

CONFIRMATION OF A QTL AFFECT MILK PRODUCTION IN BOVINE CHROMOSOME 20

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SUMMARY

The objective of this study was to confirm a quantitative trait locus for milk production described in a previous study on bovine chromosome 20 using an independent sample. A total of 1191 progeny tested bulls were analyzed for six microsatellite markers spanning bovine chromosome 20. Using multiple-marker regression, we obtained evidence ($P < 0.5$) for the presence of a quantitative traits locus in the same chromosomal region an affecting the same trait as described in the first study, therefore confirming genuine nature of this QTL.

Keywords: QTL mapping, Cattle, Milk Production

INTRODUCTION

Regions of the genome that influence quantitative traits, known as quantitative trait loci (QTL), affecting economically important traits are currently being identified in cattle using experimental crosses (backcross or F₂) or outbred populations (Weller *et al.*, 1990; Georges *et al.* 1995). Some of these QTL will be used to implement selection of animals based on their genotype at the marker linked to QTL, so-called Marker Assisted Selection. For milk production a number of QTL have been located (Bovenhuis and Weller, 1994; Ron *et al.*, 1994; Georges *et al.*, 1995). The objective of this study was to confirm, a QTL previously identified on bovine chromosome 20 using an independent sample.

MATERIALS AND METHODS

Pedigree material

A total of 1191 bulls belonging to 31 half-sibs families was analyzed in a granddaughter design for associations between markers and putative QTL (Spelman *et al.*, 1996). Average number of sons per sire was 38 with a range of 12 to 150. DNA was isolated from semen samples using standard procedures and transferred to 96 microwell format.

Marker map

A set of six chromosome 20 microsatellite markers compiled from previously published bovine maps (Barendse *et al.*, 1994; Bishop *et al.*, 1994; Georges *et al.*, 1995) was selected. PCR amplification was carried out in a reaction volume of 10 μ L using 25 ng of genomic DNA and α (³²P)dCTP as radioactive label. Map construction was performed using CRI-MAP v. 2.4 (Green *et al.*, 1990).

Information content mapping was performed according to Kruglyak and Lander (1995).

QTL Mapping

Five milk production traits were analyzed in this work: milk yield, fat yield, protein yield, fat percentage and protein percentage. All five traits are characterized by quasinormal distributions in dairy cattle. The quantitative measurements used were sires' Daughter Yield Deviations (DYDs); unregressed weighted averages of their daughter's lactation performances expressed as deviations from populations mean (VanRaden and Wiggans, 1991).

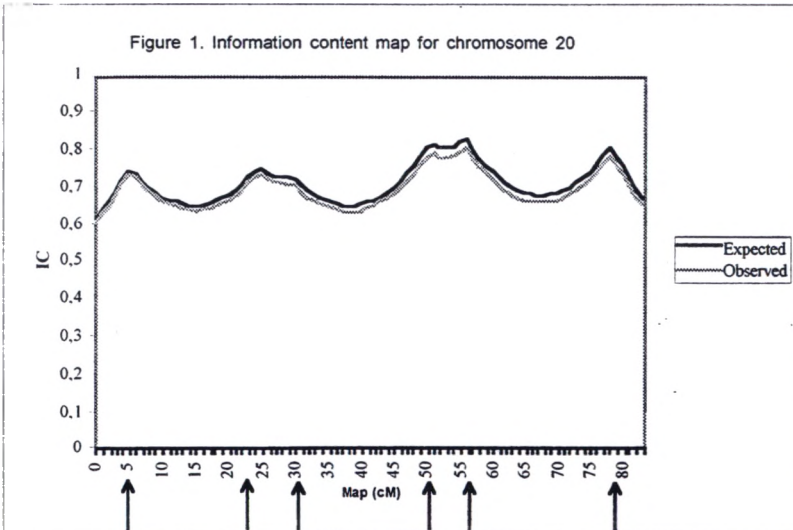
QTL analysis was done using multilinker regression (Knott *et al.*, 1996).

Chromosomal wise significance levels were determined by permutation (Churchill and Doerge, 1994). A Bonferroni correction was applied to obtain whole genome significance levels.

RESULTS AND DISCUSSION

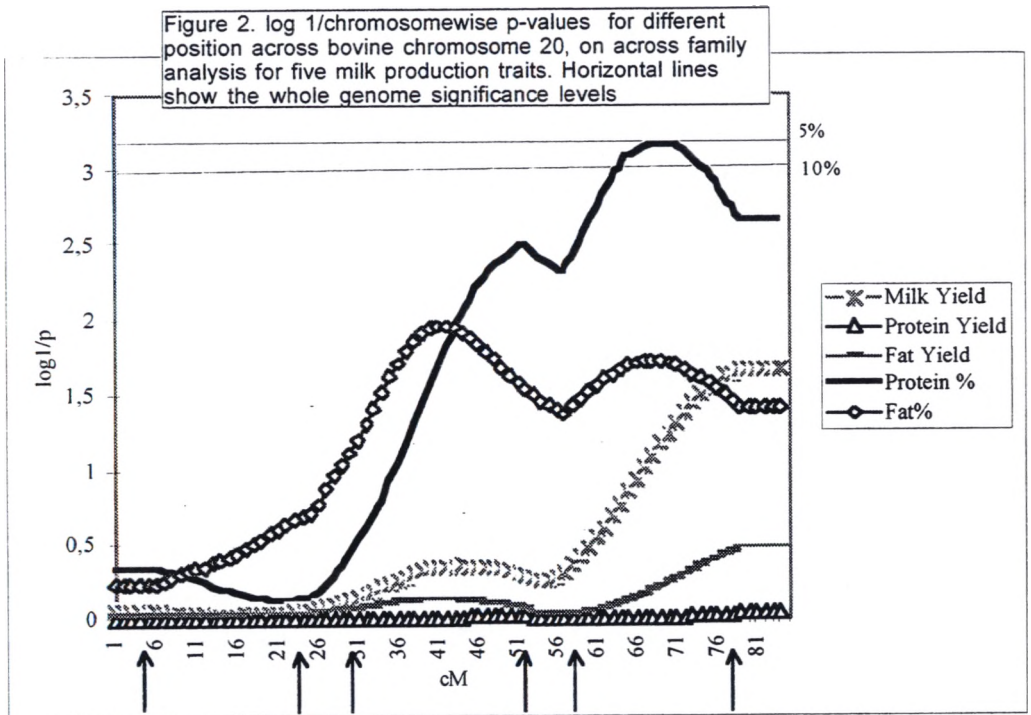
Information content map

Six markers were positioned on bovine chromosome 20 yielding a map of 73 cM (Kosambi). The mean bracket size is 12,6 cM and the range is between 19.1 to 4,6 cM. Figure 1 shows information content for chromosome 20. The information content is superior to 60% over the entire chromosome.



Mapping QTL controlling milk production

Multiple regression performed across families revealed a QTL affecting protein percentage between markers 5 and 6 (see figure 2). This QTL seems to be the same as the one reported by Georges *et al.* (1995) using a within family, maximum likelihood analysis. These authors found significant effects on the same trait (protein percent) in two families (LOD scores 3.99 and 3.20, respectively) at the same marker position. The effects on the other traits is similar in both studies: there is evidence for an effect on fat percentage and milk yield but not on fat and protein yield.



CONCLUSION

In this study we present the confirmation of a QTL affecting milk production traits on bovine chromosome 20. We are in the process of refining the map position of the corresponding QTL using IBD strategies

REFERENCES

- Barendse, W. Armitage, S.M., Kossarek, L.M. *et al.* *Nature Genetics*, 6:227-235
- Bishop, M., Kappes, S.M., Keele, J.W. (1994). *Genetics*, 136: 619-639.
- Bovenhuis, H. and Weller, J.I. (1994). *Genetics*, 137: 267-280.
- Churchill, G.A. and Doerge, R. (1994) *Genetics* 138: 963-971.

- Haley, C.S. and Knott, S. (1992). *Heredity*, 69: 315-324.
- Georges M, Nielsen, D., Mackinnon, M. *et al.*, (1995). *Genetics*, 139:907-920.
- Green, P., Falls, K. and Crooks, S. (1990). Documentation for CRI-MAP. Washington University School of Medicine, St. Louis, MO. USA.
- Knott, C.S., Elsen, J.M. and Haley, C.S. (1996). *Theor. Appl. Genet.* 93: 71-80.
- Kruglyak, L. and Lander, E.S. (1995). *Am. J. Hum. Genet.* 57:439-454.
- Ron, M., Band, M., Yanai, A. and Weller, J.I. (1994). *Anim. Genet.* 25: 259-264.
- Spelmann, R. Coppieters, W., Karim, L. *et al.* (1996). *Genetics* 144: 1799-1808.
- VanRaden P.M. and Wiggans, G.R. (1991) *J. Dairy Sci.*, 74: 2737-2746.
- Weller J.I. Kashi, Y. and Soller, M. (1990). *J. Dairy Sci.*, 73: 2525-2537.

ACKNOWLEDGMENTS

This work was funded by Holland Genetics & Livestock Improvement Corporation. J.J. Arranz is a postdoctoral fellowship of Spanish Ministry of Education (Programa De Perfeccionamiento de Doctores y Tecnólogos).