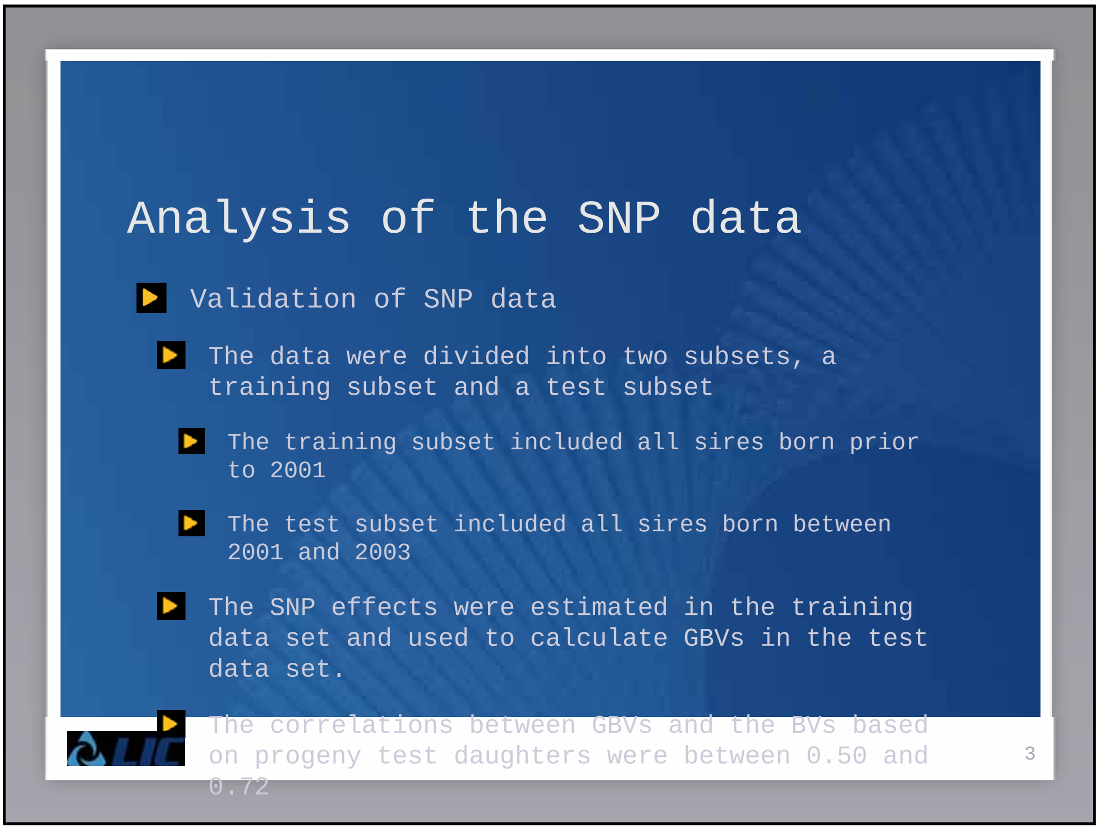
Selection in New Zealand and the implications for national genetic evaluation

B. L. Harris
D. L. Johnson
R. J. Spelman

LIC June 2008

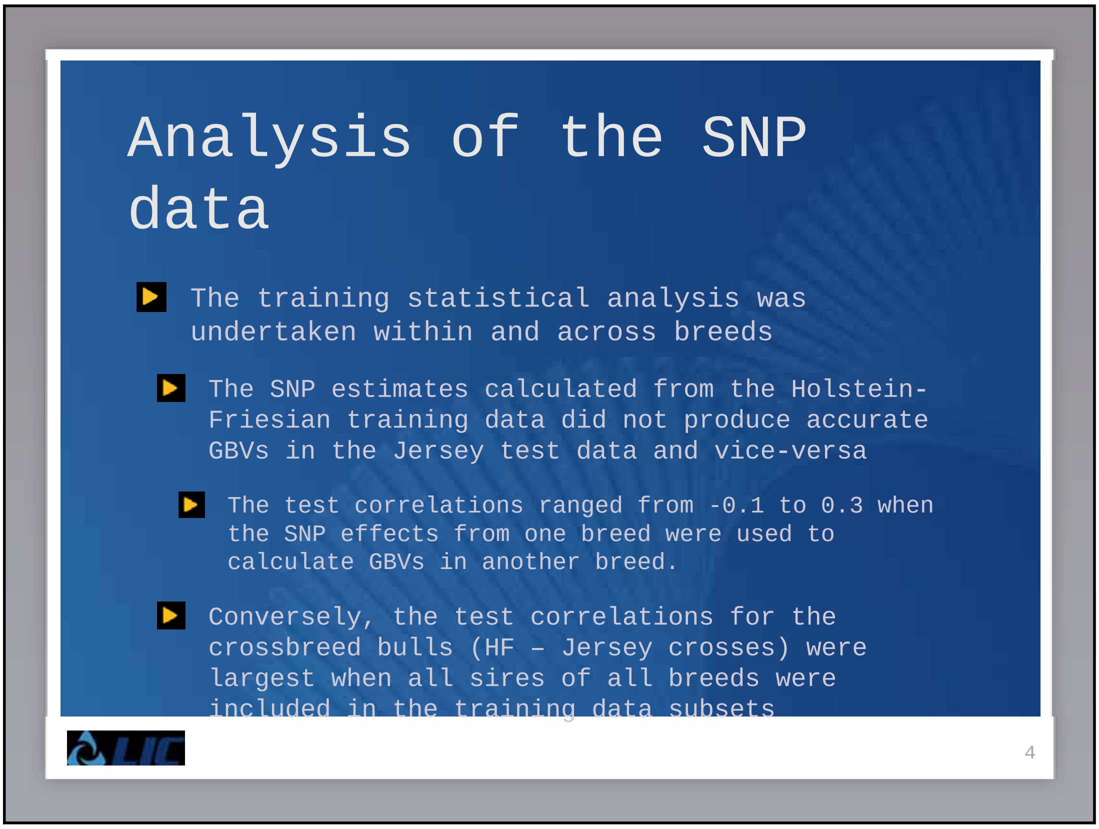
Introduction

- Genome-wide dense marker-data are available for dairy cattle
- LIC genotyped 4,500 sires born in the 1980s to the present using the BovineSNP50 BeadChip
  - The data included approximately 2,400 Holstein Friesian, 1,500 Jersey and 650 Holstien Friesian–Jersey crossbred sires
  - A total of 44,146 SNPs were retained for analysis



Analysis of the SNP data

- Validation of SNP data
  - The data were divided into two subsets, a training subset and a test subset
    - The training subset included all sires born prior to 2001
    - The test subset included all sires born between 2001 and 2003
  - The SNP effects were estimated in the training data set and used to calculate GBVs in the test data set.
  - The correlations between GBVs and the BVs based on progeny test daughters were between 0.50 and 0.72



Analysis of the SNP data

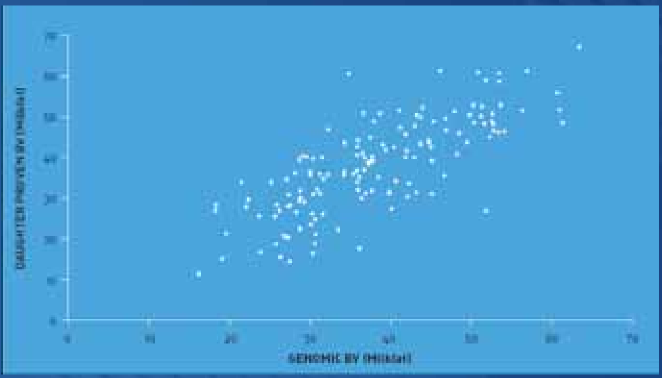
- The training statistical analysis was undertaken within and across breeds
  - The SNP estimates calculated from the Holstein-Friesian training data did not produce accurate GBVs in the Jersey test data and vice-versa
    - The test correlations ranged from -0.1 to 0.3 when the SNP effects from one breed were used to calculate GBVs in another breed.
  - Conversely, the test correlations for the crossbreed bulls (HF – Jersey crosses) were largest when all sires of all breeds were included in the training data subsets

Genomic breeding values for young sires

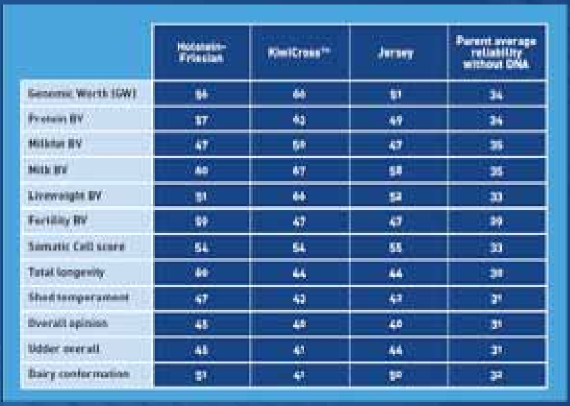
- Genomic BVs computed using genomic mixed model equations (MME) outlined by Van Raden (2007) and Habier et al., (2007)
- The input data for the models was de-regressed breeding values for proven sires and analysis was within breed for HF and Jersey sires
- This analysis the genomic relationship matrix was formed assuming equal variance for each SNP
- The reliabilities of GBVs were estimated by direct inversion of the mixed model equations

---

Genomic breeding values for young sires



Genomic breeding values for young sires



	Holstein-Friesian	KiwiCross™	Jersey	Parent average reliability without DNA
Genomic Worth (GW)	56	60	51	34
Protein BV	57	63	49	34
Milkfat BV	67	59	47	35
Milk BV	60	67	58	35
Liveweight BV	51	66	52	33
Fertility BV	59	47	47	39
Somatic Cell score	54	54	55	33
Total longevity	60	44	44	38
Shed temperament	47	43	43	31
Overall opinion	45	40	40	31
Udder overall	45	41	44	31
Dairy conformation	57	41	50	32

Genomic breeding values for young sires

- For young sires the breeding values on young sires based solely on genomic and parent information
  - Bias due overestimation of parent average as a predictor of breeding values based on progeny test for elite sires
- The overestimation is commonly caused by:
  - preferential treatment (intentional or unintentional)
    non-additive genetic effects (epistasis and dominance)
- It is important to remove the bias from the young sires genomic breeding values

LIC progeny testing program redesign

- Market the team genomic breeding values

[Teams used as]	Individual bull reliabilities	Team reliability	Size of team required
SPS bulls	35%	98%	35
Premier Sires DNA Proven bulls	60%	98%	18
Premier Sires Daughter Proven bulls	82%	99%	16

LIC progeny testing program redesign

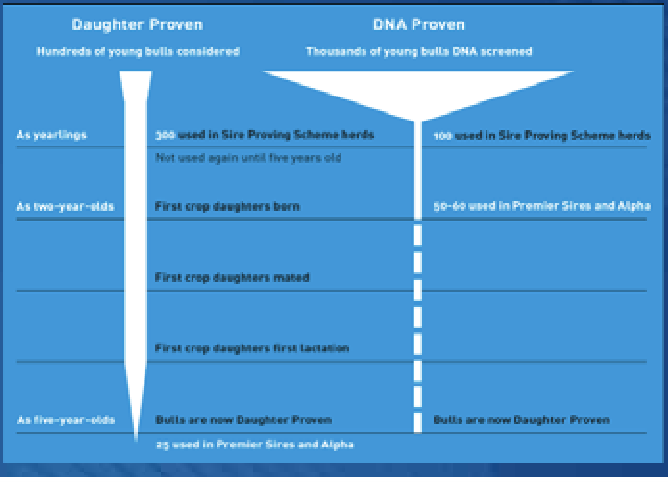
DNA PROVEN – 4 years

	YEAR -1	YEAR 0	YEAR 1	YEAR 2	YEAR 3	YEAR 4	YEAR 5
Thousands of bull calves	Cows selected for contract mating	Thousands of bull calves DNA screened. Best bulls selected	Semen from 100 elite bulls despatched into Sire Proving Scheme herds	Elite bulls available for widespread use in Premier Sires and Alpha	3 years advanced genetic gain		

DAUGHTER PROVEN – 7 years

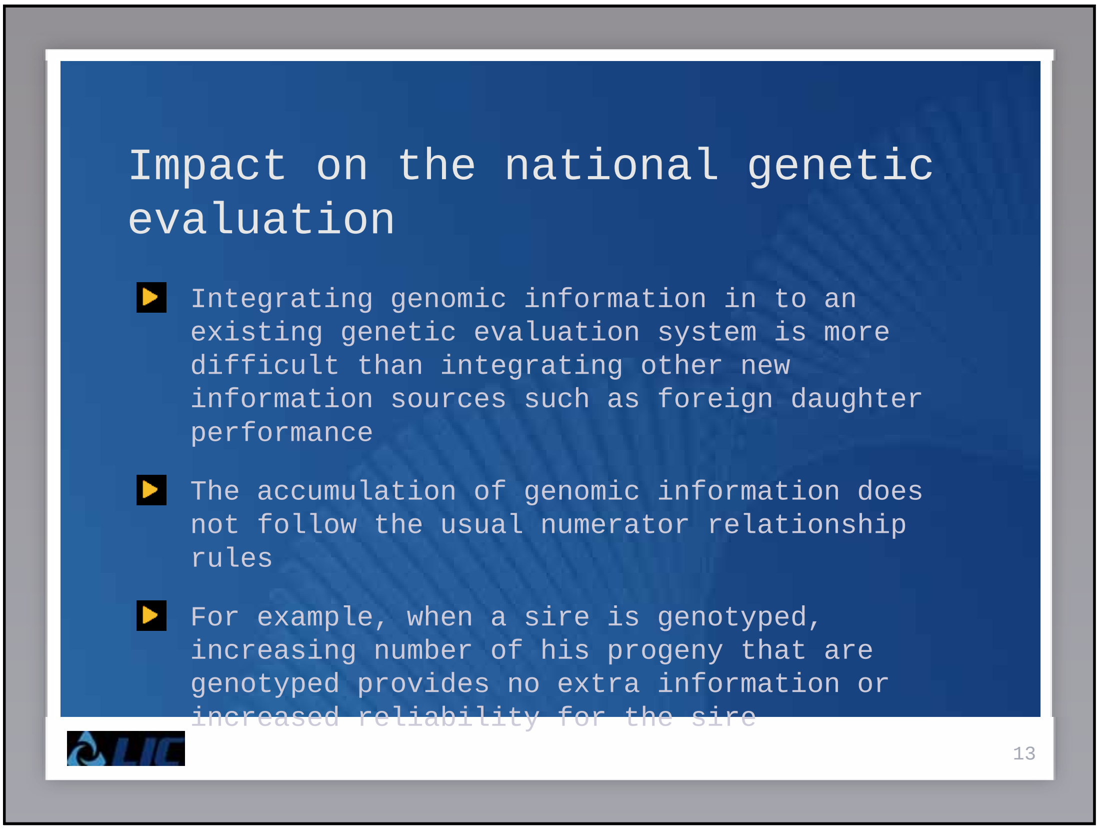
	YEAR -1	YEAR 0	YEAR 1	YEAR 2	YEAR 3	YEAR 4	YEAR 5
Hundreds of bull calves	Cows selected for contract mating	Bull calves purchased	300 bulls used in Sire Proving Scheme herds	Daughters born	Daughters mated	Daughter calves	25 elite proven bulls available for widespread use in Premier Sires and Alpha

LIC progeny testing program redesign



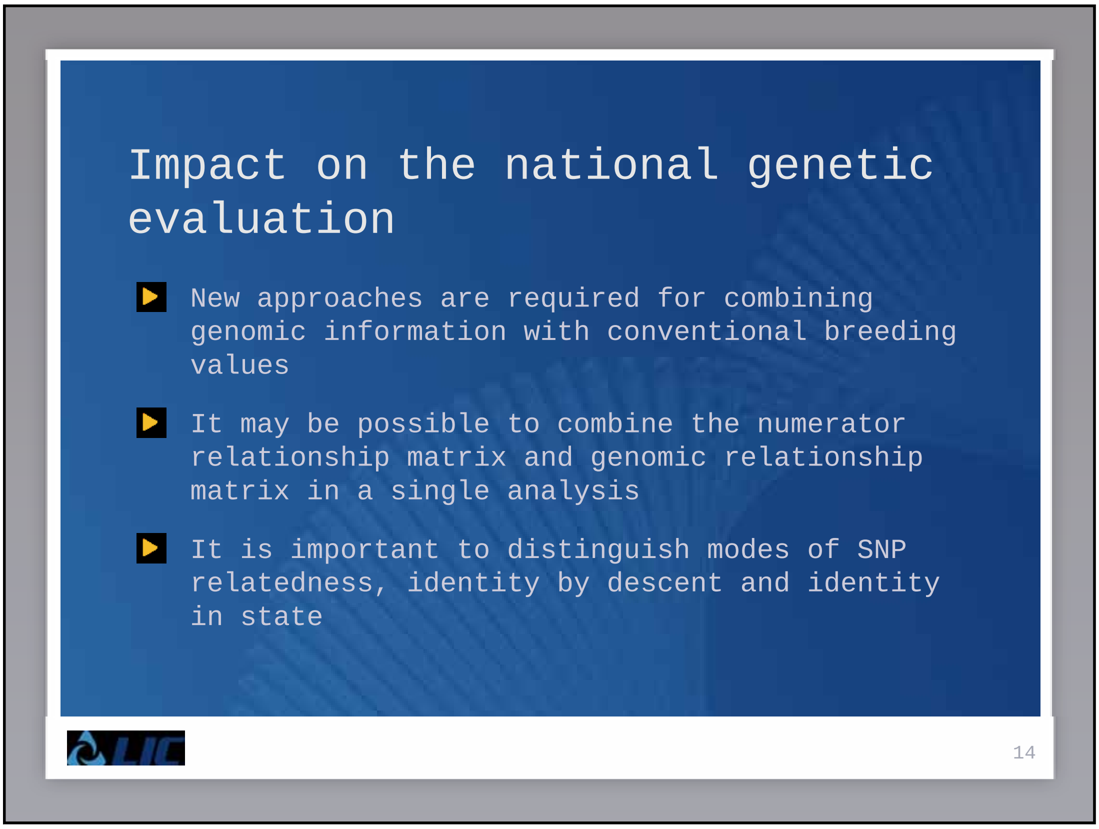
Impact on the national genetic evaluation

- The national genetic evaluation system calculates breeding values for cows and sires and is based on weighting three sources of information
  - parent information, own performance and progeny performance
- Conceptually genomic selection provides a fourth source of information, SNP or DNA information



Impact on the national genetic evaluation

- Integrating genomic information in to an existing genetic evaluation system is more difficult than integrating other new information sources such as foreign daughter performance
- The accumulation of genomic information does not follow the usual numerator relationship rules
- For example, when a sire is genotyped, increasing number of his progeny that are genotyped provides no extra information or increased reliability for the sire



Impact on the national genetic evaluation

- New approaches are required for combining genomic information with conventional breeding values
- It may be possible to combine the numerator relationship matrix and genomic relationship matrix in a single analysis
- It is important to distinguish modes of SNP relatedness, identity by descent and identity in state

Impact on the national genetic evaluation

- Semen exporting companies will want Interbull international comparisons on young sires that include genomic information
- Providing an international genetic evaluation system that combines daughter performance and genomic information from different sources will be a challenging project
- The genomic information from different countries cannot be simply treated as independent sources of information
- Presumably environment by genomic interactions will exist as well

---

Discussion

- The availability of genome-wide dense marker data for dairy cattle has allowed GBVs to estimated on young sires with no progeny information
- Farmers will want genomic information incorporated into the national genetic evaluation
- The semen exporting companies will require international genetic evaluations to include genomic information
- If genomic information is not integrated in to these systems then these systems will no longer be the primary source for selection information and their usefulness is limited

Discussion

- Technology will improve, higher density SNP chips will become available, analysis tools will improve
- In time, complete sequence data could be available on individual sires at relatively low cost
- The genetic evaluation solutions will need to evolve with the advances in DNA technology

---

THIS WILL CHANGE

DAIRY FARMING

FOREVER

Questions