

**CHARACTERISATION IN THE NEW ZEALAND DAIRY INDUSTRY OF A
POLYMORPHISM MODULATING THE TRANSCRIPTION RATE OF A CHROMOSOME
DOMAIN ENCOMPASSING *PLAG1***

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SUMMARY

Recently quantitative trait nucleotides on a region of chromosome 14 were identified to influence growth rate and height in dairy cattle. This study investigated the allelic effects of one of the reported polymorphisms in 3 dairy breeds in New Zealand for live weight and for a wider range of economic traits. Statistically significant results were identified for live weight in Jersey, Holstein-Friesian and Ayrshire breeds. The additive allelic effects varied between 11-18kg for the three breeds. The Jersey breed is near fixation for the lower live weight allele whereas the Holstein-Friesian breed is at high frequency for the high live weight allele. In the Holstein-Friesian breed there were statistically significant allelic effects for calving difficulty, rump angle, rump width, body condition score, capacity, gestation length, stature, protein yield and milk volume.

INTRODUCTION

High-density marker panels have allowed the application of genomic selection (Meuwissen *et al.* 2001) in dairy cattle breeding schemes without in-depth knowledge of the underlying causative mutations. In some cases the mutations are detected, as in the case of Karim *et al.* (2011) who have described the detection of putative quantitative trait nucleotides (QTN) on bovine chromosome 14 that have a major effect on stature and live weight in dairy cattle. Karim *et al.* (2011) demonstrated that the QTN affected live weight at birth through to 24 months of age with an allelic substitution effect of 20kgs of mature live weight and 2cms of mature stature in F₂ Holstein-Friesian and Jersey animals.

This paper outlines and describes the allele frequency and allelic effect of one of the polymorphisms (SNP FJX_250879_1:1 in *PLAG1*) as defined by Karim *et al.* (2011)) on traits of economic importance in the New Zealand population for the Holstein-Friesian, Jersey and Ayrshire cattle breeds.

MATERIALS AND METHODS

Livestock Improvement Corporation has progeny-tested approximately 200-300 bulls per year for the last 30 years. This entails the bulls being genetically evaluated on the basis of 50-85 daughters per sire. The sires are evaluated for milk fat, milk protein, milk volume and 20 non-production traits. Semen has been retained from all progeny tested sires since the early 1970s. DNA was extracted from the semen and genotyped for the *PLAG1* polymorphism. The dataset consisted of 118 Ayrshires, 2195 Holstein-Friesians and 1308 Jersey bulls.

One single nucleotide polymorphism (SNP) (FJX_250879_1:1 in *PLAG1*) was genotyped using Taqman assays-by-design using standard procedures (ABI, Foster City, CA).

Statistical analysis. Statistical analysis was undertaken using Restricted Maximum Likelihood (REML) and the average information algorithm (Johnson and Thompson, 1995). The linear model included the fixed effects of the SNP (3 classes; 0, 1 and 2 copies of the C allele) and a covariate corresponding to the proportion of genetics originating from countries other than New Zealand (overseas genetics). Each analysis was undertaken separately for each breed. The random effect was animal with a relationship matrix based on all known relationships. Estimated breeding values (EBV) were the phenotypic measures used for the analysed traits with the average accuracy of the EBVs being approximately 80%.

RESULTS AND DISCUSSION

Genotype frequency. The frequency of the C and G alleles differ significantly between the 3 breeds that were analysed (Table 1). As one would expect the C allele, which increases live weight compared to the G allele, is more predominant in the Holstein-Friesian breed whereas the G allele is near fixation in the phenotypically smaller Jersey breed.

Table 1. Genotype counts and allele frequencies of the PLAG1 SNP for the 3 main dairy breeds in New Zealand.

Breed	Genotype counts			Allele frequencies	
	CC	CG	GG	C	G
Ayrshire	12	44	62	0.29	0.71
Holstein-Friesian	1678	479	38	0.87	0.13
Jersey	0	35	1272	0.01	0.99

Phenotype effects. The effect on live weight was confirmed in this dataset for all of the three breeds (Table 2). The direction of the effect was the same in all three breeds and the size of the effect was comparable.

Table 2. Allelic substitution effect (for each addition of the C allele) of the PLAG1 SNP on live weight for the 3 main dairy breeds in New Zealand

Breed	Allelic substitution effect	(p-value)
Ayrshire	15.2	(0.05)
Holstein-Friesian	10.9	(<0.0001)
Jersey	17.9	(0.05)

Statistically significant effects for traits other than live weight were only found in the Holstein-Friesian dataset. This is due to the combination of smaller allelic substitution effects and also the small dataset for the Ayrshire breed and the near fixation of the allele in the Jersey population.

In addition to previously identified stature and live weight effects the PLAG1 SNP also has a significant effect on other body structural traits; rump angle, rump width, capacity and body condition score. For all traits the effect was an increase in value with the addition of the C allele (Table 3). In

addition calving difficulty was identified to increase with the addition of the C allele. The calving difficulty phenotype is measured in a direct effect model (Winkelman *et al.* 2010) taking into account the effect of the progeny. Karim *et al.* (2011) identified that there was an additive 2.5kg effect on birth weight, which is resulting in the increase in calving difficulty that is reported in this study. It could be postulated that in a model estimating maternal effects of calving difficulty that the C allele would reduce the incidence due to the effect on rump angle and rump width.

The SNP has a statistically significant effect on both milk volume and protein yield but not on fat yield. The allele that increases live weight also increases protein yield and live weight.

Table 3: Allelic substitution effect (for each addition of the C allele) of the PLAG1 SNP (FJX_250879_1:1) for dairy traits in Holstein-Friesian cattle.

Trait	Effect	p-value
Body Condition Score	0.03	<0.0001
Calving Difficulty	1.60	<0.0001
Capacity	0.05	0.004
Gestation length (days)	0.51	0.02
Live weight (kg)	10.9	<0.0001
Rump Angle	0.06	0.0001
Rump Width	0.15	<0.0001
Stature	0.20	<0.0001
Fat yield (kg)	0.13	0.83
Milk volume (l)	45	0.003
Protein yield (kg)	1.57	0.0003

Breeding scheme application: The potential application of the SNP in the New Zealand dairy industry is limited. Firstly the SNP is near fixation in the Jersey breed and at a high frequency in the Holstein-Friesian breed. Breeding worth (BW) is the national selection index in New Zealand dairy industry. The SNP has a non-significant effect on BW due to the negative economic outcome of increasing live weight and milk volume negating the positive protein effect. Crossbreeding of predominantly Jersey and Holstein-Friesian breeds is widespread in the New Zealand dairy industry with LIC introducing KiwiCross™ bulls to the market. Application of the SNP within the KiwiCross population has greater potential, as the allele will be at an intermediate frequency. It would be expected that the first cross KiwiCross bulls will be heterozygous but future generations that result from intercrossing have the potential to generate any one of the three genotypic classes. Given the neutral effect on BW the major application within the KiwiCross population would be positioning the population closer to either the Holstein-Friesian or Jersey populations with respect to stature and live weight and reducing the variation within the KiwiCross population by increasing the frequency of one of the homozygote genotype classes.

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