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 are 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 (i.e. more positive) PNS EBVs will produce sons with higher PNS compared to sires with lower (i.e. 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.
The Importance of Recording the Performance of Your Cattle

The saying “You only get out of something what you put into it” is particularly true of performance recording for genetic evaluation purposes. While it is possible for animals which have little or no performance data recorded to have EBVs, this TechTalk explains the benefits of recording as much trait information on your animals as practical.

Specifically, this article will discuss how we use recording to identify genetic merit, how recording more information can increase EBV accuracy, how identifying curve benders is impossible without recording, why recording is still important with genomics and how trait records can be used for non-genetic purposes. In addition, this article will discuss how to find out what traits have been recorded for each animal on the BREEDPLAN database and the value of recording traits for which BREEDPLAN does not currently calculate EBVs.

Identifying the Genetic Merit of Your Animals

With genetics, what we see is not always what we get. This is because environmental factors also have a considerable influence on most production traits. Therefore we cannot simply say that all of the observed differences in performance between animals raised in different environments and/or different management groups is due to their genetics.

In the example illustrated in Figure 1, we are comparing three bulls used on three different properties that have differing levels of feed availability. Based purely on the raw average yearling weights of each bull’s progeny, it is impossible to know whether Bull B has superior genetics or whether his progeny’s heavier weights are a function of the environment in which they were raised (on irrigated pasture). Nutrition is just one of the many environmental factors that can influence production traits. It is important to note that these factors can occur not only between properties, but between mobs and even within a single mob on a property. Two classic within mob examples are the presence of twins or individuals being sick or injured in an otherwise healthy herd.

The BREEDPLAN analysis removes the environmental factors from each animal’s raw performance and calculates Estimated Breeding Values (EBVs). To achieve this, BREEDPLAN uses three sources of information; these are pedigree, trait records (from the individual itself and its recorded relatives) and, for some breeds, genomic information.

To allow BREEDPLAN to compare animals in different management groups (e.g. the scenario given in Figure 1), there needs to be a genetic link between each group and/or property. A sire used in multiple groups passes on the same

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Figure 1. The average progeny yearling weight of Bull A, Bull B and Bull C, where the progeny were breed and raised on different properties.
genetic merit regardless of the group (or environment) he is used in. Therefore, by comparing the progeny of the link sire against the progeny of Bulls A, B and C on each individual property, we can evaluate the relative genetic merit of all the bulls involved.

As Figure 2 shows, the progeny of Bull A were 10kg heavier on average at 400 days of age than the link sire’s progeny, while the progeny of Bull B were on average 10kg lighter at 400 days of age than the link sire’s progeny. The progeny of Bull C were on average 20kg heavier than the progeny of the link sire at 400 days of age. Given that the genetic merit of the link sire does not change (e.g. any difference in average 400 day weight of the link sire’s progeny on each property is due to environmental factors), we can deduce that Bull A and C are genetically superior to the link sire for 400 day weight, and Bull B is genetically inferior to the link sire for 400 day weight. As a result, we would expect that the 400 Day Weight EBVs for Bulls A, B and C will be 20kg heavier, 20kg lighter and 40kg heavier, respectively, than the 400 Day Weight EBV of the link sire.

**Consider these animals:**

1. Animal A with no trait records (no birth weight or 200 day weight).
2. Animal B with a correlated trait record (200 day weight) but no record for the trait in question (birth weight).
3. Animal C with a record for the trait in question (birth weight) but no correlated trait records.

Indicative EBV accuracies for Animals A, B and C are displayed in Figure 3. It is important to note that these values are indicative only, as the exact EBV accuracies for an animal will vary depending on a number of factors. These factors include 1. the heritability of the trait, 2. the EBV accuracy of the parents, 3. the amount of performance information available, 4. the effectiveness of the performance information (e.g. contemporary group structure) and 5. genetic correlation with other measured traits. For example, we would expect that the EBV accuracies would be lower for traits (e.g. fertility) that are less heritable than birth weight. Equally, if the genetic correlation between the two traits was lower, then the difference in EBV accuracy between animals B and C would be greater.

**Accuracy of Your Genetic Merit Estimates and Thus the Accuracy of Your Subsequent Selections**

While it is possible to generate reliable EBVs from performance that has been recorded on correlated traits, generally speaking EBVs will be of lower accuracy if animals have not been directly recorded for the trait of interest. By definition, an EBV is an estimate of an animal’s true breeding value. The higher the accuracy, the more likely the EBV will predict the animal’s true breeding value and the lower the likelihood of change in the animal’s EBV as more information is analysed for that animal, its progeny or its relatives. Ultimately, the higher the EBV accuracy, the more informed and reliable the selection decisions are that are made, and the more genetic improvement that can be achieved.
The take home messages from these results are that EBV accuracy is improved by:

- Recording as much data as possible.
- If recording a trait is not practical (e.g. expensive or difficult to measure), then recording a correlated trait is beneficial though not as effective as recording the actual trait.
- Using information from correlated traits is also ineffective if you are trying to select against the known relationships between traits. See the following ‘Curve Bender’ section for more detail.
- To collect effective information for the BREEDPLAN analysis, breeders should aim to have a minimum contemporary group size of six animals, with at least two sires represented in each contemporary group.

BREEDPLAN can analyse up to two weights for each of 200, 400 and 600 day weights, and up to four mature cow weights per animal. Recording such repeated records can improve the accuracy of the resulting EBVs.

**Identifying ‘Curve Benders’**

‘Curve Benders’ do not follow the normal trend (e.g. high growth associated with high birth weight), but ‘bend the curve’ (e.g. high growth but low/moderate birth weight). Due to the strong genetic relationships between these trait pairings, we would typically expect that selection for growth would lead to an increase in both birth and mature weights, even if no selection emphasis is placed on birth and/or mature weight. This would have in turn have undesirable consequences for calving ease and mature cow feed requirements.

Fortunately, the correlations that govern these relationships are not absolute and are calculated from the average of the population. Therefore if a breeder records both traits, they should be able to identify individuals that deviate from the average correlation, and thus find animals that bend the growth curve. However, in situations where the breeder does not record both traits, the BREEDPLAN analysis has to rely on pedigree information and the correlations between traits to estimate the missing breeding value(s). In these circumstances, identifying curve benders is not possible. For example, if birth weight isn’t recorded then the Birth Weight EBV will be estimated based on the correlations with the 200, 400 and 600 day weight observations. Given that the correlations between the growth traits and birth weight are positive, an animal with high Growth EBVs will receive a high Birth Weight EBV. Thus, identifying ‘curve benders’ cannot occur.

**Relevance of Trait Recording When Using Genomics**

In breeds where genomic information is currently incorporated into the BREEDPLAN analysis, a genomic test will give you an estimate of your animal’s genetic merit (in the form of BREEDPLAN EBVs). However, the accuracy of the genomic EBVs for your herd will depend on a number of factors, including how closely related your animals are to what is termed the ‘reference population.’ The reference population is a group of animals which have both trait records and genotypes, and is critical for the success of genomic selection.

Recording traits for your animals in addition to having genomic tests done will mean your animals will become
part of the reference population. In turn, the genomic tests are likely to be more accurate for animals in your herd, thus increasing the accuracy of your breeding values and allowing you to make more genetic progress. For further information see the SBTS & TBTS Technical Note ‘An Introduction to Genomic Selection’.

**Recording Isn’t Just For Genetic Purposes**

The traits that you record can also serve a purpose outside of identifying the genetic merit of your herd. For example, the loss of weight in an individual can be an indicator of ill health, while weight loss in a whole mob can indicate that more feed is required. Recording your herd also allows you to benchmark where your herd is so that you can compare it against where you want to be and make appropriate management and strategic genetic decisions in order to reach your production system targets.

**How Can I Tell What Traits an Animal Has Been Recorded For on BREEDPLAN?**

The traits for which data has been submitted to BREEDPLAN are listed below the EBVs on the Individual Animal Page on Internet Solutions. An example of this is shown in Figure 4. In this particular example, the animal has had a calving ease score, a birth weight, two 200 day weights, a 400 day weight, a scrotal circumference and ultrasound scan data (eye muscle area, rib fat depth, rump fat depth and intramuscular fat) recorded with BREEDPLAN. Below the ‘Traits Observed’ listing it is also worth noticing that the animal has 688 progeny in 33 herds recorded, 351 of which have been scanned and 48 daughters with their own progeny recorded (grand progeny of the original animal listed). These progeny trait records also increase the accuracy of this animal’s EBVs.

Some breed societies display the Completeness of Performance herd rating for individual BREEDPLAN herds on Internet Solutions. For these breeds, it is also possible to look at the general recording level within a herd by checking the individual herd’s Completeness of Performance Star rating. The star rating is a 1 to 5 scale (with 5 stars being the ‘gold standard’) and reflects how much data each breeder submits to BREEDPLAN. Some breeders also make the traits recorded with BREEDPLAN available by listing the measurements taken and/or the raw observations for some traits in their sale catalogues.

**What Happens if BREEDPLAN Doesn’t Calculate EBVs for Some of the Traits I Want to Record?**

There are a number of breeds for which the full range of BREEDPLAN EBVs is not yet available. This is usually due to the lack of sufficient records within these breeds to analyse for that trait. The most commonly unavailable are the Days to Calving, Calving Ease, Structural Soundness and Temperament EBVs (either Docility or Flight Time). In addition, BREEDPLAN has recently commenced recording some new traits in some tropical breeds. These are Buffalo Fly Lesion Score, Tick Score and Coat Score.

If either of the above scenarios apply to you and you already record that trait in your herd (e.g. Calving Ease EBVS not available but you record calving difficulty scores for calves), then this data can be submitted to BREEDPLAN for storage and potential use in future BREEDPLAN analyses.

Remember, if the trait is important to you and/or your clients then make sure you are recording it! For further information on recording performance data, please contact staff at Southern Beef Technology Services (SBTS) or Tropical Beef Technology Services (TBTS).

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**Figure 4. Traits observed section on an Individual Animal Page on Internet Solutions.**
In 2017, SBTS held regional forums at a number of locations around Australia. The first regional forum was held in Armidale (NSW) in March. In April, SBTS held five Regional Forums in Albury (NSW), Seymour (VIC), Warragul (VIC), Hamilton (VIC) and Launceston (TAS). In June, three regional forums were held in Dubbo (NSW), Orange (NSW) and Goulburn (NSW). The final regional forum was run in conjunction with TBTS, and was held in Toowoomba (QLD) in July. Unfortunately, due to a lack of registrations, the planned forums for South Australia (Naracoorte & Hahndorf) and Western Australia (Albany & Bunbury) did not proceed. However, SBTS is investigating several alternative approaches to deliver the regional forum content to breeders in these areas.

Over 100 people registered for the day-long forums. Registrants were a mix of industry representatives, seedstock and/or commercial producers, with a majority (82%) being BREEDPLAN members. The producers ran a range of cattle, with 69% running British breeds, 14% running European breeds, 12% running Tropical breeds and 4% running Wagyu.

Numerous topics were discussed at each forum, some of which were even on the program. The program included the following presentations:

1. BREEDPLAN 101: Recording performance information in your herd
2. BREEDPLAN contemporary groups & genetic linkage
3. Making BREEDPLAN work for you: Common performance recording problems and how to avoid them
5. Are you making progress? Interpreting your Genetic Progress report
6. Single step BREEDPLAN: What does genomics mean for you?

As representatives from a mix of experienced and newer BREEDPLAN herds attended the forums, a lot of interesting discussing was generated. The experienced BREEDPLAN attendees were able to share tips they have learnt over the years to make collection of performance information easier on farm. Other attendees were able to offer different perspectives and approaches, which sometimes challenged the status quo. This provided a great learning opportunity for all, and, as facilitators, we were pleased to see so much interesting discussion and producer-led learning taking place at each of the forums.

Alex and Catriona with attendees at the Warragul Regional Forum in Victoria.
For the first time, SBTS was able to get anonymous audience feedback through the use of wireless “clicker” devices. These clickers allowed participants to answer multiple choice questions and proved to be extremely valuable to the presenters as they could ask a question and, based on the results, see if they needed to spend more time on the topic. The clickers also allowed a short series of benchmarking questions to be asked at the start and the end of the forums. This allowed SBTS to judge the effectiveness with which they communicated the information they were presenting.

Based on the number of participants who answered the questions incorrectly pre-forum and got the same question correct post-forum, the biggest knowledge gains were of the optimal contemporary group composition (61% improvement) and how genomics works (51% improvement). Across all questions, there was an average gain in BREEDPLAN knowledge of 33%.

When asked whether they had a better understanding of BREEDPLAN following the regional forums, 92% of all participants agreed that they did. The session that participants found most useful was the session on BREEDPLAN contemporary groups and genetic linkage, with 93% of participants rating this session as either extremely useful or very useful. 90% of all participants rated the regional forums as either excellent or very good.

The feedback provided from the 2017 SBTS Regional Forums is being used to derive content for future SBTS and TBTS workshops and forums. Some alternative venues have also been suggested, and these will be considered for any future events. To contribute feedback or to register your interest in future events, please contact Catriona or Boyd. Catriona can be contacted on (02) 6773 3357 or via email catriona@sbts.une.edu.au, and Boyd can be contacted on (02) 6773 1711 or via email boyd@sbts.une.edu.au.
The current manager of the SBTS and TBTS projects, Alex McDonald, stepped down from the role on 30th June 2017. Steven Skinner from ABRI will take over management of these two projects.

Alex moved to Armidale from Wodonga in June 1986 to take up the role of National Co-ordinator for the National Beef Recording Scheme. On a secondment from the Victorian Department of Agriculture he followed Bob Freer from NSW Department of Agriculture and Don Nicol from Queensland DPI in this role. Alex was based at ABRI in this position.

At that time the across herd genetic analysis, BREEDPLAN, was being introduced and a small Hereford analysis including five herds and the first Angus analysis including nine herds had been run and a Sire Summary published. During Alex’s 30 months as the National co-ordinator the number of herds using BREEDPLAN increased from 235 to just under 900 herds and the number of breeds running across herd BREEDPLAN analyses had increased from two to five.

Alex then became co-ordinator of the National Carcase Evaluation Project and was responsible for introducing ultrasound scanning technology to Australia which led to EBVs for carcase traits being added to the BREEDPLAN system.

In July 1992 Alex was appointed as General Manager of the Australian Limousin Breeder’s Society, a position he held for 22 years. During that time he was responsible for increasing the use of BREEDPLAN by Limousin breeders and also implemented a docility scoring system which led to the calculation of the first EBVs for docility in Australia in 2000.

Along with Bob Freer and Peter Speers, Alex was a consultant to the first SBTS project which was jointly funded by MLA, ABRI and southern breed societies. He continued as a consultant to the second and third SBTS projects.

In July 2014 Alex moved back to ABRI to manage the SBTS and TBTS projects during which time he was able to obtain MLA Donor Company funding for the current five year SBTS and TBTS projects. Alex was appointed a Fellow of the Association for the Advancement of Animal Breeding and Genetics in 2011 and was awarded the Dick Vincent award by the Australian Registered Cattle Breeders Association in 2015.

Alex and wife Judy are looking forward to joining the “grey nomad” movement with a six week trip north planned for July and August 2017. Alex will also realise an ambition to walk the Hume and Hovell track from Yass to Albury with his brother-in-law. The SBTS and TBTS team wish Alex all the best for his retirement.
Tim Emery Joins the TBTS Team

Roma based Beef Extension Officer, Tim Emery, has joined the Tropical Beef Technology Services team on a three year secondment from the Queensland Department of Agriculture and Fisheries. Tim commenced employment with TBTS in late February 2017.

Tim studied a Bachelor of Agricultural Science at The University of Queensland and during his time at university he undertook a 16 week internship at Swan’s Lagoon Beef Cattle Research Station near Ayr and work experience with CSIRO. He graduated in 2008 and was then appointed as a Beef Extension Officer at Roma in early 2009, where he has worked for the last eight years.

Tim has considerable experience and expertise in beef genetics, having been involved in the Beef CRC Champions Program as a “Genomics Champion” and more recently the Next Gen Beef Breeding Strategies Project and the current “Repronomics” Project being conducted with Brahman, Droughtmaster and Santa Gertrudis cattle.

In recent years he has delivered numerous breeding and genetics presentations over a wide area of Queensland, from Malanda in the north to Gympie in the east and Thargomindah in the west, as part of field days, workshops and the Grazing Best Management Practice (BMP) program.

Tim sat on the Future Farmers Network Board of Directors for six years and has twice been named as a finalist in the Emerging Leader Award at the Queensland Red Meat Awards. In addition, he has been on the organising committee of the widely recognised Young Beef Producers’ Forum (YBPF) in Roma for the last seven years. He is also involved in the family beef business at Wallumbilla and has his own small herd.

In his new role with TBTS, Tim will work widely with both commercial and seedstock producers in northern Australia with the goal of increasing the adoption of BREEDPLAN and its associated technologies. He will continue to be based in Roma.

Tim can be contacted on 0408 707 155 or via email tim@tbts.une.edu.au.

Boyd Gudex Joins the SBTS Team

Boyd Gudex has joined the SBTS team and will be the SBTS Technical Officer for both the Australian Limousin Breeders Society and the Australian Simmental Breeders’ Association. Previously, Boyd was employed as a BREEDPLAN Technical Consultant and has experience with BREEDPLAN analysis, BreedObject and MateSel. He will be continue to be based in Armidale.

Boyd was born and raised on a sheep and beef farm in New Zealand. He has extensive livestock genetics experience having worked for a number of seedstock companies. This includes working on the family sheep stud, Landcorp Farming Ltd, Livestock Improvement Corporation (LIC) and Deer Improvement, all in New Zealand, and the Sitz Angus Ranch in the USA.

At Landcorp, Boyd was responsible for the technical management of the five nucleus herds producing bulls for use across the company’s 100+ commercial farms. He had a similar technical management role at Deer Improvement.

Boyd received his PhD in Animal Breeding from the University of New England in 2011. He has also carried out research at the NSW Department of Primary Industries (BeefSpecs drafting calculator), LIC (Epigenetics and Mate Selection in dairy cattle) and Lincoln University (genetic tests for sheep).

Boyd looks forward to meeting Australian Limousin and Simmental breeders in the coming months, and working with them into the future. Boyd can be contacted on (02) 6773 1711 or via email boyd@sbts.une.edu.au.
In early July, the 22nd Association for the Advancement of Animal Breeding and Genetics (AAABG) Conference was held in Townsville, QLD. Held every two years, the conference attracts a mix of local and international researchers, extension personnel and producers. The three day program included sessions dedicated to beef, sheep and goats, dairy, aquaculture, industry, breeding objectives and advancements in genetic technologies. For SBTS and TBTS staff, the AAABG conference provided us with a great opportunity to hear about the latest advancements in animal breeding and genetics, while also allowing us to exchange news and ideas with colleagues from around the world.

One of the highlights of the AAABG conference is the half day field trips. This year, SBTS and TBTS staff went on a tour of the CSIRO Lansdown research station. While there, we heard about the research that is currently being conducted on the site. This included a tour of the methane chambers, where scientists are currently conducting research into whether feeding animals a special mix of grain and seaweed will reduce methane emissions. We also heard from Michael Lyons of Wambiana Brahams, who spoke about his breeding program and how he uses genomic information when making selection decisions. Lastly, we saw steers from the Spyglass Research Station Droughtmaster herd which are being utilised as part of a livestock monitoring program. CSIRO researchers are tracking the animal’s behaviour (including feeding patterns) via a solar powered wireless animal sensor node. The walk-over-weighing systems that are being utilised around water points were also on display.

Back at the conference venue, there were many interesting presentations on a wide variety of topics. We heard from Lambros Koufariotis on work being conducted at the University of Queensland, where researchers are sequencing the genome (DNA) of Brahman cattle as part of the Brahman Sequencing Project. One exciting development from this research is the discovery of the ‘Celtic’ mutation in Brahman cattle. This mutation is a genetic variant that has been found to be involved in polledness in a number of cattle breeds. It is hoped that this could lead to more accurate horn/poll DNA tests for Brahman cattle.

A number of beef researchers from AGBU also made presentations. These included David Johnston discussing the Repronomics Project and the role it will have in enabling genetic improvement in reproduction in Northern Australia. Gilbert Jeyaruban discussed his research on semen quality, which has led to the implementation of the new Percent Normal Sperm EBV for Brahman. Natalie Connors discussed the development of a beef genomic pipeline which has been critical to the implementation of the BREEDPLAN single step evaluation. Hugh Nivison, Managing Director of ABRI, gave a talk on the opportunities and challenges that genomics presents for the Australian beef industry.

On the last morning of the AAABG conference, the final plenary session was reserved for the awarding of the Helen Newton Turner medal. Dr Helen Newton Turner (1908-1995) was a former CSIRO scientist, and dedicated her career to research into the genetic improvement of sheep for wool production. The recipient of the 2017 Helen Newton Turner medal is Alf Collins Senior of CBV Brahams. Alf gave an inspiring talk on how he got to where he is today, and the people who have motivated and mentored him along his journey. Congratulations Alf.

The next AAABG Conference will be held in 2019 in Armidale, NSW.

A yard has been constructed around this water point at CSIRO Lansdown, allowing researchers to utilise a walk-over-weighing system.

Hugh Nivison, Managing Director of ABRI, presented a talk on ‘BREEDPLAN in a genomics world - Opportunities and Challenges’.
New technical notes are available for measuring traits which are important in assisting improving adaptation in tropical environments. The technical notes available are for measuring Buffalo Fly Lesion Scores, Tick Resistance Score and Coat Score, all of which have importance in the production systems for tropical environments. The technical notes can be found in the Technical Documents section on the TBTS website (http://tbts.une.edu.au/). They are also available as BREEDPLAN Tip Sheets in the Technical Section of the BREEDPLAN website (http://breedplan.une.edu.au/).

**Buffalo Fly Lesions**

Research has shown that variation exists in buffalo fly hyposensitivity between animals, and that a proportion of this variation is due to genetic differences. Trials in the wet tropics have shown that buffalo fly can reduce beef cattle production by up to 16%. Beef CRC results have also shown a correlation between high fly lesion counts and reduced lifetime fertility in Brahman cows.

Buffalo Fly Lesion Scores should be taken in late summer through to early autumn when the buffalo fly numbers are at their greatest. The approved BREEDPLAN scoring method involves scores from 1 to 5 with one being no visible lesions and five with multiple lesions or at least three sites such as neck, belly and withers.

**Coat Score**

Coat scores are a measure of adaptability of animals to tropical production systems, with sleek coated animals being more tropically adapted than woolly coated animals. Beef CRC research on Brahman and Tropical Composites found that there was a negative correlation between coat score and body condition score, indicating that genetically sleek coated animals had better body condition scores compared to animals with woollier coats. Additionally there is a positive genetic correlation between sleek coat and earlier age of puberty in Brahman females.

Coat scoring should be done at weaning in autumn and winter to gain maximum variation in spring calving herds and the first winter after weaning in autumn calving herds. Coat scores are recorded on a 1-7 scale with one being sleek and seven being woolly.

**Tick Resistance Score**

Tick resistance is recognised as an economically important production trait in grazing enterprises. Research has shown that variation exists in tick resistance between animals, and that a proportion of this variation is due to genetic differences.

Tick Scores can be taken in conjunction with 200, 400 and or 600 day weights. As a rule-of-thumb, there should be an average tick count (over at least 15 animals) of at least 20 ticks per side. Otherwise there will not be enough variation between animals for BREEDPLAN to calculate EBVs. Score using the approved BREEDPLAN 1-6 method with 1 being clean of any ticks to 6 with over 150 ticks over 4.5 mm in size per side.

The submission of scores for these traits to BREEDPLAN will be used in the development of Trial EBVs once sufficient data has been collected. For further information regarding these traits, please contact TBTS Technical Officer, Paul Williams, on 0427 018 982 or via email paul@tbts.une.edu.au.
While SBTS and TBTS offer a full day BullSELECT workshop, which has been designed for those seedstock producers who wish to further educate their commercial clients about how best to utilise BREEDPLAN information when selecting animals, we often give shorter presentations at a range of field days and other industry events. In recent months, in addition to running 10 Regional Forums, SBTS staff have attended and presented at a number of events in the eastern states of Australia.

In February, Alex presented to nearly 200 commercial beef producers at five Greenham Producer Information Days in Tasmania. These were held at Smithton, Scottsdale and Brighton, and also on King Island and Flinders Island. At each day, Alex discussed how to improve profitability using EBVs, with a focus on maximising returns on the available price grids by selecting animals with the right genetics.

In March, Carel presented at three Wagyu Breeders workshops in Ballarat, VIC, Roma, QLD and Armidale, NSW. Carel discussed a number of topics, including performance recording and genomics. Also in March, Catriona attended the 2017 Devon Cattle Breeders’ Society of Australia AGM in Tamworth, NSW, where she provided Devon members with an update on BREEDPLAN and SBTS activities. Later in the month, Catriona presented to 86 commercial beef producers at the North West Beef Producers Forum in Gunnedah, NSW. The day was organised by NSW Local Land Services and a range of topics were covered. Catriona discussed how commercial producers can utilise BREEDPLAN EBVs and selection indexes when making animal selection decisions.

Early in April, Catriona travelled to Melbourne to present on genomics at the Victorian Region of the Australian Limousin Breeders’ Society AGM. Later in the month, Catriona spoke to commercial producers at the Weetaliba Hereford Field Day in Gunnedah NSW. Several talks were presented, with the topics covered including BREEDPLAN EBVs, selection indexes and genomics.

At the start of May, Carel attended the 2017 Australian Wagyu Association Conference and Tour in Albury, NSW. At this event, Carel presented on a range of topics, including performance recording, genomics and MateSel. Also in May, Catriona spoke to commercial producers about BREEDPLAN EBVs at a field day in Tamworth, NSW.

June saw both Boyd and Catriona in Dubbo. At the start of the month, Boyd and Catriona attended the Hereford Youth Auction at the 2017 Dubbo Poll Hereford National Show & Sale, where they caught up with a number of Hereford breeders. Two weeks later, Boyd and Catriona were once again in Dubbo for the 2017 Red Angus and Simmental Show and Sale. At the end of June, Catriona was in Dubbo for the Charolais National Youth Stampede. In addition to giving several presentations on BREEDPLAN EBVs and Selection Indexes to the older attendees of the Charolais National Youth Stampede, Catriona was also part of a panel that discussed career opportunities in agriculture.

If you are interested in having a SBTS staff member present at an upcoming event, please contact Catriona on (02) 6773 3357 or via email catriona@sbts.une.edu.au to discuss your requirements.
The TBTS team, consisting of Paul Williams (Rockhampton) and newly-appointed Tim Emery (Roma), have had a busy few months presenting at numerous industry events across the state.

In early April, Brian Pastures Research Station at Gayndah played host to 65 guests, which consisted primarily of seedstock producers who had contributed genetics to the five year Repronomics Project. The event involved an array of guest speakers (including Paul who covered the Northern BIN Project), a practical demonstration of ovarian and carcase scanning, and a display of 400 head in their sire progeny groups. A few days later, Tim ventured to Clermont to co-deliver a Breeding EDGE pilot workshop to 14 commercial producers.

Later in the month, both Paul and Tim attended a large-scale industry event (100 attendees) held at Robert and Donna Rea’s ‘Lisgar’ at Gumlu in north Queensland. DAF Extension Officer, Alan Laing, organised the event and delivered multiple presentations focused on research project findings and ‘putting genetic technologies into practice’. Paul was once again asked to be one of the handful of guest speakers and he provided an overview of the Northern BIN Project, the Brahman BIN Project and the Repronomics Project.

May comprised of Paul presenting close to home (in Rocky) to a dozen seedstock producers at the Repronomics Breeder workshop, whilst Tim ventured an hour down the road from Roma to Dunkeld to deliver the ‘Animal Production’ Grazing Best Management Practice module (featuring genetics content) to 11 commercial producers.

In mid-June Tim delivered a full day of breeding and genetics content to 14 members of the Traprock Beef Group in southern Queensland. Key topics included breeding objectives, Bull Breeding Soundness Evaluation, EBVs and research project findings.

On 10th July, Belmont Australia held a ‘Production Plus’ day near Rockhampton which attracted 80 producers. Paul spoke about contemporary groups, linkage and the various BREEDPLAN traits, in particular the fertility EBVs.

If you’re keen to have one of the TBTS staff members speak at an upcoming event in your district, please get in contact with us. Tim can be contacted on 0408 707 155 or via email tim@tbts.une.edu.au, while Paul can be contacted on 0427 018 982 or via email paul@tbts.une.edu.au.
Seedstock producers in Australia who are members of a breed society with a published Selection Index are encouraged to consider using the MateSel mating optimisation tool when planning their upcoming joinings.

MateSel creates additional genetic progress within a breeding program by generating a suggested mating list from a list of sires and dams that a seedstock producer nominates as being available for use within their upcoming joining program. MateSel not only allows seedstock producers to maximise genetic progress whilst managing inbreeding, but will also save significant time previously spent compiling mating lists.

MateSel is fully customised to the breeding program of each individual seedstock operation with the seedstock producer choosing acceptable inbreeding limits by selecting one of three breeding strategies, “Genetic Diversity”, “Balanced” or “High Genetic Gain” and providing details of their desired breeding objective. Results from the MateSel analysis are returned promptly, usually within one working day.

MateSel is a valuable addition to the BREEDPLAN suite of tools that are offered by the Agricultural Business Research Institute (ABRI) in Armidale, NSW.

Seedstock members interested in learning more about MateSel should visit the BREEDPLAN website (http://breedplan.une.edu.au) and click on the MateSel icon on the right hand side, or contact staff at SBTS or TBTS.

Get Social With SBTS & TBTS

SOCIAL MEDIA

Beef producers can keep up to date with the latest developments in genetic technologies and the activities of SBTS and TBTS by following SBTS and TBTS on Facebook, Twitter and YouTube. Articles and information on upcoming events (e.g. webinar series, BullSELECT workshops) are routinely posted on Facebook and Twitter. The YouTube channel contains video presentations from past webinar series and short ‘Understanding BREEDPLAN EBVs’ video clips.

TO FOLLOW > SBTS and TBTS on Twitter, Facebook or YouTube simply go to the SBTS or TBTS website and click on the relevant icon, or go directly to the SBTS & TBTS Facebook account at http://facebook.com/SBTSTBTS, Twitter account at http://twitter.com/SBTSTBTS or YouTube Channel at http://youtube.com/user/sbtstbts.
For support and assistance in the use and understanding of the different genetic technologies that are available, such as BREEDPLAN, BreedObject Selection Indexes, Internet Solutions, TakeStock, GeneProb, Mate Selection Software & DNA based tools or to discuss any of the information included in this edition of the SBTS & TBTS Update, please contact:

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IF YOU WOULD LIKE ANY FURTHER INFORMATION ON SBTS AND TBTS PLEASE CONTACT: