DROUGHTMASTER

Australia's natural wonder

WHITE PAPER 2020

Collecting phenotypes and genotypes for the benefit of the Droughtmaster breed going forward

Prepared by Droughtmaster Australia and TBTS

In recent years, the term genomics has been the topic of conversation many times within the beef industry, creating a sense of excitement but also some confusion. Given this, this publication aims to provide Droughtmaster Australia (DA) members with:

- Background information about DNA testing and its current application within the beef industry,
- Straightforward definitions of terms commonly used in the genomics era e.g. reference population, single-step,
- A description of the many benefits of collecting performance information (phenotypes) and testing to understand the genetic makeup of an animal (genotyping), and
- An outline of key research projects involving and benefiting the Droughtmaster breed (Repronomics, Northern BIN).

By doing so, members will hopefully gain an understanding of the steps involved with the breed attaining world-leading Single-step genomic BREEDPLAN evaluation and how it will allow them to make more informed selection decisions and drive genetic gain.

DNA testing and its current application

DNA sample types

When undertaking DNA testing, producers have the ability to submit sample types to laboratories in the form of blood, semen, hair and tissue. Which sample type to use is up to the individual producer, but in some circumstances it will be determined by the situation e.g. the need to submit a semen straw from a deceased sire who wasn't otherwise sampled. When weighing up which sample type/s to use, a number of factors need to be considered: safety of sampling, risk of sample contamination (biological and chemical), sample failure and mix ups, cost, convenience, expertise of sampler, storage requirements, handling logistics and the ability to provide linkage to existing ID devices.

Some general comments about each sample type:

- *Blood*
  - Not commonly used anymore due to the higher risk of contamination, more difficult collection process and handling logistics

- *Semen*
  - Some producers have had successful breeding outcomes from semen stored for ~50 years
  - Whole straws should be thawed at room temperature and shipped either inside a pen barrel (substitute for ink tube) or placed in a slot between two ridges of cardboard; additionally, placing each straw in an individual plastic bag is ideal

- *Hair*
  - Has been the most commonly used sample type for a long time
  - Ideally should be taken from animals >60 days of age
  - Ensure that you collect an adequate amount of hair (budget ~30 hairs per test)
  - It's imperative that the sample collected and stored is dry and free of foreign matter such as manure and dirt
  - Be sure not to cut off the follicles (root bulbs) as this is where the DNA is contained
  - It's very easy to store (individual hair collection kits, room temperature, dry and away from sunlight)

- *Tissue*
  - Tissue sampling units (TSU's) are now seen by many producers and labs as the preferred sample type as:
    - The sample can be collected at birth
    - There's a reduction in failed samples, sample mix ups and risk of contamination
    - They can provide sample-to-animal linkage (can be paired to matching NLIS & management tags)
    - They're able to be processed much faster at the laboratory using a decapper machine
  - As TSU's haven't been in the market place for long (<5 years), there's still a very minor element of uncertainty about their longevity. Testing so far has shown that over a three year period, they've been able to successfully go back to the same sample four times.

Additional sampling & submission considerations

When it comes to collecting and storing DNA samples, some producers are already doing their entire herd, which is recommended. Actually testing each sample isn't going to be feasible for all producers, but having a collection and storage system in place allows for future testing to be easily undertaken if required.

Given that producers are constantly looking for ways to increase efficiency and reduce on-farm risk, service providers are heavily promoting the benefits of TSU's and uptake of the sampling method has increased significantly in recent times. It's well-known that there are additional benefits of handling TSU's at the laboratory end, and this has likely contributed to one provider now implementing additional charges for non-TSU sample types. Other providers may decide to follow suit. As a risk management strategy, some producers have opted to store hair samples at home in addition to using TSU's.

Paperwork is often considered a burden by many; however it's absolutely imperative in a beef business, especially when it comes to DNA testing. Dotting the I's and crossing the T's can be the difference between samples being accepted/declined for processing at the laboratory and continual back and forward correspondence between parties simply lengthens the time taken to receive results. Service providers generally provide detailed instructions for their submission process so be sure to locate and read them carefully. The submission process normally entails sending a hard copy form with the samples and submitting an electronic file via email.

On average, it takes four weeks from when a sample arrives at a lab to when test results become available. During busy periods though e.g. leading up to bull selling season, this timeframe can lengthen so it's important to be proactive and organised for testing, especially if you want to include genetic information into sale catalogues.

Service provider arrangements

In the current market place, there are two main, longer-term service providers offering a comprehensive range of DNA services to beef producers, Neogen Australasia and Zoetis Animal Genetics, with a couple of other companies in the early stages of offering DNA testing options. Some breed societies have been in discussions with all available options, with some deciding to align themselves with one lab in particular. For example, Angus Australia have formed partnerships with both Neogen Australasia and Zoetis Animal Genetics and so the members have the opportunity to choose which lab they undertake testing for genomics, parent verification, genetic conditions and genetic traits. The fee structure across the two labs is almost completely identical as part of the partnership arrangement. This has meant that long-standing relationships between producers and service providers have been able to remain intact as price hasn't tempted producers to cross over.

An in depth description of what services and price structure each individual service provider can offer is outside the scope of this publication, however DA members can view this information in the separate attachment provided.

Breed societies have been negotiating with service providers as to which possible tests can be bundled together so that members can benefit economically. The special bundle price is only available to members who submit their samples through the society. To date, the Droughtmaster Bundle through Neogen Australasia includes: Pompes E7, Hornpoll, Parentage (providing details of sires and dams are included) and the GGP Trop Beef 50K chip. It may be possible for this bundle to be adjusted in the future with further input from DA members. As an additional point, it's possible that transferring samples and DNA profiles across service providers can occur, however having the correct formatting is required for upload purposes. Potential costs and ramifications need to be discussed with the service providers.

Parentage verification (PV)

Parentage verification allows beef producers more certainty regarding parentage and peace of mind. With testing options available to producers, multiple sire joinings can be carried out along with mishaps identified e.g. semen straw mix ups, rogue bulls, mismothering, human error and mix-ups between AI sires and backup bulls.

A known mishap example entailed a bull travelling more than 3km and over at least five fences to get to the cows. Additionally, one of the industry's BIN research projects was shown to have 12 out of 227 calves given incorrect sires due to the other mishaps previously mentioned.

DNA parentage verification works by analysing a series of DNA markers in the progeny and in potential parents. For each DNA marker, one of the two variants observed in the progeny must have come from the dam and the other from the sire. Therefore, potential parents can be ruled out if their DNA markers do not match those observed in the progeny. In the example shown below, the calf and dam have been genotyped, as have five candidate sires.

Animal	Marker A	Marker B	Marker C	Marker D	Marker E
Calf	Aa	BB	CC	dd	Ee
Dam	aa	Bb	CC	Dd	EE
Sire 1	AA ✓	Bb ✓	Cc ✓	dd ✓	EE
Sire 2	Aa ✓	bb	CC ✓	DD	ee ✓
Sire 3	Aa ✓	BB ✓	CC ✓	Dd ✓	Ee ✓
Sire 4	aa	Bb ✓	cc	DD	ee ✓
Sire 5	AA ✓	Bb ✓	Cc ✓	dd ✓	EE

For simplicity, five different markers (Markers A, B, C, D and E) are being used. When we examine Marker A, we can see that the calf has the genotype 'Aa', and the dam has the genotype 'aa'. In this instance, the dam must have passed on 'a' to her calf. Therefore, the 'A' must have come from the sire. Sires 1, 2, 3 and 5 could have passed on an 'A' to the calf, so are potential sires of the calf. Sire 4, having the genotype 'aa', could not have passed on an 'A' to the calf, so can be ruled out as a potential sire. We can then repeat this process for the remaining markers. At the end of this process, the only sire left as a potential sire candidate is Sire 3. Note that this process does not "prove" that Sire 3 is the sire of the calf; rather, it does not eliminate him as the sire. In this simple example, five markers were enough to eliminate four of the five sire candidates from contention. In real life situations, several hundred markers are used for parentage verification.

The two types of DNA markers that have been used for DNA parentage verification in cattle are microsatellites (MiPs) and Single Nucleotide Polymorphisms (SNPs). A microsatellite is a repeat of a particular base pair sequence at a specific location in an animal's DNA e.g. CACACACA. SNPs occur where there is a difference in a single base pair e.g. A vs T. Historically, microsatellites were the DNA marker used for parentage verification. However, SNPs are replacing microsatellites as the genetic marker of choice because of their greater abundance and stability. The greater abundance of markers means more markers can be included in tests, allowing them to be more powerful and accurate, while the greater stability means the test will remain accurate over many generations.

While many beef cattle societies are moving away from microsatellite parentage verification tests to the newer SNP parentage verification test, one limitation to this upgrade is that microsatellites and SNPs are incompatible. Unfortunately, microsatellite profiles cannot be converted to a SNP profile equivalent. Therefore, animals which require parent verification via DNA need to have the same type of DNA profile as their parents. In situations where the calf is to be parent verified using a SNP profile, and the parents only have a microsatellite profile, then the parents would need to be re-genotyped to have a SNP profile.

Members are encouraged to check with their preferred service provider about the future of MiPs being offered, as one provider has stated that MiPs will be discontinued at the end of 2020.

Below is a summary of where some of the other Australian cattle breeds are up to with DNA regulations:

- **Breeds with Sires and Donor Dams needing a DNA profile on record -** Angus, Brahman, Brangus, Charolais, Hereford, Limousin, Murray Grey, Red Angus, Simmental
- **Full Parent Verification -** Wagyu, Speckle Park

Horn/poll testing

Polledness, or the absence of horns, is considered by many to be an important trait, hence it is being actively selected for within many beef breeding programs across Australia. As producers are aware, breeding for polled cattle is not always as simple as just using visually polled bulls within a breeding program and for this reason, a number of tools have been developed to enable producers to transition to a polled herd relatively quickly. One of these tools is the Australian Poll Gene Marker test that was initially released by the Beef CRC in 2010. The test was further developed by the CSIRO, with funding assistance from Meat and Livestock Australia, and a greatly improved test was released in 2013. The improved Australian Poll Gene Marker test used the same microsatellite markers as the initial test but also incorporated information from nine other markers close by in the genome.

As technology has advanced, testing has now become SNP based (SNP = single nucleotide polymorphism), with the test becoming more accurate in both Taurus and Indicus cattle. The Optimized Poll Testing (OPT) assay has increased polled prediction efficiencies and achieved a commercial poll testing success rate of 99.42% across 70,031 animals. Labs are no longer reporting a result with accuracy attached e.g. PP 98%, but instead are either including a

subscript such as PcPc / PcPf / PfPf (c = Celtic origin; f – Friesian origin) or simply reporting the result as PP – this is obviously lab dependent.

The basics still haven't changed though, with there being three possible genotypes (PP = homozygous polled; PH = heterozygous polled and HH = homozygous horned). Additionally, the polled variant of the gene (P) is usually dominant to the horned variant of the gene (H), meaning visually polled animals can either have the genotype of PP or PH. In order to increase the likelihood of offspring being polled (thus reducing the need to dehorn), PP bulls are preferable, however producers must be conscious of not falling into the trap of single trait selection and sacrificing other traits of economic importance. Understanding the genetics of scurs remains limited. It has been confirmed though that there is a relationship between scurs and sex, with male animals more likely to have scurs. Recent research indicates that scurs development is predominantly observed in heterozygous (PH) animals, but there is unexpected evidence of homozygous (PcPc) Droughtmaster bulls with a poll-shaped head with scab like scurs.

Genetic conditions

Genetic conditions or defects are caused by DNA anomalies and are present in all species, including beef cattle. The incidence of genetic conditions is normally low within a population but can rapidly escalate with inbreeding or if there's a rapid dissemination of undesirable genes through artificial breeding. 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, if a diagnostic test exists. 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 allow breeders to more easily manage genetic conditions such that production losses and spread of the mutation can be minimised.

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 three possible genotypes:

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

Genetic conditions can result in reduced performance (growth and fertility), cause structural unsoundness, and be semi-lethal or even lethal e.g. animals **affected** by Pompe's disease will typically die between 6 to 12 months of age after displaying progressive muscular weakness.

Mating a free animal to a carrier 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 25% **affected** and 75% normal calves, with two thirds of the normal calves being **carriers**.

Developments in DNA technology have resulted in diagnostic tests being available for several single gene recessive genetic conditions. Gene probability software (such as GeneProb - developed by Brian Kinghorn and licensed to ABRI) is also 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_%).

When it comes to managing genetic conditions unfortunately there is no "one size fits all" strategy. 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

Basic definition of terms used in the genomics era

Genomics – the study of an animal's genetics by analysing and interpreting the animal's genome (complete set of DNA)

- The most common current applications of genomics within the industry include parent verification, management of genetic conditions, change in qualitative traits (coat colour, polledness), genetic improvement in production traits and the assessment of breed composition.

Genotype – the genetic makeup of an organism i.e. it describes an organism's complete set of genes

Phenotype – the observable characteristics or traits (performance information) of an animal that result from the interaction between the animal's genotype and the environment

Estimated Breeding Values (EBVs) – values produced by BREEDPLAN that provide an estimate of an animal's genetic merit for a particular trait

SNP chip – a testing device used at the lab to detect variations at thousands of single sites across an animal's genome

Reference population – a group of animals which have both performance information (phenotypes) and genotypes

Single-step BREEDPLAN – genetic analysis software that uses performance, pedigree and genomic information simultaneously

How Does Genomic Selection Work? (Single-step)

When genomic information is not included in the BREEDPLAN analysis (the current situation for most Australian breeds), the BREEDPLAN analysis uses pedigree information and performance data (both on the individual and the related animals) to generate Estimated Breeding Values (EBVs). When genomic information is implemented for a breed-specific BREEDPLAN analysis, breeders are able to take an ear punch with a TSU or a hair sample on an individual animal, send the sample to the lab, and have the sample genotyped on one of the available SNP chips. The genotype information needs to be supplied to the breed society to be included in the BREEDPLAN analysis and used, in conjunction with pedigree and performance information, to generate EBVs.

For genomic selection to work, a reference population is required. The reference population consists of thousands of animals that have both phenotypes (performance data) and genotypes. Setting up a reference population has been one of the challenges in implementing genomics in many breeds of beef cattle; for most breeds to date, there simply have not been enough animals with both phenotypes and genotypes available to

form an effective reference population. The ideal reference population has phenotypes collected on all traits of economic importance and relevance to the breed, that are then SNP genotyped.

An advantage that Droughtmaster Australia has over a lot of breeds is that they have been involved in two large research projects (Repronomics and Northern BIN), where there has been the collection of large amounts of phenotypic data as well as those animals being genotyped with either the 50K chip or 35K chip. These projects will be further discussed later on in this publication.

In addition to the animals in the reference population are the animals which have genotypes, but do not have phenotypes. Typically these are young animals which have not yet reached an age where they can be performance recorded, although any animal with a genotype but no performance data fits into this group. Genomic selection uses the known relationships between the phenotypes and genotypes of the animals in the reference population to calculate EBVs for young animals.

There are several factors that will influence how well genomic selection works. Firstly, the size of the reference population is critical. For genomic selection to work successfully in Australian beef cattle, a reference population with thousands of animals with both phenotypes (performance data) and genotypes will generally be needed. Secondly, genomic selection works best when the reference population is closely related to the young animal population for which genomic EBVs are being calculated. For this reason, the reference population should be designed to represent the whole genetic pool of a breed, rather than just a subset of genetics within a breed.

This is also one of the reasons why genomics will not replace performance recording – there is a requirement that animals from the next generation have both genotypes and phenotypes coming into the reference population. It is important that seedstock producers understand genomics will not replace performance recording; the work that you do as seedstock producers to performance record your animals will be critical for the success of genomic selection in the future. Involvement in BIN projects where difficult and hard to measure traits are collected will also significantly contribute to its success.

<u>What benefits can Droughtmaster producers expect from genomics?</u>

Currently, the Droughtmaster BREEDPLAN analysis uses pedigree information and performance data (both on the individual and the progeny) to generate EBVs. When genomics is implemented for Droughtmaster, a producer will be able to take a TSU/hair sample on an individual animal, send the sample away for genotyping, and the genotype information will be included in the BREEDPLAN analysis and used to generate EBVs. This will have two main applications for Droughtmaster producers:

- *EBVs can be generated for animals which do not have performance data*

Within any breed, there will be a number of animals that do not have performance information as they are from herds which do not record performance data. In the future, with the inclusion of genomic information into the BREEDPLAN analysis, these animals could be genotyped and get EBVs for the majority of traits. These animals could be from both seedstock and commercial herds.

There are also a number of animals that are in BREEDPLAN herds but do not have performance information for some traits. This may be because:

· The animal is too young to have been measured for that trait. For example, a 200 day old calf will not have been ultrasound scanned, so it is unlikely to have EMA, Rib Fat, Rump Fat or IMF EBVs. Where the 200 day old calf does have carcase trait EBVs, these are likely to be of fairly low accuracy.

· The trait is hard and/or expensive to measure. For example, Net Feed Intake (NFI) is measured in feedlot trials where the animals are on *ad libitum* feed for nearly 100 days (including the pre-trial adjustment period). This makes NFI very expensive to measure, and thus NFI measurements are usually only collected on animals in progeny test programs. Retail Beef Yield is another good example; measuring Retail Beef Yield is very expensive because the carcase has to be completely boned out and the individual retail cuts trimmed and weighed.

· The trait is only able to be measured in one sex. For example, Mature Cow Weight is only recorded for females.

· The trait can only be measured once the animal is dead. For example, abattoir carcase information, including Retail Beef Yield and Marbling, is only measured on carcases, and not from live animals. The beef industry currently utilises live animal ultrasound scanning measurements as a way around this problem, but actual carcase measurements can only be done on dead animals.

· Even when an animal does have performance information, this information may not be able to be used effectively by the BREEDPLAN analysis. For example, when an animal is placed in a single animal contemporary group, its performance information cannot be used by the BREEDPLAN analysis to calculate EBVs. As a result, most animals in single animal contemporary groups have mid-parent EBVs until performance information can be collected on their own progeny or other relatives.

With genomics, animals can be genotyped and get EBVs for a range of reportable traits (provided that the inclusion of the genomic information into the BREEDPLAN analysis means that the EBVs reach the minimum accuracy threshold required to report). Animals that are too young to be performance recorded for a trait could be genotyped at a young age (e.g. at birth) and get EBVs that normally they would not receive until they were much older (e.g. rising 2 year olds with scan data). Similarly, where a seedstock producer wanted EBVs on stud animals for hard to measure traits, genomics would mean that relevant animals could be genotyped and EBVs generated using genomic information.

- *More accurate EBVs can be generated for animals with limited performance information*

Genomics will "boost" the accuracy of BREEDPLAN EBVs; this benefit is most pronounced when the animal has EBVs with low accuracies. For example, a young animal may have an accuracy of 30% for one trait and with the inclusion of a genomic test result, the accuracy for that EBV might become 40%. However, an older animal, which might have an accuracy of 90% for the same trait would likely only have an increase to 92% accuracy for that EBV with the inclusion of genomic information. In this way, genomics can be considered similar to the addition of progeny performance data into the BREEDPLAN analysis; when the accuracy of an EBV is low, additional data has a relatively large effect, and when the accuracy of an EBV is high, additional data has a smaller effect. Of course, the improvement in the accuracy of an EBV due to the inclusion of genomic information will vary for each trait (depending on the size of the reference population and the heritability of the trait) and for each animal (depending on how closely the animal is related to the reference population).

Also to note is that with single-step BREEDPLAN, SNP genotypes are used to determine the actual degree of relationship between individuals. In the case of full siblings, this may vary in the vicinity of 0.35 to 0.65 – rather than 0.5 (50% of genes in common) as would be assumed in a traditional genetic evaluation approach. This allows for an increase in the accuracy in the EBVs calculated, thus allowing producers to make more accurate breeding decisions early in life.

Additional single-step considerations

A further feature of the single-step process is that a genomic pipeline is used to build a single-step genomic relationship matrix for BREEDPLAN. What this means is that it allows animals to be flagged as having differences between the paper pedigree and their DNA parentage. These flagged animals are provided back to the breed society to enable them to liaise with the producer to check these animals. In some cases there may be DNA sample issues and others may require resampling or DNA parentage verification. It also may allow the paper pedigree to be corrected. This is another positive reason for Droughtmaster Australia to have in place that all sires have a DNA profile. This will allow members to identify errors that may have occurred.

It is also important to note that currently only animals that reach a required threshold of relationship to the breed's reference population will be eligible to have their genotype included in the EBV calculations.

Single-step BREEDPLAN: What have we learnt since 2017?

The following key messages have been extracted from an article written by Dr Rob Banks (AGBU) for the SBTS/TBTS Winter Update 2018.

Single-step methodology was introduced into BREEDPLAN evaluations for Brahman back in May 2017, and since then the Hereford, Angus and Wagyu BREEDPLAN evaluations have switched over to implementing Single-step BREEDPLAN routinely.

- Single-step BREEDPLAN is producing EBVs, changes in EBVs and changes in accuracy that are in line with what we expect from the theory.
- We are seeing modest increases in average EBV accuracy, somewhat larger for animals with genotypes than those without.
- We are seeing useful increases in EBV accuracy for those animals whose prior accuracy is lower.
- Single-step BREEDPLAN EBVs line up well with standard BREEDPLAN EBVs - the average change is essentially zero; but individual animals can change their EBVs quite markedly. The relationship between Single-step and standard BREEDPLAN EBVs is strong, reflected in high correlations between the two analyses.
- The amount of increase in accuracy varies between breeds and traits, and reflects the size of the genomic reference population (the animals with genotypes and performance records).
- Together, these mean that Single-step BREEDPLAN provides an opportunity to evaluate young animals for more traits, depending of course on what has been recorded in the breed's genomic reference population (what traits, how many animals).

Involvement in the Repronomics Project and Northern BIN Steer Project

How are Droughtmaster Australia and its members benefiting?

The Repronomics Project (led by Dr David Johnston, AGBU) kick-started in 2013 and has generated more than 5,800 calves (Droughtmaster, Santa Gertrudis, Brahman) representing more than 320 sires from 119 different stud prefixes. Of these calves, close to 2500 are Droughtmaster by around 130 sires, with over 30 stud prefixes represented. The Droughtmaster calves have been born alongside Brahmans and Santa Gertrudis at Brian Pastures (Gayndah) and Brahmans at Spyglass (Charters Towers). The females have fertility measurements for puberty and post-partum oestrus as well as weights, carcase, temperament, structure and other important traits as well as a 35KTropChip DNA profile. In April 2020, this research data was included in the Droughtmaster BREEDPLAN run, which is a significant positive step for the breed! In the process, the evaluation has been

upgraded to include four new BREEDPLAN traits for the Droughtmaster breed: gestation length, days to calving, shear force and flight time.

The other project that has resulted in a large increase in data going into the BREEDPLAN analysis is the Northern BIN Project of which Droughtmaster Australia is a collaborator along with Australian Brahman Breeders Association and a consortium of Santa Gertrudis breeders. This project purchases the steer portion of the Repronomics project cattle and follows them through to slaughter, collecting important data including scanning measurements for p8, Rib fat, EMA and IMF, along with weights and structural soundness measurements prior to slaughter. All steers are MSA graded in the abattoir and a meat sample sent to the meat science lab in Armidale for IMF, tenderness and meat colour measurements. This meat science data is the first data collected for the breed that will be included in the BREEDPLAN analysis.

How involvement will assist attaining Single-step BREEDPLAN into the future

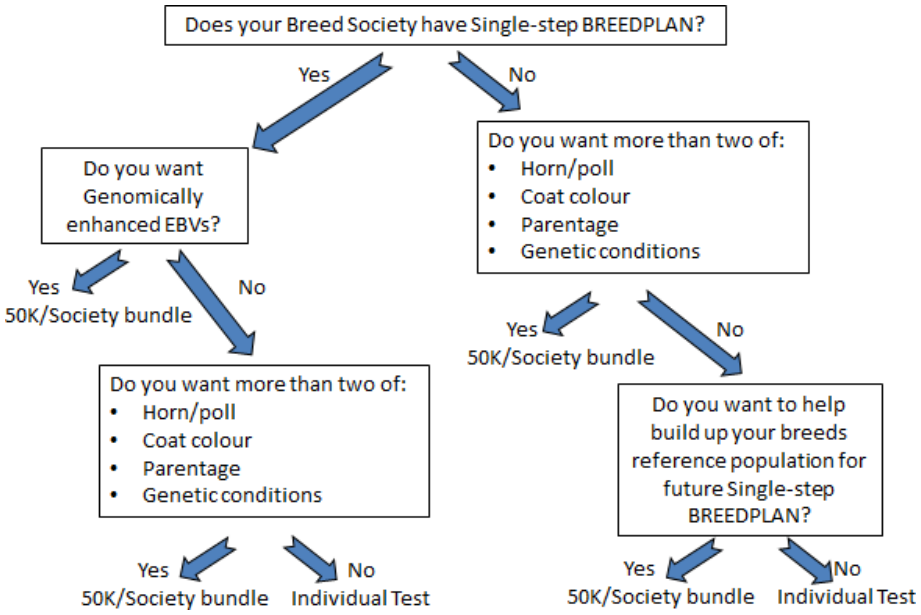
The data from the Repronomics and BIN projects will be the driving force and backbone behind Droughtmasters having a Single-step analysis in the future. With the Repronomics project having just being renewed for another five years, there will be an opportunity to purchase another five years' worth of steers and collect the carcase and meat science data to help drive the breed towards improved genetic evaluations in the future.

Going forward

As Professor Mike Coffey from the Roslin Institute in the UK once said, "In the era of genomics, phenotype is king". DA members are strongly encouraged to submit more performance information to BREEDPLAN as it allows for identifying genetic merit, increasing EBV accuracy and can also identify curve benders! This can have a positive effect in individual herds but also across the whole breed.

Genotyping strategies

When it comes to genotyping strategies, there's not really a one size fits all for producers. The genotyping strategy chosen will generally depend on both breed society regulations and the purpose of testing. Deciding which test to use can be daunting for some, however the diagram below may assist with the decision making process. Please make note that breed society regulations may override this advice.



The next decision is which animals to test and this comes down to the fact that some breed societies mandate that all calves are tested, whereas other societies ensure some or all of AI sires, sires and/or ET donors are genotyped. If you're simply testing for sire verification, then individual and all potential sires are recommended whereas for parent verification, individual and all potential parents will be done. If you're testing to get a handle on the genetic conditions within your herd, then you might look at individual parents, individuals for sale, progeny of carriers and explore the individuals that GeneProb suggests.

When heading down the Genomically Enhanced EBVs pathway, numerous potential strategies exist for those who want to maximise information for selection decisions:

- Whole herd – expensive but maximum benefit to the herd
- Influential sires and dams (particularly those with performance recorded progeny) – most value for money as less tests inform a great proportion of the herd
- Sale animals – marketing benefit (trust of tested animals, value of extra data and accuracy)
- Replacement heifers – will inform all future calves
- Animals in small contemporary groups (e.g. sick, show and/or ET animals) – these individuals would get the greatest increase in EBV accuracy within your herd

As technology continues to evolve and pricing structures change, it's advisable to regularly review and update your strategy.

In the Final Report of the Repronomics Project it has been suggested that as breeds transition to Single-step BREEDPLAN evaluation, they will benefit from additional industry genotyping to build their numbers of genotyped animals. One of the most beneficial ways would be to sample current high accuracy sires (and cows), particularly those with days to calving records that have not been genotyped.

SNP chip development, AGBU testing & quality control

Natalie Connors from AGBU recently presented on this topic at the AAABG conference in late 2019. Some of her key points include:

- The increased demand for genomic data driven by the transition of BREEDPLAN to single-step has seen an increase in the numbers of genotyping providers and SNP panels.
- It is necessary to ensure that SNP panels offered to breeders/breed societies are compatible with the genomic pipeline quality control (QC) requirements
- AGBU have developed a set of industry standards for genotype panels, along with a process of analysing new SNP panel products and validating their compatibility for the BREEDPLAN genomic pipeline.

Closing remarks

It's inevitable that genomics is part of the future of modern breeding programs and will allow producers to utilise more accurate EBVs in their animal selection. It's up to producers though to determine how genomics can be most appropriately implemented within their operation. It can't be emphasised enough that performance records (phenotypes) remain critical in the genomics era, as they drive accuracy and underpin describing an animal's breeding value.

If Droughtmaster Australia want for Single-step BREEDPLAN to be a reality in the near future and for the long-term, there will need to be an ongoing commitment to stay involved in key research work and a dedicated effort by producers to build and maintain the reference population going forward.

For more information regarding the topics covered as part of this publication, please feel free to get in contact with TBTS staff members:

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