

# Application Of Genomic Selection In The New Zealand Dairy Cattle Industry.

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## Introduction

LIC has been investing in DNA technology since the early 1990s. The first application of DNA information in the LIC breeding scheme was for parentage testing in the mid 1990s. At the same time, the detection of quantitative trait loci (QTL) for dairy cattle had just commenced (Georges et al. 1995). QTL discovered in the LIC research programme were used via marker assisted selection (MAS) in 1998 (Spelman 2002). The MAS breeding scheme relied on the generation of multiple full-sib sons from given sire and dam combinations. The resulting male offspring were genotyped and the sons that received the desirable alleles for the QTL were selected to enter progeny testing. The reproductive performance of the donor cows was poor resulting in very few of the families having enough sons to allow within-family marker-assisted selection. After two years of poor reproductive performance the within-family MAS was abandoned. LIC recommenced MAS in 2003 after the identification of both DGAT1 and GHR genes. All of the bull dams and bulls entering the progeny testing scheme were genotyped for these two genes for the next four years.

Meuwissen et al. (2001) first proposed the use of dense marker maps in a genomic selection (GS) setting. In 2006, the sequencing of the bovine genome by the international consortium was completed (Kappes et al. 2006). The sequencing generated a large number (one million plus) of single nucleotide polymorphisms (SNPs). The cost of genotyping dropped from NZ\$2.50 per marker for a microsatellite to less than one NZ cent per marker when tens of thousands of SNP are genotyped in parallel. The technology shift to large-scale SNP genotyping allowed the application of the theory that Meuwissen et al. (2001) proposed. This paper describes the application of genomic information in the LIC breeding scheme.

## Material and methods

**Genotyping.** Approximately 3300 progeny tested sires were genotyped over the Illumina 50K SNP panel. The progeny tested sires ranged in birth year from the early 1980's to the mid 2000's. Eighteen hundred Holstein-Friesian (HF) sires, 1200 Jerseys (JE) sires and 300 KiwiCross™ (KX) sires were genotyped. KiwiCross™ is the name given to crossbred animals that are less than 87.5% of one of the main dairy breeds. After removing SNP for low call rates, minor allele frequencies <2%, non-Mendelian inheritance, and failed Hardy-Weinberg tests, a total of 44,146 SNP were retained for analysis. A further 1,844 SNP that showed near perfect collinearity with another SNP ( $R^2 > 0.975$ ) were removed.

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**Statistical analysis.** The dataset was split into two: i) training dataset and ii) test dataset. The training dataset contained 2450 bulls that were progeny tested prior to 2002. The test dataset consisted of 850 bulls born after 2002 that were progeny tested. The training dataset was split into 3 components a) all 2450 animals b) 1400 HF animals and c) 1000 JE animals. Daughter yield deviations were used as the phenotype for 25 different traits. The three datasets were analysed using the methodology termed BLUP by Meuwissen et al. (2001). Validation was undertaken by comparing the genomic breeding values (BV) with the progeny test BV estimated for the relevant sires in the test dataset. The degree of accuracy of the genomic-based BVs was measured by their correlation with the progeny test BVs. Three different genomic BVs were estimated for each animal in the test dataset utilising the predicted SNP effects from the three individual training datasets.

**Genetic evaluation.** Genetic evaluation of the animals is undertaken using a genomic relationship matrix (Harris and Johnson 2010). In brief, the method utilizes a two step process. The first stage involves the prediction of genomic breeding values for genotyped individuals. Because not all ancestors of genotyped animals are genotyped, a selection index procedure is used to blend genomic predictions with traditional ancestral information that is lost between the process of deregression of the national breeding values and subsequent re-estimation using the genomic relationship matrix. Finally, the genomically enhanced predictions are filtered through to non-genotyped descendants using a regression procedure.

## Results and discussion

**Accuracy of genomic estimates.** Correlations between the DNA BV and the progeny test BV varied from 0.37 to 0.76 for the traits in the test populations (table 1). In general, the correlations for the production traits were higher than those for the non-production traits. The correlations dropped dramatically when the SNP effects were estimated from the other breed in the training dataset to the breed that they were validated in. For example, when the SNP effects were estimated in the JE training dataset the correlations between the genomic BVs and the progeny test BVs for the HF bulls in the test dataset were between -0.05 and 0.16. This was also observed for the situation where HF SNP effects were used in the JE test dataset. The results indicate that the SNP effects estimated are breed specific. However, when the combined breed training dataset was used and then validated in the individual populations the correlations were nearly identical to those presented in table 1.

**Breeding value estimation.** Up until mid 2009, three sources of information were used in the estimation of breeding values for New Zealand dairy sires; parental information, own performance and progeny performance. Genomic information is now the fourth source. Harris and Johnson (2010) showed the inclusion of genomic information for production traits in bulls without daughters increased the reliability of the estimated breeding values from approximately 35% to 55-60% when genomic information is blended with parental information. For fertility, the corresponding increase in reliability is from 31% to 50%. In contrast, sires that are progeny tested with 85 daughters have reliabilities of 75%-85%.

**Table 1: Correlations between genomic-based and progeny test BVs in the test population for the Holstein-Friesian, Jersey and KiwiCross™ breeds.**

Trait	Holstein-Friesian <sup>1</sup>	Jersey <sup>2</sup>	KiwiCross <sup>3</sup>
Protein yield	0.65	0.50	0.72
Milk fat yield	0.53	0.54	0.59
Milk volume	0.67	0.62	0.76
Live weight	0.60	0.57	0.75
Fertility	0.68	0.49	0.52
Somatic cell score	0.57	0.58	0.57
Farmer opinion	0.46	0.38	0.37
Udder overall	0.47	0.50	0.49

<sup>1</sup> SNP effects estimated from the HF training data set, <sup>2</sup> SNP effects estimated from the JE training data set, <sup>3</sup> SNP effects estimated from all of the animals in the training data set.

**Breeding scheme.** The LIC breeding scheme, which had been based on progeny testing 300 bulls per annum, has been altered to incorporate DNA information. In 2008 the number of bulls progeny tested was reduced to approximately 160. The 160 bulls were selected from 450 that were screened using the 50K panel. In 2009, genomic information was more extensively used to select the bulls entering progeny test. To select the 160 bulls, 2000 bulls were identified as the highest genetic merit animals based on their parental information. These 2000 bulls were then screened over a custom-made 384 SNP panel. The SNP panel had markers selected from the 50K panel that best described Breeding Worth (BW; the economic index in New Zealand). The 384 SNP panel had 70-80% of the predictive power of that of the 50K panel. The highest 500 bulls for genetic merit estimated from the 384 SNP panel were then screened over the 50K panel to select the 160 bulls. The 384 SNP panel has not been used since due to i) the 384 panel not being cost effective compared to the 50K panel ii) technical issues with the genotyping equipment and iii) concern that selection on a small number of markers may be reducing the genomic diversity of the breeding population too quickly. For the 2010 progeny test, 160 bulls were selected from 2000 bulls that were genotyped over the 50K panel. Genomic screening of females was undertaken in 2008 to identify the best females to generate the next crop of elite sires. These females were screened over the 384 SNP panel in that season. It has not been repeated due to the lower increase in genetic gain per dollar spent on genotyping compared to screening more young bulls over the 50K panel.

**Commercial use of genomically selected bulls.** Genomically evaluated two and three-year old bulls were first commercially released in New Zealand in 2008 with the creation of genomically selected bull teams. The genomically selected teams are marketed as “DNA Proven” whereas the teams with sires that are progeny tested are marketed as “Daughter Proven”. The DNA proven teams have a larger number of bulls compared to the daughter proven teams to reduce the risk associated with using bulls of the lower reliabilities. The DNA proven teams (separate team for each breed) are sold to the market at a NZ\$5 premium to that of the daughter proven teams to reflect the genetic superiority of the young bulls. The average cost of a daughter proven straw of semen is approximately NZ\$18. In the 2008 mating season, the genetic superiorities of the DNA proven teams over the daughter proven

teams were approximately 10, 20 and 30 BW units for the HF, JE and KX teams respectively. Ten BW is approximately equivalent to the genetic gain achieved per annum in the dairy industry. During the 2008 mating season, the HF DNA Proven team was withdrawn from the market. This was resultant from daughter information for HF bulls that entered progeny testing in 2005. The genomic proofs for the HF bulls did not predict the daughter proofs as well as had been seen in the two previous sire proven scheme years (test dataset). Given that the HF DNA Proven team had an advantage of only approximately 10 BW it appeared that there was a significant probability that the DNA Proven team could have a lower BW than the Daughter Proven team. Over the 2008 and 2009 mating seasons the three DNA Proven teams accounted for approximately 10-20% of the total inseminations. For the 2010 season, yearling bulls have been added to the DNA proven team, which has increased BW differential to 30-40 units over the daughter proven teams.

**Future direction.** The correlations presented in this study are less than those generated through stochastic simulation by Meuwissen et al. (2001). The correlations in our study are in agreement with the theoretical expectations that have been modeled recently by Goddard and Hayes (2009). Goddard and Hayes (2009) demonstrate that in order to increase the correlations to 0.75 and above, 10-20 thousand genotyped animals are needed depending on the heritability of the trait. Genotyping of this number of cows is being considered in the next twelve months. In addition, high density marker panels (expected to be released in 2010) will be utilized over a proportion of the sires that have been genotyped over the 50K panel. Statistical techniques may be used to impute the genotypes for animals that have been genotyped for only 50K SNPs.

## Conclusion

The utility of genomic information in dairy cattle breeding schemes has now reached the level of accuracy that enables dramatic changes and improvements to breeding schemes. With denser marker panels, more sophisticated statistical tools, and in the longer term, sequencing, it is expected that the accuracy of BVs will continue to improve and breeding schemes will utilize genomic information further at the expense of progeny testing.

## References

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