Lessons learnt in implementation of genomic selection in breeding dairy cattle for New Zealand

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Outline

Introduction

Initial implementation of genomics – the golden years

Initial daughter results – the dark ages

Improved implementation – the renaissance

Challenges for small populations

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

- LIC invested in a QTL discovery program that yielded a small number of QTL for milk production traits – DGAT

Introduction

- In most countries, the genomic predictions are from within-breed analyses using a single-breed reference population

- LIC – Genomic Selection across breeds

Heifers entering the herds in 2014/15

Initial implementation of genomics – the golden years

The Golden Years

- 2007: technically and financially feasible to genotype large numbers for 50K SNP

- LIC genotyped 2400 HF, 1500 Jersey and 650 crossbred sires

- We genotyped essentially all the historical sires with DNA available and all sires that were in the current breeding scheme as at 2007

The Golden Years

- We undertook genomic selection validation studies within and across breed
  - 3500 sires in the training population
  - 900 sires in the validation population
- Across breed genomic selection model gave correlations 0.50 - 0.72
- In 2007 this was considered a large training population

The initial daughter results from genomic selection – the dark ages

The Dark Ages

- By 2010-2011 the teams of genomic sires were getting breeding values based on their daughter information

- The daughter breeding values showed that the initial genomic breeding values had been biased upwards and the accuracies lower than predicted

- Genomic inflation was on average 0.7 (30% over-estimated)

The Dark Ages

- What can you do?
  - Increase training population
    - Include sire genotypes from Ireland, Australia and CRV (NZ)
    - Genotype cows
  - Increase the SNP marker density
    - Genotype using 777K HD panel
  - Statistically control the bias – this has no impact on accuracy

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The Dark Ages

- Including cow genotypes
    - 14,000 cow genotypes with phenotypes
    - Approximately 5% increase in accuracy and 20% reduction in genomic inflation
    - 6-8 cow genotypes = 1 progeny tested sire genotype
- Including CRV (NZ) sire genotypes
    - Approximately 3% improvement in accuracy

Lessons Learnt

- A training population of 4500 sires is not large enough for accurate genomic selection for a multi-breed population

- Both accuracy of prediction and prediction bias are important genomic selection performance measures

Lessons Learnt

- Including genotypes from foreign sires without NZ phenotypes did not the increase accuracy
  - Genetic correlations between countries are less than 0.95 – lose accuracy from the foreign phenotypes
- Increasing the SNP panel density requires sufficient statistical power in the training population to capture the benefits

Improved implementation – the renaissance

The Renaissance

- 2012–2016: LIC undertook to whole-genome sequencing of 600 Holstein-Friesian, Jersey and crossbred dairy animals

- By 2016: Over 120,000 cows with phenotypes genotyped

- RNA-sequencing of mammary tissue for 350 lactating cows

- Substantial genomic resource

The Renaissance

- The sequencing and genotype resource will allow genome wide association mapping to identify causal variants or markers in strong association with the causal variants which are segregating in NZ population

- Genomic selection in the future will use a custom SNP marker set derived for NZ population

The Renaissance

- Major advances in the genomic breeding value prediction procedures

- 2014: LIC improved genomic breeding value prediction system

- Current performance

    - Validation correlations 0.60 – 0.85

    - Genomic inflation range 0.9 – 1.05

The Renaissance

- 2012/13
  A new mutation appears in a genomic young sire (rare event) – 1000s of progeny born

- Dominant mutation – only one copy required to express the trait (very rare event)

- Effects heat tolerance, coat characteristics and ability to lactate

- Sequencing resource allowed us to develop a gene test to identify carriers and remove these animals from the NZ herd

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Lessons Learnt

- Sequencing data allows detection and manage of new mutations and recessive deleterious genes

- Sequencing data should allow a custom SNP marker set derived for NZ population

- Training population size is still an important consideration in NZ – we still see improvements as more cows are genotyped

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Challenges for small populations

Challenges for small populations

- The bigger the training population the better the genomic selection accuracy

- The ideal training population will be determined by the number of chromosome segments segregating in the population

- The effective population size for small populations under reasonable selection pressure is expected to be small – may require smaller training population sizes

Challenges for small populations

- Cows are an important resource for genotyping

- They can contribute to the training population size

- Our experience suggests that 6-8 cows provide a similar improvement in genomic accuracy to 1 progeny tested sire

Challenges for small populations

- Across country genomic evaluation is an important tool for small populations

- The Brown Swiss Inter-genomics has been successful genomic selection implementation

  - Common sires are used across the participating countries

  - Between country genetic correlations are close to unity

  - Pool genotypes and phenotypes

Challenges for small populations

- The cost of sequencing is decreasing rapidly

- Sequencing key sires could be a useful activity

- The sequence could be made available to 1000 bull genomics project

- Allow the smaller populations to leverage the data and tools provide by the 1000 bull genomics project to help analyse their sequence data

Questions?