

Estimation of genetic parameters of claw conformation in Holstein and Slovak Spotted breeds

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The aim of the study was to analyse the claw conformation traits in selected groups of Holstein and Slovak Spotted cows and estimate their heritability and genetic correlations between them separately for each breed. Images of the right hind claw taken during functional trimming were analysed using the NIS Elements 3.0. The pedigree database was processed by the CFC program. Genetic correlations and heritability of claw conformation traits were estimated using the generalised linear mixed model. Lower average values of claw conformation traits were found in Holstein cows compared to the group of Slovak Spotted cows. The variability of analysed traits was significantly affected in both groups by the effect of sire, calving year and season. Both positive and negative genetic correlations were observed between the claw conformation traits in the evaluated groups. In the Holstein cows, the highest positive genetic correlation was found between claw length and diagonal (0.91). In the group of Slovak Spotted cows, the highest positive genetic correlation was found between claw width and functional claw area (0.87). The heritability of tested claw conformation traits was moderate, with an average h^2 value of 0.30 ± 0.09 .

Keywords: genetic evaluation, Holstein breed, Slovak Spotted breed, claw conformation

1 Introduction

Good claw health could be achieved by regular functional claw trimming. The most commonly used approach is the so-called 5-step “Dutch” method (Sadiq et al., 2020). Claw trimming is important for even weight distribution over the contact claw area (Vidmar et al., 2021). Although various studies e.g. Burgi et al. (2017) recommend claw trimming several times a year, most farmers perform claw trimming at least once a year. However, claw trimming is not recommended during stress periods (before calving, at the beginning of lactation, and during the peak of lactation). Inadequate claw trimming can lead to several adverse effects, including various claw disorders. It is well known that lameness and claw diseases negatively affect milk production and reproduction traits, longevity and the economics of the herd. For example, Krupová et al. (2016) reported the marginal economic value of claw diseases for Pinzgau

cattle in the dairy system at 26.73 € per case per cow and year.

Claw trimming generally positively affects milk production, locomotion and behaviour. Van Hertem et al. (2014) reported that two months after hoof trimming, up to 40% of cows in the herd had normal locomotion scores, with the incidence of lame cows reduced to 5%. The effect of claw trimming on locomotion score was demonstrable after 70 days. Kibar and Çağlayan (2016) found that the milk yield increased by 0.88 kg after ten days after claw trimming. Sadiq et al. (2020) reported that claw trimming could lead to changes in behavioural activity. They found that after claw trimming, cows walked slowly, eating time and jaw movements increased, and neck activity decreased.

The economic importance of claw disorders can also be considered in selection indexes. However, the accuracy

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of such indices depends on the heritability of a particular disease. Regarding the most common claw diseases, the highest heritability was found for necrobacillosis ($h^2 = 0.94$), while the lowest for digital dermatitis ($h^2 = 0.10$) (Zavadilová et al., 2017). Heringstad et al. (2018) observed the highest heritability for interdigital hyperplasia ($h^2 = 0.39$) and the lowest for non-infectious interdigital phlegmon ($h^2 = 0.08$) and double sole ($h^2 = 0.02$).

The claw health index considering eight claw diseases (digital dermatitis, interdigital dermatitis, interdigital hyperplasia, sole ulcer, white line disease, sole haemorrhage, heel horn erosion, and toe ulcer) was launched, for example, in Canada. Estimated breeding values for each disease were combined into a sub-index, according to the occurrence and economic value. A higher value of the claw health index indicates a lower incidence of claw diseases (Malchiodi et al., 2020). Croué et al. (2019) tested the feasibility of a genomic evaluation (BLUP, GBLUP, SSSLUP) for claw health in French Holstein cows using pedigree and genomic data. They reported that the availability of genomic data increases the accuracy of genomic evaluation, mainly in the case of single-step GBLUP. Moreover, they identified several potential candidate genes and QTLs that can be responsible for the resistance to individual claw lesions.

The claw angle is also included in the breeding values estimation for conformation traits in Slovak Holstein cattle (Candrák & Lichanec, 2021). This study analysed eight claw conformation traits in Holstein and Slovak Spotted cattle in order to estimate their heritability and genetic correlations between them.

2 Material and methods

2.1 Photometry analysis

Claw conformation of 132 Holstein and 122 Slovak Spotted cows was evaluated in 2017–2019 on two farms, VPP Oponice and PD Neverice – Jelenec. Eight claw

conformation traits, (A) angle, (B) length, (C) heel depth, (D) height, (E) diagonal, (F) width, (CP) total area and (FP) functional area (Figure 1), were measured during the functional claw trimming based on the images of the right hind claw (bottom and outer lateral side) made from a distance of approximately 30–40 cm according to Vermunt and Greenough (1995). All images were then handled by the NIS Elements 3.0 software.

2.2 Pedigree information

Pedigree data were obtained in cooperation with the Breeding Services of the Slovak Republic, s.e. Pedigree database was created separately for each evaluated group (defined by breed) using the CFC program (Sargolzaei, et al., 2006) to cover at least one generation of ancestors. The pedigree databases of Holstein and Slovak Spotted cows included 280 individuals and 244 animals, respectively.

2.3 Statistical analysis

The variability of tested claw conformation traits in analysed groups was evaluated based on the calculation of average values, standard deviations (SD), minimum (min) and maximum (max). Phenotypic correlations between conformation traits were estimated according to the Pearson correlation coefficients calculated by SAS V 9.4 (SAS Institute Inc., 2009).

One-way ANOVA implemented in SAS Enterprise Guide v 7.1 (SAS Institute Inc, 2009) was then used to analyse the effect of various factors on claw conformation traits variability, including sire, date of birth, order of lactation, calving year, calving season, the season of claw trimming, trimmer, and year of claw trimming. The effects of season and year of claw trimming and trimmer were tested only in the Holstein cows group due to low observations for 2018–2019 in Slovak Spotted cows. Only factors showing statistically significant effects on the variability of claw conformation traits were used to estimate their heritability and the genetic correlation between them.

The heritability of claw conformation traits was estimated by a generalised linear mixed model and Bayesian statistics implemented in the R package *MCMCglmm* (Hadfield, 2010) based on the following model:

$$Y_{ijkl} = \mu + S_i + YS_j + YS_k + a_l + e_{ijkl}$$

where: Y_{ijkl} – the observation for one of the claw conformation traits; μ – the mean for the tested trait; S_i – the fixed effect of sire; YS_j – the fixed effect of calving year x calving season; YS_k – the fixed effect of the year of claw trimming x claw

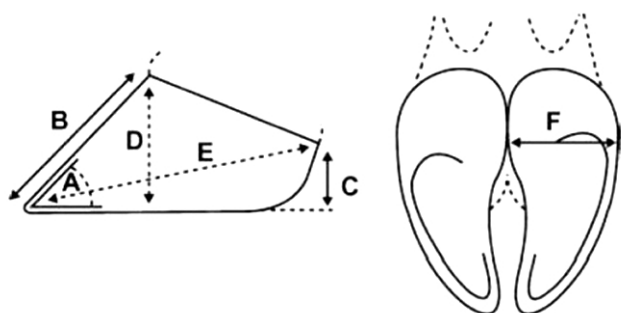


Figure 1 Claw conformation traits analysed in this study
 Source: Vermunt & Greenough, 1995
 A – claw angle, B – claw length, C – heel depth, D – claw height, E – diagonal, F – claw width

trimming season, a_i – the random additive effect of the animal, and $eijkl$ is the residual effect. In Slovak Spotted cows, the fixed effect of the year of claw trimming x claw trimming season was omitted from the model due to the limited number of observations in 2018–2019

Genetic correlations between claw conformation traits were estimated using the formula:

$$r_{xy} = \frac{COV_{xy}}{\sqrt{var_x \times var_y}}$$

where: cov_{xy} – the additive genetic covariance between variables x and y ; var_x and var_y – additive genetic variances for variables x and y

3 Results and discussion

The results of this study indicated differences in the claw conformation between Holstein and Slovak spotted cows (Table 1). In general, Slovak spotted cows showed higher average values of the analysed traits compared to Holstein cows but with similar standard deviations. In Holstein cows, the coefficient of variation ranged from 7.2% (claw diagonal) to 25.5% (functional claw area). On the other hand, in Slovak Spotted cows, the coefficient of variation ranged from 6.9% (claw diagonal) to 23.8% (functional claw area). A similar phenotypic variation of

claw conformation traits was found in the study of Duru et al. (2012). Susanto et al. (2018) reported phenotypic variation for claw angle at level 9.9% in Holstein dairy cows. Xu et al. (2022) found a lower coefficient of variation in Simmental breed, ranging between 20.0% and 22.4%. Variability of the observed claw conformation traits could be affected by genetic effects, gene variation, environmental effects (herd, order of lactation, calving season), but also by the type of floor (Burgi et al., 2017), and individuality of evaluated animals (Canatan et al., 2021).

Table 2 shows the effect of tested factors on the variability of claw conformation traits in both groups. In Holstein cows, the most significant effect showed sire (claw diagonal), date of birth (claw length, diagonal, total area and functional area), order of lactation (claw length and width) and calving year (claw length, height and functional area). The fixed effects of the season and year of claw trimming influenced length, height, diagonal, and functional claw area. The calving season did not significantly affect the variability of tested claw conformation traits. In Slovak Spotted cows, the order of lactation significantly affected heel depth, claw height, diagonal and width. The date of birth affected only claw length and width. Other effects, such as sire, calving year and season, did not significantly affect analysed claw conformation traits.

Table 1 Basic variation-statistical parameters of claw conformation traits in Holstein cows

Claw trait	N		SD	Min	Max
Holstein cows					
Claw angle (°)	132	49.88	4.51	36.28	66.72
Claw length (cm)	132	7.96	0.88	6.08	10.58
Heel depth (cm)	132	3.79	0.63	2.30	5.59
Claw height (cm)	132	6.68	0.73	4.81	8.92
Diagonal (cm)	132	12.59	0.91	10.65	15.95
Claw width (cm)	132	5.35	0.50	4.15	7.13
Total area (cm ²)	130	42.42	7.20	27.37	71.28
Functional area (cm ²)	130	23.72	6.04	13.32	43.20
Slovak Spotted cows					
Claw angle (°)	121	52.98	4.80	39.91	68.35
Claw length (cm)	121	8.42	0.71	6.75	10.91
Heel depth (cm)	121	4.10	0.57	2.45	5.47
Claw height (cm)	121	7.45	0.66	5.95	10.04
Diagonal (cm)	121	12.97	0.89	11.05	15.93
Claw width (cm)	121	5.85	0.47	4.81	7.87
Total area (cm ²)	120	46.23	6.56	31.05	65.71
Functional area (cm ²)	120	27.91	6.64	13.65	51.03

Table 2 Effect of tested factors on claw conformation traits variability

	A	B	C	D	E	F	CP	FP
Holstein breed								
Sire	0.25 0.3493	0.31 0.0768	0.27 0.2555	0.30 0.1037	0.48 <.0001	0.25 0.3555	0.36 0.0176	0.35 0.0295
Date of birth	0.03 0.8446	0.25 <.0001	0.09 0.1142	0.15 0.0035	0.30 <.0001	0.18 0.0007	0.21 <.0001	0.28 <.0001
Order of lactation	0.03 0.7266	0.22 <.0001	0.10 0.0453	0.13 0.0035	0.24 0.0068	0.17 <.0001	0.06 0.0008	0.26 0.2384
Calving year	0.02 0.6635	0.39 <.0001	0.07 0.0470	0.19 <.0001	0.14 0.0005	0.07 0.0479	0.02 0.5980	0.24 <.0001
Calving season	0.03 0.2596	0.04 0.2017	0.01 0.8446	0.03 0.2567	0.04 0.1383	0.01 0.7513	0.01 0.9958	0.03 0.3233-
Season of the claw trimming	0.01 0.5020	0.38 <.0001	0.07 0.0024	0.17 <.0001	0.13 <.0001	0.04 0.0195	0.02 0.1413	0.22 <.0001
Year of claw trimming	0.01 0.3778	0.39 <.0001	0.07 0.0076	0.24 <.0001	0.14 <.0001	0.05 0.0415	0.05 0.3402	0.25 <.0001
Slovak Spotted breed								
Sire	0.21 0.4224	0.24 0.1993	0.23 0.2783	0.25 0.1453	0.39 0.005	0.23 0.2734	0.25 0.1603	0.34 0.0071
Date of birth	0.01 0.8446	0.07 0.0024	0.03 0.1142	0.04 0.0035	0.03 0.2432	0.18 0.0007	0.02 0.4238	0.02 0.5640
Order of lactation	0.01 0.5835	0.01 0.2422	0.06 0.0304	0.06 0.0028	0.20 <.0001	0.07 0.0174	0.06 0.0209	0.07 0.0708
Calving year	0.01 0.9016	0.02 0.3467	0.04 0.088	0.02 0.3464	0.01 0.9348	0.02 0.3886	0.01 0.6990	0.01 0.9433
Calving season	0.01 0.6564	0.03 0.2798	0.02 0.6192	0.03 0.2532	0.01 0.9401	0.02 0.5467	0.02 0.4937	0.01 0.8454

It was shown that claw disease prevalence could be associated with different internal or external factors, including the age of animals as well as claw trimming (Vlček & Kasarda, 2017; Kumar et al., 2019; Ali et al., 2021). Kumar et al. (2019) reported a significantly higher incidence of claw diseases in old dairy cows. The prevalence of digital dermatitis and sole ulcer was associated with the calving season and lactation order in the study of Vlček and Kasarda (2017).

The estimated phenotypic and genetic correlations and heritabilities of claw conformation traits for Holstein group are shown in Table 3. The highest positive phenotypic correlation was found between claw length and claw height (0.87), while the highest negative correlation was observed between claw length and functional area (-0.25). Similar values of phenotypic correlations were also found in the group of Slovak Spotted cows. The highest positive correlation was estimated between claw length and diagonal (0.89), while the highest negative correlation was observed between claw angle and diagonal (-0.19). Previous studies reported high positive phenotypic correlations also between claw length and functional area (Kasarda

et al., 2018; Vlček, 2018) and claw dorsal wall length and diagonal (Canatan et al., 2021).

The genetic correlations were generally higher in the group of Holstein cows. The highest positive genetic correlation was estimated between claw length and claw diagonal (0.91), while the highest negative genetic correlation was observed between claw angle and diagonal (-0.35). A similar positive genetic correlation between claw length and claw diagonal (0.99) for Slovak Holstein cows was reported by Vlček (2018). Zavadilová and Štípková (2012) described low positive correlation between claw angle and length of production life (0.10). In the group of Slovak Spotted cows (Table 4), the highest genetic correlation was observed between claw width and functional claw area (0.87). The lowest negative correlation was found between claw angle and width (-0.34). Vlček (2018) also estimated a higher positive genetic correlation between claw width and functional claw area (0.98) in the Slovak Spotted breed. Häggman et al. (2013) describe a negative genetic correlation between claw angle and leg health.

In general, the group of Slovak Spotted cows showed higher heritability coefficients for claw conformation

Table 3 Estimated phenotypic correlation (above diagonal), genetic correlation (below diagonal), and heritability coefficients (diagonal) for claw conformation traits in Holstein cows

	A	B	C	D	E	F	CP	FP
A	0.01	-0.06	0.20	0.16	-0.03	0.07	-0.03	-0.09
B	-0.13	0.32	0.07	0.87	0.60	-0.09	0.02	-0.25
C	0.24	0.73	0.32	0.25	0.15	0.21	0.21	0.30
D	0.28	0.80	0.82	0.33	0.61	0.07	0.07	-0.11
E	-0.35	0.91	0.53	0.83	0.34	0.11	0.30	0.30
F	-0.11	0.35	0.15	0.24	0.35	0.32	0.76	0.57
CP	-0.31	0.26	0.53	0.34	0.48	0.75	0.27	0.61
FP	-0.22	0.20	0.37	0.31	0.33	0.40	0.38	0.23

Table 4 Estimated phenotypic correlation (above diagonal), genetic correlation (below diagonal), and heritability coefficients (diagonal) of Slovak Spotted breed claw conformation traits

	A	B	C	D	E	F	CP	FP
A	0.24	-0.10	0.20	0.07	-0.19	0.08	-0.09	0.06
B	-0.05	0.35	0.45	0.89	0.65	0.15	0.23	0.20
C	0.50	0.76	0.32	0.56	0.44	0.21	0.09	0.22
D	0.31	0.81	0.75	0.34	0.64	0.25	0.23	0.22
E	-0.03	0.85	0.67	0.78	0.35	0.17	0.39	0.22
F	-0.34	0.43	0.51	0.68	0.43	0.37	0.72	0.64
CP	-0.04	0.58	0.32	0.66	0.74	0.85	0.36	0.70
FP	-0.01	0.66	0.50	0.69	0.70	0.87	0.76	0.37

traits compared to Holstein. Even if the claw angle showed the lowest level of heritability in both groups, the estimated h^2 value was much higher in Slovak Spotted cows than in Holstein cows (0.01 vs. 0.24). In the group of Holstein cows, the highest heritability was found for the claw diagonal ($h^2 = 0.34$). On the other hand, the Slovak Spotted cows showed the highest level of heritability for claw width and functional area ($h^2 = 0.37$). Observed results are consistent with previous studies confirming generally medium to low heritability of claw conformation traits in beef (Giess et al., 2018) and dairy cattle breeds (Kasarda et al., 2018; Roveglia et al., 2019; Zavadilová et al., 2021).

4 Conclusions

The aim of this study was to explore the claw conformation traits in the groups of Holstein and Slovak Spotted cows. The average values of claw angle, claw length, heel depth, claw height, claw diagonal, and claw width were generally higher in the Slovak Spotted cows. The phenotypic correlations ranged from -0.25 to 0.87 in Holstein and from -0.19 to 0.89 in Slovak Spotted cows. Contrary to the phenotypic correlations, higher genetic correlations were found in Holstein cattle (-0.31

to 0.91). The genetic correlations in Slovak Spotted group ranged from -0.34 to 0.87. Claw conformation traits were found to be moderately heritable. In Holstein group, the highest heritability was observed for claw diagonal ($h^2 = 0.34$), whereas in the Slovak Spotted cows the highest heritability showed claw width and functional claw area ($h^2 = 0.37$). The results of this study can be used in the future to develop new selection indices.

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