

# Estimation of heritability for claw traits in Holstein cattle using Bayesian and REML approaches

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## Abstract

The aim of this study was to estimate the heritability of claw conformation traits in Slovak Holstein cattle by using two approaches: the Bayesian method and the restricted maximum likelihood (REML) algorithm. Overall 860 claw trimming records of 716 dairy cows were included in this study. The claw morphometric data were collected after functional trimming between 2012 and 2017. The conformation of claws was evaluated based on eight parameters (angle, length, heel depth, height, diagonal, width, total and functional areas) by digital image analysis and NIS Elements 3.0 software. The heritability of those traits was estimated using a single trait animal model including fixed effects of herd-year-season, stage of lactation and sire. Both of applied approaches indicated low or moderate level of heritability across analysed traits, in average  $0.28 \pm 0.08$  (REML) resp.  $0.22 \pm 0.09$  (Bayesian). The highest heritability was found for diagonal of claw (0.41), while the lowest one was observed for the total area of claw (0.18) and the claw height (0.12) based on the REML algorithm and Bayesian approach, respectively. The study confirmed previous assumption that the claw conformation traits are inherited in low or moderate mode. Future analysis of genetic correlations between them can be beneficial for construction of new selection indices, better responding to today's welfare requests and use of new generation indicators made possible.

**Keywords:** claw health, dairy cattle, heritability estimation, morphometric parameters

## Introduction

Functional traits of dairy cattle such as health, reproduction, and survival have become the focus of breeding strategies in last decades mainly due to their substantial effect on farm profitability. Besides fertility and udder health, locomotion problems are one of the main concern for dairy farmers worldwide (Pérez-Cabal and Charfeddine, 2015; Krupová et al., 2016).

The conformation of claws is considered as essential trait not only from an economical but also from animals' welfare point of view. Good claw conformation is important for the fitness of animals, contributing to their effective mating and

longevity. Moreover, it has been showed that strong feet and legs prolong the herd life of dairy cattle (Buitenhuis et al., 2007). On the other hand, claw disorders lead to economic losses due to the outcome of treatment dispensed for injuries as well as due to the negative consequences on milk production and fertility of lame cows (decreased expression of oestrus, increased days open, longer calving interval, involuntary culling) (Jeyaruban et al., 2012; Pérez-Cabal and Charfeddine, 2015). After mastitis and infertility, the claw disorders have been identified as the third most economically important trait in dairy farming (Häggman and Juga, 2013). Depending on the damage degree, the milk yield can decrease by 5 to 50% with simultaneous weight loss up to 1 kg per day. The production decline will usually occur during two to four months before the claw disease is diagnosed (Strapák et al., 2013). For example in Netherlands, the economic loss due to the claw disorders have been estimated at 75 \$ per cow per year (Bruijnij et al., 2010; Van der Spek et al., 2013). Krupová et al. (2016) estimated the marginal economic value of claw disorders incidence in dairy population of Slovak Pinzgau cattle to –€26.73 per case per cow and year.

For European dairy cattle the prevalence of 70% of the cows with at least one claw disorders have been reported (Van der Linde et al., 2010; Chapinal et al., 2013; Van der Spek et al., 2013). The risk of claw disorders incidence depends on various factors, including environment conditions (for example management practices and design of the facilities) and animals' genetic background (Cramer et al., 2009; Van der Linde et al., 2010). The effect of herd management on claw health is high and due to the low heritabilities of claw morphometric parameters as well as disorders, the improvement of claw health can be achieved most easily in short-term by improving only the environment conditions. But, it has been showed that being able to accurately assess claw morphometric traits could be significant benefit when determining selection strategy and gauging the impact of factors, such as the environment and nutrition (Van der Spek et al., 2013; Laven et al., 2015). Thus, in long-term perspective, direct or indirect selection of both may be the best option for improving the claw health (Häggman and Juga, 2013). There are two options; selection on claw health using data that are currently not routinely collected or indirect selection on correlated conformation traits that are currently recorded (Van der Waaij et al., 2005; Weber et al., 2013). Up to now, several studies confirmed in general low or median level of heritability for claw morphometric parameters as well as disorders (Jeyaruban et al., 2012; Chapinal et al., 2013; Oberbauer et al., 2013; Ødegård et al., 2014; Pérez-Cabal and Charfeddine, 2015).

The aim of this study was to estimate the heritability of eight claw morphometric parameters in Slovak Holstein cattle by using two approaches: the Bayesian and restricted maximum likelihood (REML) method.

## Materials and methods

In total, 860 claw trimming records of 716 Holstein cows were obtained in this study. The dataset include repeated records for a given animals due to the fact that the measured traits could change from one observation date to the next. The claw morphometric data were collected after functional trimming between 2012 and 2017. The conformation of claw after functional trimming was evaluated based on eight parameters (claw angle, claw length, heel depth, claw height, diagonal, claw width,

total and functional areas of claw) by digital image analysis. Two images per given animal on right rear leg (from bottom and outer lateral side), taken during animals' fixation in vertical trimming box, were analysed by using NIS Elements 3.0 software. All additional descriptive information was collected at the same time that claw trimming records were observed. The stage of lactation at trimming were categorized into six classes: 0–60 DIM, 61–120 DIM, 121–180 DIM, 181–240 DIM, 241–300 DIM, and higher than 300 DIM. The parity was classified into three groups: first lactation, second lactation, and third and higher lactation. The trimming records were categorized according to season of observation into four classes: spring (March, April, May), summer (June, July, August), autumn (September, October, November), and winter (December, January, February). The pedigree file consisted of overall 4841 animals. The pedigree data were provided by the Breeding Services of the Slovak Republic, s. e.

The basic descriptive statistic for evaluated morphometric parameters and Pearson correlations between each pair were calculated using SAS 9.3. In the next step, the GLM procedure was used to analyse the statistical significance of fixed effects and to determine the proportion of variability explained by them. Following fixed effects were tested by GLM models: the sire (115), the breed type (H0, H1, H2, H3), the herd-year-season (1 to 59), the claw trimmer-year-season of claw trimming (1 to 11), the type of housing (2), the parity (1 to 3), and the stage of lactation (1 to 6). Only effects of the sire, the herd-year-season, and the stage of lactation showed statistical significance ( $P < 0.001$ ) and were included in the estimation of heritability.

The heritability of claw morphometric parameters were estimated using a single trait animal model based on the two approaches: the restricted maximum likelihood (REML) algorithm implemented in ASReml v1.0 (Gilmour et al., 1999) and Bayesian method adopted in R package MCMCgmm (Hadfield, 2010).

A single trait REML animal model was used as follows:

$$Y_{ijkl} = \mu + S_i + HYS_j + LT_k + a_l + e_{ijkl}$$

where  $Y_{ijkl}$  is the observation for one of the morphometric traits,  $\mu$  is the overall mean,  $S_i$  is the fixed effect of sire,  $HYS_j$  is the fixed effect of herd-year-season,  $LT_k$  is the fixed effect of stage of lactation at trimming,  $a_l$  is the random additive genetic animal effect, and  $e_{ijkl}$  is the residual effect. The additive genetic and residual effects were assumed to be normally distributed with zero means,  $Var(a) = A\sigma_a^2$  and  $Var(e) = I\sigma_e^2$  where  $\sigma_a^2$  and  $\sigma_e^2$  are additive genetic and residual variance, respectively;  $A$  is the numerator relationship matrix and  $I$  is the identity matrix.

The REML model was also used in the Bayesian analysis. Each chain was run for 500,000 rounds with a burn-in of 50,000 rounds and a thinning interval of 100.

The heritability for each parameter was estimated according to formula

$$h^2 = \sigma_a^2 / (\sigma_a^2 + \sigma_e^2),$$

where  $\sigma_a^2$  is the variance dependent on the additive component of the genotype and  $\sigma_a^2 + \sigma_e^2$  is the phenotypic variance.

## Results and discussion

In total of 860 claw trimming records of Slovak Holstein cattle were used to estimate the heritability of claw morphometric parameters. Table 1 shows the summary statistic for each of analysed traits. The obtained average values of claw morphometric parameters reflected mainly the common practice of claw trimming on dairy cattle farms. In Holstein cattle, the claw length is usually shortened to 7.5 cm. But, the optimal claw length can differ depending on a breed. For example, due to the different body condition of Slovak Spotted and Pinzgau cattle the optimal claw length is shorter by 1 – 2 mm. The observed average value of claw angle indicated appropriate method of claw trimming applied on farms as well as correct body posture of analysed animals. The optimal claw angle is in range 45° (front legs) – 55° (rear legs) (Strapák et al., 2013).

Table 1. Claw parameters and estimated heritability in Slovak Holstein cattle

Trait	Mean $\pm$ SD <sup>a</sup>	Lower 95% CI <sup>b</sup>	Upper 95% CI <sup>b</sup>	h <sup>2</sup>	
				REML	Bayesian
Claw angle (°)	50.124 $\pm$ 5.727	49.741	50.508	0.277	0.322
Claw length (cm)	8.499 $\pm$ 1.771	8.381	8.618	0.276	0.165
Heel depth (cm)	3.909 $\pm$ 1.232	3.826	3.991	0.339	0.206
Claw height (cm)	7.467 $\pm$ 1.593	7.36	7.573	0.278	0.117
Diagonal (cm)	14.05 $\pm$ 2.659	13.871	14.228	0.416	0.4
Claw width (cm)	5.818 $\pm$ 1.136	5.742	5.894	0.306	0.226
Total area (cm)	54.83 $\pm$ 25.919	52.209	57.451	0.148	0.158
Functional area (cm)	31.87 $\pm$ 16.803	30.169	33.572	0.177	0.129

<sup>a</sup> Standard deviation; <sup>b</sup> Confidence interval

The phenotypic correlations between analysed traits are listed in Table 2. As expected, due to the physiology of dairy cattle locomotion, significant negative correlation was found between the claw angle and the diagonal as well as total area of claw. But, in general the correlations among claw angle and other morphometric traits were only weak. The highest positive correlation was found between the claw width and total area of claw.

Table 2. Phenotypic correlation between claw conformation traits

	A	B	C	D	E	F	TA
B	0.007						
C	0.031	0.536***					
D	0.001	0.851***	0.716***				
E	-0.096*	0.821***	0.713***	0.902***			
F	-0.012	0.718***	0.572***	0.815***	0.826***		
TA	-0.141*	0.809***	0.722***	0.848***	0.865***	0.949***	
FA	-0.083	0.748***	0.695***	0.79***	0.798***	0.895***	0.925***

\*  $P < 0.05$ ; \*\*\*  $P < 0.0001$ ; A – Claw angle ( $^{\circ}$ ); B – Claw length (cm); C – Heel depth (cm); D – Claw height (cm); E – Diagonal (cm); F – Claw width (cm); TA – Total area (cm); FA – Functional area (cm)

Both of applied approaches indicated low or moderate level of heritability across analysed traits, in average  $0.28 \pm 0.08$  (REML) resp.  $0.22 \pm 0.09$  (Bayesian). The highest heritability was found for diagonal of claw, while the lowest one was observed for the total area of claw and the claw height based on the REML algorithm and Bayesian approach, respectively. The level of observed heritability for claw conformation traits was comparable with previous studies (Jeyaruban et al., 2012; Häggman and Juga, 2013; Ødegård et al., 2014). Moreover, those studies indicated significant relationship between the feet and leg conformation and incidence of claw disorders. For Holstein cattle Häggman and Juga (2013) revealed that the genetic correlation among the feet and leg conformation and claw disorders ranged from -0.51 to 0.45. Similarly, Ødegård et al. (2014) reported for Norwegian Red cows the moderate level of genetic correlation between the claw disorders and the conformation of feet and leg. However, in general all of the analysed claw disorders showed significantly lower level of heritability (around 0.1) compared to foot and leg conformation traits (Chapinal et al., 2013; Oberbauer et al., 2013; Ødegård et al., 2014; Pérez-Cabal and Charfeddine, 2015).

## Conclusions

The estimates of direct heritability for claw conformation traits of Slovak Holstein cattle ranged from 0.15 to 0.42 and 0.12 to 0.4 depending on the applied methodological approach. Thus, the results clearly showed that both of methods are suitable for estimation of morphometric parameters heritability, especially in case of such low sample size. In addition, this study confirmed previous assumption that the claw conformation traits are inherited in low or moderate mode. Future analysis of genetic correlations between them can be beneficial for construction of new selection

indices, better responding to today's welfare requests and made use of new generation indicators possible.

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