Deciding which bull is mated to which cow is a standard, every-day management decision that is faced by all seedstock and commercial beef breeding enterprises. While being an every-day practice, its importance should not be understated as it is a critical decision point which has a significant impact on both the rate of genetic improvement and inbreeding levels (or genetic diversity) being observed within a herd.

MateSel is a new breeding tool shortly to be released by BREEDPLAN that enables breeders to optimise the breeding outcomes for their herd by creating a suggested mating list based on a list of candidate sires and dams.

The underlying MateSel "engine" was developed by Professor Brian Kinghorn, School of Environmental and Rural Science, University of New England. MateSel has already been implemented in the American pig breeding industry to great effect with sustainable genetic gains being achieved while maintaining genetic diversity, all resulting in improved profitability.

MateSel will be a valuable addition to the BREEDPLAN suite of tools. It will provide beef cattle seedstock producers with a mechanism by which they can objectively optimise mating allocations to reflect their breeding goals and create long term, sustainable genetic improvement within their breeding program. The optimised genetic improvement that is targeted is based on a nominated selection index, while constraints are applied on inbreeding to ensure genetic diversity is maintained or improved.

The MateSel tool is currently progressing through its final stages of field testing. Once the final revisions are implemented, a commercialisation strategy will be finalised and communicated to Breed Societies and BREEDPLAN members. It is anticipated that it will be made available to Breed Societies who both publish selection indexes and operate on ABRT’s ILR2 software program during early 2013.

In addition to the standard MateSel product, a more sophisticated “bells and whistles” version of MateSel will also be available to those breeders that want to go the extra step with designing their breeding program and mating allocations. It is envisaged that this will involve some form of consultation and be available at an additional cost. However, it is predicted that the standard version of MateSel will suit 95% of BREEDPLAN herds.

Using MateSel

One of the major benefits of MateSel is that it is entirely tailored to fit the breeding program for each individual seedstock operation. Consequently, when using MateSel, seedstock producers are required to specify a range of information regarding the structure of their breeding program and details of their breeding objective for utilisation by the MateSel program.

The information required by MateSel can be broadly broken into two key areas.

- Nomination of candidate sires and dams for use in the breeding program - The list of candidate sires and dams available for the upcoming joining season is required. This can range from a very specific list of individual animals that have already been selected for use within the upcoming season, through to a broader list of potential animals that could be used within the joining season. MateSel is fully integrated with each Breed Society database and therefore
has the ability to select default groups of animals as candidates. For example, all active females on a herd’s female inventory or all sires listed in the online semen catalogues.

■ **Outline of Breeding Program and Breeding Objective** - The specifics of the breeding program and breeding objective need to be defined. This involves such things as:
- Nominating a “target” selection index
- Selecting a breeding strategy ranging from “High Gain” to “Diversity”.
- Advising maximum numbers of matings for each sire (AI and Natural)
- Advising minimum cow mob size for the natural mating groups
- Specifying which sires can be used on heifers compared to mature cows or both.

Also, if applicable, specifying which sires and dams are dedicated to an AI program.

In the initial release of MateSel, it is envisaged that this information will be submitted to staff at BREEDPLAN using a Microsoft Excel template whereby the BREEDPLAN staff will conduct the MateSel analysis and return results to the seedstock breeder. However development is underway to provide a MateSel web-interface where seedstock breeders can enter information via a secure member login. This will allow each breeder to undertake MateSel analyses for their own herd, in their own time, without the need for a middle-man or consultant.

**Example MateSel Reports**

Following each MateSel analysis, seedstock breeders will be provided with a MateSel report that contains a suggested mating list sorted by both sire and by dam, as well as a range of summary reports illustrating the predicted outcomes of the suggested matings. A csv file containing the mating allocation list will also be provided. These reports will be made available via the secure member login facility available on the BREEDPLAN website. Some example MateSel reports are provided in the following diagrams.
New Technology - INSolutions Mobile Application

Seedstock and commercial beef producers now have a tool available that enables them to easily access a range of information on their mobile phone when evaluating prospective purchases of genetics with the release of the new INSolutions Mobile App.

The INSolutions Mobile App has been developed by the Agricultural Business Research Institute (ABRI) in Armidale as an add-on to the Internet Solutions suite of tools that are currently made available to the beef industry by Breed Societies in both Australia and overseas. The app can now be downloaded from the iTunes App Store or Google Play for a cost of $1.99. It is compatible with most iPhone and Android mobile devices.

Managing Director of ABRI, Mr Murray Scholz explained that the new INSolutions App builds on the features of the successful Internet Solutions web based service and enables a far more user friendly display of the information available regarding an animal when using a smart phone.

“When viewing sale bulls on sale day, the app enables bull buyers to view a range of information regarding each lot including a 2 generation pedigree, complete EBVs and selection index information, the popular EBV graph display, vendor comments and a photo of each animal” said Mr Scholz.

Furthermore, the INSolutions Mobile App is fully interactive enabling bull buyers to easily search and sort the catalogue on particular criteria of interest, while a favourites feature enables sale lots of particular interest to be easily highlighted and viewed in a separate list”.

Mr Scholz highlighted that while the app has been primarily designed to assist bull buyers, it is not limited to the viewing of sale catalogues, with Member Lookup, Animal Lookup and Semen Catalogue facilities also available within the app. These functions provide instant access to detailed information from the complete electronic herdbook for each registered breed organisation.

“In this manner, the app will also be of great benefit to beef producers when viewing animals in the paddock or at agricultural events and shows, or when trying to obtain contact details for an individual seedstock producer” said Mr Scholz.

Initially the INSolutions Mobile App has been enabled for all 37 Australian beef breeds that are currently utilising the Internet Solutions service, plus beef breeds in New Zealand, the United Kingdom and Hungary. Over coming months it will be expanded to accommodate other clients of ABRI who are utilising Internet Solutions such as beef clients in other overseas countries and clients in other species such as sheep, boer goats, alpaca, dairy cattle, horses and deer.

In addition, a customised version of the INSolutions Mobile App has been recently released by Angus Australia which enables access to the Angus Australia database and can be downloaded for free.

Further information regarding the INSolutions Mobile App, including a video demonstration of the app, is available from the following web page: http://abri.une.edu.au/mobile/web/
Variation in Age and Weight of Puberty in Tropical Cattle

A major research project within the Cooperative Research Centre for Beef Genetic Technologies (Beef CRC) has provided a very useful insight into the variation that exists in the age and weight at which tropical cattle reach puberty in Northern Australia. Previous to the Beef CRC, very little research had been done in this area, with one of the primary objectives of the Beef CRC project being to investigate what effect genetics had on the age of puberty and consequently what opportunities may exist to improve fertility rates in Northern Australia through genetic improvement.

Project Design
A total of 2115 heifers were involved in the project (1007 Brahmans and 1108 Tropical Composites). The heifers were born in Northern Australia on 7 co-operator properties (4 Brahman and 3 Tropical Composite (TC)) and “Belmont Research Station” which breed both Brahman and TC. Genetic linkage, across properties of origin and year within genotypes was generated by the use of AI. The heifers were born over 4 and 3 years for Brahmans and TC respectively. The heifers were allocated according to genotype, property of origin and sire to one of the following four properties “Toorak” Julia Creek, “Belmont” Rockhampton, “Swans Lagoon” Ayr and “Brian Pastures” Gayndah at weaning. Belmont and Toorak ran both Brahman and Tropical Composites while Brian Pastures only had Tropical Composites and Swans Lagoon with the harsher environment only had Brahmans. At each location all heifers from the same year of birth were managed as a single cohort.

The heifers were ovarian scanned by the use of real time ultrasound by an experienced scanner to determine when the first Corpus Luteum (CL) was observed on an ovary. When a heifer had recorded a CL she was deemed to be pubertal. The heifers were scanned every 4-6 weeks after they had reached 200 kg or at the first scanning opportunity if they were over 200 kg at their entry into the project. At each ovarian scan the heifers were weighed, P8 fat measurement was recorded and a condition score was given. All heifers were kept in the project until they had a recorded CL, which in some cases was after 2 mating opportunities.

Results
Analysis of the Beef CRC results across all four properties shows that there was a large range in both the weight and age at which the heifers reach puberty in both Brahman and TC. There was a difference of 29 months from when the youngest heifer till the oldest heifer reached puberty, whereas a difference of 289 kg was recorded between the lightest and heaviest animals when the first CL was recorded as shown in table 1.

Table 1: Mean and Range for All Heifers at Age of Puberty

<table>
<thead>
<tr>
<th>Trait</th>
<th>Mean</th>
<th>Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age at first CL (Months)</td>
<td>23</td>
<td>11 - 40</td>
</tr>
<tr>
<td>Weight at first CL (kg)</td>
<td>332</td>
<td>196 - 485</td>
</tr>
</tbody>
</table>

When looking at the distribution in age at which the heifers reached puberty, the effect of the enviroment and production system has on when the heifers cycle was can be observed. Figure 1 shows there is a small number of Brahman heifers reaching puberty in the first wet season after weaning, followed by only low numbers until the next wet season when the majority of heifers reached puberty at two years of age and are going into mating. The last heifers that did not reach puberty until the next wet season at nearly 3 years of age. The TC heifers had a similar pattern to the Brahman heifers except there were more heifers reaching puberty in the first wet season and only a few animals had not reached puberty at the end of the second wet season.
Location Difference

The location of the property on which the heifers were run had a large effect on the puberty traits in both breeds. In TC, the heifers at Toorak and Brian Pastures had a similar age and weight of first CL, whereas the heifers at Belmont were significantly older and heavier. In Brahman, the heifers at Belmont and Toorak were significantly younger than those at Swans Lagoon at the age of puberty, even though the heifers at Swans were significantly lighter when they reached puberty. At Belmont, where the Brahmans and TC were run in the same cohort there were no differences in age or weight at puberty between the breeds.

Birth-month differences

Birth month had a significant effect on the puberty traits. As the heifer’s birth month became later in the calving season (i.e. from August to April) there was a trend for age at first CL to increase. On average, early born heifers (i.e. August to September) reached puberty by approx. 20 months of age, coinciding with the end of their first postweaning wet season (i.e. May). For late-born heifers (i.e. February to March), the average age at puberty was delayed until the following May, at approx. 26 months of age, suggesting that heifers that did not achieve puberty before the start of their second postweaning dry season were significantly delayed in reaching puberty. This can have a dramatic impact on the number of heifers that have reached puberty going into mating.

Genetic Effects

One of the key outcomes of the Beef CRC research was that both age at first CL and weight at first CL were shown to be under significant genetic control in both Brahmans and TC. Heritability estimates for age at first CL were 0.57 for Brahmans and 0.52 for TC while the heritability estimates for weight at first CL were 0.56 for Brahmans and 0.46 for TC. Further analysis revealed that there was a difference due to genetics of 5.6 months in age of puberty between the top and bottom Brahman sire included in the research trial. Although not as high, there was a 3.1 month difference in age of puberty between the top and bottom sire in the TC.

Conclusions

There is a large variation in the both the age and weight that heifers reach puberty in tropical cattle, with both genetic and enviromental influences having an effect. Age of puberty can be significantly delayed in late born calves and also in enviroments that limit growth rates particularly during the dry season. Therefore, management can be used to reduce the age of puberty by controlling month of birth, duration of mating period and supplementary feeding pre-pubertal heifers prior to mating. However, significant improvement can also be made by including selection for improved reproduction into a breeding program. This can be best achieved by recording female reproductive performance information with BREEDPLAN for the calculation of Days to Calving EBVs (particularly reproductive information from maiden heifers), and careful consideration of Days to Calving EBVs when selecting both sires and dams for use within a breeding program.

Further information is available from Paul Williams at TBTS in Rockhampton on (07) 4927 6066 or paul@tbts.une.edu.au.
Software Upgrades to Internet Solutions

There have been a number of considerable software upgrades made to the Internet Solutions suite of tools over the past few months. These tools are offered by 37 Breed Societies in Australia and include the ability to search and sort an online database for each breed, view individual animal and member information, and access available sale and semen catalogues.

The software upgrades that have been implemented form part of the ongoing development and improvement to the Internet Solutions suite of tools and include:

- A significant enhancement has been made to the database management program that is used within the Internet Solutions software. This enhancement has resulted in a considerable improvement in performance in the Internet Solutions software, particularly in relation to improved speed when conducting animal and member searches.
- Users now have additional sort functionality whereby search results can be sorted in either ascending or descending order on any particular criteria by clicking on the relevant heading in the table of search results.
- The maximum number of search results that can be displayed from any particular search has been increased to 200 animals. This will greatly improve the search functionality for users attempting large searches without any noticeable effect on performance.
- Selection index information will now be automatically displayed by default within the search results. Previously users were required to select the option “Show Indexes”.
- All EBV traits will now be included in the EBV table on the individual animal page by default in a similar manner to which they display on the search results pages. Previously EBV traits were only included in the animal had EBVs reporting for that trait.
- Users now have more flexibility when conducting animal searches. In particular, the wildcard feature has been enhanced so that when looking up a member or animal, you can now use the percentage symbol (%) before and/or after a part of the name. For example, if you wish to search for an animal with “Super” in its name, just type %super% in the name search field and all animals with “Super” somewhere in their name will be displayed.
- The maximum number of dams that can be specified in the Enhanced Mating Predictor facility has been increased to 200.

The Cutting Edge - Webinar Course

With the Beef Cooperative Research Centre (CRC) formally exiting the Government’s CRC program on 30th June 2012, a range of the latest research outcomes in the area of beef cattle genetics and breeding were presented during the recent “The Cutting Edge” webinar course.

Comprised of 6 one hour presentations delivered via the internet during August and September, the webinar course was facilitated by staff from Southern Beef Technology Services (SBTS) & Tropical Beef Technology Services (TBTS), and presented by senior beef industry scientists from the Beef CRC. The webinar course was well attended with a total audience of over 500 people and 250 individual seedstock enterprises.

The topics presented during the webinar course included:

1. Genetics for Reproduction - The Female Influence
2. Genetics for Reproduction - The Male Influence
3. Relationship between Body Composition and Calving Rate
4. Effect of Genetic Differences in Fat and Net Feed Intake on Efficiency of Weaner Production
5. The Beef CRC DNA test for Growth, Feed Efficiency, Carcase and Reproductive Performance
6. The Australian DNA Test for the Polled Gene

All presentations in the “The Cutting Edge” webinar course can now be viewed from the webinars page on the SBTS (http://smts.une.edu.au) and TBTS (http://tbts.une.edu.au) websites. From either the SBTS or TBTS homepage, select “Webinars” from the left hand menu and then click on the title of the presentation that is of interest.

SBTS & TBTS would like to gratefully acknowledge the beef industry scientists, David Johnston (AGBU), Wayne Pitchford (University of Adelaide), Mike Goddard (University of Melbourne) and John Henshall (CSIRO Animal Food & Health Sciences), who generously donated their time to deliver their presentations.
All members of BREEDPLAN in Australia who have not already done so are encouraged to download their latest Completeness of Performance report, with the updating of reports for all BREEDPLAN members during July and August 2012.

The Completeness of Performance reports provide a summary of the information that each individual seedstock herd has submitted to BREEDPLAN, with a range of statistics provided within the reports including details of the pedigree, weight, carcase, birth and fertility information that has been recorded in recent years.

The Completeness of Performance reports allow members of BREEDPLAN to both routinely double check that the performance information that they have collected on their animals has been recorded with BREEDPLAN, plus importantly enable members to identify areas in which additional performance information could potentially be recorded on their animals. Recording information in these areas will improve the accuracy of the EBVs being calculated for their animals.

The latest “Completeness of Performance” reports are available for download from the Member Login area of the BREEDPLAN website. Members who don’t already have a username and password for the Member Login Area should contact staff at their Breed Society for assistance in setting one up. Alternatively, members who can not access their report in this manner should contact staff at BREEDPLAN and a printed version of the report can be placed in the mail.

In addition to the availability of updated Completeness of Performance reports, the Completeness of Performance star rating for each herd is now displayed on the Member Enquiry facility for the breeds that have elected to introduce this feature. As well as viewing the star rating for each herd, users also have the ability to limit animal and EBV searches based on a herd’s star rating.

New BREEDPLAN Promotional Brochures Available

A range of new BREEDPLAN promotional brochures are now available. The brochures provide a range of the information regarding BREEDPLAN and related genetic technologies such as BreedObject Selection Indexes, TakeStock, Completeness of Performance, GeneProb, Internet Solutions and MateSel.

The brochures are available from the technical area on the BREEDPLAN website. Alternatively, paper copies can be requested from the BREEDPLAN office.
Gains in cattle performance through genetic improvement driven by BREEDPLAN will soon be enhanced via a whole-of-life herd recording system encompassing factors like carcase performance, breeder fertility and growth for extensive beef producer, S. Kidman & Co.

While BREEDPLAN had delivered wide-ranging improvement in herd performance, the company’s livestock marketing manager, Will Abel-Smith said additional technologies would help further improve herd performance.

Mr Abel-Smith addressed the ninth Santa Gertrudis World Congress held in Brisbane during the EKKA. “We’re at the point in our business now where we have decided that if we can’t measure traits, we can’t improve,” he told the Congress.

In addition to applying selection pressure using BREEDPLAN traits, Kidman has begun performance recording using Gallagher’s TSi crushside data capture units, collecting data on every animal coming through the remote station yards on breed, age, status, weaning rates, calving rates and weight gain, allowing staff to track animals right through their productive life. Meatworks carcase data on steer progeny will be added to the data-set.

“We see it as a way of identifying those animals that aren’t performing for us and making calls on getting rid of them earlier,” Mr Abel-Smith said.

Software is also being written that will allow the company to link that performance assessment right through to carcase level, providing whole-of-cycle performance assessment potential. While that process will generate a mountain of statistical data, Kidman sees that if appropriately managed and processed, it can help target a ‘lot more’ gains in animal performance, whether it be at the meatworks chiller level, the breeding paddock level, or in the growing paddock.

Mr Abel-Smith said the company started applying more performance-based selection pressure within its Kidman Park seedstock breeding herd from about 2000 onwards, while still maintaining standards for structure and type. The company’s
stud herd contains about 1300 purebred cows, all fully-recorded on BREEDPLAN. The Kidman Park calves comprise about 20pc of all calves recorded on BREEDPLAN each year for the Santa Gertrudis breed. The calves are weighed, tagged and dam-identified, and later DNA-sire tested, even when run under quite extensive conditions, he said.

About 25 percent of the bull-producing herd are bred by AI, and heifers calve at two years. AI sires comprise a mix of breed industry leaders for desirable traits, plus semen collected from the best young bulls coming through Kidman’s own breeding program. All yearlings are measured for scrotal size, and carcase traits, and over time, the Kidman calf drop has gone from breed average, to well above, for carcase eye muscle area. Calves are now above breed average for performance in most traits.

Last year, the top 400 young Santa bulls sent to work on breeding properties were all in the breed’s top 20 percentile for growth.

Today the Kidman stud herd is managed on the company’s behalf by the Wrigley family from Moongenilla Angus near Condobolin in NSW. The Wrigleys are successful Angus bull breeders in their own right, and were now applying an ‘Angus-style’ focus on the selection process for Kidman’s Santa program, which since 2006 has produced ‘huge improvements’ in performance, Mr Abel-Smith said.

Kidman is working hard to lift the percentage of polled animals across the company’s herd.

All yearlings are scanned for carcase traits, with considerable genetic improvement for eye muscle area being observed

Last year, the top 400 young Santa bulls sent to work on breeding properties were all in the breed’s top 20 percentile for growth.

Today the Kidman stud herd is managed on the company’s behalf by the Wrigley family from Moongenilla Angus near Condobolin in NSW. The Wrigleys are successful Angus bull breeders in their own right, and were now applying an ‘Angus-style’ focus on the selection process for Kidman’s Santa program, which since 2006 has produced ‘huge improvements’ in performance, Mr Abel-Smith said.

Kidman is also working hard to lift the percentage polled across the company’s herd, and there is always great competition each year between station managers over who secures the best polled bulls. The percent polled calves have risen from 40pc in 2004-05 drop cows to around 70pc in 2009 drop cows.

Workplace health and safety and animal welfare issues, and reduced labour requirement had driven the emphasis on polled cattle, Mr Abel-Smith said.

For the past six years Kidman has minimised the use of bulls showing horn, and had more recently started DNA-testing young bulls and top sires for polled status. Bull calves are rated for horned, polled or scurred status, and homozygous polled animals are identified at about six months of age using tail-hair samples.

The strong selection pressure means about 70 percent of bull calves are now visually polled, however tests indicate that only about 20pc of those are homozygous for the polled gene, meaning there is still some considerable way to go.

While the initial selection pressure was on improving growth rates, which has largely been achieved Kidman found that there were some consequent issues with calf size and calving difficulty. As a result it has worked hard to monitor birth weights within the Kidman Park herd, with a consequent reduction in birth weight, while also succeeding in reducing gestation intervals.

“In particular, Birth Weight EBVs have helped us identify the best young bulls coming through the system, which has allowed us to mate our heifers without sacrificing growth in their progeny,” Mr Abel-Smith said. “Scrotal size is an indicator of fertility, and we have moved from breed average to above average, via measurement and selection pressure,” he said.

Ultrasound scanning has been used to lift rib-eye area and yield, with a consequent reduction in fat cover. The company’s current bull selection places an increased emphasis on rib fat, as evidence suggests this may also be related to fertility. “The evidence suggests that measurement in our stud nucleus has lifted the returns in our commercial herds – in the first instance through higher genetic potential for growth, and we look forward to seeing what gains can be made from the full herd tracking system now being activated across the business,” Mr Abel-Smith said.

He said it seemed to the company that the beef breeds with the strongest emphasis on performance recording were becoming the most successful. “We would encourage all breeders to push for continuous improvement through objective performance recording,” he said.

This article is an excerpt from an article by Jon Condon that was published on the Beef Central website on 20th August 2012. SBTS & TBTS gratefully acknowledge Jon for his assistance in reproducing this article.
Inbreeding - Be Alert but not Alarmed!

The discussion of inbreeding in bull breeder circles can lead to a broad cross section of thoughts. These range from the “we must avoid inbreeding at all costs” theory, to the “linebreeding is the best thing since sliced bread” philosophy.

Inbreeding is basically the mating of animals that are related. Within the pedigree of the mated sire and dam, one or more animals will be in common; resulting in progeny with a certain level of inbreeding. The level of inbreeding will depend on the relationship between the two mated animals. The closer the relationship, the greater the level of inbreeding that will occur in the resulting progeny.

Linebreeding is the deliberate mating of closely related animals with the perceived objective to concentrate desirable characteristics of the progeny and to breed “consistency”.

The Measurement of Inbreeding

The inbreeding level in a specific animal or mating outcome can be measured by way of an inbreeding coefficient. An inbreeding coefficient is calculated as the probability percentage (%) for any allele (i.e. pair of genes at a specific location on the chromosome) to be identical by descent.

Typical inbreeding coefficient percentages are as follows. This is assuming no previous inbreeding between any parents:

<table>
<thead>
<tr>
<th>Relationship</th>
<th>Inbreeding Coefficient</th>
</tr>
</thead>
<tbody>
<tr>
<td>Animal mated to its own parent (Sire to daughter)</td>
<td>25%</td>
</tr>
<tr>
<td>Full siblings (sire to dam with a common sire and dam)</td>
<td>25%</td>
</tr>
<tr>
<td>Half siblings (sire to dam with a common sire or dam)</td>
<td>12.5%</td>
</tr>
<tr>
<td>Half cousins (sire to dam with a single common grandparent)</td>
<td>3.1%</td>
</tr>
</tbody>
</table>

The “accuracy” of the inbreeding coefficient value that is calculated will depend on the accuracy and depth of pedigree that is recorded. For example, the accuracy of the inbreeding coefficient that is calculated would be higher in an animal with 10 generations of pedigree on both the sire and dam side, compared to an animal with 10 generations on the sire side but from a cow with little or no pedigree recorded.

Effects of Inbreeding in Beef Cattle

Inbreeding can potentially lead to three main negative outcomes being (1) inbreeding depression in production traits, (2) increased homozygosity of recessive genetic conditions, and (3) a reduction in genetic diversity.

Inbreeding depression: Generally, animals with higher levels of inbreeding have depressed performance for a range of economically important traits when compared to animals with lower levels of inbreeding (with all other factors being equal). The depression caused by inbreeding tends to negatively affect the traits which are positively affected by heterosis (i.e. crossbreeding – the opposite of inbreeding). These being fertility, survival, growth, and to a lesser extent, carcase traits.

A literature review undertaken by Burrow (1993) investigated the effects of inbreeding in beef cattle. The review revealed that inbreeding of the individual has a consistent adverse effect on growth traits from birth to maturity and on maternal traits. More specifically, for every 1% increase in inbreeding coefficient a decrease of 0.06, 0.44, 0.69 and 1.30 kg in live weight at birth, weaning, yearling and maturity respectively. Additionally, inbreeding in the dam decreased weaning and yearling weights by 0.30 and 0.21 kg respectively for every 1% increase in inbreeding coefficient, probably as a result of decreasing milk yield and reduced maternal value of the inbred dams.

The review also reported inbreeding as having a depressive effect (although the magnitudes of effect were small in some cases) on heifer conception rates, female fertility, conformation/structure, feed intake, feed conversion efficiency, carcase traits and male reproductive traits.

Recessive Genetic Conditions: Most breeds have at least one recognised recessive genetic condition. An example of these is Arthrogryposis Multiplex (AM) in Angus or Angus derived cattle or Pompes Disease in Brahman or Brahman derived cattle. An animal must carry two copies (i.e. homozygote) of the recessive genetic condition to be affected by the condition. An animal that only carries one copy (heterozygote) will not show the affects, but will be a “carrier”.

An increase in inbreeding can inadvertently lead to an increase in the likelihood of animals being affected by recessive genetic...
conditions. This is primarily through the increase in allele homozygosity as explained earlier.

**Reduction in Genetic Diversity:** Over time, higher levels of inbreeding will result in a loss of genetic diversity within the population. This can impact in both the potential loss of favourable alleles that may have existed for some traits, plus a decrease in the amount of genetic variation that exists between the animals on which future selection decisions can be made.

**Inbreeding Considerations**

Some breeders may argue that “structured” inbreeding programs can be used to produce a single “superior” individual through the stacking of desirable genes for certain production or functional traits (i.e linebreeding). This is common practice in the thoroughbred horse industry. For example, Black Caviar has common ancestry in its pedigree such as a stallion called Vain. This stallion is both Black Caviar’s paternal great grandsire and maternal great-great-grandsire. He also has a second sire, Silly Season, further back in the pedigree that appears on both sides of the pedigree.

Of course, aiming to produce one superior individual will also result in many more inferior animals through inbreeding depression or appearance of recessive genetic conditions. The aim of beef cattle breeders should be to improve the average performance of the herd. This can be achieved through objective selection and allocation of matings of breeding animals on performance traits (EBVs and Indexes) in conjunction with visual appraisal, while managing inbreeding levels. This will ensure the average performance of a herd (or breed) is improved while the inbreeding level (or genetic diversity) is maintained.

**Acceptable Levels of Inbreeding**

There is no magic level that is considered an acceptable level of inbreeding within a breeding program, with the goal in most breeding programs being to manage inbreeding rather than totally avoid it. Breeding programs that simply avoid inbreeding without considering the genetic merit of the animals used within the mating program are not likely to be economically sustainable in the long term. Ultimately, the most beneficial breeding program will be the one that results in the progeny with the highest overall genetic merit once the negative effects of inbreeding have been adjusted for.

Average inbreeding coefficient levels of less than 5% within a breeding program are considered low, with inbreeding levels of 5 – 10% generally considered more moderate levels of inbreeding and warranting more careful management. However, managing the increase in inbreeding level over time is as important, if not more important than managing the overall level of inbreeding within the breeding herd.

**Tools to Manage Inbreeding**

Bull breeders have a range of tools available to assist them with genetically improving the average of their herd for production traits while monitoring and managing inbreeding. These include:

**Mating Predictor:** The online animal search facility (colloquially known as Internet Solutions) includes an “enhanced” mating predictor option which has been implemented by most breeds. This facility includes the calculation of an inbreeding coefficient, plus details on the depth of pedigree as a pseudo “accuracy” measure, for progeny from a specified mating (See Figure 1).

**Mate Allocation Tools (Such as MateSel):** A number of computer based breeding tools are available that enable breeders to optimise breeding outcomes for their herd by creating a mating list based on a list of candidate sires and dams. These provide beef cattle seedstock producers with a mechanism for objectively optimising mating allocations to reflect their breeding goals and creating long term, sustainable genetic gains. The genetic gains are based on a nominated breeding objective, while constraints are applied on inbreeding to ensure genetic diversity is maintained or improved. More information is provided regarding one such tool, MateSel, in the article on pages 1-2.

**References:**


---

**Figure 1 – Example outcome from the mating predictor from a half-sib mating.**
The incorporation of the genomic prediction equations developed by the Beef CRC into BREEDPLAN is progressing with considerable validation work being conducted over recent months by the Animal Genetics and Breeding Unit (AGBU) at the University of New England.

The exact timeframe for the completion of this validation work is yet to be determined, however it is hoped that it will be completed prior to the end of 2012. Once completed, the subsequent incorporation of the genomic predictions into the routine GROUP BREEDPLAN analyses for each of the major beef breeds in Australia will be assessed on a breed by breed basis.

The genomic prediction equations were developed using Illumina’s new 700K SNP chips and measure more than 700,000 unique genetic variations (SNPs) within an individual animal’s genome to provide an estimate of an animal’s genetic value for a range of carcass and beef quality, feed efficiency and female fertility traits. The genomic prediction equations are applicable to most of the major beef breeds in Australia. It is hoped that the genomic prediction equations will explain up to 15% of the genetic variance for each trait in these breeds, although this is likely to vary depending on the trait and the breed of animal being tested. This is equivalent to an EBV with 40% accuracy.

The incorporation of the Beef CRC genomic predictions equations is an important step as it is now widely recognised that the best utilization of the genomic information for production traits is via incorporation into existing genetic evaluation programs such as BREEDPLAN. In this manner, the pedigree and performance information traditionally included in BREEDPLAN is combined with any genomic information that is available resulting in the calculation of EBVs with additional accuracy. The greatest value of the genomic predictions is likely to be for young animals that do not yet have any measurements on them or their progeny, for the very hard or expensive to measure traits that are generally not recorded by industry, or in small herds where it may be difficult to collect effective performance information. These scenarios present the greatest opportunity to improve the accuracy of predicting that animal’s breeding value.

### Likely Process For Inclusion of DNA Information from the Beef CRC Prediction Equation Into BREEDPLAN

1. DNA sample is collected from the animal (Hair, Blood, Semen, Tissue)
2. Sample is submitted to DNA Lab
3. DNA Lab collects animal genotype (eg. 7K or 50K SNP profile)
4. DNA Lab sends genotype to BREEDPLAN for storing on either National Beef Genomics or Breed Society Database
5. BREEDPLAN conducts data quality and parentage verification checks on genotype
6. BREEDPLAN creates 700K genotype of animal using “imputation” techniques
7. Beef CRC Prediction Equation is combined with 700K genotype to calculate Genomic Breeding Value (GBV) of animal
8. GBV in blended with traditional BREEDPLAN EBV to calculate EBV with more accuracy
A Genetic Approach to Internal Parasite Control

A recently completed research project led by Dr Peter Honey from Charles Sturt University has demonstrated that resistance to internal parasites can be improved through genetic selection, and it is likely that it is possible to select for greater resistance to internal parasites within a breeding program without compromising other commercially important traits.

The research project focussed on resistance to internal parasites in pasture based breeding herds in south eastern Australia with faecal egg count (FEC) samples taken from Angus cattle in 8 herds from Coolah in northern NSW to Mortlake in the Victorian western district. All calves were bred by AI using known fully BREEDPLAN recorded bulls with samples taken on animals between 6 and 17 months of age. Approximately 2500 samples, representing progeny from 77 different sires were evaluated in the research project.

The research showed that the resistance to parasite control was heavily influenced by genetics with a heritability of 0.37 being observed. With 37% of the total variation in faecal egg output within a group of weaners being due to genetics, ample opportunity clearly exists to improve parasite resistance through genetic selection for more resistant cattle.

Further, the research project showed that the sires in the top 10% and bottom 10% for parasite resistance had a very similar Angus Long Fed / CAAB selection index value (figure 1), providing an early indication that selection can be made for improved parasite resistance without compromising other economically important traits.

Further work will now be conducted to investigate what options may exist for BREEDPLAN to generate an EBV for parasite resistance in breeds and seedstock herds that may be interested in including selection for improved parasite resistance within their breeding program. Due to the relative difficulty in collecting performance information for this trait, future research is also likely to focus on the development of DNA based genomic prediction equations for parasite resistance.

There are now a range of DNA based technologies available that can be applied within a beef seedstock enterprise, with many more under development. Before making the decision to invest in DNA technologies it makes sense to be informed about the basic theory of DNA and the current applications available.

**The Theory of DNA**

**What is DNA?**

Deoxyribonucleic acid (DNA) is an exceptionally important molecule found in the nucleus of all bovine cells. It is often described as the ‘blueprint’ of an organism because it codes the instructions for how that organism will develop, function and appear.

In plants and animals, DNA is bundled into chromosomes. Beef cattle have 30 chromosome pairs, each pair including one chromosome inherited from the sire and one from the dam. Because the progeny inherit chromosomes from both parents, the DNA ‘blueprint’ is passed on from one generation to the next.

**DNA Structure**

DNA looks like a long twisted ladder, or double helix. The sides of the ladder are made up of alternating sugar and phosphate molecules. The rungs connect to the sugar molecules and are known as nitrogenous bases. It is the bases which provide the key functionality of DNA and exhibit variation between individuals.

There are approximately 3 billion base pairs in bovine DNA. There are four different bases, Adenine (A), Thyamine (T), Gaunine (G) and Cytosine (C). Each rung of DNA is made up of two bases linked together, either G to C or T to A. The sequences of these base pairs make up the ‘message’ of DNA, and differences in sequences provide the basis for variation between individuals.

**What is a Gene?**

A gene is a base pair sequence at a particular location on the chromosome which codes for a specific product. It is estimated there are between 22,000 and 28,000 genes in the beef animal. Genes are separated on chromosomes by areas of ‘non-coding DNA’ for which no function has been identified, but still makeup part of the animal’s genotype.

For each gene there may be 2 or more variations, known as alleles, which can result in different phenotypes or observable characteristics. For example one of the genes influencing coat colour has three alleles, the “e” allele for red coat colour, the ED allele for black coat colour and a “Wild type” E+ allele. Which alleles the animal has, and how those alleles interact with each other determines the coat colour of the animal.

**What is a Gene Marker (or DNA Marker)?**

A gene or DNA marker is a known, heritable base pair sequence which is associated with a particular gene. The DNA marker sequence does not necessarily have to be part of the gene that codes for the trait but only associated with it, therefore the value of the genetic marker will vary. There are several types of DNA markers, but those most commonly being used in the beef industry are SNPs (pronounced “snips”) and microsatellites.

**What is a Microsatellite?**

A microsatellite is a repeat of a particular base sequence at a specific location in an animal’s DNA, for example CACACACA. The number of base pair repeats differs between animals. Microsatellites form the basis for traditional DNA parent verification, which use multiple microsatellites to determine a calves parentage through exclusion of possible candidates which do not have the same microsatellites.
What is a SNP?
Single Nucleotide Polymorphisms (SNPs) are markers where there is a difference in a single base pair. For example, in the diagram, the top animal has a “C & G” base pair at the particular location in the DNA, whereas the bottom animal has a “T & A” base pair. While early DNA technology only evaluated an animal's DNA for a relatively small number of SNPs, SNP chips now routinely evaluate animals at many thousands of individual SNPs. For example, DNA chips with 7,000 (ie. 7K), 50,000 (ie. 50K) or 800,000 (ie. 800K) SNPs on them are now available.

What is a Genomic Prediction Equation?
As each production trait is influenced by many genes, inferring genetic merit for a particular trait requires the accumulated effects of many markers. Genomic Prediction Equations take the genotype of an animal as collected using dense SNP chips (eg, 50,000 SNPs) to estimate the animal’s breeding value based on the known effect of each SNP on the trait of interest.

Current Applications of DNA Technology
There are many potential applications of DNA technology within a beef seedstock enterprise. Some of the most common current applications include:

i. Parentage Verification
ii. Management of Genetic Conditions
iii. Change in Qualitative Traits (eg. coat colour/polledness)
iv. Genetic Improvement in Production Traits
v. Assessment of Breed Composition

For further information regarding the application of DNA technology, please contact staff at SBTS.

Key Terms

Trait – Attribute or characteristic of animals that can be measured and improved genetically (for example, growth rate, fertility, carcass or meat quality)

Genotype – the full genetic makeup of an animal including dominant and recessive alleles that may not be expressed

Phenotype – the observable characteristics or traits of an animal that result from the interaction between the animal’s genotype and the environment

Locus – the specific location of a gene or DNA sequence on a chromosome

Allele – one form of a gene or a genetic locus

Homozygous – animal carries identical alleles for a gene

Heterozygous – animal carries different alleles for a gene

Dominant – an allele is dominant over another so that the phenotype of the dominant allele is always expressed over the recessive allele

Recessive – an allele is recessive, so that the phenotype is only expressed when two copies of the allele are present (ie. it is homozygous).

Carrier – animal which is heterozygous and ‘carries’ a recessive allele which is not being expressed phenotypically

Enhancements to Simmental GROUP BREEDPLAN Analysis

A number of enhancements have been made to the BREEDPLAN software that is used to calculate EBVs for Simmental animals during the Spring 2012 Trans-Tasman Simmental GROUP BREEDPLAN analysis. The enhancements include:

- Upgrade to BREEDPLAN Version 6.2
- Revised method for handling different groups of “base” animals

Further information regarding these enhancements is available from the BREEDPLAN website or by contacting Christian Duff at SBTS on (02) 6773 2472 or via email christian@sbts.une.edu.au.
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, 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:

<table>
<thead>
<tr>
<th>Technical Consultant</th>
<th>Breeds</th>
<th>Contact Details</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Christian Duff</strong></td>
<td>Charolais, Red Angus, Shorthorn, Simmental, Wagyu</td>
<td><a href="mailto:christian@sbts.une.edu.au">christian@sbts.une.edu.au</a> (02) 6773 2472</td>
</tr>
<tr>
<td><strong>Andrew Byrne</strong></td>
<td>Hereford</td>
<td><a href="mailto:andrew@sbts.une.edu.au">andrew@sbts.une.edu.au</a> (02) 6773 3357</td>
</tr>
<tr>
<td><strong>Paul Williams</strong></td>
<td>Belmont Red, Brahman, Brangus, Charbray, Droughtmaster, Santa Gertrudis, Senepol, Simbrah</td>
<td><a href="mailto:paul@tbts.une.edu.au">paul@tbts.une.edu.au</a> (07) 4927 6066</td>
</tr>
<tr>
<td><strong>Gemma Wilkinson</strong></td>
<td>Blonde d'Aquitaine, Devon, Gelbvieh, Murray Grey, Red Poll, Salers, South Devon</td>
<td><a href="mailto:gemma@sbts.une.edu.au">gemma@sbts.une.edu.au</a> (02) 6773 3265</td>
</tr>
<tr>
<td><strong>Alex McDonald</strong></td>
<td>Limousin</td>
<td><a href="mailto:alex@limousin.com.au">alex@limousin.com.au</a> (02) 6771 1648</td>
</tr>
<tr>
<td><strong>Peter Parnell</strong></td>
<td>Angus</td>
<td><a href="mailto:peter@angusaustralia.com.au">peter@angusaustralia.com.au</a> (02) 6772 3011</td>
</tr>
</tbody>
</table>

If you would like any further information on SBTS and TBTS please contact:

**Southern Beef Technology Services**  
Telephone: (02) 6773 3555  
Email: office@sbts.une.edu.au  
Web: http://sbts.une.edu.au

**Tropical Beef Technology Services**  
Telephone: (07) 4927 6066  
Email: office@tbts.une.edu.au  
Web: http://tbts.une.edu.au