



A Leap Forward in Genomic Enhanced BREEDPLAN EBVs

In a first for the Australian beef industry, the BREEDPLAN analysis is now able to incorporate genomic (i.e. DNA) information for multiple traits developed from a large 50K SNP panel with the inclusion of Molecular Value Predictions (MVPs) from the Pfizer Animal Genetics (PAG) Angus 50K product into the April 2011 Angus GROUP BREEDPLAN analysis.

This follows the successful incorporation of genomic data into the Brahman BREEDPLAN analysis in October 2008 for the Shear Force EBV (i.e. tenderness). In contrast, this was for a single trait where 4 SNP's had a known effect on shear force.

The Pfizer Animal Genetics (PAG) Angus 50K product assesses the genetic makeup of Black Angus cattle at more than 50,000 locations across their whole genome. These locations are known as DNA markers or more specifically as SNPs (pronounced 'snips') which are single nucleotide polymorphisms.

In order to do this, PAG have undertaken "discovery" research in Angus cattle populations to determine the magnitude of the effects of each of the 50,000 SNPs on 13 traits analysed. Then for each animal, these effects are reported as measures of genetic merit, branded as Molecular Value Predictions, or MVPs.

Research conducted by scientists at the Animal Genetics and Breeding Unit (AGBU), with assistance from Meat and Livestock Australia (MLA), PAG and the Angus Society of Australia, has enabled MVPs for 7 of the 13 traits to be incorporated into the monthly Angus BREEDPLAN analysis, potentially increasing the accuracy of EBVs for those animals with MVP data available.

The 7 MVP traits that are being incorporated into the Angus BREEDPLAN analysis include birth weight, weaning weight, milk, carcase weight, carcase rib fat, carcase eye muscle area and carcase marbling.



Molecular Value Predictions (MVPs) from the Pfizer Animal Genetics (PAG) Angus 50K product are now included in the Angus GROUP BREEDPLAN analysis.

Angus animals with MVP data included will be identified with a trait indicator on the Angus Australia animal search facility as the PAG Angus 50K logo.

"This is an important breakthrough for industry - now all 3 sources of possible information on an animal, pedigree, its own performance and that of its recorded relatives, and its own DNA test, can be combined into a single EBV. Industry has sought this outcome, and it will help avoid confusion for breeders and producers through information overload", said Peter Parnell, CEO of Angus Australia. Only the MVPs of those animals that are submitted to Angus Australia for HD50K testing with Pfizer Animal Genetics will be used in the routine Angus BREEDPLAN analysis

This integration of Pfizer MVPs into BREEDPLAN EBVs depends on the calibration work that has been conducted by AGBU scientists. "Calibration means establishing the accuracy of the



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DNA test in relevant Australian cattle populations, and is vital in allowing breeders to make best decisions about how to use the new DNA tests”, said David Johnston, Principal Research Scientist at the Animal Genetics and Breeding Unit (AGBU). The full calibration results and explanation of the analytical components are available on the AGBU website (<http://agbu.une.edu.au>).

The current method used to incorporate the MVP data into the BREEDPLAN analysis is known as “blending”. This means BREEDPLAN EBVs are generated for all animals as normal using all known pedigree and performance data. After which, those animals with MVP data have it blended into their 7 related BREEDPLAN EBVs.

“Blending of MVPs into BREEDPLAN EBVs is a major step forward towards routine industry use of DNA testing, and would not have been possible without the cooperation between Angus Australia, Pfizer Animal Genetics, AGBU and the BREEDPLAN team at ABRI”, said Dr Rob Banks, MLA Manager of Genetics R&D.

“This will help breeders assess the technology for their own use, confident that it will fit into the BREEDPLAN framework, which is fundamental to accurate, effective genetic evaluation, and hence to the genetic improvement which is vital for our industry”, Dr Banks said.

While the incorporation of genomic information into the BREEDPLAN analysis is an exciting enhancement, particularly for increasing the EBV accuracy of “young” animals, it will be of most value when calibrated genomic information is available on economically important yet hard to measure traits such as feed efficiency and fertility.

Charolais Launch Northern Terminal Index

In March 2011, the Charolais Society of Australia implemented a new Northern Terminal Selection Index as a replacement to the Live Export Index.

The Northern Terminal Index estimates the genetic differences between animals in net profitability per cow joined for an example commercial herd in Northern Australia (i.e. Brahman cows) targeting the production of grass finished steers for the Jap Ox market. Steers are sold direct to slaughter at 630 kg (345 kg HSCW and 5 mm P8 fat depth) at 28 months. All progeny are slaughtered. In response to industry feedback positive emphasis has been placed on finishing ability.

The new Northern Terminal Index joins the Export and Domestic Indexes as the three standard selection indexes that are calculated on all Charolais animals. More detailed information is available from the Technical area of the BREEDPLAN website in the tip sheet titled “Interpreting Australian Charolais Selection Indexes” or by contacting Christian Duff at SBTS on (02) 6773 2472.



An Opportunity to be “Closer to Your Clients”

2011 will once again provide seedstock breeders with the opportunity to become “Closer to Your Clients” by hosting a workshop on-property that describes how commercial beef producers can make the best use of BREEDPLAN information when buying bulls.

The workshops are facilitated by the SBTS or TBTS team and involve a mix of practical discussions and yard demonstrations. Sessions include discussion on the effective selection of breeding cattle, an overview of the genetic selection tools available and practical demonstrations of how to use EBVs and selection indexes when choosing bulls.

Your clients will also be shown how they can use the on-line animal search facility for your breed to find the “best” bulls for their herd’s requirements.

Since this workshop initiative was released in 2007, SBTS have undertaken 32 “Closer to Your Clients” workshops across all States of Australia (apart from Tasmania). Additionally, 11 workshops have been conducted in New Zealand during 2010 and 2011.

Within Australia in 2010 “Closer to Your Client” workshops were held at:

- Belmore Shorthorns, Naracoorte SA
- Franco Herefords, Casino NSW
- Davelle South Devons, Jamestown SA
- Kevlyn Downs Shorthorns, Keith SA
- Vernola Charolais, Tandarra VIC
- Kenemere Charolais, Cobbitty NSW
- Tremere Belmonts, Moura QLD

All events were well attended by interested producers as demonstrated by the interactive discussions that took place and the multitude of questions that were asked. A highlight was the range of animals with full sets of EBVs and selection indexes on display for demonstration purposes.



A flyer providing more information regarding the “Closer to Your Clients” workshops (including an expression of interest form) has recently been emailed to all members of BREEDPLAN.

In contrast to previous years, herds will have the option to run the standard full day program (subsidised cost \$990) or up to a half day custom program by selecting from a range of informative sessions (subsidised cost \$650).

Expressions of Interest for seven “Closer to your Clients” workshops have already been received requesting this event for 2011. Any other herds that are interested in hosting this event are encouraged to submit an Expression of Interest. First in first served.

Information on the “Closer to Your Client” workshop package is also available on the SBTS & TBTS websites (<http://sbts.une.edu.au> or <http://tbts.une.edu.au>).



Measuring Birth Weight To Weigh or to Tape?

Accurately recording birth weight is important for the accurate calculation of Birth Weight, Calving Ease Direct and Calving Ease Daughters EBVs. Accordingly, a common question that is asked in the field is “are birth weights which are estimated from a hoof tape as accurate as actual birth weighing?”

The tape in question is pictured. The tape is placed around the calf’s coronet band above the hoof and provides an estimated birth weight based on a simple conversion factor from the coronet band circumference. One side of the tape is for bulls, the other for heifers. Similarly, the coronet band circumference can be measured with an ordinary dressmaker’s tape then converted to an estimated birth weight based on a conversion table. There is a different conversion for heifers and bulls.

The reasons for using the hoof measuring tape as a replacement for actual birth weighing vary but include occupational safety issues and difficulty with lifting calves, particularly heavy ones, and the cost of birth weighing devices.

To compare the accuracy of estimated birth weights from the taping technique to actual birth weights, 126 calves (62 bulls and 64 heifers) were measured within 24 hours of birth by the two methods being the coronet band circumference tape and by digital scales with a cradle device attached to the front of a quad bike. The data collection was undertaken by Tom Lawson from Paringa Livestock, Yea, Victoria (pictured). The calves measured were primarily Charolais and Angus with several Composites also included.

A simple analysis of the birth weight data provided the following descriptive statistics listed in Figure 1.

In all cases the estimated birth weights from the coronet band

circumference compared to the digitally weighed birth weight (i.e. actual) produced a higher average, more spread and higher maximum, particularly in the heifer population. A higher minimum from the tape estimates was also evident, particularly in the bull population.

Further analysis revealed that the relationship between the actual birth weights and birth weights estimated from the coronet band tape were generally quite positive.

The correlation estimates were 0.77 for heifers, 0.76 for bulls and 0.77 for all. However, while this seems encouraging it needs to be kept in context.

The analysis also reveals that there is considerable variation in the actual birth weights of calves that were estimated to have the same birth weight using the coronet band tape.

This is displayed graphically in Figure 2 which is a scatter plot of bulls measured for actual compared to estimated birth weight.

For example, this shows that calves with an estimated birth weight of 38kg from the measurement of coronet band circumference have a range in actual birth weight from 28.8kg to 41.0kg.

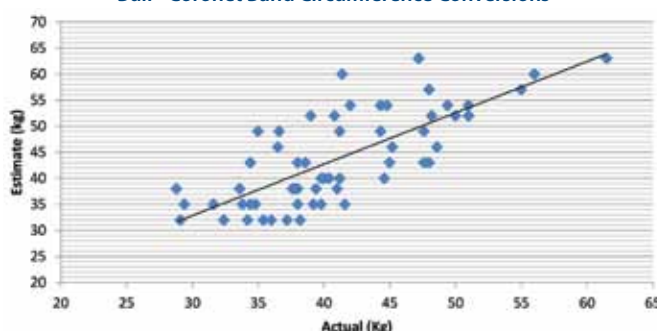
These findings are supported by research that was undertaken by Parish et al in 2009. Their study collected birth weight estimates and measurements on 587 calves within 24 hours of birth at several Mississippi research stations.

For each calf recorded, birth weights were visually estimated, then estimated using the coronet band tape and then weighed using both handheld spring scales and digital scales. The results from this study indicate that the birth weight recorded will vary depending on the collection method. Additionally,

Figure 1: Descriptive Statistics of Birthweight Data Collected

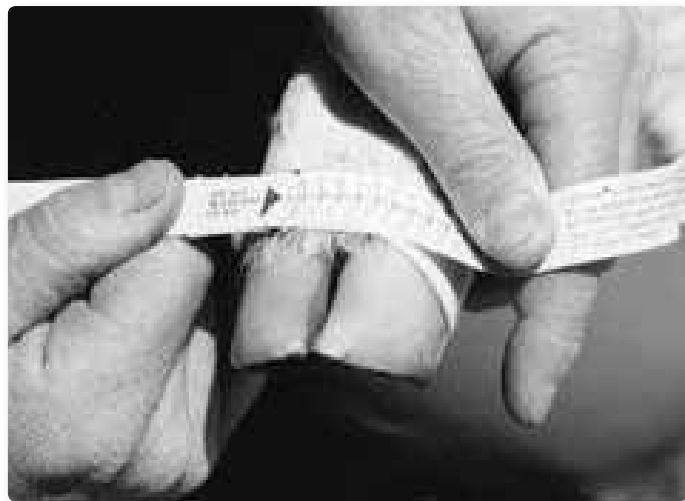
Heifers (n=64)	Average	SD	Max	Min
Actual Birth Weight (kg)	38.3	5.90	51.2	27
Coronet Band Circumference (cm)	18.2	1.37	22	16
Estimated Birth Weight (kg)	38.8	6.92	58	28
Bulls (n=62)	Average	SD	Max	Min
Actual Birth Weight (kg)	41.3	6.85	61.5	28.8
Coronet Band Circumference (cm)	19.1	1.62	23	16.8
Estimated Birth Weight (kg)	44.0	8.94	63	32
All (n=126)	Average	SD	Max	Min
Actual Birth Weight (kg)	39.8	6.53	61.5	27
Coronet Band Circumference (cm)	18.6	1.57	23	16
Estimated Birth Weight (kg)	41.3	8.37	63	2

Figure 2: Actual vs Estimated Birth Weight Bull - Coronet Band Circumference Conversions





Calves were physically weighed using digital scales.



Example of coronet band measurement.

visual estimate and coronet band tape measurement tended to underestimate high birth weights, whereas the tape also tended to over-estimate the light birth weights. Birth weight collection via either spring or digital scales resulted in more accurate measurement.

The results from both trials show that estimating birth weight from a coronet band tape should not be viewed as a replacement to actually weighing calves by spring or digital scales.

More accurate birth weight measurement will result from using scales, with the resulting Birth Weight, Calving Ease Direct and Calving Ease Daughters EBVs also being more accurate.

With further research, estimated birth weights from coronet band diameter measurement may still prove to be useful as an indirect measure of Calving Ease. At this stage however, it should not be seen as a replacement for actual birth weighing for our current genetic evaluation.

Reference - Parish, J.A, T. Smith, J.R. Parish, T.F. Best, and H.T. Boland. 2009. Evaluation of Four Different Methods of Calf Birth Weight Data Collection. The Professional Animal Scientist 25 (2009): 716-721.

TransTasman GROUP BREEDPLAN Evaluation for Devon

In May 2011, the performance data from the database of the Devon Cattle Breeders Society of Australia (including data from several American herds) was combined with the performance data from the New Zealand Red Devon Cattle Breeders Association database to conduct a joint TransTasman Devon GROUP BREEDPLAN analysis for the first time. Subsequently, the Devon GROUP BREEDPLAN analysis now enables the direct comparison of Australian, New Zealand and American Devon animals.

This now brings the total number of breeds that are conducting a TransTasman BREEDPLAN analysis to 11.

For further information, please contact Ashlee Austin at SBTS by phone on (02) 6773 3056.



Association of Breedplan EBVs with Cow Body Composition

Stephen Lee and Wayne Pitchford, University of Adelaide



Breeding herd efficiency

The Cooperative Research Centre for Beef Genetic Technologies (Beef CRC) is aiming to improve breeding herd efficiency by focussing on both productivity traits and pasture feed intake. Breeding herd efficiency can be defined as number of calves weaned plus the weight of those calves plus weight gain of the cow per megajoule of metabolisable energy consumed by each cow-calf unit over an annual production cycle.

Background

By using BREEDPLAN Estimated Breeding Values (EBVs); beef cattle breeders have the opportunity to make substantial genetic gain in many economically important traits. However, some producers have expressed concerns that breeding cattle to produce higher yielding, leaner carcasses by selecting for reduced Rump and Rib Fat EBVs may compromise a cow's ability to lay down and retain sufficient energy reserves (body condition) for timely rebreeding in management situations where nutrition is limited. Therefore, it would be good to know how BREEDPLAN EBVs for carcass traits are associated with cow body composition, and how the use of these EBVs may ultimately affect breeding herd efficiency. This article reports on the relationship between BREEDPLAN EBVs and cow body composition at pre-calving and weaning in first and second calving Angus cows. Future articles will report on results of reproductive rate and breeding herd efficiency.



Research project design

In a long-term research project across southern Australia, the Beef CRC has collected and analysed data from 7,400 pedigree recorded seedstock Angus and Hereford cows at several times during their lives. Collaborating herds were located in the New England tablelands, south west slopes of NSW, western districts of Victoria and the south east of South Australia.

For each cow, body weight and ultrasound measurements of P8 fat depth, rib fat depth, percent intramuscular fat (IMF) and eye muscle area (EMA) were measured four times over a two year period: at pre-calving and weaning for first and second calving cows (Table 1) by an accredited operator. Results presented are for Angus cows with similar results also observed for Herefords.

Table 1: Averages¹ for first and second calving cows at pre-calving and weaning

Parity	Time point	Weight (kg)	P8 (mm)	Rib (mm)	IMF (%)	EMA (cm ²)
First Calf	Pre-calving	480	6.6	4.7	4.4	53
	Weaning	510	6.8	5.2	4.8	56
Second calf	Pre-calving	551	8.3	6.0	5.6	60
	Weaning	596	11.0	8.2	6.4	66

¹Least-squares means adjusted for herd and management group effects

The relationships between these measurements and the cow's corresponding carcass EBVs, for example, average cow P8 fat depth with cow carcass Rump Fat EBV were estimated to evaluate how carcass EBVs were associated with cow body composition.

The relationships were also tested for whether they changed between pre-calving and weaning, or first calving compared with second calving cows. Summary statistics for Angus EBVs are presented in Table 2.

Table 2: Summary statistics of EBVs for Angus 2009 born calves

EBV	600 day weight (kg)	P8 Fat (mm)	Rib Fat (mm)	IMF (%)	EMA (cm ²)	Milk (kg)
Average	89	0.0	-0.1	+0.9	+3.1	12
Minimum	10	-4.7	-4.9	-1.5	-3.8	-4
Maximum	148	5.9	5.1	4.4	12.8	25

BREEDPLAN carcass EBVs are associated with differences in cow body composition

EBVs for Rump Fat, Rib Fat, IMF and EMA (adjusted to a 300kg carcass) were well correlated with cow body composition when measured either at pre-calving or weaning, for first or second calving cows. The effect of a 1 unit increase in carcass EBV on the corresponding cow ultrasound scan traits is reported in Table 3 at each of the measurement times.

At pre-calving for first calving cows a 1 unit increase in:

- Rump Fat EBV was associated with a 1.0mm increase in cow P8 fat depth
- Rib Fat EBV was associated with a 0.7mm increase in cow rib fat depth
- IMF EBV was associated with a 0.8% increase in cow IMF%
- EMA EBV was associated with an increase of 0.6cm² in cow EMA

Parity	Time point	P8 (mm)	Rib (mm)	IMF (%)	EMA (cm ²)
First Calf	Pre-calving	1.0	0.7	0.8	0.6
	Weaning	0.8	0.7	0.7	0.5
Second calf	Pre-calving	0.9	0.8	0.7	0.7
	Weaning	1.3	1.0	0.6	0.4

Association of other BREEDPLAN EBVs to cow body composition

The relationship of the cows' EBVs for 600 Day Weight and 200 Day Milk with cow body composition were also examined. Increased 600 Day Weight EBV was associated with small increases in all composition traits (Table 4). For example, at the initial pre-calving scan a 20kg increase in 600 Day Weight EBV was associated with a 0.4mm increase in cow P8 fat depth. However, the association between 600 Day Weight EBV and cow ultrasound scan varied depending on the type of analysis undertaken. When analysed at a constant weight (similar to formation of carcass EBVs), increased 600 Day Weight EBV was associated with small declines in all composition traits. Therefore, cows with higher genetic merit for 600 Day Weight EBV have more fat and muscle (ultrasound P8, rib, IMF and EMA), but when adjusted for their larger weight they had slightly less tissue relative to their weight. Importantly and as expected, the relationship between the 600 Day Weight EBV and composition traits was smaller than the direct effects associated with carcass EBVs (Table 3).

Parity	Time point	P8 (mm)	Rib (mm)	IMF (%)	EMA (cm ²)
First Calf	Pre-calving	0.4	0.3	0.1	1.8
	Weaning	0.5	0.4	0.1	1.7
Second calf	Pre-calving	0.3	0.3	0.0	2.0
	Weaning	1.1	0.7	0.1	1.9

Milk EBVs are estimates of the genetic differences between animals in milk production expressed through variation in calf weaning weight at 200 days. Milk EBV had only low associations to cow P8 fat, rib fat, IMF and EMA at pre-calving for first calving cows. However, at weaning, increased Milk EBV was associated with lower P8 and rib fat depth, IMF and EMA. The largest effects at weaning were in cow P8 and rib fat depth where a 5kg increase in Milk EBV was associated with a 0.3mm decline in P8 depth for Angus. This indicates cows with higher Milk EBVs mobilise more tissue during lactation,

particularly P8 and rib fat. Once again, like 600 Day Weight EBV, the average relationship with Milk EBV was smaller than the direct effect of carcass Rump and Rib Fat EBVs on cow P8 and rib fat depth measurements.

Another important result is that EMA EBV was not associated with cow ultrasound P8 or rib fat depth. This finding indicates that producers can select to increase carcass EMA without significantly changing cow P8 and rib fat depth.

Conclusion

BREEDPLAN EBVs for Rump Fat, Rib Fat, IMF and EMA are associated with changes in cow body composition when measured either at pre-calving or weaning, for first or second calving Angus cows. This research indicates if breeders wish to genetically change the body composition of their cow herd, they can use existing EBVs. Future articles will report on relationships between cow body composition and breeding herd efficiency.

Acknowledgment

The Beef CRC research team would like to acknowledge the considerable contribution of collaborating seed stock breeders involved in this project.

Further information

The Beef CRC website (<http://www.beefcrc.com.au/MaternalProductivityUpdates>) has further information on this project including shortly, the third edition of the 'The Maternal Journal' which will provide a comprehensive update of results.

This article was provided by Stephen Lee at the University of Adelaide. SBTS & TBTS gratefully thank Stephen for this contribution.

Key Points

- ✓ BREEDPLAN EBVs for Rump, Rib, IMF and EMA are associated with body composition in Angus and Hereford cows
- ✓ Increased 600 Day Weight EBV is associated with small increases in ultrasound P8 fat, rib fat, IMF and EMA in cows
- ✓ Increased Milk EBV is associated with mobilisation of cow P8 fat, rib fat, IMF and EMA during lactation
- ✓ EMA EBV does not influence cow P8 or rib fat depth
- ✓ Breeders can select for changes in cow body composition using existing BREEDPLAN EBVs

Producer Profile

Lisgar Droughtmasters Focus on Genetics

Robert Rea is adamant improved breeding technology will deliver the next big leap in productivity for northern beef producers.

“All of the rate-limiting factors in producing beef in northern Australia have been removed,” he says. “We’ve had the age of urea and the age of stylo – the next big thing is going to be genetic improvement. “Improved breeding means we are going to produce more kilos of beef per hectare while still maintaining carcase quality and fertility.”

Robert and Donna Rea, together with their children, Robert and Amy, run the largest performance recorded Droughtmaster herd in Australia. All 800 cows in their Lisgar herd are performance-recorded for growth and carcase data.

“We joined Breedplan about five years ago and initially, I was a sceptic,” Mr Rea said. “I am now convinced it works and am using growth rate and carcase data to source bulls and identify dam groups.

“We cull our breeders ruthlessly for fertility, temperament and susceptibility to ticks and buffalo flies. Some of them are now starting to tick all the boxes, so we’re culling on performance.”

For the past two years, the Lisgar herd has been involved in an innovative DPI trial investigating a number of reproductive technologies and genetic improvement in *Bos indicus* cattle. Each year, registered heifers are being fixed-time artificially inseminated. Half the heifers are mated to high index sires and half to breed average sires.

“This program is starting to produce some really interesting results,” he said. “We offered three bulls at the Rockhampton sale last year. All three were by the same AI sire; they were conceived the same day, born within a fortnight of each other and reared the same way. “By the time they went to Rockhampton sale, one was 150kg above our herd average, one was smack on average and one was well below average.”

Registered cows are artificially inseminated or mated in single sire groups. Commercial breeders are naturally mated in



Robert and Donna Rea, together with their children, Robert and Amy, run the largest performance-recorded Droughtmaster herd in Australia. All 800 cows in their Lisgar herd are performance-recorded for growth and carcase data.

multiple sire groups, with resulting progeny DNA tested to determine their parentage.

“This year, we found one bull had sired just five calves, even though we inspect all our bulls and semen test before mating,” Mr Rea said. “Needless to say, he found himself out of a job. Without DNA testing, we’d never have known and he’d still be here doing nothing for another three years.”

This attention to genetic improvement, combined with good nutrition and management, has helped to slash almost 18 months from the time to turn-off over the past decade.

“It used to take us three or four years to turn off four or six tooth steers for the Japanese grassfed market,” Mr Rea said. “Now we’re aiming to turn off milk and two-tooth steers capable of producing 280-300kg carcasses in less than 30 months.”

The Reas’ 11,000 hectare property stretches from the Bruce Highway to the coast and has almost every type of soil from good creek loams and heavy self-mulching black soils to coastal plains.

The 750mm average rainfall supports a range of pasture species, including Buffel grass, Urochloa, Indian Couch, Salt Couch and the legumes, Verano and Seca Stylo and Siratro.

During the dry season, weaner heifers and breeders have access to a molasses-based supplement containing four percent urea, four percent protein meal and rumen modifier Rumensin.

Article courtesy of Queensland Country Life, 3 February 2011.

SBTS and TBTS gratefully acknowledges Alan Laing and Robert Rea for their contribution.

How Accurate Is Your Pedigree Information?

One of the most fundamental jobs for a seedstock beef producer is recording the pedigree details for their animals.

Amongst other things, pedigree information is used by Breed Societies for the maintenance of their registered herd book, while also playing a critical role when EBVs are calculated for animals within the BREEDPLAN genetic evaluation.

While it is a relatively routine job, recording accurate pedigree information can be quite challenging in some circumstances.

“Mothering up” cows and calves can be difficult and compromised by cross mothering. The widespread use of artificial reproductive technologies adds another dimension of complexity. How do you know you have got what you paid for? Was there any mix up of straws during the AI process? Can you determine accurately whether the calf was sired by the AI or back up bull? And in multiple sire joining programs, individual sire identification is impossible without DNA testing.

Further complications can also arise when management hasn't always gone to plan or when human errors are made as part of the recording process.

So how accurate is the pedigree information being recorded for calves? An interesting insight into answering this question was recently provided by the Beef Information Nucleus Progeny Test Program being conducted by the Australian Limousin Breeders Society.

To ensure the accuracy of the sire information, the sires recorded for all calves from the first joining within the program were checked by DNA typing and verification through the Animal Genetics Lab at the University of Queensland.

The first joining included 10 AI sires, followed by three back up bulls.

The sire verification provided an excellent demonstration of how easily errors can occur in recording the pedigrees of



DNA Parentage Verification was used within the Limousin Beef Information Nucleus to check the accuracy of the sire information that had been recorded for calves”

animals, particularly in larger, more extensive herds.

- Two calves born on the same day had clearly swapped mothers at birth.
- The wrong straw of semen was used or the sire incorrectly recorded for three calves during the AI program
- Four calves were incorrectly assigned to the back up bull whereas they were in fact sired by the AI sire.
- Human errors occurred during the data entry for another three calves.

In total, 12 of the 227 calves (5.3%) were given incorrect sires when the pedigree information was collected for these calves. Considering the Limousin Progeny Test Program followed best practice guidelines, it is likely that this level of error is indicative of the pedigree errors currently being observed across the registered cattle industry.

The results from the Limousin program illustrate how important it is to be diligent when recording pedigree information for your animals.

They also illustrate how useful DNA parentage verification can be as a tool to maintaining accurate pedigree details.

Maximising the Value of Your Scanning Information

Many seedstock producers are now utilising live animal ultrasound scanning technology to collect objective carcass information on their animals, with animals routinely being measured for eye muscle area (EMA), rib and rump fat depth, and intramuscular fat (IMF). This article outlines some considerations that seedstock producers can make in order to maximise the value of any scanning information that is collected on their animals.

Ensure Animals Are in Adequate Condition

Ensuring animals are in adequate condition at the time of scanning is paramount to the collection of useful scanning information.

This is a particularly important consideration when scanning yearling bulls. When animals are scanned when they are not in adequate condition (ie. they are too lean), the usefulness of the fat depth and IMF measurements is considerably reduced. In particular, very little variation is observed between animals for these traits, plus the ability of the scanning machines to accurately measure IMF decreases significantly when low levels of IMF are present. In these scenarios, scanning is of little benefit as a means of identifying animals that are genetically different for fat depth and IMF%.

As a rough guide, animals would be considered to be in adequate condition if they have a minimum average rump fat depth of 4 – 5mm (or average rib fat depth of 3mm) and the majority of animals have more than 2% IMF when scanned.

Scanning animals when they meet these minimum requirements will ensure there is sufficient variation between animals to allow genetic differences to show up.

It is important to note these recommendations are only a rough guide. For example, if animals have been in lean condition and have put on the required 4 - 5 mm of fat in a relatively short period, then there may still not be sufficient variation between animals to allow genetic differences to show up, particularly for IMF.

Of course, ensuring animals are in adequate condition at scanning can be very challenging, particularly when attempting to scan bulls prior to joining as yearlings at 15 months of age. At this age, bulls are physiologically quite lean, which can be further exacerbated in tough or dry seasons.



In all scenarios, but particularly these, it is consequently of utmost importance that producers carefully consider their management practices to ensure that animals are in adequate condition so that they obtain useful results from the scanning of their animals.

Scan Your Heifers

Scanning heifers is a must for producers that are serious about improving the carcass attributes of their animals. Heifers generally mature earlier than males do, meaning they tend to lay down fat and express IMF at an earlier age than males.

The consequence of this is that heifers exhibit more variation and provide better information for identifying genetic differences between animals in the carcass traits (particularly for fat and IMF%).

This has been demonstrated previously by the Animal Genetics & Breeding Unit (AGBU) in Armidale where analysis of the scanning information collected in several large breeds showed a greater heritability in the scanning information from heifers than bulls. This clearly illustrated that the scan information collected on heifers is more valuable in identifying genetic differences between animals than the scan information collected on males.

Scanning heifers also significantly increases the amount of information available on animals for the carcass traits, which will considerably increase the accuracy of the carcass EBVs being calculated for both the animal and its relatives.

For example, the carcass EBVs being calculated for sale bulls will be more accurate if their sisters have been scanned, or likewise their dams have been scanned as yearlings.

Scan the Whole Contemporary Group

It is important to scan as many animals as possible within each contemporary group in order to maximise the usefulness of the scanning information collected. Like all performance information, it is not necessarily the measurement recorded on the animal that is important, but how the measurement compares to those of other animals. That is, how the performance of the animal compares to the performance of their peers. Put simply, the animals with inferior performance (e.g. low IMF) need to be recorded in order to identify those with superior performance (e.g. high IMF) within a contemporary group.

Only scanning a small group of selected animals (for example, only scanning bulls listed for sale or the animals within the show team) can potentially misrepresent how the performance of an animal really compares to the performance of their peers, and can lead to the calculation of carcass EBVs that do not reflect the true genetic potential of the animal.

Scan Your Animals at the Correct Age

Ensuring animals are scanned at the correct age is essential to collecting valuable scanning information. At the outside, BREEDPLAN can only accept scanning measurements on animals that have been taken between 300 and 800 days of age, therefore it is very important that all animals are scanned within this age range. However, within this age range, it is important to time scanning in accordance with the traits of particular interest. For example, if the trait of most interest is IMF, it would not be recommended to scan animals until they have matured enough so that they are exhibiting differences in the amount of IMF. Depending on the production system and breed of animals being scanned, this may not have occurred at 300 days of age.

Use an Accredited Technician

Employing an accredited scanning technician to scan animals is important in collecting valuable scanning information. Scanning technicians will have all the required equipment and are required to pass an accreditation course, which assesses them on accuracy and repeatability of measurements. It should also be noted that BREEDPLAN can only accept scanning measurements that have been taken by an accredited scanning technician. A list of accredited scanners can be accessed on the Technical page of the BREEDPLAN website (<http://breedplan.une.edu.au>), or by contacting staff at BREEDPLAN.

Provide Management Groups to BREEDPLAN

When submitting the scanning information collected on animals to BREEDPLAN, it is important that producers specify management groups for animals that have been treated differently to the rest of their peers.

Differences in treatment may include animals that have been run in different paddocks, animals that have been supplementary fed in preparation for a show or sale, bulls that have been joined as yearlings or an animal that's performance has been affected due to illness.



Ultrasound scan image of eye muscle area

By specifying management group information, producers are acting as the “eyes” for the BREEDPLAN evaluation and are ensuring that the scan information collected for an animal is not inappropriately compared to the scan information of animals that have had a different opportunity to perform.

It should be noted that the submission of scanning data to BREEDPLAN is the responsibility of the seedstock producer and not that of the scanning technician.

By carefully taking into account the above considerations, producers can be confident that they will maximise the value of the scanning information collected on their animals. In some breeds, some specific additional considerations do apply which also need to be considered. For example, there are some additional difficulties when collecting IMF information by ultrasound scanning in Brahman and Wagyu cattle.

To further discuss the collection of useful scanning information, please contact staff at SBTS or TBTS. Additionally, the accredited scanning technicians can provide guidance in this area.

Tips for Collecting Useful Scanning Information

- ✓ Ensure Animals are in Adequate Condition
- ✓ Scan Your Heifers
- ✓ Scan the Whole Contemporary Group
- ✓ Scan Animals between 300 & 800 days of age
- ✓ Use an Accredited Scanning Technician
- ✓ Provide Management Groups to BREEDPLAN

Recording Twin Calves with BREEDPLAN

When it comes to performance recording twin calves with BREEDPLAN, knowing exactly what information you need to record can be a bit of a grey area. This article provides a guide as to the information you should be providing to ensure that the performance from your twin calves is analysed correctly. The first step to correctly recording twin calves begins when the calves are registered or recorded with the Breed Society.

- When completing calf registrations, it is critical to ensure that “Number in Birth” is recorded as “2” for any calf born as a twin. The “Number in Birth” simply refers to the number of calves born during that particular birth. That is, single calves should have a “1”, twin calves should have a “2”, etc. The BREEDPLAN analysis uses the “Number in Birth” to differentiate between twin and single calves and to separate them accordingly into contemporary groups. It is important to note that the performance from twin calves will never be directly compared with the performance of single calves within the BREEDPLAN analysis.
- Both twin calves should be recorded with the Breed Society. This is particularly important in the scenario where one twin is born alive and the other twin is born dead. Most Breed Societies will record dead calves free of charge.
- In situations where one of the twin calves is removed from the dam and either fostered onto another dam or raised as a poddy calf, the Breed Society should be informed as to which calf has been removed. Further, if the calf is fostered and the foster dam has been previously recorded with the Breed Society, then it can be beneficial to notify the Breed Society of the details of the foster dam.

The second step is to correctly submit the performance data to BREEDPLAN.

- The same performance information should be recorded with BREEDPLAN for twin calves as for all your other calves. That is, twin calves should be treated no differently within your performance recording program. However, while the same performance information should be recorded, it is essential that correct management group information is submitted to BREEDPLAN in association with the performance for your twin calves. This is particularly important in situations where there are multiple sets of twins.
- In situations where one twin calf is raised on its birth dam as a single calf (as the other twin is either born dead or



removed from the dam), a management group needs to be specified with the performance for this calf so that it is not incorrectly compared with the performance of other twin calves that have been raised as twins.

- In situations where one twin calf has either been fostered onto another dam or raised as a poddy and this information has not been recorded with your Breed Society, a management group should be specified with the performance for the fostered/poddy calf. Of course, the better approach is to notify your Breed Society that the calf has been removed from its birth dam, in which case BREEDPLAN will automatically analyse the performance in a separate management group.

It is not necessary to explicitly specify a management group with the performance for twin calves that have been raised as twins. The BREEDPLAN analysis will use the birth number to automatically split them into a separate group from the single calves.

By ensuring that you complete all the steps outlined above, you can be confident that the performance for your twin calves will be correctly analysed within the BREEDPLAN analysis. Importantly, should you have any queries about the recording of your twin calves with BREEDPLAN, please contact staff at SBTS or TBTS for assistance.

Tips for Recording Twins with BREEDPLAN

- ✓ Record a “Number in Birth” of “2” when registering twin calves with your Breed Society
- ✓ Record both calves with your Breed Society
- ✓ Notify your Breed Society if one of the twin calves has been removed from the dam
- ✓ Correctly management group your twin calves when submitting performance to BREEDPLAN

Update on the Beef CRC DNA Test for the Polled Gene

As reported in previous editions, the Beef CRC, CSIRO, Meat and Livestock Australia, and the Animal Genetics & Breeding Unit, in collaboration with the University of Queensland, released a DNA test for the polled gene in August 2010 for field testing.

The DNA test was developed to assist producers who wish to increase the proportion of polled animals within their herd by enabling the differentiation between polled bulls which are homozygous or “true” polled (that is, the animal carries two copies of the polled gene) versus polled bulls that are heterozygous polled (those animals carrying one copy of the polled gene and one copy of the horned gene).



By using homozygous polled bulls (as opposed to heterozygous polled bulls), it is guaranteed that the progeny of the bull will inherit a polled copy of the gene in 100% of cases, which greatly accelerates the increase in the proportion of polled animals within a herd.

Understanding the Science

The inheritance of horned and polled genetics in cattle has long been known to be under the control of only a few genomic regions or locus, and the most important of these, the polled locus, has been mapped to chromosome 1 by a number of groups. It is not known how many genetic variants, or alleles, exist at the polled locus, but it is convenient to group them into those that are associated with horns and those that are associated with polled. Animals inherit one allele from their sire and one from their dam, and so an animal may carry two horned alleles at the polled locus (in which case the animal's genotype is homozygous horned), one horned allele and one polled allele at the polled locus (the animal's genotype is heterozygous polled), or two polled alleles at the polled locus (the animal's genotype is homozygous polled, often referred to as ‘true polled’).

The DNA test or “marker” discovered by the Beef CRC, like other tests on the market, is a linked marker. That is, it is not currently possible to directly measure the animal's genotype at the polled locus, so something that is located close by on the genome is measured. Mostly, but not always, the close by measurement is a good predictor of the unknown underlying genotype at the polled locus, with most alleles at the marker

almost always being associated with the same allele at the polled locus (either polled or horned).

Field Testing of Beef CRC DNA Marker

Since August 2010, significant efforts have been carried out to assess the usefulness of the Beef CRC marker as an indicator of the animal's genotype at the polled locus. In particular, three different sources of information have now been analysed, including animals that were DNA tested as part of the original experimental population when the test was being developed, sires for which DNA was submitted as part of the Industry Sires Genotyping Project, and lastly, animals for which individual seedstock herds have submitted DNA samples to University of Queensland for testing.

A summary of the numbers of animals included in the field testing are presented in Table 1 (see overleaf).

Results of Field Testing

Field testing has greatly increased knowledge of the usefulness of the Beef CRC DNA Test as an indicator of the genotype of an animal at the polled locus. In particular, field testing has revealed:

- Some alleles at the marker show associations with both polled and horned alleles at the polled locus. These alleles are referred to as “ambiguous” alleles and where present, pose significant challenges to the usefulness of the marker as it is not possible to determine whether the animal is carrying a horned or polled allele at the polled locus.

Importantly, the frequency of ambiguous marker alleles varies between breeds, being very high in some breeds (e.g. Limousin) versus almost non-existent in others (e.g. Brahman). Consequently, in breeds, where ambiguous marker alleles are rare the test works very well, whereas in breeds where ambiguous marker alleles are common, the test is unable to clearly predict genotype at the polled locus in a significant percentage of animals.

- In some cases, the genotype result based on the marker is not consistent with the phenotype that has been recorded for the animal. This could be due to an incorrect phenotype being recorded, to genes other than those located at the polled locus, or to a marker allele having an alternative association to that which is generally the case.

These results are illustrated in Table 2 which provides a summary of the marker results for the animals analysed during the field testing that had a polled phenotype. Similar results for the other phenotypes are available from the Beef CRC website.

In this table, P indicates a marker allele that is generally associated with a polled allele at the polled locus, H indicates a marker allele that is generally associated with a horned allele at the polled locus, and A indicates an ambiguous marker allele, which may be associated with either a polled or a horned allele at the polled locus.

As an example of the interpretation of Table 2, in Brahman animals, field testing revealed that of polled animals, in 11% of cases at least one ambiguous allele was present, meaning that in 89% of cases, the test produced an unambiguous result. Further, in 98% of cases where an unambiguous result was produced, the result was consistent with the phenotype of the animal. The conclusion that can be drawn from this is that the Beef CRC DNA test provides a useful means of identifying whether polled animals are either homozygous or heterozygous polled in the Brahman breed.

Complete details of the field testing that has been completed, including the specific results in each breed for each different phenotype are available from the Beef CRC website (<http://www.beefcrc.com.au/PolledGeneMarkerTest>).

Presentation of Results from Test

To account for the unambiguous results and those that are inconsistent with the phenotype the gene marker test results are now presented as probabilities for each genotype, rather than as a definitive genotype, as per the example below.

Homozygous PP	Heterozygous PH	Homozygous HH
91%	8%	1%

In the example above the animal has a 91% probability of being homozygous polled (or true polled), 8% probability of being

Table 1 - Counts of animals tested from each group (experimental population, industry sire or breeder submitted) for each phenotype (horned, scurred and polled) by breed.

Breed	Experimental Population			Industry Sires			Breeder Submitted		
	Horned	Scurred	Polled	Horned	Scurred	Polled	Horned	Scurred	Polled
Brahman	180	136	86	84	0	5	9	8	116
Brangus	32	27	37	0	0	0	0	0	0
Charolais	0	0	0	57	3	36	0	0	0
Droughtmaster	33	22	39	24	16	60	0	0	0
Hereford	71	27	96	105	0	109	0	0	0
Limousin	22	1	29	64	5	79	0	1	142
Santa Gertrudis	102	31	52	13	1	7	0	1	40
Shorthorn	0	0	0	3	0	105	0	0	0
Tropical Composite	116	47	84	0	0	0	0	0	0
Simmental	0	0	0	60	1	36	0	0	0

Table 2 - Results of Field Testing for Animals with a Polled Phenotype

	PP	PH	HH	PA	HA	AA	% Ambiguous	% Inconsistent with Phenotype
Brahman	84	96	4	9	10	4	11%	2%
Brangus	5	9	0	16	2	5	62%	0%
Charolais	13	13	0	8	1	1	28%	0%
Droughtmaster	34	37	1	15	7	5	27%	1%
Hereford	102	44	2	49	4	4	28%	1%
Limousin	59	38	0	102	11	40	61%	0%
Santa Gertrudis	15	60	1	16	6	1	23%	1%
Shorthorn	12	24	0	17	35	17	66%	0%
Simmental	8	12	0	14	0	2	44%	0%
Tropical Composite	43	18	1	21	0	1	26%	2%

heterozygous polled and 1% chance of being homozygous horned.

Testing Your Animals

Interested seedstock producers can currently get their animals tested through the University of Queensland's Animal Genetics Laboratory (UQ AGL) at a cost of \$33.00 per animal (inc. GST). Discounted prices apply if the tests are done through breed societies or in bulk.

To test an animal, a DNA sample from the animal and the

phenotype of the animal being tested (e.g. horned, polled, scurred or unknown) need to be provided. Hair samples are the best option (30-40 hair follicles). Contact UQ AGL or your breed society to obtain a hair collection kit. UQ AGL can also extract DNA from blood or semen for an additional charge.

The Beef CRC have recently made the test available to anyone who wishes to provide a commercial service and so it is anticipated that other DNA service providers will make the test available shortly.

Collection of Weaning Date Information

As previously reported in the Summer 2010 issue of the SBTS & TBTS Update, information regarding the date of weaning can now be collected and submitted to BREEDPLAN.

In late 2010 the Animal Genetics and Breeding Unit (AGBU) requested that members of BREEDPLAN record the date their animals are weaned and submit this information to BREEDPLAN to assist with further development and enhancement of the BREEDPLAN genetic evaluation.

While weaning date information is not being included in the BREEDPLAN analysis at this stage, once sufficient weaning date information has been recorded, AGBU will investigate using it to enhance the EBVs that are calculated by the BREEDPLAN evaluation by:

- Assisting in the correct management grouping for 200 day weight records and mature cow weights, particularly if early weaning is practiced
- Allowing the identification of data from early weaned animals to enable research into the effects of early weaning on:
 - > The partitioning of 200 day weight records into the direct and maternal components
 - > The estimation of age of dam effects and possible need for separate age of dam adjustments for 200 day weights of early weaned calves



- > The expression of female reproductive traits (e.g. days to calving) and the need to modify the definition of mating contemporary group
- > The recording and contemporary grouping of measures taken at the time of weaning e.g. docility scores, IGF-I.






Weaning date information should be submitted to BREEDPLAN in association with your 200 day weight performance which can be submitted by the paper performance recording forms, the internet performance submission facility and the BREEDPLAN compatible Microsoft Excel template.

If you are using a BREEDPLAN compatible herd recording software package (eg. HerdMaster, StockBook, CattleLink) it is advised that you contact your service provider to discuss how to record and submit weaning date information to BREEDPLAN.

For further information on collecting and submitting weaning date information, please contact staff at SBTS or TBTS.

Accessing Support in Application of Genetic Technologies

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 & 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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