Genetic Parameters of Udder Health Traits in Holstein Friesian UK Dairy Cattle

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Introduction

Mastitis is one of the most recurrent and expensive diseases affecting dairy cattle in the UK, and has an impact on production, welfare, and milk quality. Clinical mastitis (MAST) and somatic cell count (SCC) are direct and indirect measures of udder health. The udder health sub-index in the UK national profit index (£PLI) utilises test day records for SCC as well as the udder composite trait, but does not, as yet, include a direct measure of mastitis. Efforts to reduce mastitis incidence by genetic improvement are thought to be more effective if clinical mastitis were routinely recorded and evaluated, and selected for directly (Banos et al. (2006)). A lack of a national recording system for mastitis in the UK has impeded its use in genetic improvement of udder health. At present the recording of mastitis events is done voluntarily by farmers as part of their milk recording and herd management, and mastitis recording has increased in recent years with the uptake of on-farm software. The higher level of recording has brought about a rapid build up of mastitis event data that could be a valuable resource, such as being used in genetic evaluations (Zwald et al. (2006); Vallimont et al. (2009)).

The objectives of this study were to obtain variance components, correlations and heritability estimates for mastitis, SCC, and a range of type traits.

Material and methods

The recording of mastitis (MAST) events was performed by farmers on a voluntary basis as part of routine milk recording and the data was made available by milk recording organisations in the UK. In this study MAST was defined as a binary trait coded as either present (1) or absent (0) during the period 0 to 305 days after calving. Somatic cell count (SCC) was analysed as the lactation mean of the natural log of test-day somatic cell count. Ten type traits (see Table 1 for list and abbreviations) were analysed and all, with the exception of udder composite, were scored on a scale from 1 to 9, where 1 and 9 represent the extremes. Udder composite was scored on a scale from 65 to 95, which represents poor to excellent, respectively. Each type trait was measured by a classifier at inspection and records were pre-adjusted for classifier.

First lactation data were used from Holstein Friesian dairy cattle of the UK. Univariate and bivariate analyses were carried out in separately edited datasets for parameter estimation of MAST and type traits. A datafile was created from mastitis data with less strict edits to obtain a higher number of animals with both MAST, LSCC and type records for multivariate analyses. Edits on mastitis data included sires with at least 25 daughters, herd-year-season groups with at least five animals, of which had at least one mastitis case. To this SCC and type data were joined and in total there were 131,582, 122,502, and 24,388 animals, respectively for MAST, SCC, and type traits for cows in their first lactation. The incidence of mastitis in the dataset was 12.3%.

Statistical analyses. (Co)variance components and genetic parameters were estimated using a sire model in ASREML (Gilmour et al. (2006)). The fixed effects for MAST and SCC were month of calving, herd-year-season, and age in months at calving as a covariate. Each of the type traits was analysed with herd-year-visit and month of calving as fixed effects, and with age at inspection and stage of lactation (both linear and quadratic) as covariates. Multivariate analyses were carried out to estimate correlations between MAST, SCC, and each type trait, using variance components obtained from corresponding univariate analyses of each trait as starting values. Heritability estimates of MAST, SCC, and type traits were calculated as four times the sire variance component divided by the phenotypic variance (sire plus residual variance).

Results and discussion

Table 1: Heritability estimates and genetic correlations of MAST, SCC and type traits

	h^2	MAST	SCC
MAST	0.05±0.01(1)		
MAST	0.02±0.00(3)		
LSCC	0.18±0.02(1)	**0.57**±0.10	
LSCC	0.17±0.01(3)	**0.74**±0.05	
ANG	0.31±0.01(2)	**0.25**±0.10	0.15±0.08
FUA	0.24±0.01(2)	**-0.44**±0.09	**-0.33**±0.07
US	0.17±0.01(2)	-0.17±0.11	-0.15±0.09
UD	0.31±0.01(2)	**-0.50**±0.08	**-0.35**±0.06
TPR	0.27±0.01(2)	-0.19±0.10	-0.11±0.08
TPS	0.23±0.01(2)	**0.22**±0.11	**0.22**±0.08
TL	0.30±0.01(2)	0.06±0.11	0.08±0.07
RUH	0.23±0.01(2)	-0.02±0.11	0.03±0.09
LOC	0.11±0.01(2)	**-0.29**±0.13	-0.19±0.10
COMP	0.27±0.01(2)	**-0.28**±0.10	**-0.15**±0.07

$^{\alpha}$Genetic correlations in bold were significant ($p<0.05$)

ANG = angularity; FUA = fore udder attachment; US = udder support; UD = udder depth; TPR = teat placement rear; TPS = teat placement side; TL = teat length; RUH = rear udder height; LOC = locomotion; COMP = udder composite.

(1) and (2) separate datasets used for parameter estimation of MAST and type traits, respectively; (3) combined dataset used for multivariate analysis of MAST, SCC and type traits.

Heritability estimates and genetic correlations between MAST, SCC, and type traits are shown in Table 1. Mastitis had a low heritability, and differed from 0.02 to 0.05 between the two datasets for univariate, and multivariate analysis. The estimate of 0.05 is at the higher end of the range generally reported in literature using a linear model (Heringstad et al. (2000)). SCC was moderately heritable, and was similar in both datasets (0.17 to 0.18). The heritability estimate for SCC is also at the higher end of the range reported in literature (Heringstad et al. (2000)). For all type traits estimates of direct heritability were moderately to highly heritable. The heritability of COMP, a combination of traits relating to udder and teat position was 0.27. Although LOC is not an udder conformation trait, it was investigated since moderate to high genetic correlations have been reported with udder conformation traits (Boelling and Pollott (1998); Van Dorp et al. (2004)). LOC had the lowest heritability of the type traits (0.11) but the same result was also obtained by Onyiro and Brotherstone (2008) using an animal model. Literatures estimates vary widely for type traits but the heritability estimates obtained here were within the reported ranges.

Genetic correlations between MAST and SCC were high with an estimate of 0.74 obtained from the dataset used for multivariate analysis. A correlation less than one means that genetically they are not the same trait, however the high value supports the use of SCC, as a good predictor of udder health, in current evaluations. Genetic correlations between MAST and SCC with each type trait followed the same +/- direction, with the exception of RUH that was lowly correlated to both traits and was not significant ($P < 0.05$). Genetic correlations between MAST and SCC with ANG, TPS, and TL were all positive (e.g. a higher angularity score increases the risk of mastitis and higher SCC), whereas the remaining traits were negatively correlated. Not all genetic correlations of the type traits with MAST and SCC were significant ($P < 0.05$). ANG, FUA, UD, TPS, LOC and COMP were all significantly genetically correlated with MAST, and the same traits, with the exception of ANG and LOC, were significantly genetically correlated with SCC. It has been suggested that selection for improved udder conformation will reduce the increase in somatic cell count and the incidence of clinical mastitis (Lund et al. (1994)). The genetic correlation between COMP with MAST and SCC was -0.28 and -0.15, respectively, therefore is in agreement that improved udder conformation would benefit udder health. Udder depth is generally considered as the most important udder conformation trait (Boettcher et al. (1998)), and here it was the most highly correlated type trait with MAST and SCC with estimates of -0.50 and -0.35, respectively. The results show that the two most important type traits concerning udder health are udder depth and fore udder attachment, and suggest that cows with higher udders and tighter fore udder attachment are less prone to mastitis and high somatic cell counts.

Some studies have found that the relationship between some type traits with udder health or longevity are not always linear, but may have an intermediate optimum rather than the extremes of the scale (Schneider et al. (2003); Juozaitiene et al. (2006)). This may explain the low and non-significant genetic correlations between MAST and SCC with teat length. In this study only data on first lactation animals were used, whereas mastitis incidence and SCC are also problems in later lactations, and actually more so. Studies have shown greater correlations between SCC in later parities with udder depth (Evans and Berry (2005); Dube et al. (2009)). Strain upon the udder as the cow matures results in more pendulous udders that are then subject to more injury and contamination. Therefore an extension of this study could include data on MAST and SCC from later lactations.

Conclusion

Using farmer-recorded mastitis data appears promising, however standardised protocols for recording mastitis events would need to be established. Heritability estimates of mastitis are low, and genetic gain through selection upon mastitis alone would be slow, yet still positive and cumulative. By direct selection for clinical mastitis together with selection through SCC and selected type traits, particularly udder depth and fore udder attachment, an increase in disease resistance would be expected.

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