Czech Journal of Animal Science, 71, 2026 (1): 11–20 *Original Paper*

https://doi.org/10.17221/140/2025-CJAS

Genetic parameters for foot and claw disorders in Czech Holstein cattle

Ludmila Zavadilová, Eva Kašná, Zuzana Krupová, Miloslava Štípková, Michaela Brzáková*

Institute of Animal Science, Prague – Uhříněves, Czech Republic

**Corresponding author: zavadilova.ludmila@vuzv.cz*

Citation: Zavadilová L., Kašná E., Krupová Z., Štípková M., Brzáková M. (2026): Genetic parameters for foot and claw disorders in Czech Holstein cattle. Czech J. Anim. Sci., 71: 11–20.

Abstract: Our study investigated the genetic variability of specific foot and claw disorders, namely *dermatitis digitalis*, sole ulcer, and three broader categories (infectious diseases, claw horn lesions, and general claw disorder) in Czech Holstein cows. We also examined their genetic relationships with clinical mastitis and key fertility traits. Using both linear and threshold animal models, we concluded that heritability estimates for foot and claw disorders were consistently higher when employing the threshold model. A significant finding was the genetic correlation between sole ulcer and *dermatitis digitalis*, which ranged from 0.21 (calving to 305 days in milk) to 0.53 (calving to 90 days in milk). Furthermore, we observed stronger genetic correlations between clinical mastitis and overall foot and claw disorders, claw horn lesions, and infectious diseases during early lactation (calving to 90 days in milk) compared to the entire lactation period. Within this early lactation phase, the strongest genetic correlation was identified between clinical mastitis and claw horn lesions. Interestingly, our research uncovered a unique genetic link between days open and *dermatitis digitalis*, suggesting that a genetic predisposition to a higher occurrence of *dermatitis digitalis* may coincide with shorter days open. These results underscore the importance of implementing distinct genetic selection strategies for infectious claw diseases and claw horn lesions in dairy cows. This distinction is crucial due to their differing genetic correlations with other economically important traits, ultimately contributing to a better understanding of claw health genetics and its application in breeding programs.

Keywords: claw health traits; clinical mastitis; dairy cow; fertility traits; genetic correlation

Foot and claw disorders, as our study reveals, are among the primary reasons for the deterioration of dairy cow welfare (Heringstad et al. 2018; Zavadilova et al. 2021). These disorders lead to long-term and painful claw lesions, causing significant welfare problems. The consequences impact the production and reproductive system of the cow (van der Waaij et al. 2005; Kasna et al. 2023). As a result, milk production decreases, reproduction parameters worsen, and ultimately, diseased cows are culled (Koenig et al. 2005). As Koenig et al. (2005) pointed out, the relevance of involuntary culling due to foot and leg disorders is rising. The occurrence of foot and claw disorders harms the resilience of dairy cows (Kasna et al. 2022). Moreover, the increase in antibiotic use, a direct result of these disorders, has a noticeable negative impact on farm profitability, production efficiency, as well as food safety and quality (Koenig et al. 2005; van der Waaij et al. 2005).

Supported by the Ministry of Agriculture of the Czech Republic, institutional support MZE-RO0723.

Claw health traits are usually grouped according to aetiology and pathogenesis (Greenough 2007) to represent the most frequent disorders and to achieve an adequate number of records for genetic evaluation. Infectious diseases predominantly affect the skin and are related to environmental hygiene (digital dermatitis and interdigital dermatitis, interdigital phlegmon, and heel horn erosion). The claw horn disorders and lesions (ulcers, sole haemorrhage, and white line disease) are caused primarily by a combination of metabolic and mechanical factors (Greenough 2007; Rouha-Mulleder et al. 2009; Solano et al. 2015). The heritability of foot and claw disorders has been verified in several dairy cattle breeds (Koenig et al. 2005; van der Waaij et al. 2005; Laursen et al. 2009; Chapinal et al. 2013; Gernand et al. 2013). For an appropriate selection gain, additive genetic variation and genetic parameters with sufficiently high accuracy are necessary. Genetic correlations of foot and claw disorders with other traits included in a selection index serve as a tool for developing an efficient genetic process. Linear mixed models are often employed to estimate genetic parameters for claw disorders, e.g. especially when the genetic correlation with other traits is estimated (Laursen et al. 2009; Chapinal et al. 2013). In addition, threshold or logistic models are often employed due to the binary definition of foot and claw disease traits (Koenig et al. 2005; Gernand et al. 2013; Schneider et al. 2024).

Selection for decreased claw disorder incidence in cattle often means using a selection index. Apart from production traits, the main components of selection indices are functional traits, including reproductive and health traits (Krupova et al. 2018, 2024). Therefore, it is crucial to know the genetic relationship between the traits of the selection goal. The genetic relationship between foot and claw disorders and clinical mastitis is positive and moderate, but it is typically observed only for feed-related hoof diseases (0.35 and 0.32) (Buch et al. 2011). Kougioumtzis et al. (2014) found a negative phenotypic correlation between lameness and conception rate (–0.19). Zink et al. (2011) presented a negative genetic correlation between locomotion and the interval between calving and first service (–0.34). Charfeddine and Perez-Cabal (2017) confirmed the worsening effect of sole ulcer and white line disease on days open. However, Buch et al. (2011) found an unfavourable genetic correlation between claw horn lesions (sole ulcer) and days from calving to first service (0.33) and between infectious disease and a number of inseminations (0.32). Onyiro et al. (2008) found a negative relationship between *dermatitis digitalis* and calving interval; however, this relationship was mediated by milk yield, resulting in a positive genetic correlation (0.015) between the two traits. Nevertheless, a positive genetic correlation with the non-return rate after 56 days was confirmed by Onyiro et al. (2008). Schneider et al. (2024) confirmed significant positive genetic correlations between the fat-to-protein ratio and digital dermatitis, but mostly negative correlations for clinical mastitis and non-infectious claw disorders, based on the metabolic status of the cow. Genetic relationships to other traits raise questions regarding different genetic backgrounds of foot and claw disorders.

The present study aimed to analyse the genetic variability of foot and claw disorders for Holstein cows in the Czech Republic, including their genetic relationship to clinical mastitis and fertility traits.

MATERIAL AND METHODS

The raw data set included approximately 45 232 records of foot and claw disorders from 18 268 cows and 51 244 lactations monitored in 13 herds during 1998–2018. Records were from parities 1–8, but mainly from the first to the third parity (84.0%). Hoof trimmers collected data on foot health records during both regular trimming sessions and emergency visits. There were also available records on clinical mastitis and reproduction traits for every farm, provided by farmers.

The analysed dataset was limited to Holstein cows with at least 75.0% of Holstein genes and known pedigrees. Therefore, only seven herds with a sufficient number of Holstein cows were included. After editing, only 40 354 claw disorder records remained. The most frequent diseases were *dermatitis digitalis* and *dermatitis interdigitalis* (27.6%) and ulcers (28.0%). Infectious diseases, including *dermatitis digitalis*, *dermatitis interdigitalis*, interdigital phlegmon, and heel horn erosion, accounted for 41.3%. In 42.2% of records, claw horn lesions/disruptions occurred. They included toe and sole ulcers, white line disease, horn fissure, double sole and sole haemorrhage. The remaining records (8.00%) covered lameness, purulent claw diseases, interdigital hyperplasia or swelling of the coronet and/or bulb.

For analysis, three groups of foot and claw disorders were created: infectious diseases (INF), including *dermatitis digitalis* and *dermatitis interdigitalis*, interdigital phlegmon and heel horn erosion; claw horn lesions (CHL), including ulcers, white line disease, horn fissures, double sole and sole haemorrhage; and overall foot and claw disorders (OFCD), comprising all of the recorded disorders. *Dermatitis digitalis* and *interdigitalis* (DD) and ulcer (U), the most frequent foot and claw diseases, were analysed separately.

For the estimation of genetic parameters, foot and claw disorders and clinical mastitis were defined as 0/1 occurrences per lactation stage, from calving to 90 days or from calving to 305 days of lactation. Further analysis of health traits was conducted on clinical mastitis (CM) up to 305 days in milk. Lactation incidence (%) for clinical mastitis is presented in Table 1. Reproduction traits in days were the intervals between calving and first service (INT), days open (DO) and calving interval (CI). Basic statistics for the intervals between calving and first service (INT), days open (DO) and calving interval (CI) are presented in Table 2. The following linear animal model was used to estimate genetic parameters for foot and claw disorder traits and their correlations to CM and reproduction traits:

$$y_{ijklmno} = \text{parity}_i + \text{herd}_j + \text{year}_k + \text{season}_l + \text{age}_m + \text{PE}_n + \text{A}_o + e_{ijklmno} \quad (1)$$

where:

$y_{ijklmno}$ – analysed trait: the occurrence of foot and claw disorder traits (INF, CHL, OFCD, DD, U) during the first 90 days in milk or 305 days in milk; CM; reproduction traits (INT, DO, CI);

parity_i – effect of parity class i (5 levels, first, second, third, fourth, five and higher parity);

herd_j – effect of herd j (7 levels);

year_k – effect of calving year k (20 levels; 1998–2008);

season_l – effect of calving season l (4 levels, January–March; April–June; July–September; October–December);

age_m – effect of age at calving m (13 levels);

PE_n – random permanent environmental effect on cow traits across parity n;

A_o – random additive genetic effect of cow o;

$e_{ijklmno}$ – random residual effect.

The pedigree file contained 26 356 records.

A threshold methodology was employed to compare the results from linear and threshold analy-

Table 1. Lactation incidence (%) for clinical mastitis

Parity	Clinical mastitis, 90 days	Number of lactations (No.)	Clinical mastitis, 305 days	Number of lactations (No.)
1st	15.3	8 437	25.4	7 793
2nd	17.6	6 405	33.1	5 719
3rd	22.1	4 290	39.9	3 677
4th	27.0	2 314	46.2	1 895
5th and higher	33.4	1 369	59.3	1 802

Table 2. Number of lactations, mean ± SD for the intervals between calving and first service (INT), days open (DO) and calving interval (CI)

Parity	INT (days)		DO (days)		CI (days)	
	number of lactations (No.)	mean ± SD	number of lactations (No.)	mean ± SD	number of lactations (No.)	mean ± SD
1st	7 853	81.7 ± 40.6	7 272	134 ± 80.3	7 072	415 ± 75.2
2nd	5 845	81.9 ± 38.4	5 165	141 ± 75.3	5 031	423 ± 69.9
3rd	3 795	83.1 ± 36.6	3 308	147 ± 76.7	3 223	426 ± 66.9
4th	1 954	81.9 ± 33.9	1 625	144 ± 75.7	1 582	425 ± 64.7
5th and higher	1 103	83.1 ± 35.7	888	148 ± 74.7	876	431 ± 64.4

ses, given the binary nature of the claw disorder data. The statistical model was defined according to the linear animal model mentioned above. Nevertheless, the dependent variable was defined as the probability of the i^{th} parity of the o^{th} cow for the occurrence of a foot and claw disorder. The threshold model assumed an underlying continuous variable, liability (y_i), for binary traits, where the observed binary variable was defined as 1 if liability exceeded a fixed threshold and 0 otherwise. Binary models were employed to estimate genetic correlations. The genetic correlations for foot and claw disorders with other analysed traits were similar between the linear and threshold models. Therefore, only estimates from the linear analysis are presented. Data editing was performed in SAS (2016). Datasets were analysed using the DMU package (Madsen and Jensen 2010) with the RJMC (Reversible Jump Markov Chain) module so the single and multiple trait Markov chain Monte Carlo was applied. The number of burn-in rounds was 2 000, the number of sampling rounds was 100 000, and the sampling interval was 10.

RESULTS

Lactation incidence of foot and claw disorders. The lactation incidence (%) for the analysed foot and claw disorders by parity for 90 days in milk or 305 days in milk is shown in Figure 1 and in Electronic Supplementary Material (ESM) Table S1. The lactation incidences of INF and DD were almost identical in each parity, especially in the early stage of lactation. In contrast, the lactation incidence of CHL and U increased with parity, and the increase in LIR was substantial. Furthermore, OFCD increased rapidly with parity. In the fifth and highest parity, the lactation incidence of OFCD was 70%. In the higher parities, cows suffered from more diseases simultaneously during lactation than during the first lactation; therefore, the lactation incidence is lower than that of particular disorders.

Variances and heritability of foot and claw disorders. Estimates of heritability for the analysed traits are presented in Figure 2; heritability and variances are presented in ESM Table 2. Additive genetic variances were found for all analysed claw health traits. Heritability estimates for 305 days in milk were higher than those for 90 days in milk. Moreover, the heritability estimates obtained using the threshold model were higher than those obtained using the linear model. The variance of the permanent environment tends to be lower than the additive variance for almost all combinations of traits and types of analysis.

For the linear model, the heritability of foot and claw disorders (305 days) ranged from 0.08 (OFCD, DD, INF) to 0.11 (CHL). The extent of heritability estimates (305 days) for the threshold model was more substantial than that for the linear model, ranging from 0.11 (DD) to 0.21 (CHL). For the early stage of lactation (90 days), linear heritability estimates were approximately 0.05, and threshold heritability was from 0.11 (OFCD) to 0.16 (U).

Correlations between foot and claw disorders. Estimates of genetic correlations between U, DD and OFCD are presented in Figure 3. The genetic and permanent environmental correlations between foot and claw disorders are presented in ESM Table S3. Only linear estimates are presented for estimating correlations for foot and claw disorders and any other analysed traits, due to the similarity of estimates from the linear and threshold models. The genetic correlations of OFCD with INF and DD were higher for the period from calving to 90 days in milk than for the period to 350 days in milk. The strongest genetic correlations (over 0.89) occurred

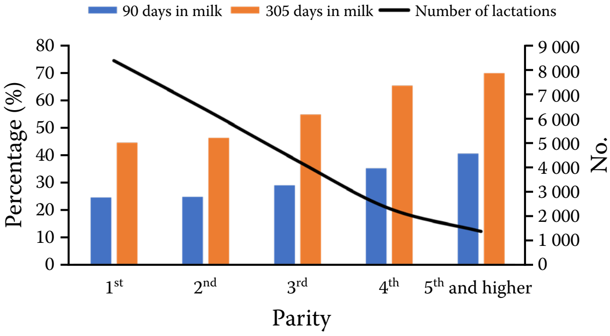

Figure 1. Lactation incidence of overall claw disorders

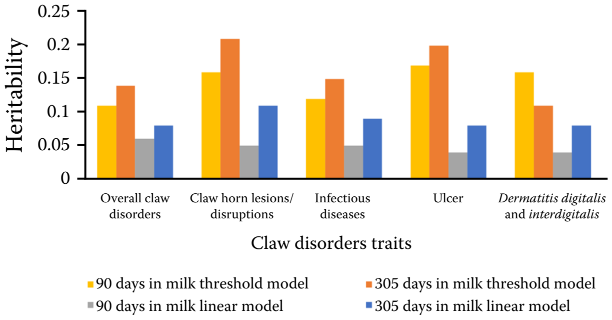

Figure 2. Heritability of analysed claw disorders

https://doi.org/10.17221/140/2025-CJAS

Hatched bars indicate a statistically significant value

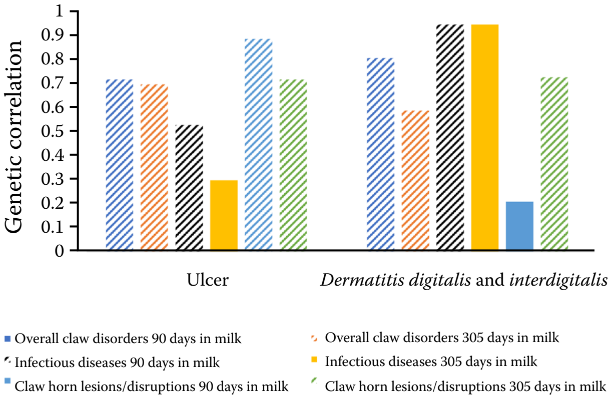

Figure 3. Genetic correlations between ulcer, *dermatitis digitalis* and *dermatitis interdigitalis* and claw disorder traits

between INF and DD and/or CHL and U. Some permanent environmental correlations were close to zero or inestimable: DD × CHL (305 d); CHL × U (90 d); INF × OFCD (90 d), apparently due to data structure. Strong genetic correlations occurred between DD and CHL (0.73) or DD and U (0.53) in the early stage of lactation. Unlike lactation, both showed a lower correlation: DD and CHL (0.21) or DD and U (0.21). Permanent environmental correlations between DD and CHL or DD and U were lower than genetic correlations for those traits.

Correlations between foot and claw disorders and mastitis. Genetic correlations between foot and claw disorders and mastitis (305 days in milk) by the linear model are shown in Figure 4. Genetic correlations and correlations due to permanent environment between foot and claw disorders and mastitis (305 days in milk) are presented in ESM Table S4 using the linear model. Only the linear estimates of correlations are presented for foot and claw disorders and CM, as the estimates from the linear and threshold models are similar. The highest correlations were present for all traits, but low genetic correlations still occurred between CM and the three groups of foot and claw traits: OFCD (0.20), CHL (0.22), and INF (0.22) over 90 days in milk. For the entire lactation period, the highest genetic correlations were observed between CM and OFCD (0.14), CHL (0.19), and U (0.12). Permanent environmental correlations between CM and foot and claw traits were negative [except CM and OFCD (0.10)] and nonsignificant.

Correlations between foot and claw disorders and reproductive traits. Genetic correlations between foot and claw disorders and reproductive traits, as estimated by the linear model, are presented in Figure 5 and 6. Genetic correlations and correlations due to permanent environment between foot and claw disorders and reproductive traits are presented in ESM Table S5. Only the linear estimates of correlations are presented for foot and claw disorders and some fertility traits, as the estimates derived from the linear and threshold models are similar. Large standard errors characterised the estimates of genetic and permanent environmental variances. Therefore, only a few estimates were statistically significant, especially with INF or DD and DO. The estimates were similar between INF and DD or CHL and U, with a tendency toward higher estimates for a particular disease (DD, U) compared with groups of foot and claw disorders (INF, CHL). Higher correlations occurred during the first 90 days of lactation, but only for some combinations of traits.

Hatched colums indicate a statistically significant value

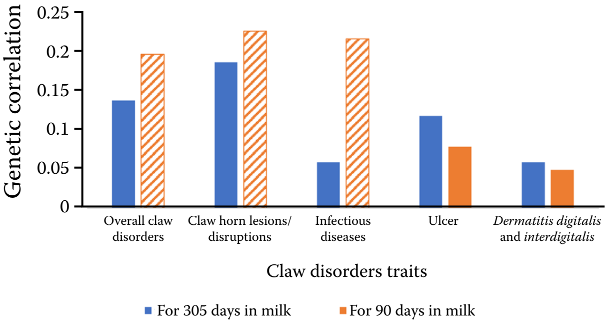

Figure 4. Genetic correlations between clinical mastitis incidence and claw disorder traits

Hatched colums indicate a statistically significant value

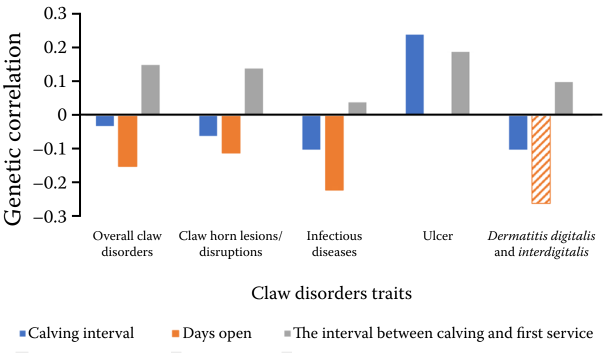

Figure 5. Genetic correlations between claw disorder traits for 90 days in lactation

https://doi.org/10.17221/140/2025-CJAS

Hatched colums indicate a statistically significant value

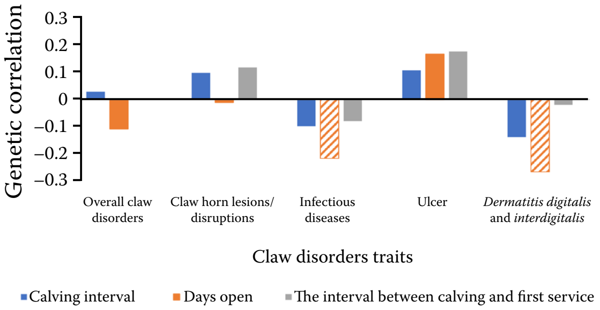

Figure 6. Genetic correlations between claw disorder traits for 305 days in lactation

The most remarkable genetic relationship seems to be between DO and INF (–0.22, –0.22) or DD (–0.26, –0.27) in both analysed time periods of lactation. These genetic correlations are negative, i.e. a genetic predisposition to a higher occurrence of the particular disease is connected with a genetic predisposition to shorter days open. In contrast, genetic correlations between U and INT are positive in both lactation periods (0.18, 0.19). This means that a genetic predisposition to a higher occurrence of ulcer disease is related to a longer interval between calving and first service. Nevertheless, those values are not statistically significant. In the 90-day segment of lactation, a remarkable increase in the permanent environmental correlations was found for DO × OFCD and DO × CHL in comparison with the 305-day segment of lactation.

DISCUSSION

Lactation incidence. The lactation incidence that we found is high but plausible. Manske et al. (2002) reported that 72.0% of the cows in Sweden had at least one claw disorder. In Norway, Sogstad et al. (2005) similarly found that 71.8% of the cows in free stalls and 47.8% in tie stalls had at least one claw lesion. In Swedish Red (SRB) cows, Buch et al. (2011) found a 25% prevalence of sole haemorrhage in the first parity. Chapinal et al. (2013) found that 40% of cows in North American dairy herds had at least one foot and claw lesion. For Spanish Holstein cows, Charfeddine and Perez-Cabal (2017) found that 30% of animals suffered from at least one claw disorder among six monitored lesions. Solano et al. (2015) reported that 36% of dairy cows (mainly Holstein breeds) showed at least one claw disorder. The low incidences of particular noninfectious claw diseases and the much higher incidences of *dermatitis digitalis* and *dermatitis interdigitalis* agreed with Heringstad et al. (2018) and Schneider et al. (2024). Solzer et al. (2022) reported a 365-day prevalence of DD at 16.0% and SU at 8.20% for cows in the first parity, which corresponds to the DD prevalence of 90 days in milk (12.30%) and to the SU prevalence of 305 days in milk (8.40%) in our study. In Czech Holstein, the frequency of claw diseases often exceeds 50% (Krpalkova et al. 2016).

Definition of foot and claw disorder traits. As it is widely done for claw health traits, we defined claw and foot disorders as binary traits due to their nature: healthy or ill. Unlike, for example, clinical mastitis, foot and claw disorders are mostly found when already developed but not at the beginning of the disease. The degree of disease is more important than the exact beginning. Claw and foot disorder reporting is mainly associated with regular trimming of claws. The incidence of claw and foot disorders related to lactation or stage of lactation provides proper and sufficient information for breeding.

Grouping of foot and claw disorders is often performed due to the high number of individual disorders and low frequency (Odegard et al. 2013). According to aetiology (Greenough 2007), the definition groups of foot and claw disorders are also justified by different occurrences of infectious and non-infectious diseases during lactation (Buch et al. 2011). Compared with claw horn lesions, infectious diseases in this study were more prevalent at the beginning of lactation, while claw horn lesions were evenly distributed throughout lactation. Odegard et al. (2013) employed a similar definition of foot and claw disorders. They defined the group of infectious diseases, including dermatitis, heel horn erosion, and interdigital phlegmon. The second group, corresponding to the claw horn lesion, included laminitis-related claw disorders such as sole ulcers, white line disease, and sole and white line haemorrhage. Koenig et al. (2005) employed a slightly different grouping for purulent and nonpurulent claw disorders. The first group primarily included digital dermatitis, sole ulcer, and phlegmon, as well as some low-incidence purulent diseases, such as sepsis or interdigital dermatitis. The second group contained laminitis, interdigital hyperplasia and other nonpurulent disorders with low prevalence, such as white line disease. The group of all claw disorders combined both previous groups. In addition, Perez-Cabal and Charfeddine (2015) classified three categories of disorder severity for six monitored claw and foot diseases. They also considered the number of disorders when creating the overall claw disorder. Schneider et al. (2024) found different local genetic correlations for digital dermatitis and several laminitis-related claw disorders, with fat-to-protein ratio and other traits representing the metabolic status of dairy cows.

Heritability of claw disorder traits. The study aimed to estimate genetic parameters, including heritabilities for foot and claw disorders, as well as genetic correlations with clinical mastitis and reproduction traits, for potential application in the genetic evaluation of foot and claw disorders in the Czech Republic. Therefore, the estimates from the linear model are more important for the whole system of routine evaluation in the Czech Republic, where a linear model is employed. As stated by Heringstad et al. (2018), linear models are fast, easy to implement and they provide similar results to more advanced models in most cases. Consequently, it is the first choice for routine estimation. The categorical model fits better for binary traits such as claw health data than the linear model. However, van der Waaij et al. (2005) affirmed that the linear model leads to satisfactorily robust estimations.

Previous studies have shown that the foot and claw disorders are characterised by low heritability, primarily due to a sizable environmental influence. Heritability published for DD was, for example, 0.10 (Koenig et al. 2005) and 0.13 (Buch et al. 2011). The values for U were 0.01 (van der Waaij et al. 2005), 0.089 (Koenig et al. 2005), 0.17 (Buch et al. 2011). Odegard et al. (2013) published a heritability of 0.20 for DD and 0.18 for sole ulcers by the threshold model. Perez-Cabal and Charfeddine (2015) reported heritability estimates of 0.02 for DD and 0.04 for sole ulcer, using a linear model, and 0.14 for DD and 0.15 for sole ulcer, using a threshold model. Similarly, Solzer et al. (2022) estimated low linear heritability for DD (0.04) and U (0.03) and higher heritability for those traits by the threshold model (DD 0.08, U 0.10). Despite using a threshold model, Schneider et al. (2024) presented heritabilities lower than 0.10 for the analysed claw diseases, except for 0.19 for interdigital hyperplasia. Solzer et al. (2022) found an important increase in heritability for the threshold model when the incidence of claw disease was low. The heritability values for ulcers were 0.03 and 0.10, and for interdigital hyperplasia 0.03 and 0.23 from the linear and threshold analysis, respectively. Similarly, the heritability of OCD estimated by Perez-Cabal and Charfeddine (2015) was 0.05 by a linear model and 0.11 by a threshold model. Odegard et al. (2013) found heritability of 0.11 for infectious claw diseases, 0.11 for laminitis-related claw disorders, and 0.13 for OCD by a threshold model. Differences between these estimates and heritability in the present study can be attributed rather to differences in the analysed data files than to differences in the analysed breeds (Holstein vs Norwegian Red).

Correlations between claw disorder traits. Stronger genetic correlations between the foot and claw disorder traits were found in the early stage of lactation than in the entire lactation period. This can be attributed to the low resistance to claw diseases, which is typically due to the high metabolic requirements of lactating cows. At the beginning of lactation, the incidence of foot and claw diseases is influenced by genes associated with the onset of dairy production and the initiation of a new reproductive cycle. We can assume that the influence of different genes is heterogeneously applied during lactation.

Regarding foot and claw disorders, we confirmed the genetic differences between infectious diseases and claw horn disorders (INF, DD vs CHL, U), especially during the lactation period. At the start of lactation, more genes are active, affecting both INF and CHL. CHL is a consequence of metabolic and environmental stress, sometimes in combination with bacterial infections. At the beginning of lactation, the metabolic stress of cows increases (Bezdicek et al. 2024), and it is known that the incidence of DD is also high. Both metabolic stress and DD can cause a high incidence of ulcers. The published genetic correlations between DD and U are miscellaneous. Koenig et al. (2005) found a genetic correlation of 0.56 between DD and U; Buch et al. (2011) −0.19; Perez-Cabal and Charfeddine (2015) −0.08; Odegard et al. (2013) 0.18.

In agreement with our results, low genetic correlations between infectious claw diseases and horn lesions (0.08) were published by Chapinal et al. (2013). Buch et al. (2011) confirmed some differences in the genetic basis between infectious diseases and claw horn disorders and they pointed out that their results indicate a partial overlap between the genetic components underlying the two groups of foot and claw diseases.

Correlations between claw disorder traits and clinical mastitis. Genetic correlations occurred more often between the groups of foot and claw disorder traits and CM than between CM and U or DD. Especially at the start of lactation, our results significantly indicated some genetic relationships between CM and foot and claw disorders. Buch et al. (2011) found a more positive genetic correlation between CM and feed-related hoof diseases, such as sole haemorrhage (0.35) and sole ulcer (0.32). These findings are similar to our study, where the genetic correlations between CM and CHL were the highest. Especially in the early stage of lactation, up to 90 days in milk, there was a high genetic correlation for INF. Buch et al. (2011) attributed it to improper feeding, possibly ruminal acidosis and laminitis induced by clinical mastitis. This is also similar to our study, where higher genetic correlations between CM and foot and claw disorders were found to occur when feeding requirements were highest at the start of lactation. Solzer et al. (2022) reported a low but unfavourable genetic correlation between DD and CM (–0.07). According to Solzer et al. (2022), there can be different genes for the respective disease, or both our estimates and those of Solzer et al. (2022) are very low and, in fact, not different from zero. Gernand et al. (2013) and Buch et al. (2011) clearly demonstrated that genetic correlations between claw disorders and diseases in the other health categories were close to zero.

Correlations between claw health traits and reproductive traits. On a phenotypic basis, Charfeddine and Perez-Cabal (2017) affirmed that *dermatitis digitalis* and *dermatitis interdigitalis*, sole ulcer and white line disease caused prolonged days open. The identified genetic correlations, especially those that are significant, suggest a shared genetic basis for the length of reproductive intervals and the prevalence of foot and claw disorders. We found negative genetic correlations between DO and two infectious diseases: INF and DD. It is unfavourable from a breeding perspective. We assume that the negative genetic correlation can be explained by a shared genetic predisposition to better reproduction, which manifests as shorter DO and higher occurrence of DD or INF, likely due to lower resiliency to metabolic stress and higher susceptibility to the disease. But perhaps DO cannot be considered as a good indicator of reproductive ability as INT. We regularly found the positive genetic correlations between CI and DD, U or CHL. The shared genetics contributes to poor reproduction and a high prevalence of U or CHL. It is favourable from a selection perspective. Onyiro et al. (2008) published negative (unfavourable) genetic correlations between DD and CI (–0.07). Kougioumtzis et al. (2014) found a negative phenotypic correlation between lameness and conception rate (–0.19). These results align with ours, indicating that a genetic predisposition to better fertility partially overlaps with a genetic predisposition to infectious diseases. But, Solzer et al. (2022) published the positive genetic correlation between DD and INT (0.12), CI (0.28), and U and INT (0.31), or CI (0.23).

CONCLUSION

The study confirmed the justified classification of foot and claw disorders in Czech Holstein cows into two categories: infectious diseases and claw horn lesions, based on their aetiology. These two categories show significantly different genetic relationships with other traits, such as clinical mastitis and fertility. Furthermore, the associations between the analysed traits vary notably between early and entire lactation periods. Overall, the genetic differences observed between infectious diseases and claw horn lesions, along with their differing genetic correlations with clinical mastitis and fertility across lactation stages, are important for effective breeding programmes. These findings highlight the need for separate genetic selection strategies specifically tailored for infectious claw diseases and claw horn lesions.

Such an improved approach will enhance the understanding of claw health genetics and its practical application in dairy breeding, leading to better animal welfare, reduced economic losses, and more sustainable dairy production systems. This is especially important because selection against foot disorders can also influence related lesion traits. Additionally, some claw disorders are genetically correlated with mastitis, emphasising the interconnectedness of various health traits in cattle.

Acknowledgement

The authors thank the Czech Moravian Breeding Corporation and Holstein Cattle Breeders Association of the Czech Republic for providing the production and reproduction data. Thanks are due to Jaroslava Šefrová and Michaela Krejčová, both of Prague Uhříněves (Czech Republic), for collecting data on farms and their vital role in this study.

Conflict of interest

The authors declare no conflict of interest.

REFERENCES

Bezdicek J, Nesvadbova A, Duchacek J, Sekaninova J, Stadnik L, Janku M. Changes in the oxidative biochemical status in dairy cows during the transition period affecting reproductive and health parameters. Czech J Anim Sci. 2024 Sep;69(9):345-55.

Buch LH, Sorensen AC, Lassen J, Berg P, Eriksson JA, Jakobsen JH, Thomasen JR, Sorensen MK. Hygiene-related and feed-related hoof diseases show different patterns of genetic correlations to clinical mastitis and female fertility. J Dairy Sci. 2011 Mar;94(3):1540-51.

Chapinal N, Koeck A, Sewalem A, Kelton DF, Mason S, Cramer G, Miglior F. Genetic parameters for hoof lesions and their relationship with feet and leg traits in Canadian Holstein cows. J Dairy Sci. 2013 Apr;96(4):2596-604.

Charfeddine N, Perez-Cabal MA. Effect of claw disorders on milk production, fertility, and longevity, and their economic impact in Spanish Holstein cows. J Dairy Sci. 2017 Jan;100(1):653-65.

Gernand E, Dohne DA, Konig S. Genetic background of claw disorders in the course of lactation and their relationships with type traits. J Anim Breed Genet. 2013 Dec;130(6):435-44.

Greenough PR. Bovine laminitis and lameness: A hands-on approach. Edinburgh (UK): Saunders; 2007. 328 p.

Heringstad B, Egger-Danner C, Charfeddine N, Pryce JE, Stock KF, Kofler J, Sogstad AM, Holzhauer M, Fiedler A, Muller K, Nielsen P, Thomas G, Gengler N, de Jong G, Odegard C, Malchiodi F, Miglior F, Alsaaod M, Cole JB. Invited review: Genetics and claw health: opportunities to enhance claw health by genetic selection. J Dairy Sci. 2018 Jun;101(6):4801-21.

Kasna E, Zavadilova L, Krupova Z, Slosarkova S, Fleischer P. The most common reproductive disorders of cows in Holstein cattle breeding. Czech J Anim Sci. 2023 Nov;68(11):433-42.

Kasna E, Zavadilova L, Vareka J, Kyselova J. General resilience in dairy cows: A review. Czech J Anim Sci. 2022 Dec;67(12):475-82.

Koenig S, Sharifi AR, Wentrot H, Landmann D, Eise M, Simianer H. Genetic parameters of claw disorders estimated with logistic models. J Dairy Sci. 2005 Sep;88(9):3316-25.

Kougioumtzis A, Valergakis GE, Oikonomou G, Arsenos G, Banos G. Profile and genetic parameters of dairy cattle locomotion score and lameness across lactation. Animal. 2014 Jan;8(1):20-7.

Krpalkova L, Cabrera VE, Kvapilik J, Burdych J. Associations of reproduction and health with the performance and profit of dairy cows. Agric Econ (Czech). 2016 Aug;62(8):385-94.

Krupova Z, Kasna E, Zavadilova L, Krupa E, Bauer J, Wolfova M. Udder, claw, and reproductive health in genomic selection of the Czech Holstein. Animals (Basel). 2024 Mar 11;14(6):864.

Krupova Z, Wolfova M, Krupa E, Pribyl J, Zavadilova L. Claw health and feed efficiency as new selection criteria in the Czech Holstein cattle. Czech J Anim Sci. 2018 Oct;63(10):408-18.

Laursen MV, Boelling D, Mark T. Genetic parameters for claw and leg health, foot and leg conformation, and locomotion in Danish Holsteins. J Dairy Sci. 2009 Apr;92(4):1770-7.

Madsen P, Jensen J. DMU – A package for analysing multivariate mixed models. Version 6, release 5.0. Foulum (Denmark): Aarhus University; 2010.

Manske T, Hultgren J, Bergsten C. Prevalence and interrelationships of hoof lesions and lameness in Swedish dairy cows. Prev Vet Med. 2002 Jul 25;54(3):247-63.

Odegard C, Svendsen M, Heringstad B. Genetic analyses of claw health in Norwegian Red cows. J Dairy Sci. 2013 Nov;96(11):7274-83.

Onyiro OM, Andrews LJ, Brotherstone S. Genetic parameters for digital dermatitis and correlations with locomotion, production, fertility traits, and longevity in Holstein-Friesian dairy cows. J Dairy Sci. 2008 Oct;91(10):4037-46.

Perez-Cabal MA, Charfeddine N. Models for genetic evaluations of claw health traits in Spanish dairy cattle. J Dairy Sci. 2015 Nov;98(11):8186-94.

Rouha-Mulleder C, Iben C, Wagner E, Laaha G, Troxler J, Waiblinger S. Relative importance of factors influencing the prevalence of lameness in Austrian cubicle loose-housed dairy cows. Prev Vet Med. 2009 Nov 1;92(1-2):123-33.

SAS Institute. SAS/STAT 9.4 User's Guide. Cary (NC): SAS Institute; 2016.

Schneider H, Krizanac AM, Falker-Gieske C, Heise J, Tetens J, Thaller G, Bennewitz J. Genomic analyses of claw disorders in Holstein cows: Genetic parameters, trait associations, and genome-wide associations considering interactions of SNP and heat stress. BMC Genomics. 2024 Mar 9;25(1):265.

Sogstad AM, Fjeldaas T, Osteras O, Forshell KP. Prevalence of claw lesions in Norwegian dairy cattle housed in tie stalls and free stalls. Prev Vet Med. 2005 Sep 12;70(3-4): 191-209.

Solano L, Barkema HW, Pajor EA, Mason S, LeBlanc SJ, Zaffino Heyerhoff JC, Nash CG, Haley DB, Vasseur E, Pellerin D, Rushen J, de Passille AM, Orsel K. Prevalence of lameness and associated risk factors in Canadian Holstein-Friesian cows housed in freestall barns. J Dairy Sci. 2015 Oct;98(10):6978-91.

Solzer N, May K, Yin T, Konig S. Genomic analyses of claw disorders in Holstein cows: Genetic parameters, trait associations, and genome-wide associations considering interactions of SNP and heat stress. J Dairy Sci. 2022 Oct; 105(10):8218-36.

van der Waaij EH, Holzhauer M, Ellen E, Kamphuis C, de Jong G. Genetic parameters for claw disorders in Dutch dairy cattle and correlations with conformation traits. J Dairy Sci. 2005 Oct;88(10):3672-8.

Zavadilova L, Kasna E, Krupova Z, Klimova A. Health traits in current dairy cattle breeding: A review. Czech J Anim Sci. 2021 Jul;66(7):235-50.

Zink V, Stipkova M, Lassen J. Genetic parameters for female fertility, locomotion, body condition score, and linear type traits in Czech Holstein cattle. J Dairy Sci. 2011 Oct; 94(10):5176-82.

Received: October 10, 2025
Accepted: December 11, 2025