

Genome-wide Associations for Milk Production and Somatic Cell Count in Irish Holstein-Friesian Cattle

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1. Key Message

- We have identified numerous quantitative trait loci (QTLs) associated with milk production and somatic cell score (SCS).
- These QTLs will undergo further investigation to determine the basis of the phenotypic variation seen in these genomic regions.

2. Introduction

- Genomic information can supplement traditional methods of genetic evaluation.
- Discovery of QTLs may also aid in the identification of genes and gene pathways associated with lactogenesis and immunocompetence.

3. Objective

- To identify QTLs associated with milk production and somatic cell count in Irish Holstein-Friesian cattle.

4. Materials and Methods

- 40,668 SNPs were genotyped in 914 Holstein-Friesian AI sires with daughters in Ireland using the Illumina Bovine50 Beadchip.
- Daughter yield deviations (DYD) were the dependent variables;
 - Milk yield
 - Fat yield and concentration
 - Protein yield and concentration
 - Somatic Cell Score (= $\log_e$ Somatic Cell Count)
- Only sires of high reliability
 - Deregressed reliability $\geq 80\%$ for milk production (n=914)
 - Deregressed reliability $\geq 70\%$ for SCS (n=776)
 - Dependent variable weighted by deregressed reliability

• Statistical Analysis

3 linear models

a) SSR (NP) - (Single SNP Regression No-polygenic) regression on each SNP individually in a fixed effect model (e.g. no polygenic effect).

a) SSR (P) - (Single SNP Regression Polygenic) regression on each SNP individually in a linear mixed animal model accounting for relationships between animals (e.g. polygenic effect included).

b) SW - (Sliding Window) linear mixed animal model regressing on a window of 7 SNPs sliding across the genome

2 Bayesian models

d) BayesA (NP) - (BayesA No-polygenic) Bayesian model without a polygenic effect accounted for assuming many QTLs with small effects and few QTLs with large effect.

e) BayesA (P) - (BayesA Polygenic) Bayesian model with a polygenic effect assuming many QTLs with small effects and few QTLs with large effect.

- False discovery rates (FDR) of 5% and 0.1% calculated based on q-value.

5. Results

- **Figure 1:** $-\log_{10}$ of P values from the single marker mixed model analysis. Autosomes are arranged from left to right.

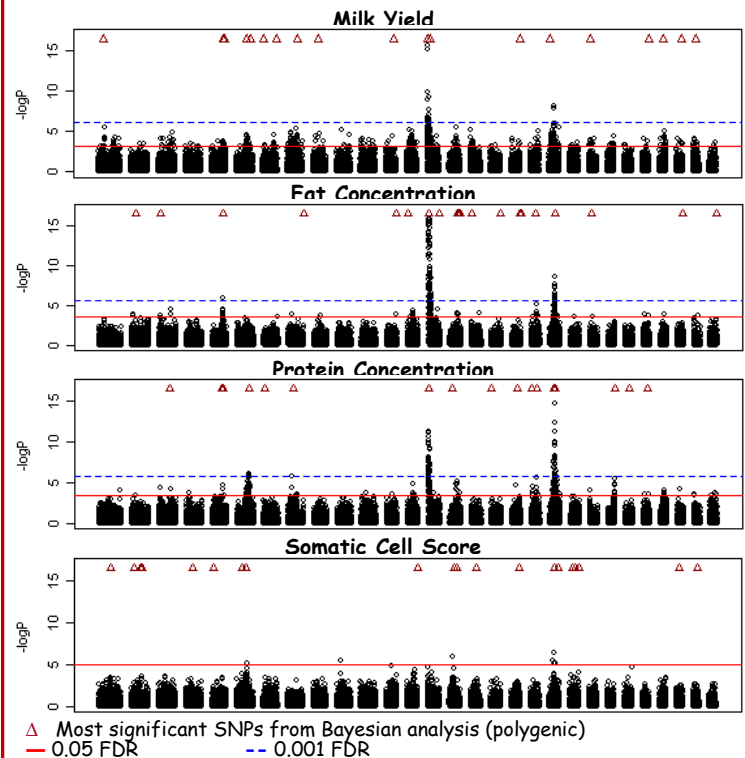


Table 1: Number of SNPs exceeding the 0.05 ■ and 0.001 ■ FDR for the different models

	SSR (NP)*		SSR (P)		SW	
Milk Yd.	31738	20908	364	20	255	10
Fat %	18701	6230	214	114	186	100
Protein %	24313	11515	230	67	182	63
SCS	6151	498	9	0	3	0

Table 2: Pearson ■ and rank ■ correlation between SNP effects across the different models

	SSR (NP)	SSR (P)	SW	Bayes (NP)	Bayes (P)
SSR (NP)		0.29	0.25	0.17	0.15
SSR (P)	0.64		0.90	0.44	0.41
SW	0.51	0.82		0.40	0.30
Bayes (NP)	0.20	0.29	0.24		0.80
Bayes (P)	0.20	0.29	0.23	0.91	

6. Conclusion

- For each trait numerous QTLs were found to be associated with phenotypic variation (Table 1).
- Strong correlations existed between SNP effects estimated within the linear models (0.51 to 0.82) and within the Bayesian models (0.91).
- Correlations between SNP effects estimated in the linear and Bayesian models were weak (0.20 to 0.29).
- However the ranking of SNPs between the 2 polygenic linear models (SSR (P) and SW) and the Bayesian models (Bayes (NP) and Bayes (P)) were more similar ($r=0.3$ to 0.44).
- Greater amounts of SNPs were significant for non-polygenic models as the test statistic is substantially inflated when pedigree is not accounted for.
- The positions of the detected QTLs will require further refining.