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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



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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 ($\text{Adj-EBV}_{\text{temp}}$) 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 $-\log_{10}(1e^{-4})$ and $-\log_{10}(5e^{-5})$ 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 ± 0.239) followed by XB (0.0079 ± 0.217) and HF bulls (-0.0402 ± 0.256). PLINK analysis show BTA 4 to contain genome-wide significant genomic regions across all three breeds for $\text{Adj-EBV}_{\text{temp}}$. 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).

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“...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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LIST OF ABBREVIATIONS

Abbreviations

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