INTERBULL BULLETIN NO. 43. Stavanger, Norway, August 26-28, 2011

Genetic Evaluation of Claw Health in Denmark, Finland and Sweden

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Abstract

A Claw Health Index (CHI) was developed and included in the Nordic Total Merit Index (NTM). The index combined information from a multiple trait evaluation that contained 7 claw trimming traits in each of the first 3 lactations. Genetic parameters for the 21 traits were estimated for Holstein and Red Dairy Cattle (RDC). Heritabilities ranged from 0.01 to 0.07 for both breeds. Correlations between CHI and health indices as well as between CHI and NTM were all favorable.

Introduction

Claw diseases are a problem in dairy production today both economically and from animal welfare point of view (Buch et al 2011). Further the gradual shift from tie stalls to loose house barns in the Nordic countries leads to an increase of infection related claw diseases i. e. dermatitis, heel horn erosion and skin proliferation. The first evaluation of claw trimmers' reports was done in Sweden in 2006 (Eriksson 2006). It was based on claw trimming reports on 4 claw trimming traits from first lactation cows. This study presents the development of a genetic evaluation of 7 claw trimming traits in the first 3 lactations, which is now routinely run in the joint genetic evaluation for Denmark, Finland and Sweden.

Material and Methods

Data collection started 2003 in Sweden, 2004 in Finland, and 2010 in Denmark and data for the most recent evaluation (August 2011) was extracted from the data bases in June 2011. Data is recorded by professional claw trimmers, during their routine trimming visits in the herds. In general, trimmings are made twice a year, so that a cow can have several trimming records in each lactation. Table 1gives the definitions, abbreviations and coding of the traits. The traits can be grouped into 3 groups. The first consists of the infection related traits (DE, HH and SP), the second of feed related traits (SH, SU and WLS), the third of malformation traits (CSC).

Genetic evaluation model

All traits were pre-corrected for heterogeneous variance due to year of trimming, breed and country. The evaluation was done within breed, HOL, RDC and Jersey (JER). The model for estimation of breeding values was a multi-trait, multi-lactation model with repeated observations within lactations. The model contained the following effects:

Effect	Type
Herd*period (period=five years)	Fixed
Calving age*country	Fixed
Year*month of calving*country	Fixed
Lactation stage(weeks)*country	Fixed
Herd*year*season (spring and autumn)	Random
Permanent environment	Random
Animal	Random
Residual	Random

Maximum three trimming records were allowed per lactation. A trimming was used when it was made within 430 days after calving and at least 12 weeks after preceding trimming within lactation. Uninformative records were removed from data. A record was considered to be uninformative when its herd-year-season contained no disease code even though the probability for a specific code, as judged by the frequency and number of observations in the herd-year-season, exceeded 95%. The number of resulting observations in total over all three lactations after deletion of uninformative record is given in table 1. In Table 2 the total number of trimmed and evaluated cows and the frequency of each trait are given for year 2010. The latest years roughly 40, 10, and 50 percent of the cows in Denmark, Finland and Sweden were trimmed and their data used in the evaluation.

Table 1. Trait definitions and the number of trimming records in the evaluation

Abbreviation	**Disorders**	**Coding**	**Holstein**	**RDC**	**Jersey**
DE	Dermatitis: Interdigital (1), digital (2)	(0-1-2)	550533	350407	23404
HH	Heel Horn Erosion	(0-1-2)	473012	358026	12998
SP	Skin Proliferation: (interdigital hyperplasia, wart)	(0-1)	561041	337844	25189
SH	Sole Hemorrhage	(0-1-2)	594433	412268	24035
SU	Sole Ulcer	(0-1-2)	600078	403521	28534
CSC	Cork screw claws	(0-1)	537909	371915	28575
WLS	White line separation, double sole	(0-1)	591868	396490	27588

Table 2. Number of trimmed and evaluated cows totally and percent disorder records in each lactation in year 2010

Number	**Holstein**			**RDC**			**Jersey**		
of cows	296904			179240			22057		
Lactation	1	2	3	1	2	3	1	2	3
DE	19	20	19	11	11	11	14	12	10
HH	18	23	28	20	24	28	7	8	14
SP	3	6	8	2	5	6	1	1	1
SH	24	21	26	24	17	20	8	6	8
SU	5	6	9	4	3	4	5	5	7
CSC	1	2	2	3	4	4	0	1	1
WLS	5	7	10	4	4	7	3	4	7

Estimation of genetic parameters

Genetic parameters were estimated using restricted maximum likelihood (Madsen and Jensen, 2000) for Holstein and RDC on the Swedish data from 2006 to 2010. The analyses were made, within breeds, on data from around 160000 Holstein and 110000 Swedish Red cows (SR). The model used was a sire model but with all other effects as in the evaluation model described above. Several multiple trait models were run, each containing 2 claw traits and 3 lactations, thus in total 6 traits. The analysis was based on cows with first lactation present in data.

Results and Discussion

Genetic parameters

Genetic parameters averaged over lactations are presented in tables 3 and 4 for infection related and feed related traits and CSC respectively. Genetic correlations and heritabilities were similar in all three lactations with a few notable exceptions. Following frequency increase, the heritability for skin proliferation increased with lactation number, starting with low heritabilities in lactation 1, 0.02 for Holstein and 0.01for RDC, to 0.07 and 0.05 in lactation 3. The genetic correlations between infection related traits are rather high. Also for feed related traits and CSC correlations are high. Genetic correlations between the same traits in different lactations are high. For DE, HH, SP, SH and SU correlations ranged from 0.79 to 0.99. CSC and WLS correlations were lower, from 0.66 to 0.99.
The correlations between infection related and feed related traits and CSC were varying, ranging from -0.13 to 0.40 with a mean of 0.13. The genetic parameters are presented in detail in Johansson, 2011.
Repeatability increased with lactation, 0.15, 0.21 and 0.24 for first second and third lactation respectively. Skin proliferation had the highest repeatability, 0.35 on average.

Table 3. Genetic parameters for infection related traits as an average over lactations. Heritabilities on, genetic correlations below and permanent environmental effects above each sub diagonal.

	DE	HH	SP
		Holstein	
DE	**0.04**	0.38	0.23
HH	0.58	**0.04**	0.18
SP	0.67	0.45	**0.02**
		RDC	
DE	**0.04**	0.35	0.24
HH	0.77	**0.07**	0.20
SP	0.66	0.57	**0.03**

Table 4. Genetic parameters for feed related traits and CSC as an average over lactations. Heritabilities on, genetic correlations below and permanent environmental correlations above each sub diagonal.

	SH	SU	CSC	WLS
		Holstein		
SH	**0.04**	0.39	0.27	0.39
SU	0.74	**0.04**	0.10	0.22
CSC	0.49	0.50	**0.02**	0.15
WLS	0.73	0.78	0.28	**0.01**
		RDC		
SH	**0.05**	0.51	0.38	0.40
SU	0.68	**0.02**	0.12	0.31
CSC	0.37	0.27	**0.03**	0.10
WLS	0.62	0.74	0.08	**0.01**

Genetic evaluation

Relative breeding values including all lactations was computed for each trait by weighing absolute breeding values from each lactation using 0.5, 0.3 and 0.2 for lactations 1, 2 and 3 respectively.
Economic weights for claw traits were calculated by Pedersen et al, 2011. Using those a Claw Health Index (CHI) was developed and included into NTM in

August 2011. In the claw health index, sole ulcer is dominating because of the high economic costs caused by this disorder. The economic weights used to weigh claw traits into a claw health index, the same for Holstein and RDC, are presented in their absolute form in table 6. CHI is then weighted into NTM using 0.08 for Holstein and 0,05 for RDC and Jersey.

Table 5 gives the number of daughters per AI-sire, the average reliability and the average index level for each country. The reliability values are rather high despite of the low numbers of daughters per sire, boosted by repeated observations especially in first lactation where the repeatabilities were low. Also the favourable genetic correlations within the feed and infection trait groups contribute to the high reliabilities. Official breeding values are published when reliability is higher than 40%. This level is reached by all progeny tested Swedish and Danish bulls. In Finland a little more than 80% of the progeny bulls reach this level.

In table 6 correlations from the August 2011evaluation of NTM with claw health index and claw traits are shown. In both breeds Sole Haemorrhage and Sole Ulcer were positively correlated to NTM. CHI was also positively correlated to NTM. This was also shown in Eriksson, (2011) where there were low favourable correlations between CHI and the NTM sub traits: Selection for claw health was favourable for all health traits (longevity, other diseases, udder health and feet&legs). Thus it will be relatively easy to improve the claw health.

Table 5. Number of sires (NS), number of daughters per AI-sire (NDPS), average reliability (R2) and average level of claw health index (CHI) for young sires (born 2004-2006)

	Denmark			**Finland**		**Sweden**		
	Holstein	RDC	Jersey	Holstein	RDC	Holstein	RDC	Jersey
NS	1525	144	233	172	368	277	248	13
NDPS	22	19	22	13	11	44	59	7
R2	62	54	56	52	48	73	78	65
CHI	99	98	100	98	102	99	103	99

Table 6. EBV-correlations between NTM and claw health index (CHI) and claw traits (August 2011)

	Economic weights	**Correlations**	
		RDC	Holstein
DE	0.22	-0.06	0.20
HH	0.22	-0.05	0.19
SP	0.39	-0.11	0.07
SH	0.13	0.24	0.18
SU	1.00	0.15	0.28
CSC	0.13	0.03	0.03
WLS	0.15	0.14	0.23
CHI		0.09	0.30

Conclusions

Claw health information is included into NTM. Most progeny tested bulls will have an official CHI in first lactation. The EBV-correlations between CHI and NTM as well as between Claw Health Index and health traits are favourable

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