Current Status of the Use of Genomic Information in the National Genetic Evaluation in New Zealand

B. L. Harris[1] and W. A. Montgomerie[2]
[1]LIC, Private Bag 3016, Hamilton, New Zealand
[2]NZ Animal Evaluation Unit, Hamilton, New Zealand

Who provides the resources for genotyping?

The genotyping is not a service organised or provided by the national genetic evaluation unit. Commercial laboratories are contracted by the individual breeding companies or by individual breeders to undertake the genotyping of their animals. There are two technologies being used in New Zealand, Customized CRV Illumina 60K and the Illumina Bovine SNP50 BeadChip. The use of the two technologies is likely to result in added compexity to the use of genomic information in the national genetic evaluation systems.

Who owns the genomic data?

The individual breeding companies or an individual breeder will organise their own genotyping and therefore own their genomic data.

Who has access to genomic data?

Obviously the owners (individual breeding companies or an individual breeder) have access to their genotypes. The national genetic evaluation unit will have access to genotypes from individual breeding companies or an individual breeder if the breeding company or breeder has agreed to provide the genomic information for national genetic evaluation. The genotypes will stay in-house with the breeding companies, while the national centre provides the software for creating the GRM coefficients for input to the national evaluations. The SNP prediction equations will be available in the individual breeding companies from there own analysis of their own data. The national genetic evaluation system will provide genomic estimated breeding values (GEBV) for proven and unproven sires. The GEBVs for sires will be publicly available using similar criteria to that used for publication of EBVs.

A brief description of training data sets?

All LIC progeny test sires from sires born 1980s through to 2000 were used for initial training and the test data set was sires born 2001-2003 as outlined by Harris *et al.* (2008). The initial training data set contained: 1450 Holstein Friesian sires, 980 Jersey sires and 60 Jersey-HF crossbred sires. The GEBV estimation initial testing has been undertaken using all LIC progeny test sires born in 2005 or earlier. From the SNP data on the 4,500 sires approximately 1400 loci had a deletion or an identified third allele which resulted in lower than average call rates and these SNPs were removed. SNPs were removed for low call rates, minor allele frequencies less than 2%, non-Mendelian inheritance and failed Hardy Weinberg tests. A total of 44,146 SNPs were retained for analysis. Genomic breeding values (GBVs) were estimated for 25 traits; milk volume, milkfat, protein 270-day yields, live weight, fertility, somatic cell score, longevity, 12 linear conformation traits, 4 farmer scored linear traits, calving difficulty and gestation length. The input data for the analysis was additive component of the de-regressed breeding values (genetic groups were removed). The de-regression of breeding values avoids double accounting of genetic relationships in both the numerator relationship matrix and the SNP effects. The SNP effects were estimated in the training data set and then these estimated effects were used to estimate GBVs in the test data set. The accuracy of the GBVs was estimated by the correlation between these GBVs and the BVs based on progeny test daughters.

A brief description of SNP effects estimation method?

To compute GEBVs for proven and unproven sires the genomic mixed model equations (MME) outlined by VanRaden (2008) will be used. The input data for the models was de-regressed breeding values for proven sires. The MME uses a genomic relationship matrix rather than a numerator relationship matrix. The method for obtaining the genomic relationship outlined by VanRanden (2008) that does not require allele frequencies but instead adjusts for mean homozygosity by regression techniques has been extended to account for multibreed populations. The extension allows the covariance between relatives in a multibreed population to take account of the differences in allele frequency among breeds. This algorithm is similar to that for forming the relationship matrix in a purebred population except that when forming the diagonals we partition into breed fractions to account for different variances among breeds and include segregation variances due to different allele frequencies among breeds. In the MME analysis all the progeny tested sires data is used. Current testing of the model is using LIC progeny test sires born in 2005 or before, and contains 1995 Holstein Friesian sires, 1295 Jersey sires, 334 Jersey-HF crossbred sires The genomic relationship matrix is adjusted to take account of the differences in allele frequency among breeds and crosses. The reliabilities of GEBVs are estimated by direct inversion of the mixed model equations. The GEBVs for young bulls do not contain all the parent information that is contained in the national genetic evaluation. To incorporate the parent information from the national genetic evaluation a selection index approach will be used. The parent information from the national genetic evaluation and the GBV are not independent sources of information. The covariance between the parent information and the GBV was approximated by the reliability of the parent information in the genomic MME with a numerator relationship matrix replacing the genomic relationship matrix. The equations are given by Berry *et al.* 2009 in appendix 1.

What is the publication policy?

The GEBVs for sires will be publicly available using similar criteria to that used for publication of EBVs. The GEBVs for cows will available to the cow owners through the same processes as EBVs for cows are currently published.

What is the time frame to release genomic evaluations?

In June-July 2008 unofficial GEBVs and genomic evaluations based on national breeding objective economic values were released by the breeding companies. The official GEBVs are planned for release in May-July 2009 from the national genetic evaluation unit.

What is the attitude towards Interbull/International evaluations accounting for genomics?

New Zealand would welcome international evaluations that account for genomics provided that between country/farming-sytem GxE was taken into account appropriately. Interbull appears to be the logical choice for an international repository of genotypes.

Collaborations

At present CRV and LIC are collaborating with the national genetic evaluation unit by providing genomic information for an official NZ GEBV release in May-July 2009. LIC and ICBF have exchanged genotypes and phenotypes for Holstein Friesian sires and are working towards producing a prototype joint across country GEBV estimation for NZ and Ireland.

References

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