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Genome Wide Association Studies for Temperament in New Zealand Dairy Cattle

A thesis presented in partial fulfilment of the requirements for the degree of Master of Science in Animal Science in Animal Breeding and Genetics

at

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New Zealand

Massey University

Fei Yi Chan
2012
DEDICATION

To my parents
ABSTRACT

The aim of this thesis was to identify genomic regions associated with cow temperament in New Zealand dairy cattle. The data set used was provided by the Livestock Improvement Corporation, and contains estimated breeding values (EBV) for temperament of 3140 bulls of three breeds; Holstein-Friesian (HF), Jersey (JE) and Crossbreed (XB) born between 1994 and 2006. Biallelic genotype data were also provided containing 700,000 single nucleotide polymorphism (SNP) markers. Estimated breeding values for cow temperament were adjusted (Adj-EBV<sub>temp</sub>) for age, percentage of North American Holstein genes (NAH%), percentage of New Zealand Holstein-Friesian (HF%) and percentage of Jersey (JE%). Using PLINK, the association between individual markers and temperament was investigated. PLINK was also used to produce output with genomic corrected p-values (GC) which adjusts for inflation based on the median chi-square statistic. Suggestive and genome-wide significance thresholds were set at $-\log_{10}(1\times10^{-4})$ and $-\log_{10}(5\times10^{-5})$ respectively. From literature review, the average estimate of heritability of temperament was 0.17, and average genetic correlation with milk yield was 0.165. JE bulls had the highest average EBV for temperament ($0.0352 \pm 0.239$) followed by XB ($0.0079 \pm 0.217$) and HF bulls ($-0.0402 \pm 0.256$). PLINK analysis show BTA 4 to contain genome-wide significant genomic regions across all three breeds for Adj-EBV<sub>temp</sub>. Further investigation on individual chromosomes provided no further information on significant genomic regions affecting temperament. A closer look at many of these regions show they are in domains known as “Junk DNA”. Results suggest that although genomic selection for temperament in dairy cattle is plausible, genetic gain via direct selection for this trait will be slow and desired effects may not be immediate.

Keywords: Temperament, dairy cattle, genomic selection, quantitative trait loci (QTL).
ACKNOWLEDGEMENTS

“...but those who hope in the LORD

will renew their strength.

They will soar on wings like eagles;

they will run and not grow weary,

they will walk and not be faint.” Isaiah 40:31

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The Lord is my strength and my shield; my heart trusts in Him, and He helps me. My heart leaps for joy, and with my song I praise Him. Psalm 28:7
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## Abbreviations

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<tr>
<th>Abbreviation</th>
<th>Description</th>
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<tbody>
<tr>
<td>AEU</td>
<td>Animal Evaluation Unit</td>
</tr>
<tr>
<td>AI</td>
<td>Artificial Insemination</td>
</tr>
<tr>
<td>BLUP</td>
<td>Best Linear Unbiased Predictor</td>
</tr>
<tr>
<td>BTA</td>
<td>Bos taurus Autosome</td>
</tr>
<tr>
<td>BW</td>
<td>Breeding Worth</td>
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<tr>
<td>DNA</td>
<td>Deoxyribose Nucleic Acid</td>
</tr>
<tr>
<td>EBV</td>
<td>Estimated Breeding Value</td>
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<tr>
<td>EV</td>
<td>Economic Value</td>
</tr>
<tr>
<td>GBV</td>
<td>Genomic Breeding Value</td>
</tr>
<tr>
<td>GC</td>
<td>Genomic Corrected p-value</td>
</tr>
<tr>
<td>GWAS</td>
<td>Genome Wide Association Studies</td>
</tr>
<tr>
<td>HF</td>
<td>Holstein-Friesian</td>
</tr>
<tr>
<td>JE</td>
<td>Jersey</td>
</tr>
<tr>
<td>LD</td>
<td>Linkage Disequilibrium</td>
</tr>
<tr>
<td>LIC</td>
<td>Livestock Improvement Corporation</td>
</tr>
<tr>
<td>LW</td>
<td>Lactation Worth</td>
</tr>
<tr>
<td>MAS</td>
<td>Marker Assisted Selection</td>
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<tr>
<td>PW</td>
<td>Production Worth</td>
</tr>
<tr>
<td>QTL</td>
<td>Quantitative Trait Loci</td>
</tr>
<tr>
<td>SNP</td>
<td>Single Nucleotide Polymorphism</td>
</tr>
<tr>
<td>TE</td>
<td>Transposable Element</td>
</tr>
<tr>
<td>TOP</td>
<td>Traits Other than Production</td>
</tr>
<tr>
<td>XB</td>
<td>Crossbreed (Holstein-Friesian x Jersey, a.k.a. KiwiCross)</td>
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