

FACT SHEET

Genomic Tools – What do I put in and what do I get back?



FAST FACTS

- **Breed societies and TBTS/SBTS can provide information about different service providers, hair collection kits and DNA tests available**
- **When collecting a hair sample, it is important to follow the correct procedure outlined by the service provider**
- **At the lab, DNA is extracted from the sample and is analysed using a SNP Chip, leading to the generation of an animal's raw genotype**
- **Using the genotype information, prediction equations are generated that will underpin more accurate EBVs.**
- **Incorporating prediction equations with phenotypic and pedigree information in BREEDPLAN will deliver the single best estimate of an animal's genetic merit**
- **Genomic breeding values are based solely on prediction equations**

Historically, estimating the genetic merit of an animal has required recording an animal's performance and the performance of its relatives and progeny. Technology developed by the Beef CRC will enable genetic progress to be fast-tracked by predicting an animal's genetic merit based on DNA. This fact sheet describes the steps involved in genomic testing.

Who do I talk to about the process?

It is recommended that you contact either your breed society or regionalised (Tropical/Southern) Beef Technology Services as a first point of call. They will be able to provide you with information about the different service providers, the various avenues to obtain a hair collection kit, the DNA tests available and potential end results. Other fact sheets in this series detail the commercial DNA tests available to producers and the value of the Beef CRC's prediction equations.

Collecting a hair sample

Upon receiving your hair collection kits, firstly make certain that the animal's identity (tattoo or ear tag) is *accurately* recorded on the ID label provided. Next, select 50-60 hairs from the switch/brush of the animal's tail, ensuring that the hair is clean and dry. Pluck the hair with a rapid, sharp motion. Wrapping the hair around your finger or a pen can assist with this. The hair roots must be visible (see picture) as bulbs at the end of the hair. DNA is only contained in the root of the hair. Attach the hair to the collection card as directed and trim the excess. The collection kit is now placed in the supplied plastic bag

and with a completed application form is sent to the service provider.

An animal's genetic makeup may also be determined by testing a blood or semen sample

At the laboratory

Once the sample is received, the next step is to extract the DNA. This process is made up of several steps, some of which include cleaning the material, adding a number of chemicals, incubating the sample, and then finally checking the quality of the extracted DNA. After the DNA has successfully been extracted, the sample is processed on a genotyping platform. Genotyping identifies the individual sequence data or genetic variants at many sites across the genome and is referred to as genomic data. For a 50K SNP Chip, this process identifies genetic variants in DNA at 50,000 sites across an animal's genome.



Figure 1: Hair sample with clearly visible roots at the end of hair (top of picture)

Genomic selection and prediction equations

Genomic selection involves using genetic markers scattered randomly over the entire genome to identify genes associated with a desired trait. For example, for a trait like marbling, no matter where the genes

controlling this trait are located in the genome, they will be identified by using many genetic markers. To identify the location within the genome for these genes, variations known as single nucleotide polymorphisms (SNPs), which are associated with desired traits within the genome, are marked. Prediction equations generated by the CRC quantify the importance of each SNP and the overall value of all SNPs associated with a certain trait.

Generation of a genomic value

The generation of a genomic value requires genotyping providers to send the raw genotype to the Animal Genetics and Breeding Unit (AGBU) in Armidale. At this stage the genotype is quality checked and stored on file. Genomic prediction equations are then applied to the genotype to generate a genomic value, which estimates the breeding value based on DNA information alone.

BREEDPLAN EBVs and genomic values

The purpose of prediction equations is to estimate the breeding values of individual animals, so that cattle breeders can select the best animals. BREEDPLAN already performs this task for phenotypic measurements and pedigree information. The genetic evaluation system is now in place such that if an animal is recorded in BREEDPLAN, its genomic value is integrated with pedigree and phenotypic information. This process produces a BREEDPLAN Estimated Breeding Value (EBV) for this particular animal. Adding in genomic data simply increases the accuracy of that BREEDPLAN EBV. A symbol affixed with the animal's EBVs denotes that genomic values have been integrated (see symbol in example below). The increased accuracy of such BREEDPLAN EBVs allows producers to be more confident in their selection. Further information on BREEDPLAN EBVs and incorporation of genomic information is available in the fact sheet, 'Beef CRC prediction equations: improving productive traits with DNA.' and start of joining details on all cows. It is strongly recommended that seedstock herds supply DC EBVs with sale bulls and females, and that bull buyers request DC EBVs. This will enable beef producers to select animals with superior merit for reproductive rate.

Table 1: An example of BREEDPLAN EBVs where Beef CRC genomic prediction equation information has been incorporated.

Further information

The Beef CRC website (<http://www.beefcrc.com>) and the SBTS/TBTS webinar series (<http://sbts.une.edu.au/Webinars/webinars.html>) have additional information on BREEDPLAN EBVs and the use of DNA technology for beef cattle breeding.

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	Calving Ease Dir (%)	Birth Wt. (kg)	200 Day Wt. (kg)	400 Day Wt. (kg)	600 Day Wt. (kg)	Milk (kg)	Scrotal Size (cm)	Carcase Size (cm)	Eye Muscle Area (sq. cm)	Rib Fat (mm)	Rump Fat (mm)	Retail Beef Yield (%)	IMF (%)
EBV	+1.3	+4.3	+42	+77	+102	+17	+2.8	+59	+7.8	+0.3	+0.6	-0.2	+3.8
Acc	39%	64%	59%	55%	53%	50%	50%	54%	51%	57%	53%	42%	43%
Breed Avg. EBVs for 2009 Born Calves													
EBV	+0.0	+4.6	+37	+70	+89	+12	+1.3	+49	+3.1	-0.2	+0.0	+0.3	+0.9

Traits Observed: BWT, 200WT

