Single-step genetic evaluation for claw health traits in Switzerland

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Abstract

In Switzerland, a resource project was launched in 2019 to improve claw health in Swiss cattle. This project marked the beginning for the development of the first genetic evaluation for claw health traits in Swiss dairy cattle. Data recorded by claw trimmers during routine care was used to develop a single-step genetic evaluation for the most common dairy cattle breeds Holstein, Swiss Fleckvieh, Simmental, Brown Swiss and Original Braunvieh.

A key advantage of this dataset is its comprehensive inclusion of all healthy cows observed during routine care. From 2019 to 2024, a total of 104,276 records were collected for the multi-breed evaluation of Holstein cattle (encompassing Holstein, Swiss Fleckvieh, and Simmental), while 33,464 records were documented for Brown Swiss (Brown Swiss and Original Braunvieh). Breeding values were predicted for four distinct traits: dermatitis digitalis (DD), white-line disease (WL), other infectious claw diseases (INF), and other non-infectious claw diseases (NINF). The prevalence rates of DD, WL, INF, and NINF were observed as 20.9%, 9.9%, 45.8%, and 20.7% respectively in the Holstein evaluation, while in the Brown Swiss evaluation, they were found as 7.8%, 10.2%, 37.6%, and 13.5%.

A multi-trait animal model with binary coding of the trait was fit in the ssGTaBLUP evaluation, with heritability estimates ranging from 3% to 9% determined for the four traits across both populations. A top-bottom comparison revealed that daughter prevalence among sires with the highest and lowest estimated breeding values (EBV) varied by 14% to 35%. An index incorporating breed-specific weights for the four traits has been developed and is now published for all Swiss breeders.

A primary challenge in developing the genetic evaluation was the scarcity of phenotypic data alongside a substantial population of genotyped animals that exhibited limited genetic correlation with individuals supplying phenotypic records.

Key words: Claw health, single-step genetic evaluation, dairy cattle, multi breed evaluation

Introduction

Claw health represents the third leading cause of culling in Swiss dairy cattle, following mastitis and fertility challenges. Claw diseases and the resultant lameness significantly affect animal health and welfare as well as herd productivity, primarily due to treatment costs and decreased milk yield. Previous research has estimated that associated economic losses can range from several hundred to over one thousand dollars per case and animal (Dolecheck and Bewley, 2018).

A resource project was initiated in 2019 to enhance claw health in Swiss cattle. The main objective was to implement systematic recording of claw health data by hoof trimmers during routine care. Hoof trimmers received training to ensure standardized and consistent documentation of claw diseases. In addition to advancing management practices, a key objective of the project and this study was to establish the first Swiss genetic evaluation for claw health traits and to improve dairy cattle's claw health. Utilizing the comprehensive genomic data available for dairy cattle, a single-step evaluation was developed to maximize the utility of this information. The resulting breeding values will support breeders in sustainably improving the claw health of Swiss dairy cattle through breeding.

Materials and Methods

Data

Data recorded by claw trimmers during routine care was collected through the resource project ‘Gesunde Klauen’ (https://gesundeklauen.unibe.ch, access date 2025/07/30) for multiple cattle breeds. The raw data set included 286,138 records of both diseased and healthy cases from 2019 to 2024. Thus, having all sound and diseased records solved the question of reconstituting the contemporary groups. Disease recording was done according to ICAR definitions (ICAR, 2020). Pedigree and genotype data were obtained from the three Swiss cattle breeding organizations: Braunvieh Schweiz, swissherdbook, and Holstein Switzerland.

During quality control, records lacking identity information, herd information or disease codes were excluded. Data pertaining to the principal dairy cattle breeds in Switzerland – Holstein, Swiss Fleckvieh, Simmental, Brown Swiss, and Original Braunvieh – were retained. Typically, animals underwent trimming twice annually. Phenotypic data were compiled as records per month and animal. For Holstein multi-breed evaluation, 104,276 records were analysed (including Holstein, Swiss Fleckvieh, and Simmental). 33,464 records were used for Brown Swiss evaluation (Brown Swiss and Original Braunvieh).

Genotype data obtained through standard imputation included 114,640 SNPs for 490,761 animals from Holstein dataset and 146,609 animals corresponding to Brown Swiss evaluation. The Holstein dataset contained 5,284 cows with both phenotype and genotype records, while the Brown Swiss dataset comprised 2,894 cows with these records.

Trait definition

Due to low prevalence of certain diseases, genetic evaluation was limited to dermatitis digitalis (DD) and white-line disease (WL) as individual traits. Remaining diseases were combined into two groups: other infectious diseases (INF) and non-infectious diseases (NINF). INF comprised heel horn erosions, interdigital dermatitis, and interdigital phlegmon. NINF included interdigital hyperplasia (limax), asymmetric, corkscrew, and scissor claws, concave dorsal wall, double sole, axial, horizontal, and vertical horn fissure, thin sole, sole hemorrhage, sole bulb and toe ulcer, and toe necrosis.

Genetic model

A linear multi-trait repeated animal model was implemented to estimate variance components and genomic breeding values. Fixed effects included parity, trimmer by year, stage of lactation, year-month. Recombination and heterosis were also incorporated as fixed effects into the Holstein multi-breed evaluation. The random effects comprised herd-year-season, permanent environment, and animal genetic effect. Traits were coded as binary variables (0 or 1).

Variance components were estimated with the VCE software (version 6.0.2; Neumaier and Groeneveld, 1998) and the four-trait animal model, applied separately to the Holstein and Brown Swiss datasets.

Genetic evaluation

Single-step genomic breeding values were predicted using the ssGTaBLUP model (Mäntysaari et al., 2017) implemented in the MiX99 software package (Strandén and Lidauer, 1999). Reliability estimates for these breeding values were assessed with snp_blup_rel (Zaabza et al., 2020), executed within the MiX99 environment. Estimated breeding values (EBV) were standardized to a mean of 100 and a standard deviation of 12 for publication.

Validation of genetic evaluation

A top-bottom comparison was performed to validate the genetic evaluation process. The average prevalence among daughters was calculated for sires with high reliability (Brown Swiss ≥ 0.35, Holstein ≥ 0.6). These averages were then compared between the sires within the top 10% and bottom 10% of EBV.

Results & Discussion

Prevalence rates for the traits DD, WL, INF, and NINF were observed at 20.9%, 9.9%, 45.8%, and 20.7% respectively in the Holstein evaluation, and at 7.8%, 10.2%, 37.6%, and 13.5% in the Brown Swiss evaluation. The prevalences of DD, WL, and NINF align with findings from Holstein and Brown Swiss populations in other countries (Johansson et al., 2011; Köck et al., 2019; Malchiodi et al., 2018). The comparatively higher prevalence of INF may be attributed to trimmers being instructed to record heel horn erosion with high sensitivity.

Heritability estimates for the four evaluated traits and two assessments of Holstein and Brown Swiss ranged from 3% to 9%, as detailed in Table 1. The highest estimate was recorded for DD in the Holstein evaluation, while the lowest was noted for DD in Brown Swiss. These findings are consistent with previously reported heritability values from studies conducted in other countries (Chapinal et al., 2013; Charfeddine et al., 2018). The highest heritability estimate for DD in Holstein is expected, owing to the more extensive dataset and greater prevalence observed in the Holstein evaluation compared to the Brown Swiss assessment. Additionally, the trait is specifically characterized as a single disease rather than a group trait, enhancing the precision of the evaluation.

Table 1: Heritability estimates and standard errors for claw health traits in the two evaluations

Trait	Holstein	Brown Swiss
Dermatitis digitalis	0.09 (0.003)	0.03 (0.006)
White-line disease	0.05 (0.004)	0.07 (0.009)
Other infectious diseases	0.04 (0.002)	0.04 (0.004)
Other non-infectious diseases	0.06 (0.004)	0.04 (0.007)

The EBV of genotyped sires for the four assessed traits ranged from 53 to 139 in Holstein and from 68 to 123 in Brown Swiss, following standardization. Among Holsteins, the mean reliabilities for DD were 0.84 for proven bulls with a minimum of 20 phenotyped daughters in 10 herds, and 0.43 for selection candidates (Figure 1). In the Brown Swiss evaluation, these averages were 0.67 and 0.24, respectively (Figure 2). The reliability estimates were comparable across all four traits. Generally, the reliabilities observed in Holstein evaluations exceeded those for Brown Swiss, a difference attributable to the greater number of phenotypic records and genotyped animals available for Holstein analyses.

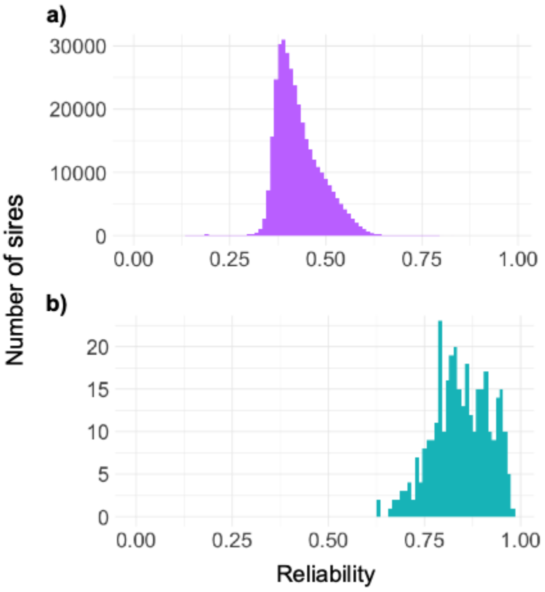

Figure 1. Reliability estimates for dermatitis digitalis (DD) in Holstein for selection candidates (a) and proven bulls (b).

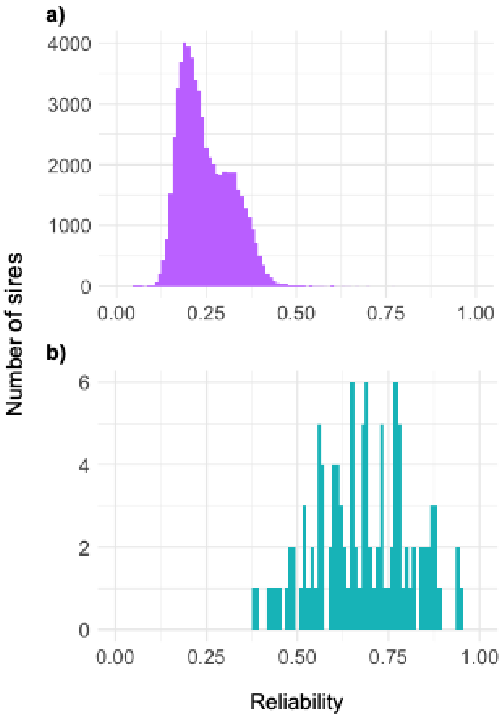

Figure 2. Reliability estimates for dermatitis digitalis (DD) in Brown Swiss for selection candidates (a) and proven bulls (b).

Validation of the EBV through top-bottom comparison revealed differences in daughter prevalence ranging from 14% to 35% across various traits and evaluations. These results are influenced by the average prevalence of the specific disease or disease group under consideration. For example, the top-bottom comparison for DD in Holstein indicated a 32% difference in prevalence between top and bottom sires (Figure 3), while in Brown Swiss cattle, the same trait demonstrated a 14% difference (Figure 4). Both figures illustrate a distinct separation between the two groups, providing strong evidence for the validity of the genetic evaluation for claw health traits. These findings confirm that selecting sires with higher EBV will contribute to genetic improvement in claw health traits.

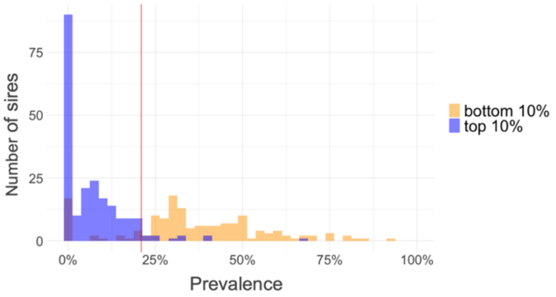

Figure 3. Top-bottom comparison for dermatitis digitalis (DD) in Holstein. The red line indicates the population mean prevalence.

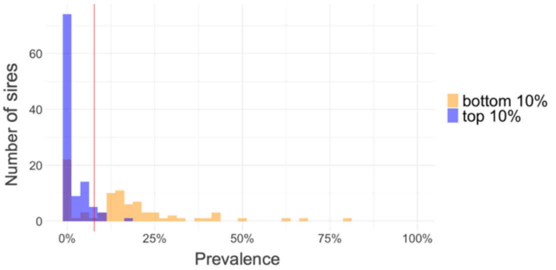

Figure 4. Top-bottom comparison for dermatitis digitalis (DD) in Brown Swiss. The red line indicates the population mean prevalence.

In pursuit of enhanced overall claw health, the EBV of the four traits were consolidated into an index. This EBV index is intended to streamline farmers' selection process during mating decisions. The index weights for these traits were determined specifically for each evaluation and established through consultation with veterinarians involved in the resource project. Weightings were calculated based on both the prevalence of each trait within the respective evaluation and their relative economic significance.

For the Brown Swiss evaluation, all four traits were assigned equal weight in the final claw health index. In contrast, within the Holstein evaluation, DD received a weight of 0.5, WL and INF each received 0.125, and NINF was weighted at 0.25. A modest positive genetic trend is evident for the Brown Swiss breed (Figure 5), with approximately 8 index points gained over the past 20 years – representing three-quarters of a standard deviation. For the Holstein breed, the trend is more pronounced, with a gain of 13 index points or roughly one standard deviation over the same period (Figure 6). Despite the absence of a dedicated selection tool during this time frame, farmers recognized the importance of claw health and made intuitive decisions accordingly. While indirect selection through other traits is theoretically possible, it is considered unlikely. No high genetic correlations with previously selected traits could be identified.

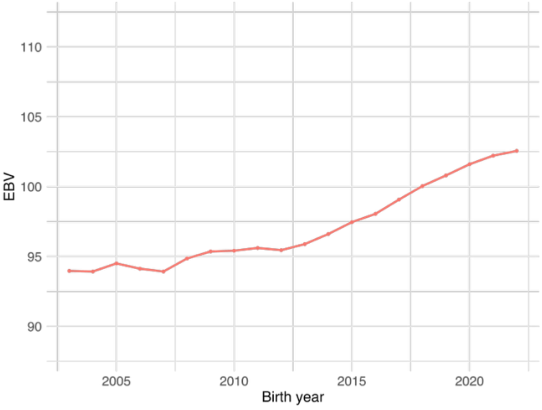

Figure 5. Genetic trend in the claw health index of Brown Swiss for individuals born from 2003 to 2022.

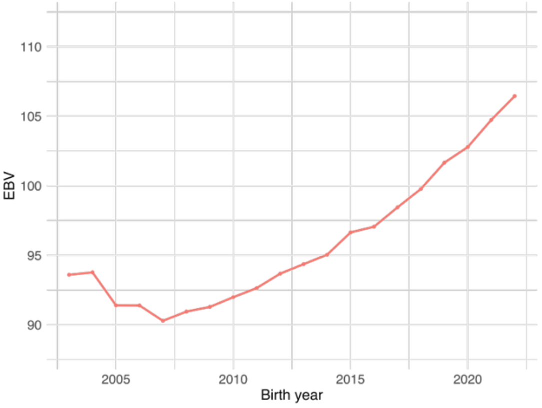

Figure 6. Genetic trend in the claw health index of Holstein for individuals born from 2003 to 2022.

By providing specific EBV for claw health traits, this positive trend can be sustained. Achieving the long-term objectives of the resource project and study is possible through careful consideration of the proposed index and the potential future integration of EBV into the overall selection index for Swiss dairy cattle breeds.

The primary challenge in developing the genetic evaluation was the limited availability of phenotypic data. Despite having five years of recorded information, the database remained constrained due to the small number of participating hoof trimmers, the relatively low population of animals in Switzerland, and their distribution across various breeds. The genetic evaluation was made possible by employing the single-step method and leveraging genomic information. Nevertheless, the abundance of genotypes presented an additional challenge, as most genotyped animals showed weak genetic and genomic connections to those with available phenotypic records. The majority of genotypes were sourced from international bulls through genotype exchange programs.

Conclusions

The first single-step genomic EBV for claw health traits in Switzerland have been predicted. Heritability estimates for four distinct traits ranged from 3% to 9%, based on data from the five major Swiss dairy cattle breeds: Holstein, Swiss Fleckvieh, Simmental, Brown Swiss, and Original Braunvieh. These EBV were used to develop a claw health index, considering evaluation-specific weights to provide Swiss dairy breeders with a straightforward selection tool. Given the observed positive genetic trend, there is potential to further strengthen the genetic improvement of claw health in the future. The next phase involves participating in the development of the new MACE EBV for claw health traits. Following successful validation, we intend to integrate the MACE EBV into our single-step pipeline, leveraging international data to further enhance our genetic evaluation.

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