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Claw Trimming Records and Locomotion Can Improve Selection for Feet and Legs

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Abstract

Since lameness is an increasing problem in modern dairying, efforts have been made to improve the trait genetically. In the Nordic countries, first indices included feet and leg traits from the linear assessment scheme. Recently, other traits requiring more logistic recording challenges have been collected, like veterinary treatments for claw disorders, locomotion in Denmark, and disorders treated by claw trimmers in Sweden. This study presents genetic parameters and different index scenarios for these traits estimated on first lactation Danish Holstein cows. Estimated heritabilities were 0.01 for all subcategories of claw- and leg disorders, 0.09 for locomotion, between 0.13 and 0.27 for linear feet and leg traits, and about 0.06 for claw trimming data (Swedish estimate). The genetic correlation for claw disorders and locomotion was 0.46, while those between leg disorders and hock quality or bone structure were 0.42 and 0.26, respectively. Different selection indices including disorders, claw trimming, locomotion and rear leg rear view were developed. The index including claw trimming and locomotion showed the highest accuracy, especially for small daughter groups. Generally, claw trimming data achieved a higher accuracy than claw disorder data, and locomotion is more advantageous than rear leg rear view. The collection of claw trimming data and locomotion and their inclusion in a feet & leg index are recommended.

Introduction

Lameness has been on the rise in modern dairy cattle production over the last two decades. Scientists have taken up the topic and conducted research on improving the trait genetically. In the Nordic countries, the first selection indices for feet and legs included feet and leg traits which are part of the linear assessment scheme. Over the last decade, other traits requiring more logistic recording challenges and involving other people than field inspectors, have been collected on a large scale, like veterinary treatments for claw and leg disorders in the Nordic countries, locomotion in Denmark, and most recently, claw disorders treated by claw trimmers in Sweden, the latter two on research basis only so far. In Denmark, a sub-index for “Other diseases” which contains, among others, breeding values on feet and leg health based on veterinary records is included in the total merit index. As information on different and maybe more appropriate traits are becoming available, the question arises whether a new index based on these new traits would not be more suitable for selecting the best sires.

The aim of this study was to present genetic parameters and accuracy of claw health for different selection indices.

Material and Methods

The data set consisted of 429,877 Danish Holstein Friesian in 1st lactation, data recorded between 2004 and 2007. The data set contained three groups of data: health data recorded by veterinarians (422,095 records), linear type traits and locomotion collected by field inspectors (56,438 records). Claw records were collected by claw trimmers in Sweden and were analysed there. Assuming the resulting genetic parameters would also fit the Danish Holstein population, they were used in the various index calculations.

The veterinary disorders were divided into three sub-categories: Claw Disorders consisting of heel horn erosion, interdigital dermatitis, interdigital phlegmon, interdigital hyperplasia, laminitis, and sole ulcer; Leg Disorders including hock infection, swollen hocks, and bruising; and finally All Disorders comprising the previous two groups plus a category with all undefined feet and leg disorders. Claw disorders constituted 56 % of all feet and leg disorders, while leg disorders represented 22 %. In order to ascertain that the herds and veterinarians participated fully in the health recording scheme, the herds had to meet the standard of at least 0.3 registered treatments of any disease per calving, otherwise the herd was excluded from the data set. Repeated recordings of claw or leg disorders were omitted, i.e. only the first record was used for analysis. The disorders were defined as binary traits, recorded as 0 (diseased) or 1 (healthy).

Locomotion was scored by six trained field-officers in combination with linear type traits. All traits were recorded on a scale from 1 to 9. The feet and leg traits rear leg side view (RLSV), rear leg rear view (RLRV), hock quality (Hocks), bone structure (Bones), and foot angle (FA) were used in this study. Only those records, where both linear type traits and Locomotion were available, were kept in the data set. Table 1 presents means and standard deviations of all traits.

Table 1. Mean and standard deviation of health traits and linear traits collected in Denmark

Trait	Mean	Std. Dev.
Claw disorders	0.035	0.18
Leg disorders	0.014	0.12
All disorders	0.063	0.24
RLSV	5.23	0.79
RLRV	6.06	1.02
Hocks	5.90	0.15
Bones	6.79	0.79
FA	5.25	0.85
Locomotion	5.31	1.82

Estimation of genetic parameters for claw health, conformation traits and locomotion was carried out by using the AI-REML procedure (Jensen et al., 1997). The following bivariate sire model was applied:

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_2 \end{bmatrix} \begin{bmatrix} \mathbf{s}_1 \\ \mathbf{s}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix}$$

where $\mathbf{y}_1$ stands for the observations of the health trait of interest and $\mathbf{y}_2$ stands for the observations of one of the conformation traits or locomotion.

The random effect of sire is expressed by $\begin{bmatrix} \mathbf{s}_1 \\ \mathbf{s}_2 \end{bmatrix} \sim \mathrm{N}(\mathbf{0}, \mathbf{G}_0 \otimes \mathbf{A})$ where: $\mathbf{G}_0 = \begin{bmatrix} \boldsymbol{\sigma}^2_{\mathbf{s1}} & \boldsymbol{\sigma}_{\mathbf{s12}} \\ \boldsymbol{\sigma}_{\mathbf{s21}} & \boldsymbol{\sigma}^2_{\mathbf{s2}} \end{bmatrix}$, and $\mathbf{A}$ is the additive genetic relationship matrix among sires. Relationships were traced five generations back.

The random residual is described by $\begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix} \sim \mathrm{N}(\mathbf{0}, \mathbf{R}_0 \otimes \mathbf{I})$ where $\mathbf{R}_0 = \begin{bmatrix} \boldsymbol{\sigma}^2_{\mathbf{e1}} & \boldsymbol{\sigma}_{\mathbf{e12}} \\ \boldsymbol{\sigma}_{\mathbf{e21}} & \boldsymbol{\sigma}^2_{\mathbf{e2}} \end{bmatrix}$, and $\mathbf{I}$ is the identity matrix of appropriate size.

$\mathbf{X}_1$ and $\mathbf{X}_2$ are design matrices associating the fixed effects $\mathbf{b}_1$ and $\mathbf{b}_2$ to $\mathbf{y}_1$ and $\mathbf{y}_2$, respectively. The design matrices $\mathbf{Z}_1$ and $\mathbf{Z}_2$ associate sires to observations.

The fixed effects ($\mathbf{b}_1$) for the health trait of interest were herd-year, season (4 classes), age at calving in months (20-35 months), calving year-6 month period.
The fixed effects for the conformation traits and locomotion ($\mathbf{b}_2$) comprised herd-year, month of calving (12 classes), age of calving in months (20-35 months of age), stage of lactation in months (1-14 months in lactation), classifier-year-month, and year-region. Denmark was divided into ten regions.

The genetic parameters for traits collected by claw trimmers were taken from Sweden. The following four claw diseases were recorded and analysed separately (frequency in parentheses): dermatitis (5-10 %), heel horn erosion (15-20 %), sole haemorrhage (25-30 %), and sole ulcer (5 %) (Naeslund, 2008). For Holstein, the heritabilities varied between 0.035 for sole ulcer and 0.079 for dermatitis. In our analysis, we assumed a rough estimate for heritability of 0.06 for any claw disease.

The different index scenarios were calculated by using SIP (Selection Index Program). The desired gain was totally placed on claw health either recorded by veterinarians or claw trimmers, with linear type traits or locomotion acting as correlated informative traits. Different combinations of traits and an increasing number of daughters per sire (10, 25, 50, 75, 200) were tested.

Results

Heritabilities for all disorders and type traits including locomotion are shown in Table 2. The heritabilities for health traits were 0.01 for all subcategories. The heritabilities for the linear type traits varied between 0.09 for Locomotion and 0.27 for bone structure.
Furthermore, Table 2 represents the genetic correlations between the health traits and linear type traits. Both Claw Disorders and Leg Disorders were highly correlated with the traits All Disorders. Moreover, Claw Disorders were significantly associated with Locomotion and RLRV, while Leg Disorders showed a significant correlation with hock quality and bone structure. All Disorders were significantly correlated with Locomotion, hock quality and bone structure. Neither rear leg side view nor foot angle showed a significant correlation to any of the disease traits. Phenotypic

correlations (not shown here) were generally small, ranging between 0.01 and 0.09 and statistically not significant.

Table 2. Heritabilities and genetic correlations for different claw diseases and linear type traits

	Claw	Leg dis	All dis.	Loc	RLSV	RLRV	Hocks	Bones	FA
h^2	0.01	0.01	0.01	0.09	0.19	0.14	0.22	0.27	0.13
Claw d.		0.35*	0.92*	0.46*	-0.07	0.21*	0.12	0.14	0.02
Leg dis			0.71*	0.09	-0.14	-0.07	0.42*	0.26*	-0.17
All dis.				0.31*	-0.12	-0.12	0.30*	0.23*	-0.04

* significantly different from zero

Table 3 presents the key parameters for running the Selection Index Program (Wagenaar et al., 1995). The correlation between Claw Trimmer data in Sweden and Locomotion in Denmark was calculated by establishing the correlation between the breeding values of sires of sires used in both countries, adjusted for reliability. Claw trimming data showed a higher correlation to Locomotion than claw health data.

Table 3. Parameters applied in SIP. Heritability (h^2) (diagonal), genetic correlations (r_A) (above diagonal), phenotypic correlations (r_P) (below diagonal), and phenotypic standard deviations.

	Claw health	Locomotion	RLRV	Claw trim	σ_P
Claw health	**0.01**	0.46	0.21		0.24
Locomotion	0.09	**0.09**	0.73	0.79	1.73
RLRV	0.02	0.02	**0.14**		0.96
Claw trim		0.09		**0.06**	0.18

Six different indices were constructed (Table 4). In all indices, all economic emphasis was placed on claw health either based on veterinary records (Index 1 to Index 4) or based on claw trimming records (Index 5 and 6). The linear type traits with the highest genetic correlation to claw health, Locomotion and RLRV were added as correlated informative traits. Not surprisingly, the accuracy of any particular index increased with increasing number of daughters per bull. The index only based on veterinary records had the lowest accuracy, which was increased by roughly one third by adding Locomotion. Adding only RLRV as an informative trait had a lower effect, while Locomotion and RLRV together yielded nearly the same results as only Locomotion. The index based on claw trimming records produced higher accuracies than any of the previous scenarios. Especially for small groups of daughters, this index was even more accurate when including locomotion.

Table 4. Accuracy for different indices for different daughter group sizes

No. of daughters	**Index 1**	**Index 2**	**Index 3**	**Index 4**	**Index 5**	**Index 6**
	Claw health	Claw health Locomotion	Claw health RLRV	Claw health Locomotion RLRV	Claw trim.	Claw trim. Locomotion
10	0.16	0.24	0.19	0.25	0.36	0.46
25	0.24	0.35	0.28	0.35	0.53	0.62
50	0.33	0.44	0.36	0.44	0.66	0.74
75	0.40	0.49	0.42	0.49	0.73	0.79
200	0.58	0.63	0.59	0.64	0.87	0.89

Discussion

The genetic parameters for the health traits and type traits were in line with previous estimates on a similar data material (Aamand et al., 2008). Estimates for health traits were low, due to the nature of the trait. Data were recorded by veterinarians, i.e. only the worst cases where the farmer thought it inevitable to call the veterinarian for help, were recorded, thereby creating low frequencies for health records which resulted in low heritabilities. Locomotion had the lowest heritability of the other feet and leg traits, which is also in agreement with previous analyses (Boelling et al., 2007). Estimates of genetic correlations between locomotion or feet and leg traits and claw health were moderate, indicating a favourable relationship between the different traits. The moderate genetic correlations between claw disorders and rear leg rear view (0.21) and claw disorders and locomotion (0.46) suggest that locomotion and RLRV are applicable indicator traits for improvement of claw disorders. Locomotion and RLRV show a high correlation of 0.73 which lets the question arise whether these two traits are in fact the same. The index calculations showed that locomotion yielded more precise results than RLRV and seems to be more appropriate in predicting good claw health.

In this study, recording of claw health was performed by veterinarians. The drawback of this approach is that only the severe cases of lameness are recorded. Recordings of claw characteristics by claw trimmers will presumably extend the data material, and make future estimation of genetic parameters more reliable. Results indicated that indirect selection for improved claw health using locomotion and conformation traits is possible. One approach might be to incorporate Locomotion and conformation traits in a selection index. By doing so, conformation and locomotion can account for some of the genetic variation associated with claw health.

The parameters for claw trimming data were based on Swedish results but are assumed to be comparable in Denmark. The frequency for single diseases was up to 30 % and thereby a good deal higher than those computed from veterinary records. The advantage of claw trimming data is that usually all cows in a herd are trimmed and thus all cases, also the most sub-clinical ones, are found and recorded. This higher frequency results in a higher heritability. Claw trimming data are more precise and represent the state of claw health in a herd better than veterinary records where only the most severe cases are documented.

Locomotion has also the ability to describe sub-clinical lameness. A low locomotion score (score 1 to 4) describes bad locomotion, i.e. ab- and adduction of the rear legs, short steps and an uneven gait. In young animals like cows in their first lactation, bad locomotion is usually due to some claw health problems, not yet severe enough to make the animal completely lame, but critical enough to impair her walk. Therefore, both locomotion and claw trimming data are much more precise in describing the state of claw health of an animal than veterinary records or linear type traits. This is reflected in the higher accuracies of the different index scenarios tested in this study.

Conclusion

Currently, indices for claw health or absence of feet and leg problems are based on linear type traits and veterinary records which describe claw health only to a certain degree. Recently, better traits have become available, although only on a research basis so far. Preliminary analyses suggest that these traits are more apt to describe claw health and yield indices with a higher accuracy, thus giving the possibility to select sires more exactly. Sweden has started to collect claw trimming data a few years ago, Denmark plans to start collecting claw trimming data from late autumn onwards. The results of this study indicate that indices based on both claw trimming data and locomotion yield better results. Therefore, the collection of these two groups of data on an official basis is highly recommended. When these data are available, development of a new index for claw and leg health is a logical consequence and highly encouraged.

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