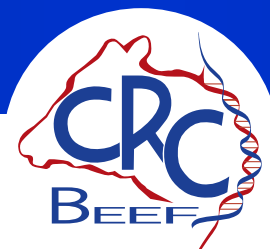


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Background Paper: Sequencing the Brahman genome

What is the Beef CRC Brahman sequencing project?

The Beef CRC, in partnership with CSIRO Livestock Industries and the Victorian Department of Primary Industries, selected a Brahman bull, whose semen is widely used in Australia, to have its genome sequenced.

This bull is the first bovine bred in Australia to have its genome sequenced. The name of the bull has not been published for commercial considerations.

A popular Australian Brahman sire was chosen for sequencing so the Australian beef industry could reap maximum benefit from the development of future new genetic improvement tools.

Information about the unique variation of the Brahman genome identified from this bull will be added to the publicly-available international bovine genome database.

The project will ensure that genes associated with important production traits, such as beef quality and fertility, are identified and included in new commercially-available DNA marker panels.



Why was a Brahman bull sequenced?

The Beef CRC believes it is important to capture the unique genetic information of breeds that are important to Australian production systems. The *Bos indicus* breeds like the Brahman are particularly important for Australia, so it is critical that unique DNA markers from their sequence are included on future new DNA marker panels.

The Brahman and other *Bos indicus* breeds are not as significant in the beef production systems of other developed countries as they are in Australia.

Brahmans and Brahman-cross cattle comprise over half Australia's cattle population. The breed performs well in tropical northern Australia, whereas traditional British breeds are unsuited to the harsh northern Australian environment.

Most of the gene mapping of important production traits of the bovine genome has, to date, focused on the Hereford and beef and dairy breeds, which are suited for temperate climates. Sequencing the Brahman genome is an important addition to these initiatives, particularly for the future of the Australian beef industry.

Have other Australian cattle been sequenced?

The Beef CRC project also sequenced the genomes of Australian-bred bulls from two un-related Southern African Sanga breeds that are also adapted for harsh climates. These are the Tuli and Africander breeds, which are both *Bos taurus* breeds that evolved quite separately to the British and European breeds and which are more adapted to harsh tropical environments than the traditional *Bos taurus* breeds.

Collectively, the Brahman, Africander and Tuli provide a range of industry-applicable breeds that will best service the requirements of breeding programs directly designed for northern Australian production systems. The genetic information from bulls of these three breeds will be included in information about the genetic variation in different animals and cattle breeds stored in new high-density ‘SNP chips’.

What are the new high-density ‘SNP chips’?

The new high-density Single Nucleotide Polymorphisms (SNPs – pronounced “snips”) contain **variations in DNA sequences** which distinguish the genes of one animal from another.

These chips are a powerful new research tool which will provide a detailed genome-wide analysis of genetic variation between animals and breeds that researchers can use to map to important production traits.

Such traits may include carcass and beef quality (beef tenderness, marbling and retail beef yield), growth and feed efficiency, parasite resistance and other adaptive traits, and female reproductive performance (age at puberty, postpartum re-conception and lifetime reproductive performance).

It is unlikely that ‘a’ single gene for these important production traits will be found; rather hundreds, or even thousands and tens of thousands, of genes may influence the performance of an animal for each trait.

The new dense SNP chips will contain at least half a million variations in DNA sequences between animals and across breeds. Researchers can use this information to develop genetic improvement tools such as DNA marker panels to predict animals that will perform best in particular environments, and for particular markets. Producers will then use these genetic tools to select animals for breeding purposes, or to manage animals to better meet the specifications of premium beef markets.

Ultimately, the tools developed from these high density SNP chips will enable producers to more accurately predict the performance of their animals for important production traits than is currently possible. An example is cow fertility, which is an important production trait that is currently difficult for producers to select for, as the animal’s fertility and lifetime reproductive performance is not known at the time a producer needs to make selection decisions on which animals should go into the breeding herd.

How will producers use these new high density SNP chips?

Use of the high-density SNP chips will lead to more profitable and sustainable beef production.

However, producers are unlikely to use these chips directly. Rather, the high-density chips are an entirely new **research** tool. They will help scientists develop smaller, more targeted and cost-effective panels of DNA markers applicable to commercial production systems.

It is these DNA marker panels that industry can then use to predict the breeding or market value of their animals.

The Beef CRC proposes that genetic predictions of breeding value developed from these panels, once extensively evaluated in independent Australian cattle populations, are fed directly into the BREEDPLAN beef genetic evaluation scheme, to seamlessly incorporate DNA information with other performance and pedigree data recorded for animals.

The combination of genetic information and phenotypes has already been successfully incorporated into BREEDPLAN with the development of ‘shear force’ EBVs for Tenderness – known as ‘marker-assisted EBVs’ (EBV^m) – which were launched for the Brahman breed in 2008.

Beef CRC cattle genomics Frequently Asked Questions: <http://www.beefcrc.com.au/genomicsFAQ>