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
- DNA information used in the LIC breeding scheme was for parentage testing in the mid 1990s
- In the late 1990s LIC began a QTL discovery program

Introduction

- QTL discovered in the LIC research program were used via marker assisted selection (MAS) in 1998 and 1999
- In 2000 the MAS program was stopped when the cost of the program became greater than its economic return

Introduction

- In 2001 Meuwissen et al. first proposed the use of dense marker maps in a genomic selection setting
- In 2006, the sequencing of the bovine genome by the international consortium was completed
- The sequencing generated a large number of single nucleotide polymorphisms (SNPs)

Introduction

- 2006 onwards
- The cost of genotyping dropped dramatically when tens of thousands of SNPs could be genotyped in parallel
- The technology shift to large-scale SNP genotyping allowed the application genomic selection

- This paper describes the use of genomic information in the LIC dairy cattle breeding scheme

Genotyping

- Genotyping was done using two different marker panels

- Illumina 50K panel: approximately 23,000 animals have been genotyped using the 50K panel

- Illumina 777K high density panel: 3,000 animals have been genotyped using the HD panel

Genotyping

- The genotyped population includes all of the sires that have been progeny tested since 1995 and 50% of sires progeny tested 1985-94

- 5538 Holstein-Friesian (HF) sires
- 2861 Jerseys (JE) sires
- 723 KiwiCross (KX) sires

- The majority of the females that have been genotyped are daughters of sires that were progeny tested in the last five years.

Genomic Evaluation

- Use a two-step process that incorporates information from the genomic relationship matrix with the traditional BVs

- The first stage involves the prediction of genomic breeding values for genotyped individuals.
- The second stage blends the genomic predictions with parent information from non-genotyped ancestors

Genomic Evaluation

- The genomic breeding values of parent animals are applied to their non-genotyped descendants
- The descendants breeding values and reliabilities are updated for the ancestors genomic information

Application of Genomic Selection

- Commercial use of genomic evaluated (GE) bulls

- In 2008 2-3 year old GE bulls were first released as a team of bulls
- In 2010 yearling bulls were selected for commercial use

Application of Genomic Selection

- Commercial use of genomic evaluated (GE) bulls
- The teams are marketed as “DNA Proven”
- The DNA proven teams have a larger number of bulls (25) compared to the daughter proven teams to reduce the risk associated with using bulls that have reliabilities that are lower than that of the progeny-tested bulls.

Application of Genomic Selection

- Commercial use of genomic evaluated (GE) bulls

- The DNA proven teams are sold at a NZ$5 premium to reflect the genetic superiority of the young bulls
- The average superiority of the DNA proven team is equivalent to 2½ years of genetic improvement
- The use of DNA proven sires has increased over the last 5 years, increasing from 15% of inseminations in 2008 to just over 40% in 2011

Application of Genomic Selection

- Breeding scheme

- Prior to the genomic selection, LIC had been progeny testing 300 bulls per annum
- In 2008, the number of bulls progeny tested was reduced to approximately 160 bulls
- The 160 bulls are selected from approximately 2000 to 3000 bulls with 50k genomic information
- The low-density (12K) panel will likely be used in 2012

Application of Genomic Selection

- Performance of genomics

- Genomic information was included in the national evaluation in 2009
- Subsequent analysis by NZAEL in 2010 identified that the genomic estimates were biased upwards
- In 2010-2011 adjustments were introduced to reduce the bias
- The majority of the adjustment factors now range from 20 to 40 BW units

Application of Genomic Selection

- Performance of genomics

- 2011, NZAEL decided to remove genomics from the main index (Breeding Worth) but continue to publish a secondary index that includes genomic information

Application of Genomic Selection

- Commercial use of genomic evaluated (GE) bulls

- The first two crops of DNA-proven sires, used in 2008 and 2009, have now received their progeny test proofs
- The initial GEBVs of these sires were found to be over-estimated and LIC credited the $5 premium that the farmers paid
- The adjustments have been re-estimated so the over-estimation should not occur in the forthcoming years

Application of Genomic Selection

- Improving genomic estimation

- Considerable effort to improve the accuracy and reduce the bias of the genomic evaluations

- Increasing the number of genotyped animals
- Better genomic evaluation systems to decrease the genomic bias

Application of Genomic Selection

- Improving genomic estimation

- Genotypes have been exchanged with Ireland, Australia and CRV Ambreed (NZ)
- Genotype-by-environment interactions have reduced the utility of the genotypes from both Australia and Ireland
- The exchange of NZ progeny-tested bulls with CRV resulted in increases in accuracy of approximately 3% for the milk production traits

Application of Genomic Selection

- Improving genomic estimation

- LIC has genotyped 25,000 females from the NZ dairy herd and is in the process of genotyping another 25,000 cows
- Most of the females that have been genotyped are the daughters of progeny-test sires
- Integration of the female genotypes into the genetic evaluation has been challenging

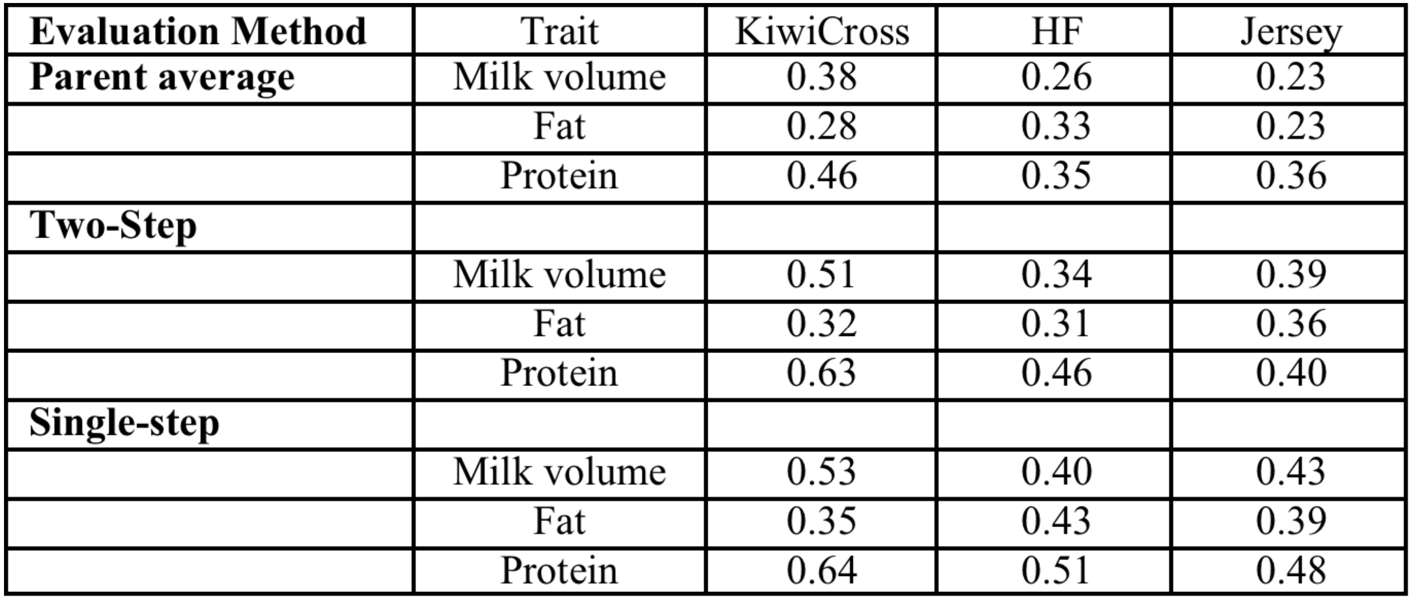
Application of Genomic Selection

- Improving genomic estimation

- Statistical tool development has focused on the single-step method for the NZ multi-breed population
- The single-step method has resulted in increases in accuracy over the current two-step method and in a reduction in the bias

Application of Genomic Selection

- Improving genomic estimation
- Increase in realized reliability between parent average, two-step and single-step genomic prediction

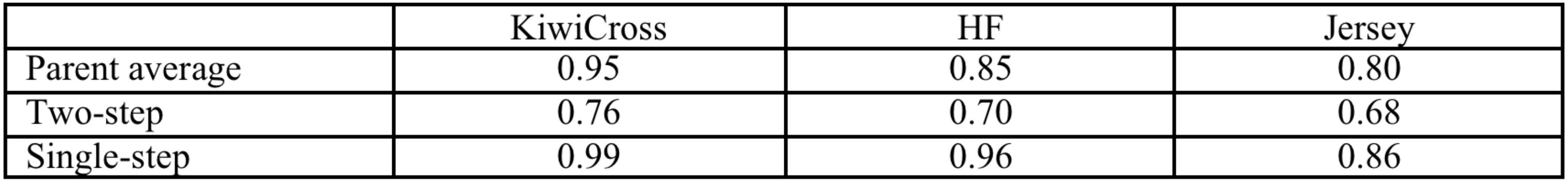


Evaluation Method	Trait	KiwiCross	HF	Jersey
Parent average	Milk volume	0.38	0.26	0.23
	Fat	0.28	0.33	0.23
	Protein	0.46	0.35	0.36
Two-Step				
	Milk volume	0.51	0.34	0.39
	Fat	0.32	0.31	0.36
	Protein	0.63	0.46	0.40
Single-step				
	Milk volume	0.53	0.40	0.43
	Fat	0.35	0.43	0.39
	Protein	0.64	0.51	0.48

Application of Genomic Selection

- Improving genomic estimation

- Average inflation estimates for the three milk production traits for each breed



	KiwiCross	HF	Jersey
Parent average	0.95	0.85	0.80
Two-step	0.76	0.70	0.68
Single-step	0.99	0.96	0.86

Future Direction

- LIC will continue to invest into improving the accuracy of genomic evaluation
- The current focus is on increasing the number of genotyped animals and increasing the density of genetic markers
- Active in whole genome sequencing
- Integrating biological information to identify markers that have causative effects

Conclusion

- The introduction of genomic information into LIC dairy cattle breeding scheme has been a steep learning curve over the last five years

- Dairy farmers have utilised the new technology and to date have not benefited to the degree that was expected, which is a common situation with new technology

Conclusion

- Ongoing investment will be required to continue to improve and maintain the accuracy of genomic selection
- With this investment, it is expected that the accuracy of genomics will continue to improve and breeding schemes will utilize genomic information further at the expense of progeny testing

Questions?