Phenotypic And Genetic Relationships Between Clinical Mastitis And Udder Conformation Traits In Austrian Fleckvieh Cattle

C. Fuerst[*], C. Egger-Danner[*], A. Koeck[†], and B. Fuerst-Waltl[†]

Introduction

Breeding for mastitis resistance is becoming increasingly important, because of its effect on farm economy and animal welfare and also because consumer demands for healthy and naturally produced products increase. Most countries performing genetic evaluations for mastitis resistance lack records of clinical mastitis (CM) as disease recording systems are not well developed. Thus, most commonly SCC is used as an indirect measure. In Austria, genetic evaluations for udder health are based on SCC and have been carried out since 1998. SCC is included in the total merit index, currently with a relative weight of 9.7% for Fleckvieh cattle (Fuerst et al. (2010)). In a review, Mrode and Swanson (1996) reported that the average estimated genetic correlation between CM and SCC based on literature values was approximately 0.7. Until now genetic evaluations of CM are carried out only in the Nordic countries, where health traits are routinely and widely recorded for more than 30 years. Studies on the relationship between mastitis and conformation traits are limited (e.g. Rupp and Boichard (1999)). Results of these studies and others, investigating the relationship between conformation and SCC, suggest that clinical mastitis incidences can be reduced by selection for certain udder conformation traits.

In 2006, a project to establish a nation-wide health monitoring system for cattle started in Austria (Egger-Danner et al. (2007)). Udder conformation traits are on average recorded for 40-60 daughters of each Fleckvieh test bull. Thus, the objectives of this study were to calculate phenotypic and genetic associations of CM with udder conformation traits in Austrian Fleckvieh (dual purpose Simmental) cows.

Material and methods

Data. CM data were collected within the Austrian project “Health monitoring in cattle” in which diagnoses from veterinarians are recorded. A detailed description of the health recording system and data validation is given by Egger-Danner et al. (2007) and Koeck et al. (2010). CM was defined as a binary trait (0 or 1) within the interval from -10 to 50 d after calving. All cows culled due to udder problems within the investigated time period were considered as diseased even if they did not have a record of veterinary CM treatment. Cows culled because of other reasons were included as healthy if they had no CM treatment.

---

[*] ZuchtData EDV-Dienstleistungen GmbH, Dresdner Str. 89/19, A-1200 Vienna, Austria.

[†] University of Natural Resources and Applied Life Sciences Vienna, Division of Livestock Sciences, Gregor Mendel-Str. 33, A-1180 Vienna, Austria.

Udder conformation data were taken from the routine conformation recording system. Only conformation data from first parity cows from herds actively participating in the health recording system were considered. Age at first calving was restricted to 19 and 43 months. In total, records from 5,426 Austrian Fleckvieh (dual purpose Simmental) cows calving between 2007 and 2009 were available. The pedigree file had information on 52,358 animals.

Model. Phenotypic relationships between the traits were calculated using the MIXED procedure (SAS (1990)). The variance components were estimated from a linear animal model using the program VCE6 (Kovac and Groeneveld (2007)). In total, 11 bivariate analyses were carried out with CM and one of the udder conformation traits each.

The model for CM was as follows:

$Y_{ijklmn} = \mu + Year_i{*}Season_j + Age_k + Herd_l + Animal_m + E_{ijklmn}$

Where: Y_{ijklmn} = observation of CM between –10 and 50 days after calving (0 or 1)
μ = overall mean
$Year_i{*}Season_j$ = fixed effect of interaction between calving year (2007-2009) and season (4)
Age_k = fixed effect of calving age (5 classes)
$Herd_l$ = random herd effect
$Animal_m$ = random genetic effect of recorded animal (cow)
E_{ijklmn} = random error effect

The following model was applied for udder conformation traits:

$Y_{ijklmno} = \mu + Classifier_i{*}Year_j + Age_k + Time_l + Herd_m + Animal_n + E_{ijklmno}$

Where: $Y_{ijklmno}$ = observation of udder conformation trait (11 traits)
μ = overall mean
$Classifier_i{*}Year_j$ = fixed effect of interaction between classifier and year (98)
Age_k = fixed effect of calving age (5 classes)
$Time_l$ = covariate of time after last milking in hours
$Herd_m$ = random herd effect
$Animal_n$ = random genetic effect of recorded animal (cow)
$E_{ijklmno}$ = random error effect

Results and discussion

Phenotypic relationships. Average incidence of CM (-10 to 50 days after calving) was 4.0% over all cows in the data set. Linear and quadratic regressions of CM on each udder conformation trait were analyzed. All quadratic regression coefficients except for teat thickness ($P<0.05$) were above significance level. Linear regression coefficients were significant to highly significant for fore and rear teat placement ($P<0.05$), fore udder attachment ($P<0.01$), udder score, suspensory ligament and udder depth ($P<0.001$). As an example the relationship between overall udder score and CM is shown in Figure 1. Higher udder scores are related with fewer CM diagnoses. Figure 2 shows the relationship of udder thickness with CM. An average thickness of the teats (score 5=2.5 cm) leads to the lowest number of CM cases. Too thin and too thick teats result in clearly more udder health problems. Very thin teats are related to a lower milking speed which leads to a longer milking time resulting in a higher mechanical stress during the milking process. On the other hand thicker teats might lead to an easier entry of pathogens.

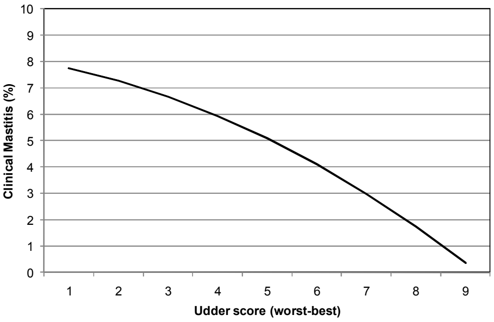

Figure 1: Phenotypic relationship between overall udder score and CM.

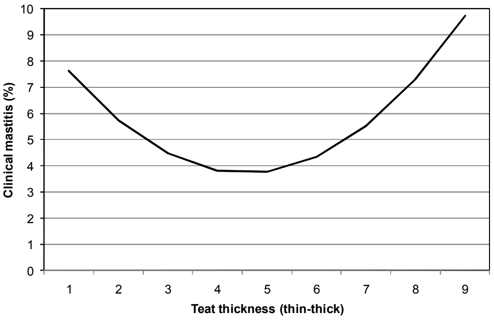

Figure 2: Phenotypic relationship between teat thickness and CM.

Genetic correlations. Genetic correlations between all estimated pairs of traits are presented in Table 1. Interpretation of (linear) genetic correlations is rather difficult when the true relationship is obviously nonlinear. From phenotypic analyses this is particularly the case for teat thickness (see Figure 2).

Table 1: Genetic correlations (r_g, SE in parenthesis) between CM and udder conformation traits and corresponding heritabilities for each bivariate run.

Trait	r_g (SE)	h^2 CM[a]	h^2 conform.[b]
Udder score (worst-best)	-0.42 (0.29)	0.021	0.307
Fore udder length (short-long)	-0.30 (0.24)	0.022	0.210
Rear udder length (short-long)	0.51 (0.34)	0.014	0.294
Fore udder attachment (loose-strong)	-0.65 (0.28)	0.022	0.181
Suspensory ligament (weak-strong)	-0.02 (0.05)	0.020	0.229
Udder depth (deep-high)	-0.45 (0.25)	0.022	0.257
Teat length (short-long)	-0.01 (0.24)	0.020	0.382
Teat thickness (thin-thick)	-0.05 (0.26)	0.020	0.366
Fore teat placement (outwards-inwards)	-0.07 (0.24)	0.019	0.345
Rear teat placement (outwards-inwards)	-0.45 (0.27)	0.023	0.331
Additional teats (less-more)	-0.19 (0.26)	0.020	0.212

[a] *SE for h^2 CM was 0.02 in all cases*

[b] *SE for h^2 of conformation traits varied between 0.03 and 0.04*

Genetic correlation between overall udder score and CM is markedly negative (-0.42), indicating that classifiers give the highest scores for functional, ‘healthy’ udders. Somehow surprising is the result that CM is negatively related to a longer fore udder (-0.30) but positively with a longer rear udder (0.51). The positive relationship with rear udder length might be due to the relationship with milk production. Longer fore udders are also related with a higher milk yield on the one hand but on the other hand correlated with a stronger attachment which shows a significantly negative correlation (-0.65) with CM. Although phenotypic analyses show that a stronger suspensory ligament leads to fewer CM diagnoses, the genetic correlation is not significant. In accordance to Rupp and Boichard (1999), fore udder attachment and udder depth are among the most important conformation traits with regard to udder health (-0.65 and -0.45, respectively).

Genetic correlations of CM with teat length and thickness show no significant correlation, but phenotypic analyses indicate that there is an intermediate optimum for teat length and thickness. Slightly inwards placed teats also lead to fewer CM cases.

Results suggest that cows with higher udders that are more tightly attached and have slightly inwards placed teats have less mastitis treatments. Similar associations of udder conformation traits were shown in earlier studies for CM traits (Rogers et al. (1998); Sørensen et al. (2000)). Similar genetic correlations of these conformation traits were also reported for longevity (Fuerst and Fuerst-Waltl (2006)).

Conclusion

Based on the findings it is feasible that conformation traits are included in a future udder health index. Fore udder attachment, udder depth and rear teat placement could be considered as auxiliary traits in order to select for mastitis resistance. However, analyses should be repeated as soon as more data are available.

Acknowledgements

This work was financed by the Federal Ministry of Agriculture, Forestry, Environment and Water Management (BMLFUW) of Austria and the Federation of Austrian Cattle Breeders (ZAR). Birgit Fuerst-Waltl was supported by the Austrian Science Foundation (FWF; Elise-Richter Program V43-B12).

References

Egger-Danner, C., Fuerst-Waltl. B., Holzhacker, W. *et al.* (2007). In: *Book of Abstracts of the 58th Annual Meeting of the EAAP*, page 363.

Fuerst, C., Dodenhoff, J., Emmerling, R., *et al.* (2010). http://www.zar.at/download/ZWS/ZWS.pdf.

Fuerst, C., Fuerst-Waltl, B. (2006). *Züchtungskunde* 78:365-383.

Koeck, A., Egger-Danner, C., Fuerst, C. *et al.* (2010). *J. Dairy Sci.*. (accepted).

Kovac, M., Groeneveld, E. (2007). VCE6, User's guide and reference manual, V. 6.1.

Mrode, R. A., and Swanson, G. J. T. (1996). *Anim. Breed. Abstr.* 64:847-857.

Rogers, G. W., Banos, G., Nielsen, U.S. *et al.* (1998). *J. Dairy Sci.* 81:1445-1453.

Rupp, R., and Boichard, D. (1999). *J. Dairy Sci.* 82:2198–2204.

SAS (1990). SAS Inst. Inc., Cary, NC. User's Guide.

Sørensen, M. K., Jensen, J. and Christensen, L.G. (2000). *Acta Agric. Scand. A Anim. Sci.* 50:72-82.