Significant Changes to Brahman GROUP BREEDPLAN

Significant changes have been introduced to the BREEDPLAN software used to calculate EBVs for Australian Brahman animals. These changes have been applied in the April 2017 Brahman GROUP BREEDPLAN analysis and will apply to subsequent analyses.

The Australian Brahman Breeders' Association (ABBA) has worked collaboratively with staff at the Animal Genetics & Breeding Unit (AGBU) and the Agricultural Business Research Institute (ABRI) to implement a new approach for incorporating genomic information into the calculation of Estimated Breeding Values (EBVs) within Brahman BREEDPLAN. This technology is known as "Single Step" BREEDPLAN and heralds a new age in BREEDPLAN genetic evaluation and the implementation of genomic selection for the Australian beef industry, and specifically the Brahman breed.

What is Single-Step BREEDPLAN?

Single-Step BREEDPLAN is a new genetic analysis where the pedigree, performance and genomic (DNA) information is processed and analysed all together.

This is different from the blending methodology which has been used to incorporate genotype information into Brahman BREEDPLAN. In the blending approach:

- a Direct Genomic Value (DGV) is calculated using a prediction equation derived from research data, and
- the DGV is then combined with the existing EBV for the animal, using the derived genomic accuracy for each trait and the existing accuracy of an animal's EBV for that trait.

The single-step analysis is a significant improvement on the blending approach, in that it takes account of each animal's <u>actual</u> genetic relationship based on its genotype with all other genotyped animals, including those in the reference population. In the blending approach, each animal with a DGV is assumed to have the same genetic relationship with the reference population. The reference population is the set of Australian Brahman animals that have genotypes (SNP data) and phenotypes (performance records) for a particular trait. Currently the reference population for Australian Brahman includes animals measured and genotyped in the CRC, along with animals genotyped and recorded in the Brahman BIN program and current R&D projects and in industry herds.

Overall, the most important effects of the switch to Single-Step BREEDPLAN are that:

- Genomic information will contribute to all EBVs that are calculated within the main multi-trait BREEDPLAN analysis.
- Animals that had previously obtained Blended EBVs will now show a range of accuracies in their EBVs for 200-Day Weight and Days to Calving. That range reflects the genomic relationship between the animal and the reference population, and will vary from animal to animal.

- The Days to Calving EBV now incorporates information from research data on two genetically correlated traits – first lactation anoestrous interval and heifer age at puberty. This data will ensure that the single-step analysis includes the same data previously used to derive the prediction equations and then to generate the DGV for Days to Calving.
- Unknown parents may be identified (provided the animals have genomic information available).
- Genomic information will contribute to not only the EBVs of the animal that has been genotyped, but will also contribute to the EBVs for the animal's relatives (e.g. parents, progeny). This is unlike blending where the genomic value was only included into the individual's own EBV (not its parents or progeny).
- The need to regularly re-calibrate the prediction equations that are used to calculate genomic predictions is removed, with genomic effects being updated each time that a Brahman Single-Step BREEDPLAN analysis is conducted.
- With a traditional pedigree based approach, the relationships between animals within Brahman BREEDPLAN are determined by pedigree alone. For example, pedigree would predict that the genetic relationship between full siblings (i.e. animals with the same sire and dam) is 0.5. This means that full siblings are predicted to have 50% of genes in common when calculating traditional pedigree-based breeding values. Now in single-step the relationship between individuals is determined using their SNP genotypes and will vary from the previously assumed average relationship. In the case of full-sibs this may now vary from 0.35 to 0.65.

    Similarly, pedigree may assume that two animals are unrelated, but in reality, the animals may share common genes, and have a genomic relationship greater than 0.

Other Changes to the Brahman Analysis

In addition to the introduction of the single-step technology, a number of other changes were introduced in the April Brahman BREEDPLAN analysis. These included:

- The calculation and reporting of the EBV for Carcase Intra Muscular Fat (IMF). Note that only IMF measurements derived from abattoir data are used in the calculation. Scan IMF measurements are not used in the Brahman analysis.
- The introduction of a new male reproduction trait, Percent Normal Sperm (PNS). PNS is measured as part of the bull breeding soundness evaluation (BBSE) at around 2 years of age. It is expected that sires with higher (ie more positive) PNS EBVs will produce sons with higher PNS compared to sires with lower (ie more negative) PNS EBVs.
- The elimination of the blending of DGVs. With the inclusion of the genotype information in the single-step analysis, it is no longer possible to blend the DGVs for 200-Day Weight and Days to Calving.

A key requirement for the single-step analysis is the formation of the genomic data. The software to analyse this data also checks for pedigree and breed composition. Currently, only animals identified as purebred Brahmans (ie greater than 80% Brahman) are eligible to have their genotypes included in the analysis. Further, this software will also identify possible discrepancies between the paper pedigree and the genomic pedigrees and breeders will be approached to re-sample the animals to ensure DNA integrity and in some cases pedigrees may need to be corrected by the ABBA.

Summary

The April Brahman BREEDPLAN analysis included significant changes. These included:

- the introduction of the Single-Step BREEDPLAN software,
- the inclusion of additional traits, and
- the cessation of the blending of DGVs.

For most animals these changes will not have resulted in significant changes to EBVs and Selection Index values. However, in some cases, the rankings of animals may have changed.

The important message from the introduction of the single-step analysis is that the greatest change in EBVs and accuracies was for:

- animals that had a genotype record used in the analysis and, in particular, animals with lower accuracy EBVs – in general younger animals. Once an animal has its own record for a trait, or has progeny recorded for a trait, the additional information coming from genomic relationships with the reference population will be reduced, and
- the 200-Day Weight and Days to Calving EBVs for animals that previously had DGVs blended but which are now ineligible for the incorporation of their genotypes.

If you have any questions regarding the changes to Brahman BREEDPLAN or to changes in EBVs resulting from the new analysis, please contact Paul Williams, Brahman TBTS Technical Officer (P: 07 4927 6066, E: paul@tbts.une.edu.au) or Brahman BREEDPLAN (P: 02 6773 3555, E: brahman@breedplan.une.edu.au)