy Science, 71, 223–231.

Harris B.L., Freeman A.E., Metzger E. (1992): Genetic and phenotypic parameters for type and production in Guernsey dairy cows. Journal of Dairy Science, 75, 1147–1153.

de Haas Y., Janss L.L.G., Kadarmideen H.N. (2007): Genetic and phenotypic parameters for conformation and yield traits in three Swiss dairy cattle breeds. Journal of Animal Breeding and Genetics, 124, 12–19.

Interbull (2010): National GES Information. Available from http://www.Interbull.slu.se/national _ges_info2/framesida-ges.htm

Lawstuen D.A., Hansen L.B., Johnson L.P. (1987): Inheritance and relationships of linear type traits for age groups of Holsteins. Journal of Dairy Science, 70, 1027–1035.

Misztal I., Lawlor T.J., Short T.H., VanRaden P.M. (1992): Multiple-trait estimation of variance components of yield and type traits using an animal model. Journal of Dairy Science, 75, 544–554.

Misztal I. (1999): REMLF90 Manual. Available from http://nce.ads.uga.edu/~ignacy/numpub/blupf90/docs/remlf90.pdf

Meyer K., Brotherstone S., Edwards M.R., Hill W.G. (1987): Inheritance of linear type traits in dairy cattle and correlations with milk production. Animal Production, 44, 1–10.

Pérez-Cabal M.A., Garcia C., Gonzalez-Recio O., Alenda R. (2006): Genetic and phenotypic relationships among locomotion, type traits, profit, production, longevity, and fertility in Spanish dairy cows. Journal of Dairy Science, 89, 1776–1783.

Rogers G.W., McDaniel B.T. (1989): The usefulness of selection for yield and functional type traits. Journal of Dairy Science, 72, 187–192.

Schaeffer G.B., Vinson W.E., Pearson R.E., Long R.G. (1985): Genetic and phenotypic relationships among type traits scored linearly in Holsteins. Journal of Dairy Science, 68, 2984–2988.

Short T.H., Lawlor T.J. Jr., Lee K.L. (1991): Genetic parameters for three experimental linear type traits. Journal of Dairy Science, 74, 2020–2025.

van der Waaij E.H., Holzhauer M., Ellen E., Kamphuis C., de Jong G. (2005): Genetic parameters for claw disorders in dutch dairy cattle and correlations with conformation traits. Journal of Dairy Science, 88, 3672–3678.

Wiggans G.R.,Gengler N., Wright J.R. (2004): Type trait (co)variance components for five dairy breeds. Journal of Dairy Science, 87, 2324–2330.

Wiggans G.R., Thornton L.L.M., Neitzel R.R., Gengler N. (2006): Genetic parameters and evaluation of rear legs (rear view) for Brown Swiss and Guernseys. Journal of Dairy Science, 89, 4895–4900.

Received: 2010–04–14
Accepted after corrections: 2010–10–14

Corresponding Author

Ing. Ludmila Zavadilová, Institute of Animal Science, Přátelství 815, 104 00 Prague-Uhříněves, Czech Republic
Tel. +420 267 009 608, fax +420 267 710 779, +420 267 711 448, +420 267 770 779, e-mail: zavadilova.ludmila@vuzv.cz