

Current News & Events

Latest News

It's a World First! Multi-Country Single-Step BREEDPLAN analysis for the Hereford breed 8 November 2017 BREEDPLAN is pleased to announce the release of a world first: a multi-country Single-Step BREEDPLAN analysis for the Hereford breed, released as the mid-October 2017 Hereford GROUP BREEDPLAN analysis. "This will allow the Hereford breed in Australia, New Zealand and Namibia to take advantage of cutting-edge analytical software that now includes genomics," said Dr. Brad Crook, BREEDPLAN (ABRI). The release of Single-Step BREEDPLAN heralds a new age in genetic evaluation technology available to the beef cattle industry, and specifically the Hereford breed in Australia, New Zealand and Namibia. This new genetic analysis combines pedigree, performance and genomic (DNA) information together in a complete multi-trait BREEDPLAN analysis of birth, growth, fertility, carcass and feed intake traits. Genomic information now contributes to the EBV and accuracy calculations of genotyped animals and their relatives. What is Single-Step BREEDPLAN? Single-Step BREEDPLAN is a new genetic analysis where pedigree, performance and genomic information is processed and analysed all together. The single-step analysis takes account of each animal's actual genetic relationship based on its genotype with all other genotyped animals, including those in the reference population. The reference population is the set of Hereford animals within the Hereford BREEDPLAN analysis that have genotypes (SNP data) and phenotypes (performance records) for a particular trait. "Single-Step doesn't remove the need for ongoing collection of accurate phenotypes," said Dr. Alex Ball, Strategic and Innovation Manager at Herefords Australia. "It is important that breeders embrace genotyping if they are going to extract any benefit from Single-Step". Overall, the most important outcomes of introducing Single-Step BREEDPLAN are:

- Genomic information will contribute to all traits that have EBVs calculated within the main multi-trait BREEDPLAN analysis.
 - Unknown parents may be identified (providing animals have genomic information available).
 - Genomic information contributes not only to EBVs of genotyped animals but also contributes to EBVs of their relatives (e.g. parents, progeny).
 - With a traditional pedigree based approach, the relationships between animals within Hereford 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. In Single-Step BREEDPLAN, however, SNP genotypes are used to determine the actual degree of relationship between individuals. In the case of full siblings, this may now vary from 0.35 to 0.65 – rather than 0.5 as would be assumed in a traditional approach to genetic evaluation. This will allow for improved accuracy in the EBVs calculated.
- Summary With the release of the mid-October 2017 BREEDPLAN results, the Hereford breed in Australia, New Zealand and Namibia has become the first breed worldwide to implement a multi-country Single-Step BREEDPLAN analysis. Genomic information as well as pedigree and performance data is now being used to calculate Hereford BREEDPLAN EBVs and accuracies.

Australian Bazadais Cattle Society Inc. Join BREEDPLAN In August 2017, the Australian Bazadais Cattle Society Inc. became the latest Australian Breed Society to join BREEDPLAN, with the purpose of running a national genetic evaluation for the Bazadais breed. A national genetic evaluation offers Australian Bazadais breeders several opportunities, these include:

- The ability to identify genetically superior sires and dams for breeding purposes.
- The ability to make objective selection decisions for traits of economic importance.
- The ability to benchmark the genetics of their herd against other Australian Bazadais herds for a range of economically important traits. These opportunities will allow Australian Bazadais breeders to identify areas in which their herd is performing well, and areas in which there is an opportunity for genetic improvement. Equally, Australian Bazadais breeders will now be able to identify animals which have the genetic package to complement their breeding programs and improve their herd. Together, this will allow Australian Bazadais breeders the opportunity to increase the rate of genetic improvement within the breed. Those interested in joining Bazadais BREEDPLAN can find an enrolment form [here](#), and a fee schedule [here](#). Further information can also be found in the Technical section of the BREEDPLAN website or by contacting BREEDPLAN staff on (02) 6773 3555.

Introduction of Single-Step to Brahman GROUP BREEDPLAN Exciting times ahead for members of the Australian Brahman Breeders' Association with the introduction of significant changes to the BREEDPLAN software used to calculate EBVs for Australian Brahman animals. These changes were applied in the April 2017 Brahman GROUP BREEDPLAN analysis and is now incorporated into the monthly analysis. This has resulted from the implementation of 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. The single-step analysis is a significant improvement on the blending approach, in that it takes account of each animal's actual 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. 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).

- 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. 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. Summary The 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 200-Day Weight and Days to Calving EBVs.