



# Optimise Your Joinings With MateSel

**R**unning out of time to plan your upcoming joinings? Looking to identify the best sires for your herd to manage inbreeding and maximise genetic progress?

All members of breed organisations that have selection indexes available and have upgraded to ABRI's new generation of breed registry software known as ILR2 are encouraged to consider the use of the new MateSel mating allocation tool when planning their upcoming joinings. This includes members of the Angus, Brahman, Brangus, Charolais, Hereford, Limousin, Murray Grey, Red Angus, Santa Gertrudis and Wagyu breeds.

MateSel not only allows breeders to maximise genetic progress whilst managing inbreeding, but will also save significant time previously spent compiling mating lists. MateSel creates additional genetic progress within a breeding program by generating a suggested mating list based on breeder nominated sires and dams. Breeders choose acceptable inbreeding limits by selecting one of three breeding strategies, "Diversity", "Balanced" or "High Gain" and their desired breeding objective. A flat fee of \$165 (inc GST) applies to access a MateSel analysis, and results are returned promptly, usually within one working day.



## 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.
- **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.

# WINTER 2013 UPDATE

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This information is submitted via email to staff at BREEDPLAN using a Microsoft Excel template whereby the BREEDPLAN staff will conduct the MateSel analysis and promptly return results to the seedstock breeder, usually within 24 hours.

## Example MateSel Reports

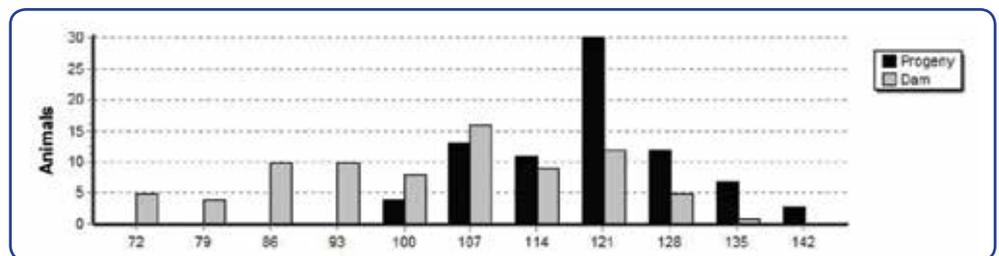
Following each MateSel analysis, seedstock breeders will be provided with a MateSel report that contains a suggested mating list sorted by both sire and by dam, as well as a range of summary reports illustrating the predicted outcomes of the suggested matings. A csv file containing the mating allocation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

Some example MateSel reports are provided in the diagrams below.

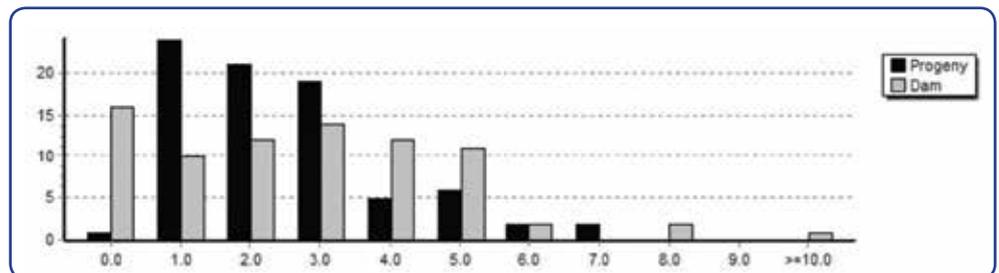
To learn more about MateSel, or to download the excel template for submitting a list of candidate sires and dams, visit <http://breedplan.une.edu.au> and click on the MateSel icon on the right hand side, or contact the designated SBTS or TBTS Technical Officer for your breed (see back page for contacts).

DAMS		SIREs		POTENTIAL PROGENY MID-PARENT VALUES																	
Catv. ID	ID	Name	Prog. Ind. %	Non. Index	3yr. Days	GL	Best	200	400	800	Mat	Mil.	SS	DC	Cut	EMA	Rib	PS	RFY	BMF	
2000	xxxxE156	xxxP243	4.0	109.5	0.9	1.4	-2.2	3.6	37.7	71.9	85.7	80.5	14.1	1.0	-5.2	49.8	6.4	0.1	-0.1	1.3	1.8
2000	xxxxE159	xxxP242	4.0	114.5	0.9	1.4	-3.3	4.6	42.8	79.4	100.9	91.1	14.3	1.2	-4.9	57.3	6.7	-0.6	-1.0	1.8	1.3
2000	xxxxE17	xxxD131	2.3	118.5	2.9	2.6	-4.9	2.7	38.3	79.1	96.8	82.8	18.3	2.8	-4.4	58.4	6.9	-0.6	-0.2	1.0	1.8
2000	xxxxE174	xxxD131	3.7	107.5	2.9	2.3	-4.2	2.6	38.9	72.1	92.6	78.4	14.2	2.1	-3.8	56.5	4.6	-0.5	-0.3	0.4	1.7
2000	xxxxE175	xxxD90	7.7	118.0	1.6	1.6	-3.6	4.1	48.2	77.9	93.6	87.9	17.9	2.9	-4.4	59.2	6.3	-0.3	0.2	1.1	1.7
2000	xxxxE18	xxxP243	2.5	117.9	1.3	1.2	-2.7	3.8	48.4	75.7	95.2	75.1	16.5	1.0	-4.9	61.0	6.8	0.5	0.9	0.8	1.8
2000	xxxxE181	xxxP243	4.0	106.5	2.2	1.9	-2.9	2.4	33.4	66.6	85.2	83.5	12.5	1.1	-5.1	53.8	6.3	-0.4	-0.9	1.4	1.4

Example Mating List Sorted by Dam



Example Selection Index Distribution of Potential Progeny Compared to Selection Index of Candidate Dams



Example Distribution of Inbreeding of Potential Progeny Compared to Inbreeding of Candidate Dams

## View the Winter 2013 SBTS & TBTS Update Electronically

Would you prefer to view the Winter 2013 SBTS & TBTS Update on your smart phone or tablet?

If so, simply scan the following QR Code using your device.



# Variation in Lactation Anoestrus in First Calf Cows in Tropical Cattle

A major research project within the Cooperative Research Centre for Beef Genetic Technologies (Beef CRC) has provided very useful information on the success of lifetime production in Brahman and Tropical Composite cattle in Northern Australia. One of the primary objectives of the Beef CRC project was to investigate what effect genetics had on the Post-Partum Anoestrus (period between calving and a return to cycling) in first calf cows and consequently what opportunities may exist to improve fertility rates in Northern Australia through genetic improvement.

## Project Design

A total of 2137 cows were involved in the project (1020 Brahman and 1117 Tropical Composites (TC)). The cows (also used in the age of puberty studies) were bred on 7 co-operator properties (4 Brahman and 3 TC) and at “Belmont Research Station” which bred both Brahman and TC. Genetic linkage, across properties of origin and year within genotypes was generated by the use of AI. The cows were generated over 4 and 3 years for Brahman and TC respectively. The cows 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 Brahman.

The project continued until all the cows were around 8.5 years of age and had been given the opportunity to have 6 calves and had been mated for the 7th time. The cows stayed in the project unless they failed to wean a calf in 2 consecutive years or were culled on management decisions (eg. temperament, udder etc.) Cows were naturally mated for 12 weeks and during this period the cows were ovarian/pregnancy scanned at 4 week intervals from joining by the use of real time ultrasound by an experienced scanner. The cows were also scanned a further 4 times after mating and prior to calving. These were half way between mating and weaning, weaning, half way between weaning and pre calving and around 3 weeks prior to calving. Other data collected at each scan was live weight, condition score and a P8 fat measurement.



## Results

### Resumption to Cycling in First Calf Cows

The research showed that 52% of the Brahman cows had cycled by weaning compared to 80% of the Tropical Composites. It must be mentioned that about 40% of the Brahman were run on the harsher conditions at Swans Lagoon. Of the 48% of Brahman cows that did not cycle before weaning, most cycled within 100 days post weaning but there were a percentage of cows that did not cycle until the start of the next wet season or later as shown in figure 1. The 18% of Tropical Composites that did not cycle before weaning cycled within 100 days after weaning.

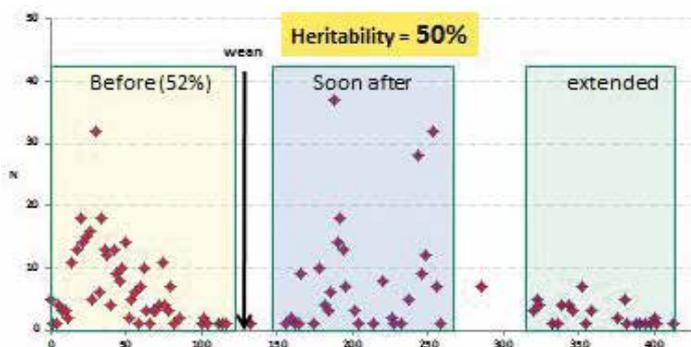


Figure 1. Wet First Calf Cow Resumption of Cycling in Brahman

### Genetic Effects

One of the key outcomes of the Beef CRC research was that lactation anoestrus interval in first calf cows was shown to be under moderate to high genetic control in both Brahman

and TC. Heritability estimates for lactation anoestrous interval in 3 year old first calf cows were 0.51 for Brahmans and 0.26 for TC. Further analysis revealed that there was a difference due to genetics of 4.4 months in lactation anoestrus between the top and bottom Brahman sire included in the research trial as shown in Table 1. Although not as high, there was a 2.8 month difference in lactation anoestrus between the top and bottom sire in the TC. This had a major effect on the ability of daughters from bulls with the increased post-partum anoestrus to conceive during the joining period as first calf cows. This was illustrated by only 5 out of 37 daughters of Belmont 79/96 reconceiving as first calf cows.

Brahman sires	
LANCEFIELD 4999M	-3.3
MR VB 797/3	-3.1
TARTRUS 3886	-2.9
CONA CREEK 2722	-2.3
NEWCASTLE WATERS TOBY	-2.1
LANCEFIELD 4461	-2.0
McKELLAR RICARDO	-1.9
TARTRUS ABEL MANSO	-1.8
.	.
TARTRUS 2415	+1.9
TARTRUS 3292	+2.0
JDH DENVER DE MANSO	+2.1
LANCEFIELD AMBITION	+2.1
LYNDHURST 1660/7	+2.4
WAVERLEY SUPREME DE MANSO	+2.6
TARTRUS MR MANSO 025	+3.8
BELMONT 79/96	+5.6

lactation anoestrus interval EBV (days)  
(Wet 1<sup>st</sup> calf cow)

4.4 month difference in time 1<sup>st</sup> calf daughters to resume cycling

Table 1 Difference in lactation anoestrus between top and bottom Brahman sires in months

## Conclusions

The results emphasise the substantial opportunity that exists to improve conception rates in tropical beef cattle breeds by focusing recording and selection on early in life female reproduction traits, particularly in Brahman for traits associated with lactation anoestrus.

Culling first calf cows that do not conceive or not retaining replacement progeny from those animals will have a positive impact in the improvement of conception rates. The results show these cows are more likely to have progeny that will not conceive as first calf cows as well.

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 for maiden heifers and first calf cows), 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](mailto:paul@tbts.une.edu.au).

# SBTS & TBTS Get Social



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SBTS & TBTS



sbtstbts

Beef producers can now keep up to date with the latest developments in genetic technologies and the activities of SBTS and TBTS by following SBTS and TBTS on Facebook, Twitter and YouTube.

SBTS and TBTS have set up social media accounts with the aim of making technical information and updates more accessible to seedstock producers. Information will be routinely posted on Twitter and Facebook such as articles, webinars and event details, while the YouTube channel will contain video

presentations such as webinars from past webinar series and short “Understanding BREEDPLAN EBVs” video clips.

To follow SBTS and TBTS on Twitter, Facebook or YouTube simply go to the SBTS or TBTS website and click on the relevant icon, or go directly to the SBTS & TBTS Facebook account at <http://facebook.com/SBTSTBTS>, Twitter account at <http://twitter.com/SBTSTBTS> or YouTube Channel at <http://youtube.com/user/sbtstbts>.

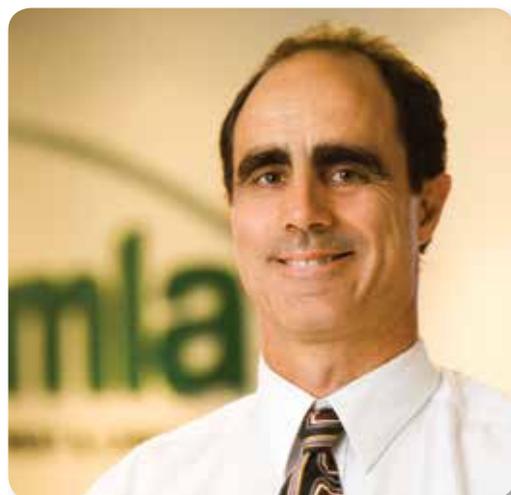
# Dr Robert Banks Appointed Director of AGBU

The organisation responsible for the research and development behind BREEDPLAN, the Animal Genetics and Breeding Unit (AGBU) at the University of New England (UNE) has a new Director with the appointment of Dr Robert Banks. The appointment of Dr Banks follows the retirement of long serving Director, Dr Hans Graser at the end of last year.

Dr Phil Wright, NSW DPI's Chief Scientific Officer, and Professor Annabelle Duncan, UNE's Deputy Vice-Chancellor, Research, welcomed the appointment.

Dr Wright said "Dr Banks has an excellent reputation in Australia's sheep and cattle industries as a genetic innovator. His technical and communication skills will ensure AGBU continues to be the leading group for genetic evaluation in Australia and internationally."

Professor Duncan said AGBU has been serving Australian agriculture since 1976 as a joint venture between UNE and DPI. "It is exciting to announce the appointment of Dr Robert Banks to continue the role of applying the science of genetics to Australia's livestock industries," Professor Duncan said. "I would also like to pay tribute to outgoing Director, Dr Hans Graser, who has made an enormous contribution;" she added.



Dr Banks commented: "The role is a great privilege. I am looking forward to ensuring that our livestock industries take full advantage of the genomics revolution." He added: "There will be significant challenges around ensuring that breeders, commercial producers and the community as a whole can obtain the full benefits of genomics R&D, and this area will be a key focus for me."

A PhD graduate of UNE, Dr Banks has a long history in the genetic improvement of Australia's extensive livestock industries. He has worked for Meat and Livestock Australia for nearly 25 years. In the late 1980s he led the development of the genetic evaluation system for the Australian Meat Sheep industry.

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## Monthly GROUP BREEDPLAN analyses for Hereford

Herefords Australia (HAL) have joined the Angus, Brahman, Brangus, Charolais, Droughtmaster, Limousin, Murray Grey, Red Angus, Santa Gertrudis and Wagyu breeds in upgrading the software used to manage their pedigree and performance database to ABRI's new generation of breed registry software known as ILR2. The new software includes several new features such as the running of monthly GROUP BREEDPLAN analyses and production of enhanced BREEDPLAN reports. This will significantly enhance the BREEDPLAN service that is provided to members of Hereford BREEDPLAN.



It is anticipated that the Australian Simmental Breeders Association and the South Devon Cattle Breeders Society will upgrade to the ILR2 software before the end of 2013.

# Managing Genetic Conditions

**G**enetic conditions or defects are caused by DNA abnormalities and are present in all species, including beef cattle. The incidence of genetic conditions is normally low within a population but increases in inbreeding, or the rapid dissemination of genes through artificial breeding, can lead to an escalation in the prevalence of a condition.

Over 400 genetic conditions have been identified in beef cattle. Approximately one quarter of these are caused by a single gene mutation, making them easy to manage through DNA testing. Historically, genetic conditions were managed by extensive progeny testing or by eradicating all known relatives of the affected animal. This resulted in production losses and the potential loss of superior genetics. Developments in DNA testing and gene probability technology now allows breeders to more easily manage genetic conditions such that production losses and spread of the mutation can be minimised.

## Recognising Genetic Conditions

Genetic conditions generally result in:

- Poor growth and fertility performance. For example, calves with Protoporphyrria (photosensitivity) develop scabs and open sores when exposed to sunlight and have reduced liver function, which in turn decreases their overall performance.
- Structural unsoundness. For example, animals with Snorter Dwarfism have a short, blocky appearance with deformed bone growth in the nose, causing difficulty breathing.
- Semi-lethal - Not all affected individuals survive to maturity. For example, many calves affected by Contractural Arachnodactyly (CA) will die shortly after birth because they are unable to stand and suckle. Those calves who are able to stand will often survive to maturity but have poor growth performance.

- Lethal - No affected animals survive to maturity. For example, animals affected by Pompes will typically die between 6 to 12 months of age after displaying progressive muscular weakness.

The symptoms of genetic conditions can be quite nonspecific. When large numbers of calves are dying or being born with similar abnormalities, both environmental and genetic causes are suspected. Consequently, there is a need for the surveillance and reporting of abnormal calves to Breed Societies, veterinarians or beef technical officers if genetic conditions are to be identified. Photographs and DNA samples from affected animals should be collected to aid in the identification of the condition.

## Mode of Inheritance

Genetic conditions have different modes of inheritance. Many have a simple recessive inheritance of a single gene mutation making them easy to manage. These single gene recessive genetic conditions result in 3 possible genotypes:

- > *Free* - animal carries two normal genes and no copies of the mutation
- > *Affected* - affected or abnormal animal which carries two copies of the mutation
- > *Carrier* - animal which looks normal but carries one copy of the mutation which can be passed onto offspring

As illustrated in Figure 1, mating a carrier animal to a free animal will avoid production losses, with 100% of calves being unaffected by the genetic condition. But, 50% of the resulting offspring will still be carriers. Mating carrier to carrier will result in 75% normal calves and 25% affected, with two thirds of the normal calves being carriers.

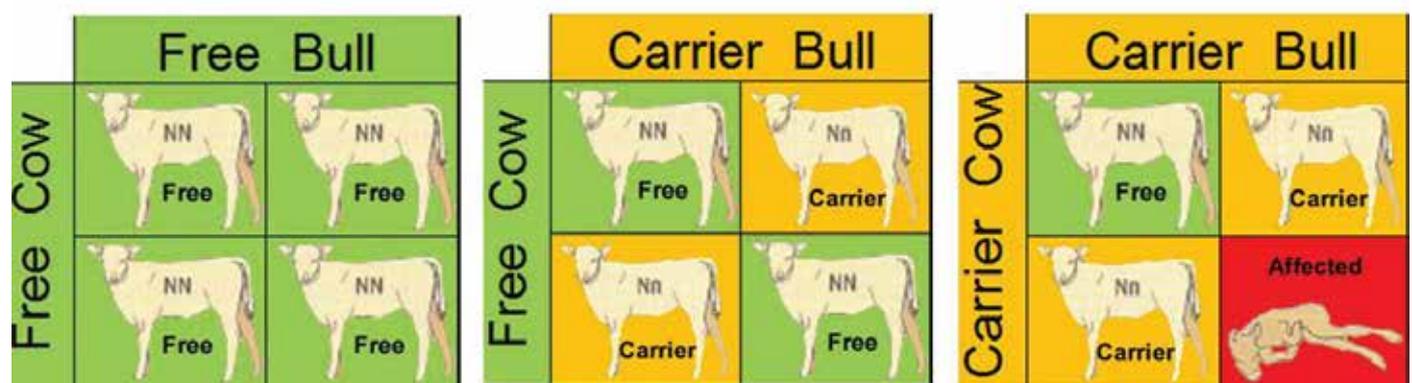


Figure 1 provides an illustration of the possible mating outcomes from different mating combinations for a single gene recessive genetic condition.

## Tools Available to Manage Genetic Conditions

Developments in DNA technology have resulted in diagnostic tests being available for several single gene recessive genetic conditions. The ability for beef producers to collect a DNA sample (either hair, semen, blood or tissue) and send it to a DNA lab for testing has significantly assisted the management of genetic conditions.

In addition to the development of DNA tests, a range of gene probability software (such as GeneProb) is now available to estimate the probability that an untested animal is a carrier, based on their pedigree and the known DNA test results for animals within that pedigree.

Results from gene frequency software such as GeneProb identify animals as either being free untested (XXFU) or the percentage chance of being a carrier (XX\_\_%) as illustrated in the example in Figure 2.

Code	Description
AMF	Tested Free
AMFU	Not Tested, based on pedigree expected to be free.
AMC	Tested Carrier
AM __%	Not tested, based on pedigree information the animal has the indicated percentage chance to be a carrier.
AMA	Tested Affected

Figure 2. The possible genotype results for Arthrogryposis Multiplex (AM). DNA testing reports AMA, AMF and AMC while the GeneProb predictions report AMFU and AM\_\_% (eg. AM25%).

## Managing Genetic Conditions

There is no “one size fits all” strategy for managing genetic conditions. Before embarking on a management strategy producers should consider:

- The economic impact of the condition
- The frequency of the condition within the herd
- The availability and cost of DNA tests
- Researching the genetic condition status of any animals being brought into the herd
- Their legal obligations about disclosing the carrier status of sale animals
- The relevant Breed Society regulations

Generally, the management of genetic conditions can be broken into two components.

**Managing the Incidence of Affected Animals** – In simple terms, the incidence of animals affected by the genetic condition can be managed by avoiding mating carrier dams to a carrier sire. This may be relatively easy to manage in seedstock herds, but can be extremely difficult in commercial herds which keep no pedigree records. For this reason it is recommended that

## Key Facts

- ✓ There are over 400 genetic conditions identified in beef cattle. DNA tests are currently available for several of the most prevalent genetic conditions.
- ✓ DNA testing identifies 3 possible genotypes – Free, Carrier and Affected.
- ✓ The incidence of affected offspring can be eliminated by avoiding carrier to carrier matings.
- ✓ There is no “one size fits all” approach to managing the incidence of carrier animals within a breeding herd.

commercial herds, or seedstock herds that have done minimal DNA testing, should always use bulls that are tested free.

**Managing the Incidence of Carriers** – Managing the frequency of carrier animals is important in seedstock operations. Where available, the use of DNA testing to determine if an animal is either free or a carrier for a genetic condition broadens the options for breeders looking to manage or eradicate the mutation. Use of software like Geneprob to calculate the risk of particular untested individuals being carriers enables DNA testing efforts to focus on the most high risk animals.

Breeders should carefully consider and develop a management strategy that will be used to manage each genetic condition. Some examples of management strategies are as follows:

- DNA test all animals in the breeding herd to identify and cull carrier animals.
- Conduct strategic DNA testing of highly influential animals (eg. sires, donor dams) to calculate the probability of animals being carriers, and better identify the “at risk” bloodlines. Further testing can then be conducted to better isolate the carriers present in the herd.
- Continue to use carrier animals in the breeding program by joining them only to tested free sires/dams and routinely testing the progeny. As outlined previously, mating a carrier to a free animal will result in 100% of calves being unaffected by the genetic condition, with 50% of the resulting offspring being free of the condition and 50% being carriers. This approach is of particular benefit when the carrier animal is of high genetic merit and the producer wants to utilise these desirable genes in the breeding program.
- Only use sires that are tested free or are expected to be free by inheritance to ensure that the incidence of the condition does not increase. This is a common approach for genetic conditions of low economic impact.

In all situations, if carrier animals are sold, full disclosure of their genetic condition status should be provided.

For further advice regarding the management of genetic conditions, contact your designated SBTS or TBTS Technical Officer.

# Maximising Genetic Improvement in a Seedstock Beef Breeding Enterprise

One of the key measures of the success of any seedstock beef breeding enterprise is the genetic improvement that is made within their breeding program from one year to another. In a climate of declining terms of trade, genetic improvement provides an important tool that can be used to facilitate an improvement in the phenotype, performance and ultimately profitability of animals in both seedstock and commercial beef herds.

Genetic improvement is achieved when the average genetic value of the progeny is higher than the average genetic value of the parents from which they were selected, with the rate or amount of genetic improvement achieved being determined by the degree of superiority of the progeny relative to their parents.

Having a good understanding of the factors that influence the rate of genetic improvement is consequently an important consideration for all seedstock beef breeding enterprises.

## Factors Influencing the Rate of Genetic Improvement

Most seedstock beef producers will have an understanding of the factors that influence the rate of genetic improvement (or response to selection) being achieved each year within their breeding program, however this can be more formally defined by the following equation. This equation equally applies to the genetic improvement that is made for an individual trait, selection index or the overall breeding objective.

$$R = \frac{i \times r \times \sigma_g}{L}$$

Where:

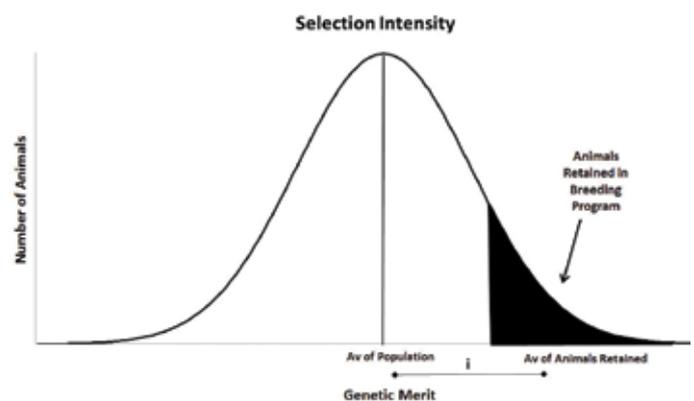
- R** = Response to Selection
- i** = Selection Intensity
- r** = Accuracy of Selection
- $\sigma_g$**  = Genetic Variation
- L** = Generation Length

Seedstock beef producers need to appreciate how these factors interact in the dynamics of a breeding herd to ensure that long term sustainable genetic improvement is achieved within their breeding program.

## Selection Intensity (i)

The selection intensity is the difference in the average genetic value of the animals selected for breeding versus the average genetic value of all animals in the population from which they were selected (see diagram). The higher the selection intensity (or the degree of superiority), the higher the rate of genetic improvement that will be achieved.

The practices conducted within a beef seedstock enterprise have a large influence on the selection intensity within a breeding



program. When a large proportion of animals are selected as parents, as is normal for selecting replacement heifers, the resulting selection intensity will be small. Conversely, when a smaller proportion of animals are selected as parents, such as is normal when selecting bulls, the resulting selection intensity will potentially be quite large. In general, the smaller the proportion of animals selected, the higher will be their relative genetic superiority, therefore the higher the selection intensity.

Use of reproductive technologies such as artificial insemination and embryo transfer provide seedstock beef producers with powerful tools that can be used to increase selection intensity and hence the genetic improvement that is achieved.

## Accuracy of Selection (r)

Accuracy of selection is determined by the magnitude of the correlation between the true breeding value of the animal's available for selection as parents, and the information on which the selection decisions are based. The accuracy of selection will be influenced by such factors as the heritability of the individual trait, the quantity and quality of information



## Generation Length (L)

Generation length is defined as the average age of the parents in a population at the time that their progeny are born, with a shorter generation length resulting in greater genetic improvement being achieved.

Beef animals are somewhat constrained in contrast to other livestock species (eg. poultry) due to an older age of puberty and longer length of gestation, however generation length can be reduced through use of younger animals within a beef breeding program. This includes strategies such as retaining a higher proportion of replacement heifers, ensuring heifers have their first calf at 2 years of age and the use of yearling sires.

## The Trade Off

As with many of the economically important traits that exist within a breeding objective, an antagonistic relationship also exists between many of the factors which influence the rate of genetic improvement achieved in a beef breeding program. For example, shorter generation length may result in a lower accuracy of selection. Seedstock beef producers need to carefully consider how these factors interact to ensure that overall genetic improvement is maximised.

In conclusion, knowledge of the factors that influence the rate of genetic progress and how they interact is important for all beef seedstock producers. By increasing selection intensity, increasing the accuracy of selection decisions, increasing the genetic variation and decreasing the generation length, a greater rate of genetic improvement can be achieved within both individual seedstock beef breeding enterprises and across the Australian beef industry as a whole.

available, the availability of selection tools, and the accuracy of these selection tools. The higher the accuracy of selection, the more informed and correct the selection decisions are that are made, and the more genetic improvement that is achieved.

In a modern beef seedstock operation, accuracy of selection can be maximised by:

- accurately performance recording and measuring all animals within the breeding program
- accurately performance recording and measuring as many traits as possible within the breeding objective
- utilising genetic tools such as BREEDPLAN EBVs and selection indexes when making selection decisions
- using proven sires as opposed to younger bulls
- considering the use of DNA based technologies where available.

## Genetic Variation ( $\sigma$ )

The amount of genetic variation that exists within the population of animals that are available for use within the breeding program influences the amount of genetic improvement that is possible, with greater genetic variation providing a greater potential to make genetic improvement.

The amount of genetic variation that exists is difficult for a seedstock enterprise to influence, but careful management of inbreeding is important in ensuring the genetic variation does not diminish. In practice, the degree of genetic variation can be increased by expanding the gene pool from which animals are selected, such as through sourcing genetics from herds or bloodlines not previously utilised or from overseas countries. Strategies such as crossbreeding can also be used to increase genetic variation, particularly in commercial operations.

## Fast Facts

- ✓ Understanding the factors that influence the rate of genetic improvement is important to a seedstock producer
- ✓ Greater genetic improvement will be achieved by:
  - > Increasing selection intensity
  - > Increasing the accuracy of selection
  - > Increasing the amount of genetic variation
  - > Decreasing the generation interval

### References:

*Applied Animal and Plant Breeding, School of Environmental and Rural Science, UNE, GENE 251/351 Course Notes and Reading Guide.*  
*Genetic Evaluation and Breeding Program Design, School of Environmental and Rural Science, UNE, GENE 422/522 Course Notes and Reading Guide.*

# Breed Societies Participate in Genetic Progress Benchmarking Workshop

Southern Beef Technology Services (SBTS) recently facilitated a Genetic Progress Benchmarking Workshop for the 15 Breed Societies participating in the SBTS project.

Attended by Breed Society Managers plus representatives from each breed organisation's Board or Technical Committee, the workshop presented a series of new benchmarking statistics and reports that have been developed by SBTS which evaluate the genetic improvement that has occurred in the Australian beef seedstock industry since 1990.

Topics were covered including:

- What is genetic improvement and what is the role of the Breed Society in facilitating genetic improvement?
- Detailed analysis of the genetic improvement that has occurred within each breed
- Benchmarking of the genetic improvement that has occurred between breeds and breed groups (eg. British, European)
- Discussion of what strategies can be implemented within each breed to increase the rate of genetic improvement



Manager of the ABRI Beef Breeding Extension Division, Christian Duff commented that the workshop enabled Breed Societies with the opportunity to carefully evaluate and benchmark the genetic progress that has been achieved within their breed in a similar fashion to the financial benchmarking that is routinely conducted. Importantly, the designated SBTS Technical Officer will now work with each Breed Society to both further digest the messages from the workshop and progress the strategies that were identified to increase the rate of genetic improvement being achieved within each breed.

A similar exercise is now being planned for Breed Societies participating in the Tropical Beef Technology Services (TBTS) project.

## Revision to Reportability of Australian Simmental Weight EBVs

The criteria used to determine the reportability of Weight EBVs for Simmental animals (i.e. 200 Day Growth, 400 Day Weight and 600 Day Weight) was revised in the 2013 Autumn TransTasman Simmental GROUP BREEDPLAN analysis.

The reportability criteria used for Simmental Weight EBVs will now follow the industry standard of “linking” the reporting of the three Weight EBVs. That is, if one weight EBV meets the minimum accuracy threshold to report then all three Weight EBVs report. Previously, the reporting of the weight EBVs were not linked, therefore each EBV needed to reach its own



independent level of accuracy before reporting. Individual EBVs with accuracy less than 20% will still not be reported.

If you have any questions about this revision please contact Christian Duff, Simmental SBTS Technical Officer - (02) 6773 2472 or [christian@sbts.une.edu.au](mailto:christian@sbts.une.edu.au)

# Have You Downloaded the INSolutions Mobile App?



Seedstock and commercial beef producers who use a smart phone or tablet are encouraged to download the new INSolutions Mobile App.

The INSolutions App builds on the features of the successful Internet Solutions suite of web based tools and enables users of a smart phone or tablet to view information about a particular animal or seedstock operation in a user friendly manner.

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.

Technical Officer within the SBTS project, Andrew Byrne said the INSolutions Mobile App is 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”.



“The app enables users to pull out their phone and view a range of information regarding each animal including a 2 generation pedigree, complete EBVs and selection index information, the popular EBV graph display, vendor comments on sale animals and a photo of each animal” said Andrew.

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

Andrew explained that a number of important features have been added to the INSolutions Mobile App since it was initially released in 2012. “Of most consequence is the ability to download sale catalogues and then view them offline when attending sales where there is no mobile phone coverage”.

The INSolutions Mobile App enables users to view animal and member information for all breed organisations that are currently utilising the Internet Solutions service. In addition to over 35 Australian beef breeds, this includes beef breeds from a range of overseas countries, plus breed organisations 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 also been made available 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/>*



# Understanding EBV Accuracy

While many beef producers may look at EBV accuracy in relation to an individual animal, it is also worthwhile considering how accurate the EBVs are in describing the genetics of groups of animals within a breeding program (eg. all bulls in this joining season's bull team). In order to consider this concept, it is important to better understand the principles behind EBV accuracy.

## What is EBV Accuracy?

By definition, an Estimated Breeding Value (EBV) is an estimate of an animal's true breeding value. The "accuracy" figure produced with each EBV provides an indication of the amount of information that has been used in the calculation of that EBV. The higher the accuracy, the more likely the EBV is to predict the animal's true breeding value and the lower the likelihood of change in the animal's EBV as more information becomes available for that animal, its progeny or its relatives.

## How is Accuracy Reported?

Accuracy figures are reported as a percentage (%) between 0 – 99. In most cases where an EBV is presented, the accuracy of the EBV will be reported in either the column immediately following the EBV or the row beneath the EBV (figure 1).

Name/ID	Calving Ease Dir (%)	Calving Ease Dis (%)	Gestation Length (days)	Birth Wt (kg)	200 Day Wt (kg)	400 Day Wt (kg)	600 Day Wt (kg)	Mat. Cow Wt (kg)	Milk (kg)	Scrotal Size (cm)	Days to Calving (days)	Carc. Wt (kg)
NJRG398	+1.6	-0.1	-5.4	+5.0	+49	+87	+111	+96	+13	+1.9	-5.2	+6
Accuracy (%)	48%	41%	68%	78%	73%	72%	68%	58%	44%	75%	37%	61%

Figure 1. EBV accuracy figures are reported as a percentage (%) between 0 and 99.

## Interpreting EBV Accuracy

The following guide is recommended when interpreting accuracy on an individual animal:

- less than 50% accuracy - the EBVs are preliminary. In this accuracy range the EBVs could change substantially as more direct performance information becomes available on the animal.
- 50-74% accuracy - the EBVs are of medium accuracy. EBVs in this range will usually have been calculated based on the animal's own performance and some pedigree information.
- 75-90% accuracy - the EBVs are of medium-high accuracy. EBVs in this range will usually have been calculated based on the animal's own performance coupled with the performance for a small number of the animal's progeny.



- more than 90% accuracy - the EBVs are a high accuracy estimate of the animal's true breeding value. It is unlikely that EBVs will change considerably with addition of more progeny data.

## What Influences the Accuracy of an EBV?

A range of factors influence the accuracy of an EBV including:

- > **The heritability of a trait:** Heritability is defined as the proportion of observable differences in a trait between individuals within a population that is due to genetics. The higher the heritability of a trait the higher the EBV accuracy, all other variables being equal. This is one of the reasons why higher accuracies are generally seen for for the Weight EBVs (e.g. 400 Day Weight) compared to the Days to Calving EBV.
- > **The accuracy of the parents:** An animal that has sire and/or dam with high EBV accuracy will generally have higher accuracy EBVs compared to an animal with parents of lower accuracy as more information is known about the relatives of the animal.
- > **The amount of performance information available:** EBVs accuracies will increase as more performance information is analysed for a specific trait. This includes performance information on the animal itself, as well as progeny records. EBV accuracies of 90% and greater are generally only observed on animals that have had progeny with performance recorded for the specific trait.
- > **Effectiveness of performance information:** Animals that are in large contemporary groups will generally have higher EBV accuracy compared to those in small or single animal contemporary groups.

> **Genetic correlation with other measured traits:** As BREEDPLAN uses a multi-trait model, genetic correlations between traits are utilised to calculate EBVs and associated accuracies. For example, recording 200 day weight will also add information to the generation of the 400 Day Weight EBV. Therefore herds that are recording a range of traits (e.g. calving ease, weight, fertility, carcass) will have higher EBV accuracies than a herd that is undertaking limited recording (e.g. 200 day weights only).

## Considering EBV Accuracy for a Group of Animals

In conducting a breeding program where multiple animals influence the genetics of the breeding herd, the accuracy of the EBVs describing the breeding value for a group or team of animals is also important.

For example, the EBV accuracy for the team of females being flushed in an embryo transfer program, or the team of bulls being joined. This may be a group of bulls used in a specific joining (e.g. Spring/Summer 2013) or a group of bulls used over subsequent joinings (e.g. all bulls used over last 3 years).

Figure 2 illustrates the EBV accuracy for a group (or team) of animals with an average EBV accuracy of 30% for a trait. While individual bulls within the team may have “low” EBV accuracy, the accuracy of the EBVs describing the breeding value for the entire team of animals will be considerably higher.

Put in practical terms, while individually some bulls within the team will perform above expectation, some will perform below expectation and some will perform exactly as expected, across the entire team, the EBVs will describe the breeding value of the team of bulls with considerably higher accuracy.

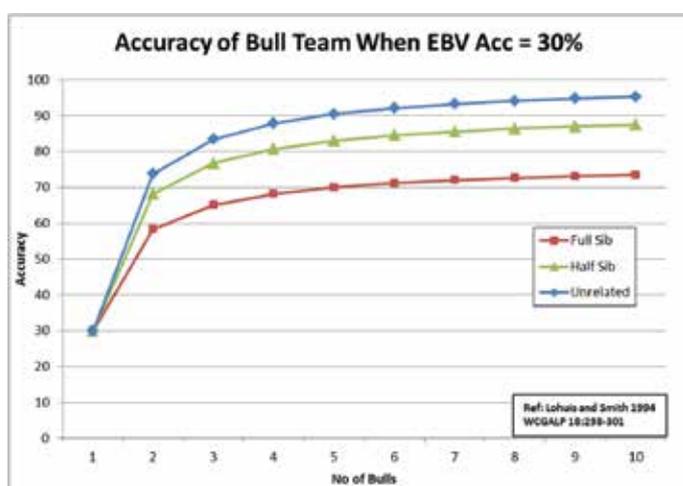


Figure 2 - Accuracy of a Bull Team when EBV Accuracy of Individuals is 30%

For example, an individual bull with an EBV of relatively low accuracy of 30% has some level of risk attached as the EBV could change significantly as more information is analysed.

If there is a bull team of two, both with 30% accuracy for the EBV, the EBV accuracy for the bull team is considerably higher at 58% for a team of full sibs, 68% for half sibs and 74% for unrelated bulls.

Similarly, if there is a bull team of ten, all with 30% accuracy for the EBV, the EBV accuracy for the bull team is 74% for a team of full sibs, 88% for half sibs and 95% for unrelated bulls.

For the same situation, but all with 60% accuracy for the EBV, the EBV accuracy for the bull team is 90% for a team of full sibs, 93% for half sibs and 97% for unrelated bulls.

The reason higher bull team EBV accuracy is observed for unrelated bulls, compared to half sib or full sibs, is due to there being less chance of a bias affecting the EBVs for all bulls in the team.

This shows that the risk of using bulls with relatively low individual EBV accuracy (e.g. yearlings) can be overcome by considering them in a bull team context, rather than individuals. This is a result of “spreading-the-risk” across the team, rather than “putting-all-your-eggs-one-basket” approach.

This also suggests that a team of younger “unproven” bulls can be competitive, in terms of EBV accuracy, to an individual “proven” sire.

## Considering Accuracy in Selection

Although the accuracy of an EBV should be considered, animals should generally be compared on EBVs regardless of accuracy.

In the case where animals have similar EBVs, the animal with the higher accuracy would be preferable because the results can be predicted with more confidence (i.e. less risk).

If seedstock producers prefer to minimise risk through the use of animals with higher accuracy EBVs, consideration could be given to:

- Undertaking a higher level of performance recording across a range of traits and managing their seedstock herd to maximise contemporary group size.
- Sourcing bulls, females and genetics (e.g. semen, embryos) from herds with a history of performance recording.
- Using high accuracy proven sires (e.g. AI sires) or dams.
- Spreading the risk of using younger, lower accuracy animals by utilising the bull “team” approach.

# Barriers to Adoption of Genetic Technologies Surveying Project for Northern Australia

**A** BRI's Beef Breeding Extension Division is currently facilitating a surveying project, on behalf of Meat and Livestock Australia (MLA), titled "Barriers to Adoption of Genetic Technologies in northern Australia".

The objectives of the project are to identify:

1. The current and perceived future selection criteria for bulls by producers in northern Australia;
2. What is currently working well with BREEDPLAN and other related genetic technologies;
3. What is not working well and could be changed for greater adoption across both the seedstock and commercial breeding sectors.
4. A strategy to address the barriers to adoption identified from the survey.

A standardised telephone survey will be employed as the main research method with several target groups located in (or providing genetics to) northern Australia. Northern Australia is defined as Queensland, the Northern Territory and the northern rangelands of Western Australia.

The target groups are stratified into five distinct groups being (i) seedstock herds that are BREEDPLAN members (ii) seedstock herds that are not BREEDPLAN members (iii) very large northern Australian commercial breeding herds (>5400 head) (iv) large northern Australian commercial breeding herds (1600 to 5400 head), and (v) small to medium northern Australian commercial breeding herds (100 to 1600 head).



Overall, 450 businesses will be surveyed in this project, which is based on 90 randomly selected businesses per target group. The surveying will be undertaken in mid-2013 by an independent surveying team, with the project outcomes to be analysed and reported by the end of the year.

The senior investigator for the project is John Bertram. John also has an integral part time role as a Technical Officer in the TBTS project. Along with this project, both the TBTS and SBTS projects are managed under ABRI's Beef Breeding Extension Division.

## Tips on Using Twitter

**An interesting webinar was recently jointly facilitated by Beef Central and Future Beef titled "Beef Up Your Twitter Effectiveness".**

**The webinar would be of great value to any seedstock producers that are considering how to use and get the most out of Twitter.**

**The webinar can be viewed from the Future Beef website:**

**<http://futurebeef.com.au/resources/multimedia/#twitter>**



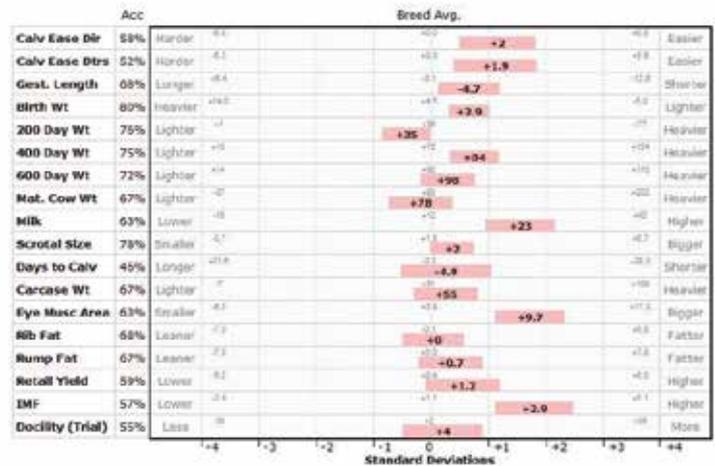
# Understanding the EBV Standard Error Graph

A new graph when viewing animals within the EBV Enquiry facility on Internet Solutions is now available for implementation by Breed Societies that have upgraded to ABRI's new generation of breed registry software known as ILR2.

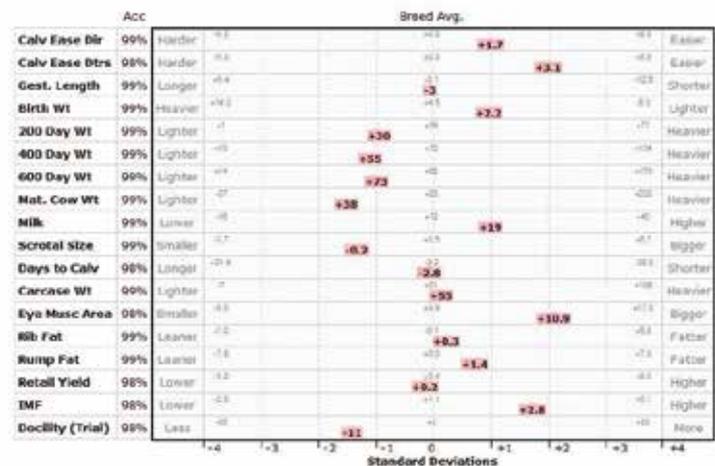
The EBV Standard Error graph provides seedstock and commercial beef producers with an indication of the possible change in an animal's EBVs for each trait. The horizontal bar for each trait displays one standard error either side of the current EBV value, meaning that statistically, there is a 67% chance that the true breeding value for this trait will be within this range. Another way of looking at this is to consider that as more performance information is added for the animal, the EBV would be expected to fall within the EBV range displayed in the graph 67% of the time.

Of course, as the EBV takes into account all the pedigree and performance information that is available at the current point in time, the EBV is still the most reliable indication available of the animal's breeding value for each trait at the current point in time. The EBV Accuracy for each trait is shown at the left side of the graph.

To access the EBV Standard Error graph for an animal, users need to click on the animal of interest from within the EBV Enquiry facility and then click either "EBV Graph" or the graph icon as they would normally do to display the EBV Percentile graph. At the bottom of the EBV Percentile Graph, a button will display titled "Switch Graph". Clicking on this button will display the EBV Standard Error graph for the animal.



Example EBV Standard Error graph for Young Animal



Example EBV Standard Error graph for Proven Sire

Examples of the EBV Standard Error graph are provided in the attached diagrams. As the EBVs of the proven sire have higher accuracy, the graph demonstrates that there is less possible change in EBVs as more information becomes available than for the young animal.

## Enhanced Mating Predictor for Gelbvieh

The mating predictor facility available within the Internet Solutions suite of tools that is offered by the Australian Gelbvieh Association now has the extra capability to calculate the expected level of inbreeding in the progeny from a specified mating. This enables members to carefully analyse and monitor the level of inbreeding that exists within their Gelbvieh animals.

Similar functionality also exists within the mating predictor tool that is offered by many of the other breed organisations. Further information regarding the use of the mating predictor tool is available from the BREEDPLAN Booklet page within the Technical area of the BREEDPLAN website in the document titled "A Guide to Internet Solutions".

# 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:

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