Genome-wide associations for fertility traits in Holstein-Friesian cows using data from four European countries

D.P. Berry[1], J.W.M. Bastiaansen[2], R.F. Veerkamp[3], S. Wijga[2], E. Wall[4], B. Berglund[5] and M.P.L. Calus[3]

[1]Teagasc, Moorepark, Ireland. [2]Wageningen Uni. The Netherlands, [3]Wageningen UR Livestock Research, The Netherlands, [4]Scottish Agricultural College, UK, [5]Swedish University of Agricultural Sciences, Uppsala, Sweden

1. Introduction

- Low heritability of fertility traits makes genetic selection, using traditional means, more difficult
- Options: increase heritability and/or use genomic information

2. Objective

- To identify regions of the bovine genome associated with fertility

3. Materials and Methods

- Primiparous Holstein-Friesian cows from experimental farms in Ireland (Teagasc), the UK (SAC), The Netherlands (Wageningen UR Livestock Research), and Sweden (Jälla).
- Fertility traits:
  - Calving to first heat interval (CFH)
  - Calving to first service (CFS)
  - Calving interval (CI)
  - Number of services (NS)
  - Pregnancy rate to first service (PRFS)
  - Post partum commencement of luteal activity (CLA) – 2-3 times weekly
- Illumina Bovine50 Beadchip genotypes on all animals
  - 37,590 single nucleotide polymorphisms on up to 1,570 animals after edits
- Genetic parameters estimated using linear mixed model analysis
- Univariate and bivariate genome-wide association analysis undertaken using Bayesian stochastic search variable selection performed using Gibbs sampling.

4. Results and Discussion

- Heritability estimates of traditional fertility measures varied from 0.03 to 0.16; heritability of CLA was 0.13 (SE=0.06)
- Posterior QTL probability for traditional fertility measures were less than 0.021
- Posterior QTL probabilities of >0.04 were observed for CLA on BTA 2 (BTA-49769-no-rs; posterior probability of 0.060) and BTA 21 (BTA-12468-no-rs; posterior probability of 0.045)
  - rs numbers of both SNPs were rs41579201 and rs29024420, respectively
- BTA-49769-no-rs explained 0.51% of the genetic variance in CLA while BTA-12468-no-rs explained 0.35% of the genetic variance in CLA
- The posterior probability of 0.060 for CLA at SNP BTA-49769-no-rs was increased to 0.094, 0.121, 0.162, 0.662 and 0.162 when CLA was included in a bivariate genome wide association analysis with CFH, CFS, NS, CI and PRFS, respectively
- The posterior probability of 0.045 for CLA at SNP BTA-12468-no-rs on BTA 21 was increased to 0.052, 0.152, 0.072, 0.123 and 0.135 when CLA was included in a bivariate genome wide association analysis with CFH, CFS, NS, CI and PRFS, respectively
- Of the 16 genes near BTA-49769-no-rs three have functions that relate to fertility: Bos taurus inhibitor of DNA binding 3, dominant negative helix-loop-helix protein (ID3), fucosidase, alpha-L-1, tissue (FUCA1), and E2F transcription factor 2 (E2F2)

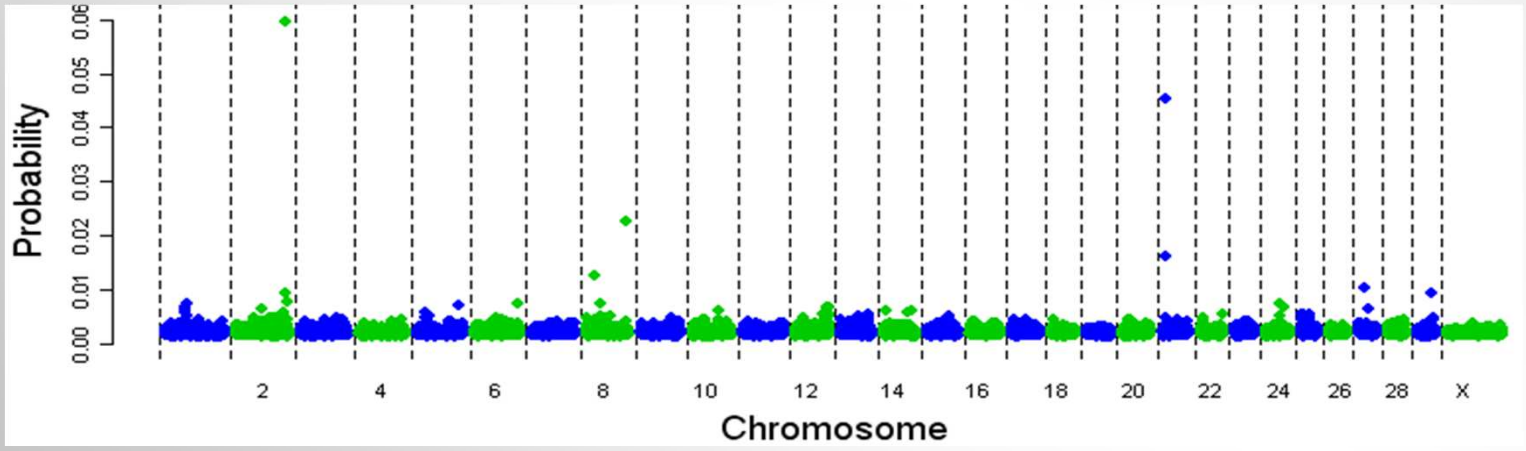

Figure 1. *Posterior QTL probabilities for post-partum commencement of luteal activity for each of the autosomes from left (BTA 1) to right (BTA29) and the X-chromosome at the far right*

5. Conclusions

- Two regions of the genome potentially harbouring a mutation associated with CLA were identified

6. Acknowledgements

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