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

<table>
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<tr>
<th>Evaluation Method</th>
<th>Trait</th>
<th>KiwiCross</th>
<th>HF</th>
<th>Jersey</th>
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<tr>
<td>Single-step</td>
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<td>0.43</td>
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Application of Genomic Selection

:utf-8解读:-

Improving genomic estimation

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

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<th>HF</th>
<th>Jersey</th>
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<tr>
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<tr>
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<tr>
<td>Single-step</td>
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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?