Lameness Evaluations for the UK Dairy Industry

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Abstract

Lameness has been recorded by Milk Recording Organisations (MRO) in the UK for a number of years, either as a feet problem event or lameness event. A pilot study based on data from one UK MRO was carried out to estimate genetic parameters. The data set consisted of 425 000 records from 46 000 Holstein cows, of which 21 000 records were flagged as having a lameness event. From this data a heritability of 0.04 for lameness was estimated using an animal repeatability model, treating lameness as a binary trait. Using the genetic parameters estimated from this restricted data set, preliminary Estimated Breeding Values (EBVs) for 55 000 bulls were produced ranging from -0.64 to 0.55 from a data set consisting of 946 000 animals contributing 8 700 000 records, of which 322 000 records recorded a lameness event.

Key words: Lameness, dairy, genetic evaluations

Introduction

Lame cows produce between 300 and 600 fewer litres of milk per lactation (Coulon *et al.,* 1996; Amory *et al.,* 2008), take 20 to 40 days longer to get back in calf (Argaez-Rodriquez *et al.,* 1997; Hernandez *et al.,* 2001), and are more likely to be culled (Machado *et al.,* 2010). This makes lameness one of the most costly challenges faced by British dairy farmers today as well as a major welfare concern of the industry. Numerous studies taking place over a number of years from 1989 to 2014 have found a range of average prevalence of lameness in the UK dairy herd from 18% to 37% (Rutherford *et al.,* 2009; Barker *et al.,* 2010).

In 2011, AHDB Dairy launched the Healthy Feet Programme to assist farmers in reducing lameness in their herd. A recent study on 44 dairy farms showed that there was a reduction of lameness events by one fifth after one year of implementing the Healthy Feet Programme. Although these industry measures are reducing incidence levels in the UK dairy herd, they are only addressing the cause at the management level.

The UK has improved health traits in the dairy herd through breeding since 1999 with the inclusion of lifespan, SCC and daughter fertility in the national breeding index. Selection on these low heritability traits has seen improvement in the national herd with a reduction in SCC and improvements in fertility traits and productive lifespan. Previous studies have found lameness to be a low heritability trait, ranging from 0.10 to 0.19 (Boettcher *et al.,* 1998; Kadarmideen *et al.,* 2000). Therefore the development of a breeding index for lameness will further assist the improvement that has already occurred as a result of better management practices. This paper will outline the work undertaken thus far to develop such a breeding index for the UK dairy industry.

Materials and Methods

Data Sources

Farmer recorded lameness events were available through UK Milk Recording Organisations (MROs); National Milk Records (NMR) and Cattle Information Services (CIS). These events indicate if the cow had a foot problem or was lame at milking. Conformation data was also available from the Holstein UK herdbook classification records. The conformation records used in the analysis included rear leg side view, foot angle, body condition score, locomotion, overall feet and leg score and bone quality.

Methods

Genetic parameter estimates

All Holstein cows with lactation 1 to 5 data were selected if they had experienced a lameness event, along with their contemporaries. This gave ~169 000 animals which had experienced at least one lameness event, ~325 000 lameness events, ~818 000 contemporaries contributed ~5.9 million records. For parameter estimation, the following restriction criteria were applied;

1. Dropped records with unknown sire or dam
2. Sire had at least 10 daughters in data
3. Oldest 500 daughters were retained
4. Dropped animals with missing heifer conformation classifications
5. Retained animals with first and consecutive lactations
6. Dropped contemporary groups without a lameness event
7. Dropped contemporary groups containing less than 5 records

This left a data set containing ~425 000 records, of which ~21 000 were lameness events. These records related to ~46 000 animals of which ~11 000 had experienced at least one lameness event. Table 1 outlines the mean, median, range and standard deviation of events per animal in the data set, along with, the percent of animals experiencing at least one lameness event.

Table 1. Descriptive statistics of final genetic parameter data set.

Mean no events	Median no events	Range	St Dev	% animals >0 events
0.46	0	0 – 24	1.15	24.2

EBV estimates

The same raw data set had the following criteria restrictions applied;

1. Dropped records with unknown sire
2. Dropped contemporary groups without a lameness event

3. Dropped contemporary groups containing less than 5 records

These restrictions resulted in a data set containing ~946 000 animals, of which ~167 000 had at least one lameness event. In total the data set contained ~8.7 million records and ~322 000 lame events. The mean median, range and standard deviation of lameness events in the data set are given in Table 2, along with the percent of animals in the data set observed as lame on at least one occasion.

Table 2. Descriptive statistics of final EBV estimation data set.

Mean no events	Median no events	Range	St Dev	% animals >0 events
0.34	0	0 – 25	1.01	17.6

Model terms

An animal repeatability model was fitted for both the genetic parameter and EBV estimates. Lameness was treated as a binary trait with 0 indicating that the animal was not lame and 1 indicating that she was lame at the time of milk recording. The full model fitted was as follows;

$$y = Xb + Za + Zp + e$$

where y is a vector of lameness observations coded as 0 for not lame and 1 for lame, b is a vector of fixed effects consisting of the herd-test-month of observation, season of calving, days in milk, lactation number and age at calving in months, a is a vector of random animal effects with an assumed distribution of $N(0,\sigma^2_a A)$, p is a vector of random permanent environmental effects with an assumed distribution of $N(0,\sigma^2_p A)$, e is a vector of residual effects with an assumed distribution of $N(0,\sigma^2_e I)$, and X and Z are incidence matrices.

Results

Genetic parameter estimates

A heritability of 0.04 with 0.007 standard error was found. This result was comparable to a heritability of 0.08 found in a pilot study when

a sire model was fitted using data from one MRO.

Figure 1 illustrates the prevalence of lameness found in the data set used for the genetic parameter estimates.
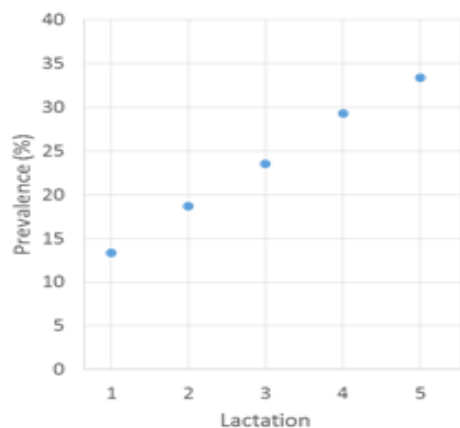

Figure 1. Prevalence of lameness by lactation in genetic parameter estimation data set.

EBV estimates

EBVs were estimated for ~55 000 sires, ranging from -0.64 to 0.55. Figure 2A illustrates the distribution, with a median of 0.001 and standard deviation 0.06.

Reliabilities ranged from 0 – 0.999 with median 0.35 and standard deviation 0.21. Figure 2B illustrates the distribution of reliabilities.

Phenotypic correlations

Phenotypic correlations between lameness events in lactation 1 to 5 and the conformation traits were calculated (Table 3) as well as correlations between lactation 1 to 5 lameness events (Table 4).
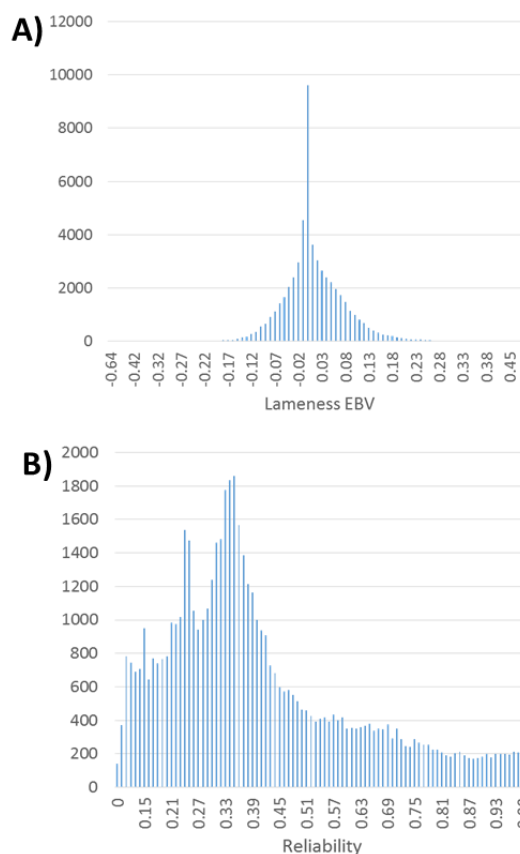

Figure 2 A) Distribution of lameness EBVs for ~55 000 sires, and B) Distribution of lameness reliabilities for ~55 000 sires.

Table 3. Phenotypic correlations between lameness events within lactation and heifer conformation classifications.

	LSV	FA	BCS	Loco	OLS	BQ
L1	0.03	-0.02	0.01	-0.11	-0.10	-0.04
L2	0.01	0.00	-0.02	-0.02	-0.02	-0.02
L3	-0.01	0.03	-0.04	-0.04	-0.05	0.00
L4	0.00	0.02	0.01	0.00	0.00	-0.01
L5	-0.02	0.00	-0.01	-0.01	0.01	-0.01

LSV – rear leg side view, FA – foot angle, BCS – body condition score, Loco – locomotion, OLS – overall leg score, BQ – bone quality, L1-L5 – lameness events in lactation 1-5.

Table 4. Phenotypic correlations of lameness across lactations 1 to 5.

	Lact 1	Lact 2	Lact 3	Lact 4	Lact 5
Lact 1		0.12	0.11	0.09	0.05
Lact 2			0.19	0.19	0.15
Lact 3				0.25	0.16
Lact 4					0.26

Discussion

The trend shown in Figure 1 for prevalence of lameness across lactations in our data set closely reflects the trend shown in the UK national herd. This indicates that the data set used for parameter estimates is representative of the national population.

The EBVs expressed in Figure 2 relate to the percent of daughters which will experience a lameness event in their lifetime. For example, using a bull with -0.1 lameness EBV it is expected that 10% fewer daughters of this bull will experience a lameness event in their lifetime compared to a 0 lameness EBV bull.

A minimum restriction on reliability is proposed before publishing a lameness EBV. In the case of the preliminary lameness EBVs, around 47 000 of the 55 000 sires with a lameness EBV had a reliability greater than 20%, which is recommended as the publication cut-off.

Conclusions and future work

We have shown that lameness as a binary trait recorded by MROs is a lowly heritable trait, and we believe that the development of national genetic evaluations for lameness may be possible given the volume of data now available from UK MROs.

Work is ongoing to estimate genetic correlation between lameness events, with the aim to improve the accuracy of lameness EBVs. In addition, Digital Dermatitis has been recorded as part of the Holstein UK classification system and is intended to be reviewed and included in further analyses.

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