56th Annual Meeting of the European Association for Animal Production, Uppsala, Sweden, June 5th – 8th, 2005, Commission on Animal Genetics, Session GPh1.4

Quantitative Trait Loci Affecting Fertility and Calving Traits in Swedish Dairy Cattle

M. Holmberg and L. Andersson-Eklund

Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences
Box 7023, 75007 Uppsala, Sweden.
Corresponding author, e-mail: Mia.Holmberg@hgen.slu.se

Introduction

Reproduction traits, including fertility and calving traits, are of significant economic importance in dairy cattle production. Poor reproductive performance is the most common reason for culling, today 26% of all disposals in the Swedish red and white breed (SRB) are due to impaired fertility (Swedish Dairy Association, 2004). The consequences of low fertility include additional inseminations, higher veterinary costs, increased culling rate and higher replacement costs. Calving performance and calf viability are important traits not only for economical reasons but also for animal welfare. Reproduction traits have a low heritability and are thus demanding to improve by traditional selection on phenotypes. Molecular techniques have made it possible to locate loci (QTL) involved in the expression of a quantitative trait by combining information on genetic markers and phenotypic information on a trait. A few studies have described QTL for reproduction traits in different populations (Schrooten et al., 2000; Kuhn et al., 2003; Schulman et al., 2003). The objective of this study was to map QTL contributing to the genetic variation in fertility and calving traits in the Swedish dairy cattle population.

Material and methods

Resource Population and Marker Data. Ten paternal half-sib families were included, nine of the Swedish red and white breed and one of the Swedish Holstein breed. The total number of genotyped bulls was 417 and the number of sons per grandsire ranged from 21 to 58 with a mean of 42. DNA from all bulls was extracted from semen samples that were obtained from the Swedish breed organization, Svensk Avel. In total 20 chromosomes were included in the study and 145 genetic markers were genotyped. Marker maps were established by using the CRI-MAP program, version 2.4 (Green et al., 1990) and the Haldane map function.

Phenotypic data. Data on a total of 11 traits were analyzed in this study. Phenotypic traits considered were non-return rate of 56 days, number of inseminations, fertility treatments, interval calving to first insemination, heat intensity score, stillbirth (direct and maternal), and calving performance (direct and maternal). Direct effect is calving when the evaluated bull is the father and maternal effect is when the bull is grandfather to the calf. For the traits non-return rate of 56 days and number of inseminations the heifer and cow performance were treated as separate traits. Non-return rate of 56 days is based on whether or not the heifer/cow had a second insemination within 56 days after the first insemination. Fertility treatments were defined as veterinary treatments for fertility disturbances from 10 days before until 150 days after the first calving. Data on heat intensity score and calving difficulty are generated by the individual farmer who subjectively scores the performance in predefined categories. Stillbirth includes calves dead at birth or within 24 hours. The calving traits are based on first calvers only and twin calvings are excluded.

The phenotypic data was obtained from the national genetic evaluation. Daughter group averages, based on a minimum of 50 daughters per bull and adjusted for systematic environmental effects, were available for all fertility traits except heat score. For the calving traits and heat score, estimated breeding values were obtained from the national genetic evaluation and were used as phenotypic records in the analyses.

Statistical Analysis

The QTL analyses were performed for each trait separately with a multimarker regression approach (Knott et al., 1996; Vilkki et al., 1997). On each chromosome at every cM, the phenotypes were regressed on the probability of transmission of alternative paternal QTL alleles to sons. The analysis is nested within families to allow for different linkage phases between markers and QTL between grandsires. First, the chromosomes were analysed individually to identify candidate regions for QTL. To increase the power of the analysis, QTL that reached a chromosomewise significance of $P < 0.10$ in the across-family analysis were included as cofactors in the further analyses (de Koning et al., 2001). The analyses were repeated until no new QTL were found and the estimated locations of the identified QTL were stable. Permutation tests of 10,000 rounds were performed for each trait separately to set significance levels for analyses within and across families (Churchill and Doerge, 1994).

Results and Conclusions

Association between markers and traits were tested on 20 chromosomes for a total of 11 traits. In the initial analysis without inclusion of cofactors we detected a total of 13 QTL that exceeded the 5% chromosomewise significance level in the across family analysis. These QTL were located on eight chromosomes (6, 7, 9, 11, 13, 15, 20, and 29). Two QTL were significant at the genome level, affecting the traits non-return rate in heifers and non-return rate in cows on chromosomes 9 and 20, respectively. When including possible QTL from the initial analysis as cofactors in the following analyses, both the number of QTL detected and the test statistics increased in most cases. In total we found 30 QTL at the 5% chromosomewise significance level when including cofactors, and 15 of these reached genomewise significance.

In conclusion we found that it is possible to identify chromosome regions with effect on fertility and calving traits in the Swedish dairy cattle population. Our results provide a basis for further work to narrow down the QTL regions before the results can be used in practical breeding.

Acknowledgments

The study was partly financed by Swedish Farmer’s Foundation for Agricultural Research. The Authors are grateful to the Swedish Dairy Association for providing the phenotypic data, to the breed organization Svensk Avel for providing the semen samples and to the Agricultural Research Center MTT in Finland for supplying the QTL analysis program.

References

Churchill, G. A. and R. W. Doerge. 1994. Empirical Threshold Values for Quantitative Trait Mapping. Genetics. 138(3):963-971.

de Koning, D. J., N. F. Schulman, K. Elo, S. Moisio, R. Kinos, J. Vilkki, and A. Maki-Tanila. 2001. Mapping of multiple quantitative trait loci by simple regression in half-sib designs. J. Anim. Sci. 79(3):616-622.

Green, E., K. Falls, and S. Crooks. 1990. Documentation of CRI-MAP, Version 2.4. Washington University School of Medicine, St Louis, MO.

Knott, S. A., J. M. Elsen, and C. S. Haley. 1996. Methods for multiple-marker mapping of quantitative trait loci in half-sib populations. Theor. Appl. Genet. 93(1-2):71-80.

Kuhn, C., J. Bennewitz, N. Reinsch, N. Xu, H. Thomsen, C. Looft, G. A. Brockmann, M. Schwerin, C. Weimann, S. Hiendieder, G. Erhardt, I. Medjugorac, M. Forster, B. Brenig, F. Reinhardt, R. Reents, I. Russ, G. Averdunk, J. Blumel, and E. Kalm. 2003. Quantitative trait loci mapping of functional traits in the German Holstein cattle population. J. Dairy Sci. 86(1):360-368.

Schrooten, C., H. Bovenhuis, W. Coppieters, and J. A. M. Van Arendonk. 2000. Whole genome scan to detect quantitative trait loci for conformation and functional traits in dairy cattle. J. Dairy Sci. 83(4):795-806.

Schulman, N. F., S. Viitala, D. J. de Koning, A. Mäki-Tanila, and J. Vikki. 2003. Mapping of quantitative trait loci affecting fertility traits in Finnish Ayrshire. Proc. 54th Annu. Mtg. of the Eur. Assoc. of Anim. Prod., Rome, Italy.

Swedish Dairy Association. 2004. Husdjursstatistik (Cattle statistics). Svensk Mjölk, 631 84 Eskilstuna, Sweden.

Vilkki, H. J., D. J. deKoning, K. Elo, R. Velmala, and A. MakiTanila. 1997. Multiple marker mapping of quantitative trait loci of Finnish dairy cattle by regression. J. Dairy Sci. 80(1):198-204.