CASE STUDY

# MLA case study: Beef Information Nucleus Project

**What:** **Nation-wide progeny test**

**Who:** **MDC and five cattle breed societies**

**Why:** **Improve information for economically important genetic traits**

Australia's cattle breeders are backing their future with nation-wide progeny testing to identify which genetics make good economic sense.

The Beef Information Nucleus (BIN) initiative is a portfolio of projects established through the MLA Donor Company and co-funded by five of the major breed societies.

The BIN project is delivering more accurate and extensive estimated breeding value (EBV) information to validate gene markers so producers can improve animal selection.

The project is collecting information about the economically important traits (such as fertility, growth and eating quality) of the progeny from numerous sires:

- **Angus:** 140 sires, 4,000 progeny over three generations
- **Brahman:** 65 sires, 2,000 progeny over three generations
- **Charolais:** 50 sires, 405 progeny in southern Australia (from Angus females), 485 progeny in northern Australia (using Brahman females), three generations
- **Hereford:** up to 15 sires each joining, 425 progeny over three generations
- **Limousin:** 10 sires/year, 220 progeny/year, four generations

The accuracy of genomic EBVs, which to date is typically in the 30 to 45% range, is completely dependent on how many animals have been recorded and genotyped in reference populations – as this population rises, so does the accuracy of genomic EBVs.

The BIN progeny testing programs are therefore essential to genomic progress and are already impacting the genetic evaluation system, BREEDPLAN, used for beef cattle in Australia.

## Fast facts:

- Five breed societies involved
- More than 300 sires and nearly 8000 head of their progeny
- Carcase and reproductive traits targeted
- Eating quality and methane emissions traits also assessed
- Will guide development of DNA technology for economic traits

As a result of the BIN initiative, feed efficiency EBVs are coming on line for some breeds, and the accuracy of EBVs for some sires are now between 90 and 100%.

Other outcomes from BIN projects is the clear message that pasture based production systems should chose positive fat EBVs and select for docility to improve meat quality.

Using phenotypic carcase data to verify genomic predictions is also an opportunity to improve marbling and retail beef yield.

And it's not just about measuring reproductive and carcase traits. One BIN project is linked to an assessment of methane emissions, involving the Trangie Agricultural Research Centre's Angus herd.

This Genetic Improvement of Beef Cattle for Greenhouse Gas Outcomes project has demonstrated a direct correlation between lower feed intake animals and lower methane emissions. The next step is to measure methane emissions of cattle from other beef breeds, to see if genetic variation exists. This will underpin the development of methane EBVs.

The BIN projects are generating grassroots interest, demonstrating a huge level of interest from producers and the wider industry and underpinning the breed societies' commitment.

The flow-on effect for commercial producers is new knowledge which they can use to select more productive genetics which allow cows to produce more calves in their lifetime.

# Beef Information Nucleus Project

## *BIN project snapshot 1: Brahmans*

The Australian Brahman Breeders Association established the breed's largest progeny test program in 2014, with funding from MDC. It involves 2000 animals in two commercial herds in Queensland. Over seven years, 73 Brahman sires will be evaluated. The project has already achieved 20% improvement in the accuracy of Brahman-sire EBVs. It aims to improve the accuracy of existing EBVs and collect valuable data on hard-to-measure traits, such as eating quality and female reproduction.

## *BIN project snapshot 2: Herefords*

Since 2010, the Hereford project has been collected from the progeny of about 50 Hereford and Poll Hereford sires considered in the top 25% for important traits. Twelve herds, from south-west Queensland to South Australia, have been measured for birth weight, calving difficulty, gestation length, 200, 400 and 600-day weights, structural soundness, docility, net feed intake and carcase traits. Full sets of Meat Standards Australia chiller assessment data have been collected, and meat samples analysed for tenderness, cooking loss and intramuscular fat. In anticipation of future genomic-based technologies, tail hairs and blood samples have been collected from all progeny to use as a source of DNA information and genotyping.

## Further information

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