



Final report

Building and delivering effective genomic selection for northern Australia cattle

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Dedication

This report and research outcomes are dedicated to the memory of four very significant people who died during the course of this project. Firstly, Dr Steve Barwick a long-term AGBU colleague who co-designed the project and whose scientific prowess was world renowned for putting an economic framework to beef cattle selection. Secondly, Professor Bernie Bindon, CEO of the Beef CRC, a huge supporter of this research and a scientific mentor to many. Thirdly, Burnett Joyce, former principal of Gyranda Santa Gertrudis stud, a huge supporter of beef genetics research, especially female reproduction and was an early adopter, innovator and key collaborator in this project. Finally, and most tragically my wife Kimberly, her unwavering support and love of this project enabled all that has been achieved

Abstract

This project has been very successful in building the size of genomic reference populations of Australia's main tropical beef cattle breeds. This has enabled northern beef producers to access more individuals that are genetically described. Commercial producers can now benchmark their herds and match genetics with increased precision to their production systems and markets. Seedstock breeders have increased capacity to make faster rates of genetic progress across the range of economically important traits, particularly female reproduction. This has been achieved by generating and intensely recording more than 5,700 genetically relevant animals from Brahman, Santa Gertrudis and Droughtmaster breeds. All this data, coupled with high density DNA SNP profiles, have been submitted to the BREEDPLAN genetic evaluation of each breed where it has added significantly to the genomic reference population data, underpinning the genomically-configured single-step evaluations. The project has increased EBV accuracies and greatly expanded the number of animals available with a full suite of BREEDPLAN EBVs, with many generated from a DNA profile only. The project has developed first-ever across-breed research EBVs, allowing direct comparisons of genetic merit across Brahman, Santa Gertrudis and Droughtmaster. The project has developed novel traits creating opportunities to expand genomic evaluations to identify genetics more suited to northern Australia environments.

Executive summary

Background

- Genetics is a vital tool available to the beef industry to boost productivity, increase profitability and improve environmental and social viability. However, to use genetics effectively requires the accurate prediction of genetic merit of populations, breeds and individual candidates for selection. This research used precision experimental design and recording to maximise the impact of the project on the genetic evaluation of Australia's most influential tropically adapted beef breeds.
- The improvements to the genetic evaluation as a result of the project will benefit tropical beef breeders in both the commercial and seedstock sectors. The benefits will also flow through the supply chain with backgrounders, feedlotters and consumers all potentially benefiting from the enhanced genetic evaluation for tropical beef breeds.
- Phenotypic and genomic data collected in the project will directly drive increased EBV accuracies across the range of economically important traits, especially for female reproduction. The results of the project will help inform improvements to BREEDPLAN genetic evaluations, including the development of new EBVs targeting profitable northern production systems.

Objectives

Delivering enhanced genetic products to industry and removing barriers to adoption in northern Australia through:

- a) Recording high precision phenotypes, particularly traits related to female reproduction on approximately 2,000 additional females, across 3 tropically adapted breeds in northern Australia.
- b) Generating new knowledge and improved systems through;
 - i) evaluating the magnitude of genotype x environment (GxE) interactions
 - ii) trialling novel recording technologies which have potential to reduce costs of recording
- c) Establishing and fostering collaboration through working with service providers, breed societies and northern seedstock breeders.

Methodology

Key activities for the project include:

1. Intensive recording of female traits (approximately 550-650 new females per year).
2. Identification and use of new AI sires (10-20 new per year).
3. Sourcing and use of natural mate bulls (10-15 new per year).
4. Accurately recording all calves generated (approximately 1,000/year) and trial new experimental measures.
5. Generation of across-breed (genomic) data to inform EBV.
6. Establishment of key project linkages and development of further research collaboration/opportunities.
7. Product development and rapid industry implementation.

Results/key findings

The project has successfully increased the accuracy of the prediction of genetic merit of selection candidates (most critically, young sale bulls) especially for female reproduction EBVs. For genotyped Brahmans, the inclusion of the project data in BREEDPLAN increased their accuracies across all EBVs with the largest increases observed for gestation length (18%), days to calving (48%), heifer age at puberty (48%) and lactation anoestrous interval (48%). Similar to larger magnitude increases in accuracies were observed for Droughtmaster EBVs. For

Santa Gertrudis the increases in accuracies were lower as a result of smaller numbers in the project and higher average existing accuracies. The project recorded large amounts of data on more than 20 new or emerging traits, and these could be included in future genetic evaluations to allow (genomic) selection for additional traits affecting profitability. The project increased adoption of genetic technologies with more animal evaluated, many with EBVs generated from genomics only.

The project design has allowed the development of an across-breed evaluation, which produced research EBVs that allows the northern beef industry to capture both the within and between breed genetic variation for the full suite of economically important traits for Brahman, Santa Gertrudis & Droughtmaster.

The project has enhanced the genetic evaluations of tropical breeds by providing critical reference population data to drive the recently implemented BREEDPLAN single-step genomic evaluations. The project has increased genetic linkage across herds and improved BREEDPLAN's ability to remove non-genetic sources of variation when estimating breeding values, which is critical in allowing comparisons of genetics across herds. Finally, the project has shown that, for a range of key traits, *GxE* interactions were not evident. This is critical knowledge in designing the BREEDPLAN analysis, and provides a current answer to a common question raised by BREEDPLAN users.

Benefits to industry

The main benefits to the industry has been the increased numbers of animals (particularly young bulls) in northern Australia that are now genetically described by BREEDPLAN EBVs and selection indexes, especially for the key profit driver traits of female reproduction. More than 88,000 animals have been genotyped and included in the BREEDPLAN single-step evaluations during the course of this project. The project enhances the ability of commercial producers to buy genetics that are better suited to their productions systems (and markets) and now have the ability to make those comparisons across breeds with the development of first-ever across-breed research EBVs. Critically, the seedstock industry has increased capacity to make faster rates of genetic gain, through increased accuracy (and spread in EBVs) and across a broader suite of traits driving profitability, especially the key traits of female reproduction. The computation of EBVs directly comparable across breeds is a major development allowing commercial breeders to directly compare across the three breeds. This will also allow for more effective implementation of new composite breed development programs, particularly as the evaluations progress from across-breed to full multi-breed configurations.

Future research and recommendations

The project has clearly shown the benefits of using genomics in northern Australia through the increased accuracy and spread in BREEDPLAN EBVs. However, the magnitude of the improvement is a direct function of the size of the genomic reference population in each breed, the heritability of the traits recorded (which can be heavily impacted by experimental design and recording precision) and the relevance of the genetics represented in the reference. Therefore, to further increase EBV accuracies and drive faster rates of genetic progress the size of the reference populations in each of the tropical beef breed needs to continue to increase, particularly for traits with high economic value that currently have lower numbers. It is also important to ensure the recording is done on the latest, most relevant genetics in each breed. Commonly, in the north the key profit-driver traits are difficult or costly to measure in industry herds so the importance of recording these in an effective reference population is of particular importance. Additionally, the project has provided a means to test novel phenotypes as candidate traits for future genomic selection. The other critical design aspect of this project was the running of the breeds head-to-head to generate the necessary data to allow the development of across-breed (and multi-breed) evaluations. In the future this needs to continue to maintain and improve the accuracy of the current breed comparisons for all important traits and include the addition of other breeds relevant to northern Australia.

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1. Background

1.1 Genomic selection

Genomic selection has changed livestock breeding programs worldwide. Dairy breeding programs have shown 2-4 fold increase in rates of genetic progress (e.g. Garcia-Ruiz *et al.* 2016). This phenomenal change has occurred through the advent of low-cost high density SNP microarrays and the application of genomic selection (Meuwissen *et al.* 2001). However, the benefits achieved currently in beef cattle breeding programs have been less pronounced. This was primarily due to delays in the development of routine genomic evaluations e.g. single-step (Legarra *et al.* 2014) but was addressed for Australian beef cattle evaluations with development of BREEDPLAN single-step evaluations in 2017 (Johnston *et al.* 2017). The results of Johnston *et al.* (2023) showed that the BREEDPLAN genomic evaluations were starting to show significant increases in EBV accuracies, but it was observed the benefits for many beef breeds were constrained by the low numbers of animals with a phenotype and a SNP genotype. The accuracy achieved from genomic evaluations for each EBV is a function of the size of the reference, the heritability of the trait (Goddard and Hayes 2009) along with the relatedness of an individual to the breed's reference population (Habier *et al.* 2010).

Genetics is a vital tool for the beef industry to boost productivity, increase profitability and improve environmental and social viability. However, to achieve this the accurate prediction of genetic merit of populations, breeds and individual candidates for selection is required. This research applied precision experimental design and recording, and the latest genomic technologies to directly improve the genetic evaluations for Australia's tropically adapted beef breeds. This will benefit both commercial and seedstock sectors that select bulls in their breeding programs. The benefits will also flow through the supply chain with backgrounders, feedlots and consumers all potentially benefiting from the enhancement to the genetic evaluation of tropical beef breeds.

1.1.1 Genomic reference populations

The construction of genomic reference populations is critical for the development of genomic evaluations and ultimately the success of genomic selection. For tropical beef cattle in Australia, it was recognised that the recording in seedstock herds was considerably less representative of their population than was the case for temperate breeds and the predecessor project (MLA B.NBP.0759) set out to address this shortfall. Whilst that project was very successful, the number of records was not yet enough to generate an EBV with sufficiently high accuracies, particularly for genomics-only EBVs.

Many of the traits with high economic values in northern beef breeding objectives are often not recorded or are costly to measure in industry herds (often both), for example female reproduction and carcass and meat quality traits. Therefore these important traits generally have low accuracies, particularly in young sale bulls and thus are clear candidates for recording in the reference populations to enable genomic selection. To assist with this the project has been recording new traits and helped determine their suitability for future genetic evaluations with the potential to develop new EBVs targeting profit drivers for northern production systems.

1.1.2 Single-step genomic evaluations

Incorporation of DNA based information into BREEDPLAN genetic evaluations is now occurring through the development and implementation of single-step methodology that enables genomic information from high density SNP genotypes to contribute to the EBVs (and accuracies). This occurs through the inclusion of genotyped animals in the genomic relationship matrix (that replaces the conventional pedigree of those individuals). However, the increased EBV accuracies (and spread in EBVs) is generated by these genotyped

animals also having phenotypic data in the analyses. These individuals are commonly referred to as genomic reference animals or members of the breed's reference population.

This project will directly influence the single-step BREEDPLAN evaluations of the three dominant tropical breeds, Brahman, Santa Gertrudis & Droughtmaster, through the regular submission of both the phenotypic and genomic data collected from the project, thus building the size of their genomic reference populations. This will result in increased EBV accuracies across the range of economically important traits, especially for female reproduction for all new animals entering the evaluations, especially those which rely on genomics only (i.e. no own performance data).

2. Objectives

The project objectives were to deliver enhanced genetic products to industry and remove barriers to adoption in northern Australia through:

- a) Recording high precision phenotypes, particularly traits related to female reproduction on approximately 2000 additional females, across three tropically adapted beef breeds in northern Australia.
- b) Generating new knowledge and improved systems through;
 - i) evaluating the magnitude of genotype x environment interactions,
 - ii) trialling novel recording technologies which have potential to reduce costs of recording,
- c) Establishing and fostering collaboration through working with service providers, breed societies and northern seedstock breeders.

Each of these objectives have been achieved, with the overall numbers being met even though the project experienced some very challenging seasons that affected conception rates and maiden heifer growth rates. GxE analyses have been performed across a large number of sires with progeny across locations. Recording of new traits has been successful with statistical models used to determine significant fixed effects and heritability estimates of each of the traits, with resultant across-breed research EBVs generated for all sires used in the project.

All the phenotypic and genomic data generated by this project describe current genetics in each breed and has been used by the three breed societies to implement and enhance their BREEDPLAN single-step evaluations. This has allowed large numbers of northern bull breeders to access genetic evaluation for the first time, offering their genetics for sale with the full suite of BREEDPLAN EBVs, often generated from genomics-only information. This has increased adoption of genetics through the increased numbers of bulls in northern Australia with BREEDPLAN EBVs.

3. Methodology

3.1 Experimental design

The project used existing Queensland Department of Agriculture and Fisheries (DAF) and the Northern Territory Department of Primary Industries (NTDPI) cow herds generated in MLA B.NBP.0759 to undertake recording and create new calf crops over the five years of the project. This had the benefit that several cohorts of females existed in Year 1 of the project that could be continued, or started recording that already had full recording history (i.e. birth details, fixed effects) as well as pedigree and genomic profiles. This phase of the project saw the addition of a NTDPI developed Tropical Composite breed. This composite was previously run at a separate research station in the Northern Territory and for this project heifers were relocated to Douglas Daly and run alongside the selected Brahman herd that was part of the B.NBP.0759 project. This has enabled head to head

comparisons of the NT Tropical Composite with Brahmans in the same environment and the subsequent computation of across-breed research EBVs from that data.

3.1.1 Recording

Intensive recording was completed at each project site (approx. 550-650 new females per year), including accurate recording of date of birth and all known fixed effects. Each year approximately 1,000 new calves were generated in the project and at each site and year were all managed together with no drafting, culling or sorting. This was important to generate data suitable for genetic analyses and for the project to generate across-breed comparisons and the resultant across-breed EBVs.

The project measured a very large number of traits from birth, weaning, post-weaning, puberty and through rebreed, mating and calving outcomes. Measurements included: weights, scores, ultrasound scan (carcase and ovarian) measures and mating and calving outcomes. The precision recording and management coupled with a high frequency of recording and the application and evaluation of cutting edge measurement technologies ensured the traits being recorded in the project were of the highest precision. This meant that heritabilities, while within the range of expectations, were high, reducing the total number of records required to achieve higher levels of genomics-only EBV accuracies.

3.1.2 Sire selection

New genetics were sourced each year from industry herds for each breed and included the identification of new AI sires (approx. 10-20 per year) and the sourcing of natural mate sires (approx. 10-20 new/year) usually as two year old sale bulls. Both the AI and natural mate sires were chosen to maximise the future relatedness of young selection candidates (e.g. future two year old sale bulls) to the genomic reference for that breed. This involved sourcing AI sires that were previously not represented in the project that had large numbers of progeny registered in the breed in the last five years (or a natural mate son). Also considered were emerging sires (i.e. young sire with progeny or a recent sale topping bull) that were likely to have large numbers of progeny in next few years.

Natural mate sires were used in large multi-sire single breed mating groups that included all maiden heifers and first-calf cows. Mating ratios were at 3-4% with an 11-12 week joining period. AI sires were used in two rounds of fixed-time AI programs over all second-calf cows and older. Most sires had progeny generated across years and locations to ensure strong genetic linkage and this enabled the estimation of genotype x environment interactions i.e. GxE across sites.

3.2 Data management and industry implementation

All data on individuals recorded at the research stations was submitted regularly to the project central database throughout the year where it was checked and loaded. Regular data downloads of latest phenotypic data on BREEDPLAN traits and all genomic information were provided to ABRI for all BREEDPLAN traits to be loaded onto their northern multi-breed research database and made available to each breed's monthly BREEDPLAN run. This ensured a very short time between latest recording and inclusion in the genetic evaluation, thus allowing for up to date contributions of an expanding genomic reference population and increased EBV accuracy of the latest project sires.

3.3 Project linkages and collaborations

The project design included linkage through common sires across sites and years, including Brahmans used across the NT DPI and DAF herds. Beefmaster sires were used over Droughtmaster cows to provide a benchmark

of this US performance tropical breed. This project was also linked through common Brahman sires with the Southern Multi-Breed Projects (SMB) P.PSH.1261 Grafton site (Walmsley *et al.* 2021). And in the final year of the project (#24 cohort) Angus and Hereford sires were used that were predominantly from the SMB project to generate F1 progeny out of a subgroup of the project Brahman cows.

Project cattle were also a valuable resource to other projects. The most important collaboration was with the Industry-driven MLA MDC project that purchased all steer cohorts from the DAF sites to include in the Northern Steer BIN project (MLA P.PSH.0743, P.PSH.0774, P.PSH.1386 & P.PSH.1408). This project has collected critical post-weaning steer growth, abattoir carcass and meat quality traits. Several cohorts of steers at weaning have been recorded for immune competence phenotypes using the recently developed CSIRO test (Hine *et al.* 2019) and a subset of the Spyglass steer cohorts have been recorded for feed intake at pasture, GreenFeed methane production and feedlot feed intake at UQ Gatton.

Project cows in the DAF herds have also been used in several outside projects including: a DAF camera imaging project, nitrogen use efficiency studies, and in recent years, the heifer cohorts at Brian Pastures and Spyglass have been recorded for methane production at pasture as part of the Northern Methane project (UQ/MLA project *“Reducing methane emissions and improving profitability in northern Australian beef 2022-2027”*, P.PSH.1406)

Project data has been used by AGBU researchers in the improvement of BREEDPLAN evaluations (as part of MLA L.GEN.2204 project) including the development of single-step methodology, turning on existing traits (e.g. days to calving EBV in Droughtmaster), re-estimation of breed genetic parameters, and the latest research into the development of a cow body composition EBV and BREEDPLAN multi-breed genomic evaluations.

4. Results

4.1 Recording levels achieved

The experimental design of the project has focused on the generation and intensive recording of more than 5,700 animals at Queensland DAF and Northern Territory DPI research facilities. The experimental animals generated were as genetically relevant to the existing breeds as possible, thus maximising the benefits to current and future industry selection efforts. This was mainly achieved by the careful sampling of new sires used each breeding season, including the mix of AI and natural mate sires.

Precision recording methods and protocols were a key feature of the project and were done to maximise the genetic expression of a trait, thus reducing the number of records required to achieve higher levels of genomic accuracies (see results in section 4.3.1). The project generated annual calf crops from 2019 born (2020 weaned cohort) through to 2023 born (2024 weaned cohort) with numbers of animals and records presented in section 4.1.1.

In addition to the new project animals generated, there were also existing cohorts of females available from Phase 1 of the project (MLA B.NBP.0759) that were recorded in this project for the key female reproduction traits. Heifer cohorts were scanned for age at puberty and were subsequently mated in this project to generate lactation anoestrous interval and calving traits.

4.1.1 Number of project animals generated

The total number of calves generated in the project by location and year are presented in Table 1. The DAF sites included Brian Pastures research facility (east of Gayndah) and Spyglass research facility (north of Charters Towers). The NTDPI herd was located at the Douglas Daly research farm (near Douglas-Daly), but also included weaner heifers born at the two feeder-herds of Kidman Springs research station (Brahmans) and Beatrice Hill research farm (NT Tropical Composites).

Table 1. Number of animals generated in the project by year and research station

Year (of weaning)	DAF – Brian Pastures	DAF - Spyglass	NTDPI – Douglas Daly	Total
2020	409	547	162	1,118
2021	305	416	274	995
2022	377	433	237	1,047
2023	432	585	286	1,303
2024	392	535	341	1,268
Total	1,915	2,516	1,300	5,731

4.1.2 Cohorts & traits recorded

During the project the data recorded was collated and checked by the project technicians and then sent to the project's central database at AGBU. This included all phenotypic data and all SNP genotypes sent directly from the DNA lab. Tables 2a and 2b provide a summary of the cohorts and trait blocks recorded during this project. It includes cohorts 2017, 2018 and 2019 that were born as part of Phase 1 that were measured for female reproduction traits in this current project. Cohorts 2020, 2021, 2022, 2023 and 2024 were born and recorded as part of this project.

All calf cohorts and new sires each year were genotyped using the GGP TropBeef 35K or GGP TropBeef 50K chip bundle. The genotyping included: SNP genotype, parentage verification, Pompe's E7 and bovine horn/poll tests. Sharefiles of results were provided by the DNA company and data loaded onto the project database.

The breadth of recording is a key feature of any reference population, thus enabling genomic selection across the range of economically important traits, particularly those traits that are expensive or difficult to measure in industry herds. Listed below in Table 3 is the total number of records for each of the calf and cow measures at DAF and NTDPI herds. Calf measures were recorded on the cohorts described previously in Table 1. For the cow measures it also included the existing 2017-2019 cohorts for the female reproduction traits. Many of the measures had repeat records taken at different ages/physiological states and some of the cow traits also included repeat records for cows that calved across years.

Table 2a. Number of records by cohort and traits recorded at DAF research stations

Cohort	Project	N animals	Trait block [#]	genotyped
BP17	born previous, recorded current	155	LA, DC1, DC2, MCW	all
SP17	born previous, recorded current	230	LA, DC1, DC2, MCW	all
BP18	born previous, recorded current	160	AP, LA, DC1, DC2, MCW	all
SP18	born previous, recorded current	278	AP, LA, DC1, DC2, MCW	all
BP19	born previous, recorded current	188	AP, LA, DC1, DC2, MCW	all
SP19	born previous, recorded current	279	AP, LA, DC1, DC2, MCW	all
BP20	born and recorded current	207	B,W,Y,AP, LA, DC1, DC2, MCW	all
BP20-steers*	born and recorded current	202	B,W	all
SP20	born and recorded current	237	B, W,Y,AP, LA, DC1, DC2, MCW	all
SP20-steers*	born and recorded current	310	B,W	all
BP21	born and recorded current	136	B, W,Y, AP, DC1, LAI	all
BP21-steers*	born and recorded current	169	B,W	all
SP21	born and recorded current	204	B, W,Y, AP, DC1, LAI	all
SP21-steers*	born and recorded current	212	B,W	all
BP22	born and recorded current	167	B,W,Y,AP	all
BP22-steers*	born and recorded current	210	B,W	all
SP22	born and recorded current	230	B,W,Y,AP	all
SP22-steers*	born and recorded current	203	B,W	all
BP23	born and recorded current	223	B,W,Y,AP	all
BP23-steers*	born and recorded current	209	B,W	all
SP23	born and recorded current	306	B,W,Y,AP	all
SP23-steers*	born and recorded current	279	B,W	all
BP24	born and recorded current	223	B,W	all
BP24-steers*	born and recorded current	209	B,W	all
SP24	born and recorded current	270	B,W	all
SP24-steers*	born and recorded current	265	B,W	all

B=birth measures; W=weaning measures; Y=yearling measures; AP=heifer puberty scanning; LA=first-calf cow lactation anoestrous scanning; DC1=days to calving first mating record; DC2=days to calving second natural mating record; MCW=cow weight record.

*sold at weaning to the Northern Steer BIN MDC project

Table 2b. Number of records by cohort and traits recorded at NT DPI research station

Cohort	Project	N animals*	Trait block [#]	genotyped
DD17	born previous, recorded current	134	LA, DC1, DC2, MCW	all
DD18	born previous, recorded current	264	AP, LA, DC1, DC2, MCW	all
DD19	born previous, recorded current	279	AP, LA, DC1, DC2, MCW	all
DD20	born and recorded current	207	B,W,Y,AP,LA,DC1,DC2,MCW	all
DD20-bulls	born and recorded current	90	B,W,Y,PNS	all
DD21	born and recorded current	242	B,W,Y,AP,DC1,LAI, DC2	all
DD21-bulls	born and recorded current	151	B,W	all
DD22	born and recorded current	238	B,W,Y,AP, DC1	all
DD22-bulls	born and recorded current	125	B,W,Y, SC, PNS	all
DD23	born and recorded current	261	B,W,Y,AP	all
DD23-bulls	born and recorded current	147	B,W	all
DD24	born and recorded current	165		all
DD24-bulls	born and recorded current	176		all

* heifers coming from the feeder herds of Kidman Springs (Brahmans) and Beatrice Hill (Tropical Composite) have limited recording

B=birth measures; W=weaning measures; Y=yearling measures; AP=heifer puberty scanning; LA=first-calf cow lactation anoestrous scanning; DC1=days to calving first mating record; DC2=days to calving second natural mating record; MCW=cow weight record SC=scrotal size PNS=percent normal sperm.

Table 3. Number of records for calf (#20-#24 cohorts) and cow measures

Calf measures	N	Cow measures	N
<i>DAF herds</i>			
Birth weight	4,343	Live weight	63,016
Weaning weight	4,039	Buffalo fly lesion score	646
Vigour score	4,418	Navel size score	1,842
Coat colour	3,093	Body condition score	53,240
Calving difficulty score	4,420	Hip height	26,239
Dehorn score	4,040	Lactation status	5,489
Horn status	4,393	Fungal infection score	137
Coat length score	4,026	Calf mothering score	4,389
Flight time	3,995	Ultrasound scan EMA	3,254
Calf loss code	4,418	Ultrasound scan P8	26,253
		Ultrasound scan rib	3,257
		Teat scores B&F, L&R at birth	4,316
		Teat score B&F, L&R at weaning	1,505
		Udder score at birth	4,316
		Ovarian scan follicle right	17,796
		Ovarian scan follicle left	18,327
		Pregnancy test	7,612
<i>NT DPI herd</i>			
Birth weight	1,034	Liveweight	4,280
Weaning weight	1,991	Body condition score	3,921
Condition score	6,566	Ultrasound scan P8 fat	226
Liveweight	8,173	Ovarian scan right	3,590
Scrotal size	746	Ovarian scan left	3,993
Flight time	1,373	Lactation status	4,001
		Pregnancy test	4,108

4.1.3 Mating data – natural and AI

The calves generated in the project resulted from a combination of natural (maiden heifers and first calf cows) and AI matings (all second calf and older cows). Tables 5 and 6 shows the numbers of females by DAF and NT DPI locations, years and breeds, respectively.

Table 5. Numbers of females total and by AI and natural mating across DAF locations and cohorts

Mating Group	Total Females Used	Entered Natural Mating	Natural Sires Used	Females used for AI	AI total inseminations	AI Sires Used
BP18_BB	197	98	6	99	132	8
BP18_DM	146	75	4	71	97	9
BP18_SG	197	114	5	83	112	5
BP19_BB	185	101	5	84	134	11
BP19_DM	150	76	5	74	111	9
BP19_SG	181	86	5	95	158	6
BP20_BB	163	109	6	54	71	8
BP20_DM	124	80	5	44	64	11
BP20_SG	165	101	6	64	96	6
BP21_BB	198	116	5	82	108	9
BP21_DM	251	200	6	51	67	10
BP21_SG	328	254	6	74	99	5
BP22_BB	194	102	6	92	126	27
BP22_DM	145	74	4	71	99	11
BP22_SG	184	96	5	88	119	6
Total Brian Pastures	2,808	1,682	79	1,126	1,593	141
SP18_BB	403	219	9	184	250	10
SP18_DM	357	196	9	161	227	11
SP19_BB	397	234	11	163	230	11
SP19_DM	359	206	8	153	233	10
SP20_BB	321	206	10	115	150	8
SP20_DM	299	193	9	106	152	10
SP21_BB	536	367	10	169	239	10
SP21_DM	685	518	10	167	238	12
SP22_BB	885	711	11	174	224	33
SP22_DM	893	706	10	187	263	18
Total Spyglass	5,135	3,556	97	1,579	2,206	133
Total DAF	7,943	5,238	176	2,705	3,799	274

Table 6. Numbers of females total and by AI and natural mating across NTDPI breeds and cohorts

Mating Group	Total Females Used	Entered Natural Mating	Natural Sires Used	Heifers used for AI	AI instances	AI Sires Used
DD18_BB_2-3yo	268	268	6	0	0	0
DD18_BB_yearling	143	143	18	0	0	0
DD18_TC_yearling	107	107	16	0	0	0
DD19_BB_2-3yo	252	252	6	0	0	0
DD19_BB_yearling	136	136	15	0	0	0
DD19_TC_2-3yo	104	104	3	0	0	0
DD19_TC_yearling	117	117	14	0	0	0
DD20_BB_2-3yo	232	202	6	30	30	2
DD20_BB_yearling	106	106	15	0	0	0
DD20_TC_2-3yo	195	195	6	0	0	0
DD20_TC_yearling	93	93	15	0	0	0
DD21_BB_2-3yo	205	187	5	18	18	2
DD21_BB_yearling	124	124	15	0	0	0
DD21_TC_2-3yo	188	188	5	0	0	0
DD21_TC_yearling	107	107	15	0	0	0
DD22_BB_2-3yo	214	192	6	22	22	2
DD22_BB_yearling	107	107	14	0	0	0
DD22_TC_2-3yo	187	187	7	0	0	0
DD22_TC_yearling	115	115	15	0	0	0
Total NT	3,000	2,930	202	70	70	6

The total number of AI sires represented at DAF herds was 99 (see Appendix 9.1.1 for full list by breed) and included two Brahman sires (viz. DRF16024 and DRF16454) from the NTDPI herd. The six AI sires used at NTDPI included four new industry sires from a leading performance herd and two link sires (viz. CBE070192 and KAI147250) heavily used in the first phase of this project. The natural sires totalled 85 at DAF and 162 in the NTDPI, with a grand total of **351** sires used to generate the #20-#24 cohorts and represents an increased sampling of the genetics across all breeds.

4.1.4 DNA diagnostic tests

All project generated calves (#20-#24 drop) at DAF and NT sites and all new sires were SNP genotyped (N=5,307) using GGP TropBeef chips. The test also included diagnostic tests for DNA parentage, Pompe's disease and polled/horn genotypes. In addition, in conjunction with Overarching BIN project (MLA L.GEN.2007/L.GEN.2201) a subset of animals from this project and from Phase 1 were tested for the nine commercially available SNP-based myostatin mutations.

a) Poll/horn DNA test

All project animals were scored for horn/poll status (i.e. horns, poll or scurs) in the branding cradle prior to dehorning at approximately five months of age. Those animals with a P/H genotype and a horn/poll score are shown in Table 6 (DAF herds) and Table 7 (NTDPI herds) by breed and sex. For simplicity, the two versions of polled mutation (Pc and Pf) present only in Santa Gertrudis were recoded to P.

Results showed across all breeds in DAF herds a total of 1,962 calves were phenotypically poll or scurs (49%) however, Brahmans had a lower frequency of polled than the other two breeds. Results for NTDPI herd

showed very similar patterns to those observed in the DAF herds, albeit with lower frequency in the Brahman with only 34% of animals that were either polled or scurred.

The horn/poll phenotypes of PH genotype animals suggests a scoring inaccuracy with a small percentage of animals being scored as horned which should have been recorded as scurs (cells shaded in green). This was not surprising given the very young age at scoring where the differentiating between horn and a scur was often quite difficult. Likewise there were very small numbers of HH animals that were scored as scurs and even smaller numbers as polled (these may have developed horn later in life). Essentially all genotypic PP animals were scored as phenotypically polled with only three exceptions (shaded pink). The occurrence of scurs in PH genotype animals was different across the sexes. Scurs in all three breeds was more prevalent in bull calves compared to heifers (shaded yellow). This suggests a possible difference in the mode of gene action, with the scur gene(s?) being dominant in males and (partially) recessive in females. However, it appears the inheritance of scurs in Santa Gertrudis may be slightly different to the other breeds suggesting the frequency of the scur gene(s) is lower and possibly fully recessive in females.

Table 6. Frequency of phenotype vs DNA genotype for horn and poll in DAF herds by breed and sex

breed	sex	SNP genotype	Horn	Poll	Scur	Total
BRAHMAN			911	422	345	1678
	B		470	187	198	855
		HH	413	2	12	427
		PH	57	134	185	376
		PP	0	51	1	52
	H		441	235	147	823
		HH	404	1	10	415
		PH	37	197	136	370
		PP	0	37	1	38
DROUGHTMASTER			314	1004	326	1644
	B		170	402	231	803
		HH	130	0	2	132
		PH	40	150	228	418
		PP	0	252	1	253
	H		144	602	95	841
		HH	128	2	13	143
		PH	16	326	82	424
		PP	0	274	0	274
SANTA GERTRUDIS			129	422	68	619
	B		69	206	55	330
		HH	63	0	4	67
		PH	6	131	51	188
		PP	0	75	0	75
	H		60	216	13	289
		HH	58	3	11	72
		PH	2	153	2	157
		PP	0	60	0	60
		total	1363	1887	775	4025

Table 7. Frequency of phenotype vs DNA genotype for horn and poll in NTDPI herd by breed and sex

breed	Sex	SNP genotype	Horn	Poll	Scur	Total
BRAHMAN			387	117	105	609
	B		208	49	60	317
		HH	189	3	16	208
		PH	19	33	44	96
		PP	0	13	0	13
	H		179	68	45	292
		HH	173	1	24	198
		PH	6	56	20	82
		PP	0	11	1	12
TCOMP			100	207	68	375
	B		57	90	34	181
		HH	41	1	0	42
		PH	16	41	34	91
		PP	0	48	0	48
	H		43	117	34	194
		HH	37		6	43
		PH	6	64	28	98
		PP	0	53	0	53
total			487	324	173	984

- b) **Myostatin mutations.** Observations over the course of the project noted the increasing numbers of cattle with increased visual muscularity of calves at DAF sites, including several animals each year with an extreme double-muscling phenotype. As the numbers continued to increase it became apparent that a double-muscling gene mutation (known to exist in other beef breeds) was segregating in the project population. There was concern that it was impacting performance, in particular double-muscled heifers were observed to be extremely old for age at puberty. It was also apparent this was impacting the sire's LSMs for heifer age at puberty and for other related traits. Conversations with industry suggested this was being observed in seedstock and commercial tropical breed herds. Therefore, in conjunction with the MLA L.GEN.2007/L.GEN.2201 project, a large number of animals from this project and Phase 1 of the project were genotyped for myostatin mutations and subsequent analyses were undertaken to quantify the effects of the myostatin mutation using data collected in the project on these animals.

A total of 5,646 of the Repronomics project animals were genotyped for nine different SNP-based myostatin gene mutations (C313Y, D182N, E226X, E291X, F94L, NT419, NT821, Q204X, S105C) using the commercially available DNA tests and existing SNP profiles of each animal. Analyses have been completed and currently collated into a scientific publication. Gene frequency estimates for each mutation were presented in Moore *et al.* (2025a) and shown in Table 8. Analyses on the sizes of effects has been completed and this new research is in the process of being written into a series of scientific publications. Results of the gene frequencies shown in the Brahman population from this project indicated they were not segregating for any of the myostatin mutations, whereas, for both Droughtmaster and Santa Gertrudis they have low frequencies of the NT821 mutation and very low frequencies of the F94L mutation, with a cumulative 20% of all project animals across the two breeds with one or two copies of NT821 and/or F94L mutations.

Table 8. Frequency of myostatin alleles for the NT821 and F94L myostatin variant in project Brahman, Droughtmaster and Santa Gertrudis animals*

Breed	NT821					F94L				
	0	1	2	N animals	Freq(p)	0	1	2	N animals	Freq(p)
Brahman	2,554	0	0	2,554	0.000	2,554	0	0	2,554	0.000
Droughtmaster	1,852	331	5	2,188	0.078	2,138	48	0	2,186	0.011
Santa Gertrudis	697	199	8	904	0.119	872	32	0	904	0.018

*Table 2 from Moore *et al.* 2025a

4.2 New traits and across-breed comparisons

A key objective of the project was to use the herds as a resource to record new traits, potentially leading to the development of new EBVs for economically important traits for the northern industry, particularly driven by genomics. The main focus was on additional cow traits associated with survival and adaptation, with recording occurring at different ages and physiological states e.g. heifer vs lactating cow (see Table 9). Several of the new traits commenced recording in Phase 1 of the project (MLA B.NBP.0759) and continued to be measured in this project. The adaptation trait buffalo fly lesion score was modified in this project to standardise the scoring to occur at the start of mating of maiden heifers. It was determined that the heifers in these cohorts had not undergone any culling at this stage and had not been administered chemical control through fly tags (that were used on older cows). Therefore, data on this trait was limited to more recent years and also for cohorts where the incidence of lesions were apparent. Heifer navel score was also recorded on the same cohorts of heifers. The other cow traits were recorded at the first and second calving and included scores of all four teats, udder and mothering behaviour. Calf traits included a vigour score at birth and a coat length score at weaning. For three years the steer cohorts (2022, 2023 and 2024) were measured for new immune competence traits as part of the Northern Steer BIN project (MLA P.PSH.0743 and P.PSH.0744).

Key to the development of any new trait is the accumulation of sufficient numbers of records that have been recorded with a clear trait definition (i.e. consistent scoring/measuring methods). Statistical analyses were performed to understand, and quantify, any fixed effects associated with each trait. This was done so robust genetic modelling can occur and potentially develop a new EBV. Also, the ability to quantify the magnitude of the important non-genetic effects could help with future implementation.

For the most accurate estimation of variance components and the prediction of project EBVs, all analyses used the maximum amount of data available for each trait by combining the data across Phase 1 and records taken in this project. Pooling data allowed more accurate partitioning of fixed effects and modelling of maternal effects for some traits. Standard BREEDPLAN traits were not considered but data on those traits from this project, and Phase 1, have been pivotal in the re-estimation of genetic parameters underpinning the BREEDPLAN evaluations for each breed e.g. new Brahman parameters implemented November 2024 (MLA L.GEN. 2204).

Project data for each trait was pooled across breeds to develop the genetic analyses and a breed term was included as a fixed effect in the model. All analyses were re-run removing the breed term from the model, and given the project management that maintained direct breed comparison of performance (within same fixed effects) the resultant genetic parameter estimates captured breed effects. Across-breed research EBVs were then generated from each of the analyses using genetics parameters from the pooled breed analyses (that included breed), with the resultant project research EBVs directly comparable across all sires and breeds.

4.1.1 Development of new female traits

Each new trait was analysed separately with initial editing of data and raw data description. Full fixed effect modelling occurred using step-down approach from full models (all known effects and interactions) to yield final models which contained only significant terms ($P < 0.05$). These were then analysed in ASReml (Gilmour *et al.* 2009) to estimate variance components and genetic parameters (e.g. heritability estimates). These analyses resulted in an understanding of both the genetic and non-genetics effects for each new trait.

Individual trait reports including least squares means for breed effects and other important fixed effects (e.g. location, age of dam) are presented in Annex A. A summary of all heritability estimates are presented in Table 9. Results show all the new traits were moderate to highly heritable with large amounts of genetic variation and many of the traits also exhibited significant breed differences. The only trait exception was calf vigour score that was estimated to be the only lowly heritable trait (9%). This score was developed in an attempt to capture calf loss data on calves that at birth exhibited an industry observed condition called “dumb calf syndrome”. However, in this project we do not believe we observed this condition and the vigour score (or activeness) of the calf in this study, whilst variation existed, was most likely a function of how many hours the calf had been born when being observed. Therefore, it appears this trait was not suitable for determining any genetic differences in calf survival and the scoring of the trait would need to be redefined for any future development of a trait for genetic evaluation.

Removing the breed term from the statistical models generally resulted in slight increases in additive variances and heritabilities, with the largest increases observed for those traits with a large estimated breed effect e.g. navel score. Each of the ASReml analyses were then rerun as a BLUP model using genetic parameters from initial models (that included breed), this yielded solutions for the random animal effect (i.e. EBVs) that were comparable across-breed (see section 4.1.3).

The data and genetic estimates from the various ultrasound carcass scans on the project females at different stages helped inform the development of a new cow body composition EBV in BREEDPLAN as part of MLA L.GEN.2204 project (Wolcott *et al.* 2023). This new EBV is primarily related to the genetic difference in potential survival of first-calf cows when at their most vulnerable state as first-lactation three-year old cows at the beginning of the wet season (going into their 2nd mating). The EBV is especially important as northern breeding objectives have increased focus on improving female reproduction as it is therefore critical to quantify any underlying genetic relationships with cow body composition that might be detrimental to cow survival. All data from this project was used in the research of the new EBV and will be an important source of reference data for genomic evaluations of this trait in the future for each of the breeds.

Table 9. Additive variances and heritability estimates for all new traits with (+ breed) and without (- breed) a breed term fitted in the model

Recording age/status	Trait	V _A	h ² + breed	V _A	h ² - breed
Yearling heifer	Live weight	230.1	0.49	262.4	0.53
	Hip height	7.27	0.51	8.25	0.55
	Body condition score	0.015	0.31	0.018	0.34
	Scan P8 fat	0.56	0.41	0.58	0.42
Into mating 1	Live weight	589.7	0.62	625.2	0.63
	Hip height	10.58	0.64	11.09	0.66
	Body condition score	0.031	0.36	0.031	0.36
	Scan P8 fat	2.93	0.52	3.24	0.56
	Scan rib fat	0.64	0.52	0.72	0.55
	Scan eye muscle area	15.91	0.43	16.42	0.44
	Navel size score*	1.16	0.53	2.55	0.71
	Buffalo fly lesion score*	1.18	0.51	1.39	0.55
Into mating 2	Live weight	843.4	0.57	934.8	0.61
	Hip height	10.49	0.61	11.21	0.64
	Body condition score	0.054	0.37	0.060	0.40
	Scan P8 fat	1.97	0.40	2.00	0.40
	Scan rib fat	0.51	0.40	0.49	0.39
	Scan eye muscle area	17.91	0.36	21.19	0.42
At 1 st calf	Mothering score*	0.29	0.18	0.30	0.19
	Teat size score*	0.48	0.32	0.52	0.33
	Udder size score*	1.00	0.49	0.99	0.49
At 2 nd calf	Teat size score*	0.36	0.25	0.41	0.28
	Udder size score*	0.70	0.39	0.72	0.40
Calf at birth	Vigour score	0.11	0.09	-	-
Calf at weaning	Coat length score	0.96	0.49	2.03	0.67

* estimates on the underlying scale

Bivariate analyses were performed for the same measure that were recorded at different ages. The results of the genetic analyses generally showed an increased in the genetic variance of the trait as age increased (and change of physiological state) and genetic correlation estimates were often less than 1.0. For all measures, the correlations were highest (i.e. closer to 1) between those recorded at Yearling heifer and M1, and the lowest were between Yearling heifer and M2 (see Table 10). This reflects the increased age between the two measures but also at the M2 measure the females were now lactating. Hip height had the highest correlations across measurement times, whereas body composition traits had the lowest, illustrating the potential for the re-ranking of sires for these body composition traits across measurement times.

Table 10. Genetic correlations between pairs of the same measure across time

Measure	Heifer & M1	Heifer & M2	M1 & M2
Live weight	0.95	0.80	0.89
Hip height	0.98	0.93	0.99
Body condition score	0.78	0.70	0.74
Scan P8 fat	0.90	0.76	0.82
Scan EMA			0.76
Scan rib fat			0.75

4.1.2 Development of new male traits

The NTDPI breeding programs have made significant gains in improving female reproduction through selection using a phenotypic selection index (Schatz *et al.* 2010). The index included measures taken on young males in the selection program and recorded in this project. The aim of this work was to quantify the underlying genetic bases, and associated genetic changes in the male reproduction traits. These are crucial genomic reference data for these male traits in Brahman, particularly since all male calves in the DAF herds were castrated.

The data used were from Brahman and NT Tropical Composite (TCOMP) bulls, weaned from 1995 to 2022 with more than 60% of the data being recorded during this project and in Phase 1 of the project. Recording occurred at approximately yearling age (**Y_**) when animals were on average 395 days of age, and again at 18 months (**F_**) when average age was 582 days. Scrotal size (**SS**) was recorded using a scrotal tape and measured as the circumference of the two testicles at the widest point. All bulls that were cryptorchids and had only one testicle were removed (for all data). Semen samples were obtained using manual palpation or electro ejaculation and sperm morphology assessments were done using a microscope crush-side by department staff to determine percent normal sperm (**PNS**). Since 2019, the recording of percent normal sperm included an additional lab morphology assessment (n = 975) conducted on both breeds for the 18 month semen testing, and this data was submitted to Brahman BREEDPLAN. Table 11 presents the numbers of records and raw means for each of the male reproduction traits.

Table 11. Raw means for scrotal size (SS) and percent normal sperm (PNS) measured at yearling (Y_) and 18 months (F_) in NTDPI Brahman and TCOMP.

Trait	N	Mean	Std	Min	Max
Y_SS	3,180	21.7	3.8	12.4	38.0
Y_PNS	1,754	19.5	27.1	0	100
F_SS	2,919	26.1	3.8	13.7	42.5
F_PNS	2,282	44.8	31.1	0	97
F_PNS*	975	60.8	28.8	0	99
Y_age	3,225	394.8	28.2	249	491
F_age	2,940	582.3	35.8	431	705

* Morphology assessments by a commercial lab.

Given the low total numbers of records all genetic analyses were performed using a pooled dataset across the two breeds. Preliminary univariate analyses revealed that crush-side assessed percent normal sperm at 18 month (F_PNS) was not heritable, indicating possible issues with how that trait has been recorded and therefore only the laboratory morphological assessment recorded during this project was used for the 18 month PNS (F_PNS) and the crush side assessment is not suitable for future genetic evaluation.

All traits were modelled with fixed effects for contemporary group (year, herd of origin), breed and linear and quadratic regressions for age of animal and age of dam. Models were re-run removing the breed term for each trait. All models included a pedigree constructed using up to five generations and included a total of 6,200 animals.

Genetic parameter estimates were obtained from univariate analyses and these were compared to estimates when the primary trait was analysed in various combinations of bivariate and trivariate analyses with the other traits. This was done to investigate if there were changes in variance components resulting from accounting for selection that might have been generated by the common practice of culling on scrotal size at yearling. This may also affect the variances of scrotal traits, but more importantly, impact the variance components of the PNS traits.

Additive variances and heritabilities for each trait from models including a fixed effect term for breed (Table 12) and without breed (Table 13) are presented. Results shows scrotal circumference measurement at 12 and 18 months were highly heritable with slight increases in additive variances when breed was not fitted. Slight increases in estimates were also observed for F_SS when Y_SS was included in the bivariate model, thus accounting for any culling that was occurring at the yearling measurement time.

Percent normal sperm traits had lower heritabilities and tended to increase when the breed term was removed from the models. However, the largest impact on estimates was observed when other traits (in particular yearling scrotal) were included in the estimation. Generally, there was an increase in the additive variance and heritability of the PNS traits. PNS at 18 months had a slightly higher heritability than at yearling age, albeit with considerably fewer records. Yearling PNS was heritable but runs increased risk of more data censoring as non-pubertal/small scrotal fail to provide a semen sample, this would reduce effectiveness of any genetic evaluation. Genetic parameter estimates obtained from this study are in very close agreement with estimates published from the Brahman and Tropical Composite breed from the Beef CRC (Corbet *et al.* 2013). **BREDPLAN TRAIT?**

Table 12. Additive variances (V_A) and heritabilities (h^2) from univariate and multi-variate analyses with a breed term included in the models.

Trait combinations	Y_SS		Y_PNS		F_SS		F_PNS	
	V_A	h^2	V_A	h^2	V_A	h^2	V_A	h^2
Y_SS	3.00	0.48 (0.05)						
Y_PNS			68.1	0.16 (0.05)				
F_SS					3.50	0.52(0.05)		
F_PNS							111.1	0.17(0.08)
Y_SS & Y_PNS	3.02	0.48	71.8	0.16				
Y_SS & F_PNS	3.00	0.47					134.8	0.20
Y_SS & F_SS	3.08	0.49			3.64	0.52		
Y_PNS & F_PNS			69.9	0.16			114.5	0.17
F_SS & F_PNS					3.49	0.52	125.4	0.19
Y_SS & F_SS & F_PNS	3.07	0.49			3.65	0.52	121.1	0.18
Y_SS & Y_PNS & F_PNS	2.99	0.48	72.6	0.17			135.1	0.20
Y_SS & Y_PNS & F_SS	3.05	0.49	66.6	0.15	3.64	0.52		

Table 13. Additive variances (V_A) and heritabilities (h^2) from univariate and multi-variate analyses without a breed term in the model

Trait combinations	Y_SS		Y_PNS		F_SS		F_PNS	
	V_A	h^2	V_A	h^2	V_A	h^2	V_A	h^2
Y_SS	3.23	0.50 (0.05)						
Y_PNS			107.0	0.24(0.06)				
F_SS					3.55	0.52 (0.05)		
F_PNS							110.9	0.17 (0.08)
Y_SS & Y_PNS	3.21	0.50	104.6	0.23				
Y_SS & F_PNS	3.20	0.52					135.6	0.20
Y_SS & F_SS	3.32	0.52			3.68	0.53		
Y_PNS & F_PNS			110.7	0.25			115.3	0.18
F_SS & F_PNS					3.54	0.52	122.5	0.18
Y_SS & F_SS & F_PNS	3.31	0.51			3.68	0.53	124.5	0.18
Y_SS & Y_PNS & F_PNS	3.18	0.50	106.4	0.24			138.9	0.20
Y_SS & Y_PNS & F_SS	3.26	0.51	95.4	0.21	3.67	0.52		

Table 14. Genetic correlations between SS and PNS at yearling and 18 months for models including breed.

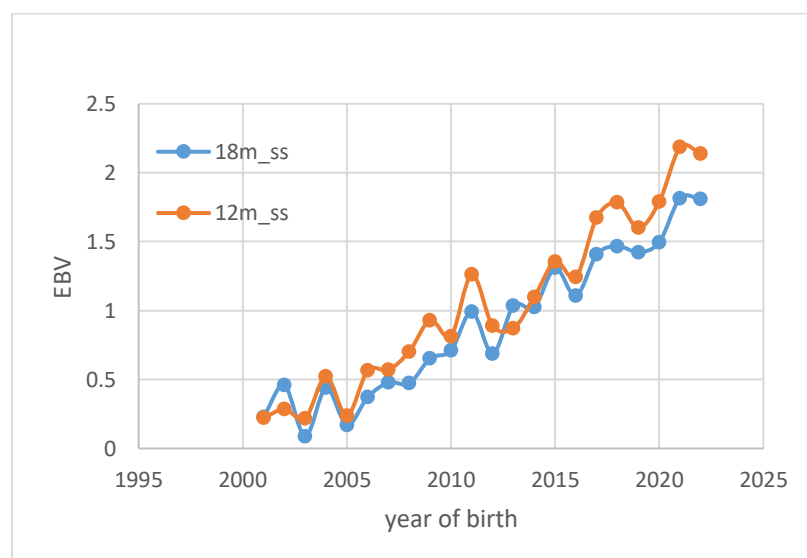
	Y_PNS	F_SS	F_PNS
Y_SS	0.70 (0.12)	0.89 (0.02)	0.59 (0.17)
Y_PNS		0.51 (0.13)	0.74 (0.24)
F_SS			0.37 (0.18)

Table 15. Genetic correlations between SS and PNS at Yearling and 18 months for models without breed (from trivariate analyses)

	Y_PNS	F_SS	F_PNS
Y_SS	0.71 (0.09)	0.88 (0.03)	0.57 (0.16)
Y_PNS		0.47 (0.12)	0.62 (0.23)
F_SS			0.38 (0.18)

Genetic correlations between traits were estimated from bivariate and trivariate models with breed (Table 14) and without a breed term fitted (Table 15). All traits were positively correlated and fitting breed had little effect on the estimates. Across time periods SS were highly correlated ($r_g = 0.88$) and PNS slightly lower ($r_g = 0.74$). SS and PNS were also positively correlated with estimates ranging from 0.38 to 0.71.

Project EBVs were generated for each of the traits using the most appropriate multivariate model and are presented from models where breed was not included in the model (i.e. across-breed EBVs). Table 16 presents statistics for EBVs for all animals in the evaluations and shows considerable spread in EBVs for all traits. Genetic trends for scrotal EBVs (Fig. 1) and PNS (Fig. 2) were for these male traits in this herd, and highlight that whilst the selection was based on a phenotypic index for many decades, there has been a clear underlying genetic improvement occurring in these male reproduction traits.

**Figure 1. Genetic trends in scrotal size at 12 months (Y_SS) and 18months (F_SS) in NT DPI Brahman and Tropical Composite.**

These results support the use of these male data in genomic evaluations and are critical for BREEDPLAN genetic evaluations as they represent an important source of genomic reference data (in Brahmans) for these male reproduction traits. The traits were not generated at the DAF sites because all males were castrated. An example of an animal from the NT Douglas Daly herd included in the Brahman BREEDPLAN evaluation is shown in Fig. 3 and shows the recording of the two male reproduction traits and that its genomics has also been included.

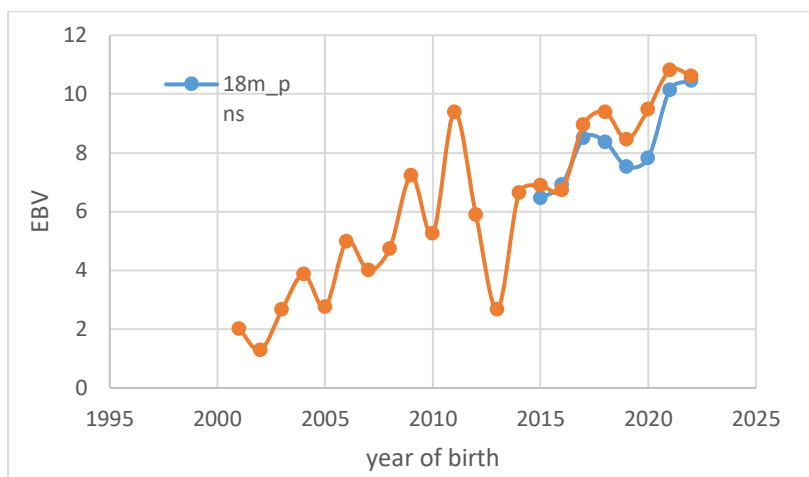


Figure 2. Genetic trend in percent normal sperm at 12 months (Y_PNS) and 18 months (F_PNS) in NT DPI Brahman and Tropical Composite.

Table 16. Summary statistics for trait EBVs for SS and PNS at Yearling (12m) and Final (18m) stages

EBV	Mean	Std	Min	Max
Y_SS	0.97	1.40	-4.47	5.51
Y_PNS	5.57	7.48	-16.5	31.5
F_SS	0.85	1.36	5.26	6.14
F_PNS	5.05	5.88	-15.9	27.3

Brahman Animal Details
DDRF 51704 (H) (COM)

[Animal Enquiry](#) [EBV Enquiry](#) [Mating Predictor](#) [Member Enquiry](#) [Sale Catalogues](#) [Semen Catalogues](#) [Download Files](#) [Online Register](#)

Identifier: DRF51704M
Sex: Male
PH No.: 51704
Birth Date: 02/11/2020
Calving Year: 2021
Status: Active
Registration Status: Commercial
Sire: [DDRF 50633 \(H\) \(COM\)](#)
Dam: [DDRF 50430 \(H\) \(APX B\)](#)
Breeder: [DEPT OF AGRICULTURE AND FISHERIES](#)
Current Owner: [DEPT OF AGRICULTURE AND FISHERIES](#)
Horn: Horned
Colour: Red
DNA Status: POLL/HORN (HH)
Pompe Status: Tested Free
DNA Genotype: SNP(GGP50K-TB Ref:1352921) SNP(SEEKSIRE Ref:1352921)
Parent Verification: Parent Verified
Progeny: None
Pedigree: [\[View\]](#)
EBV Graph: [\[View\]](#)

January 2025 Brahman BREEDPLAN																		
	Gestation Length (days)	Birth Wt (kg)	200 Day Wt (kg)	400 Day Wt (kg)	600 Day Wt (kg)	Mat Cow Wt (kg)	Milk Size (kg)	Scrotal Size (cm)	Days to Calving (days)	Carcass Wt (kg)	Eye Muscle Area (sq.cm)	Rib Fat (mm)	Rump Fat (mm)	Retail Beef Yield (%)	IMF (%)	Percent Normal Sperm (%)	Flight Time (secs)	Shear Force (kgs)
EBV	-5.5	-5.5	-16	-8	-14	-50	-5	+4.3	-26.1	-27	-1.4	+2.0	+1.9	-0.3	+0.2	+21.9	-0.16	-0.33
Accuracy	57%	77%	79%	80%	79%	75%	66%	76%	60%	67%	51%	61%	60%	40%	53%	62%	69%	46%
Breed Avg. EBVs for 2023 Born Calves Click for Percentiles																		
EBV	-0.4	+2.5	+20	+28	+39	+44	-2	+1.2	-2.8	+22	+2.8	-0.3	-0.5	+0.6	-0.2	+1.6	+0.00	-0.01

Traits Analysed: 200WT,400WT,600WT(x2),SS,PNS,Genomics

Figure 3. An example NT DPI DRF animal with male reproduction traits recorded and genomics included in latest Brahman BREEDPLAN evaluation (source: <https://abri.une.edu.au/online/cgi-bin/>)

4.1.3 Project across-breed research EBVs

A critical design feature of the project was that the various breeds at both the DAF and NTDPI herds have been run together and managed exactly the same throughout the project. This has been a very important feature of the project to enable the generation of large amounts of data across all traits that is suitable for the estimation of breed differences and the development of across-breed genetic comparisons and across-breed EBVs. The project has kept the northern industry informed of this unique feature of the project and encouraged discussion on future implementation strategies, in particular with each of the three breed societies. Field days have been conducted showing the breeds with their head-to-head performance, including the steers performance postweaning and through to carcase and meat quality data. This has been achieved through a unique collaboration of the Brahman and Droughtmaster breed societies and Performance Santa group (and MLA MDC) that have continued to buy the project each year and maintained the direct breed comparisons. This initiative demonstrates the level of cooperation necessary to allow implementation of across-breed EBVs for the northern breeds. The project data is proving seminal in the latest AGBU research into the development of to develop to necessary methodology for the development and implementation of full genomic across-breed EBVs BREEDPLAN (MLA L.GEN.2204). And when implemented the across-breed evaluation will rely almost exclusively on the inclusion of the project data to allow the alignment of breeds into a single set of EBVs.

4.2.3.1 New cow traits – DAF herds

Analyses performed in 4.2.1 to generate animal solutions (EBVs) that were comparable across all animals in the analysis, including the sire's EBV that were directly comparable across-breed. Listed in Annex B and C are the project generated across-breed research EBVs using genetic parameters and models determined in the univariate analyses above for all the new traits recorded in the project. However, for completeness a few key BREEDPLAN traits were also included for traits where the data were predominantly recorded in the reference populations *viz.* gestation length, birth weight, weaning weight (direct and maternal), carcase weight and shear force.

These across-breed research EBVs produced by the project are a very unique set of results and a major achievement of the project. The genetic merit described by the EBVs are across a large range of growth, reproduction, carcase and meat quality traits and captures both the within breed and between breed genetic differences in a single EBV. For some traits the between breed differences are quite large (e.g. coat length score), whereas for many other traits the within breed variation was larger than any breed differences.

In recent years the experimental design of the project was expanded to include new sire breeds. The first was an international benchmarking initiative using the US Beefmaster breed. This is a stabilised tropical composite breed developed primarily in Texas and has a long history of performance recording. A sample of sires were used in AI over project Droughtmaster cows. Subsequently, the progeny have been backcrossed to both Droughtmaster and Beefmasters. All progeny are performance recorded head-to-head with other breeds and all data submitted to the Droughtmaster BREEDPLAN evaluation. Also as part of an industry initiative to benchmark Brahmans from Australia with South Africa & Namibia the progeny of four nominated link sires that were generated in Phase 1 of the project continued to be recorded for their maternal traits and progeny performance in this phase of the project.

In 2023, the AI matings included Angus and Hereford sires mated to Brahman cows to generate the F1 progeny. Although only small numbers of progeny exist at this stage it is expected these numbers will increase in future years. The experimental design will also allow the future pooling of data from the Grafton site of the Southern Multi-breed Project data, through the use of common Angus, Hereford and Brahman

sires across the two projects. The performance of the F1 progeny in this project have been recorded head-to-head with Brahman, Droughtmaster and Santa Gertrudis and the first cohort of steers have gone to the Northern Steer BIN project. All F1 females have been retained and will be recorded for puberty and mated to generate reproduction records. It is planned the Angus F1 will be mated to BREEDPLAN recorded Brangus sires and the F1 Herefords to BREEDPLAN recorded Braford sires.

4.2.3.2 Heifer and bull traits – NTDPI herd

Across-breed research EBVs from NTDPI herd for male traits (*viz.* sperm morphology and scrotal circumference measured at yearling and 18 months) are presented in Appendix 9.3.1. for sires with accuracy greater than 60%. The EBVs show a large spread however there was clear overlap of the Brahman and NT Tropical Composite breeds for all four traits. Brahman sire DRF16764M and TCOMP sire DRF30902 were superior for all four EBVs.

Heifer data from NTDPI herd was extracted to construct a phenotype for heifer age at puberty. This included a combination of ovarian scans taken before or early in the mating season as well as pregnancy test and foetal age data. However, it is important to note that this was not the same trait as DAF herds due to the age at puberty phenotype being generated from significantly less frequent ovarian scanning and with a greater reliance on foetal ageing results. This occurred due to the constraints of mustering during wet season in this site over both Phase 1 and this project. The data in this project also included phenotypes from NT Tropical Composite that were relocated to the Douglas Daly research farm and run with the selected Brahmans.

Two analyses were performed using the age at puberty data, the first used all Brahman data across both phases of the project to generate the largest possible dataset to estimate genetic parameters. The second analyses were just the data from this phase of the project that included the Brahmans and the NT Tropical Composite that were managed as contemporaries. Fixed effects models for each trait and dataset were developed in SAS and included all main effects and all first-order interactions. Final models for full Brahman data included: cohort, origin, birth-month and cow-age-group and interactions. The same effects were significant for the pooled breed dataset however cow-age-group was not significant ($P>0.05$).

Table 17. Genetic parameters for heifer age at puberty for NTDPI breeds from two dataset

Dataset	Model	V_A	V_E	h^2
All Brahman		6,332	9,413	0.40 (0.06)
Brahman & NT TCOMP	With breed	4,414	8,127	0.35 (0.06)
	Without breed	4,320	8,329	0.34 (0.06)

Results in Table 17 show heifer age at puberty was moderately heritability in both datasets, with a larger additive variance in the Brahman only dataset compared to the pooled breed dataset. These estimates are lower than age at puberty from Beef CRC and Repronomics DAF herds, most likely reflecting the reduced precision in recording the trait.

Project across-breed research EBVs for sires with daughters with an age at puberty record from the pooled breed analysis are presented in Appendix 9.3.2 and show a spread in EBVs from -103 days to +173 days in these Brahman and NT Tropical Composite populations.

4.1.4 Calf losses

Calving records from all 2020 to 2024 born calves at DAF locations and calf losses were collated and percentage of losses computed for a total of 384 dead calves. This equated to an 8.7% calf loss which was similar to the long term average of about 10% in northern Australia. Figure 4a shows the proportions of all reported losses, and Fig. 4b gives the ratios for the subset of losses from known/preventable causes. Clearly, deaths associated with

dystocia was the major cause of losses and highlights the need for recording the trait or correlated traits (e.g. birth weight and gestation length) in genomic reference populations. This would allow selection pressure to be placed on these traits, especially as tropical breeds continue to select for higher growth rates.

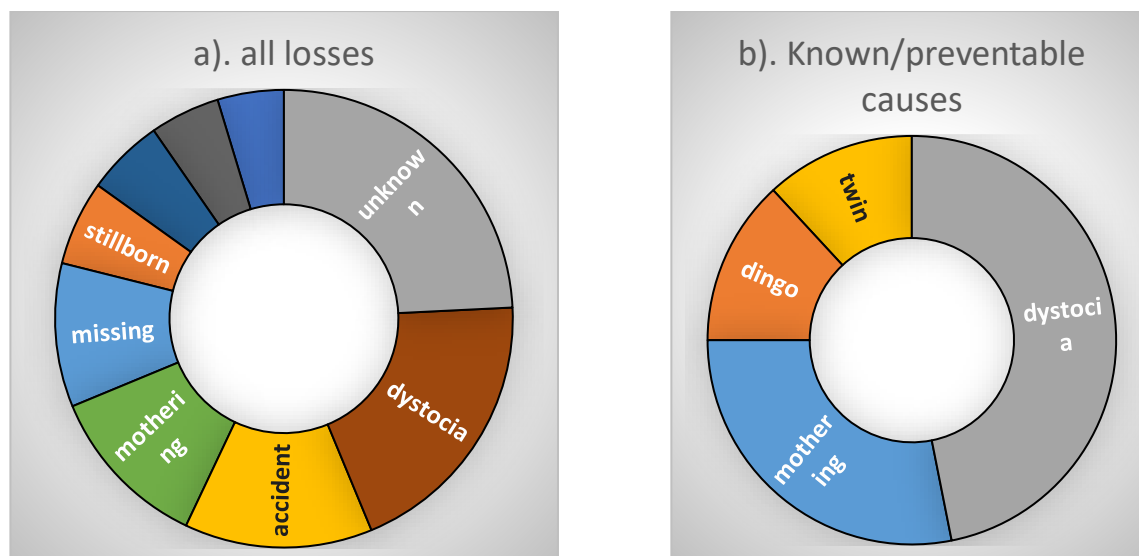


Figure 4. Percentage cause of calf losses a). all and b). known/preventable cause in project recorded calves

4.3 Project impact

The primary objective of the project was to build and deliver effective genomic evaluation for northern Australia. For this to be achieved both bull buyers and breeders need to be able to access more genetically described animals, with higher accuracy EBVs for the main tropical beef breeds used in northern Australia. This project has achieved this through the increased capacity of Brahman, Droughtmaster and Santa Gertrudis (i.e. the three most numerically popular breeds) to genetically evaluate animals through their single-step genomic BREEDPLAN evaluations. This was particularly important for young sale bulls, many of which now have genomics-only generated EBVs. The single-step evaluations also provides the opportunity for herds to genetically benchmark themselves and this gives them the power to identify future herd improvers based on a full suite of trait EBVs and \$Indexes. The improved EBV accuracies across the full range of economically important traits is also enabling seedstock herds to make faster rates of genetic progress, which can now be achieved with better balance across traits in the breeding objective. This is a direct result of the increase in accuracy for key profit EBVs (many of which were of low accuracy) which the phenotypes and genotypes collected as part of this project, combined with the recently implemented single-step evaluation for tropical breeds, has enabled.

4.3.1 Improved EBV accuracies

A series of full BREEDPLAN single-step evaluations for each of the three breeds were performed to quantify the effect of the project data (both phenotypes and genotypes) on their evaluations. To achieve this all records on animals from both Phase 1 and this project were removed from the evaluations of each of the three breeds, this included the removal of their genotypic data (i.e. all project animals removed from the breed's GRM). However, removing all genotypes on sires with progeny in the project and those genotyped by the project in Industry herds was not possible. This means the results presented are likely an underestimate of the total impact of the project on the genetic evaluations of the three breeds. Also not valued was the benefits the project has had on improving across-herd linkage, critical for enabling accurate comparison of animals across herds. Statistics were generated on the changes in all trait EBVs and accuracies for all animals but the crucial subset of animals to examine were those included in the evaluation

with a SNP genotype. Changes in their EBVs and accuracies generated through the single-step evaluations will quantify the contribution of the project data to the genomic reference population of each breed.

- a) **Brahman.** Brahman was the breed with the largest number of animals genotyped (total in GRM=66,643) and also the largest breed in the project. The analyses showed that the inclusion of the project data had little effect on EBV means (Table 18) of these animals, indicating the project data did not introduce any bias in their EBVs. However, the addition of the project data did increase the standard deviations of most traits (Table 18) resulting in a greater spread in trait EBVs.

Table 18. Brahman single-step EBVs for genotyped non-project animals (N=61,938) without (NO) and with (WITH) inclusion of project data in the analyses

EBV*	NO project data				WITH project data			
	mean	std	min	max	mean	std	min	max
GL	-0.93	2.00	-8.9	8.5	-0.77	2.07	-11.2	9.3
BW	2.46	2.39	-7.5	10.5	2.49	2.73	-8.2	11.7
WW	20.36	9.41	-30.3	56.1	20.03	9.85	-32.5	58.1
YW	27.57	11.76	-27.4	76.7	27.34	11.97	-26.2	78
FW	38.12	16.16	-43.2	106.3	38.02	16.44	-43.2	111.1
MCW	43.7	28.34	-92	160.3	43.12	29.11	-91.5	170.5
GLM	0.02	0.28	-1.2	1.1	0.1	0.31	-1.7	1.5
BWM	0.08	0.84	-2.3	3.4	-0.01	0.84	-2.7	4.4
WWM	-0.7	2.52	-26.1	12.5	-0.65	2.58	-26.5	12.6
ScS	0.71	1.27	-3.7	6.9	0.68	1.31	-3.6	6.9
DTC	-1.57	9.09	-38.8	23.5	-1.13	9.60	-40	26
HIM	0.13	0.13	-0.5	0.7	0.12	0.16	-0.5	0.9
HEA	2.49	1.69	-5	9.9	2.52	1.74	-5.3	10
HRF	0.05	0.52	-1.9	3.2	0.03	0.58	-2	3.1
HP8	0.06	0.82	-3.6	4.5	0.03	0.94	-3.6	4.5
BEA	2.32	1.70	-6.8	10.1	2.3	1.73	-6.5	10.3
BRF	0.08	0.23	-1	1.3	0.08	0.25	-1	1.4
BP8	0.2	0.45	-2.2	2.6	0.19	0.47	-2.1	2.7
CWT	26.46	12.37	-40.1	76.3	24.96	12.77	-40.3	74
CEA	2.25	1.93	-7.3	12.3	2.22	2.13	-7.6	12.7
CP8	-0.41	1.39	-5.7	6.6	-0.48	1.44	-5.8	6.5
CRF	-0.42	0.95	-3.9	4.4	-0.35	1.02	-3.8	4.4
CMY	0.66	0.53	-3.2	3.2	0.52	0.57	-3.3	3.5
CIM	-0.02	0.23	-1	1.5	-0.08	0.26	-1	1.4
SHF	0.06	0.19	-0.69	1.32	0.07	0.23	-0.72	1.26
FLT	0.00	0.09	-0.54	0.69	0.00	0.10	-0.53	0.68
PNS	0.35	4.74	-15.4	19.2	0.44	5.56	-17	23.3
AP	-13.97	54.36	-204.6	140.1	-13.62	67.62	-276.9	184.3
LAI	-1.25	25.91	-103.6	95.7	0.14	31.75	-125.7	107.5

*birth weight (BW), gestation length (GL), 200d weight (WW), 400d weight (YW), gestation length maternal (GLM), birth weight maternal (BWM), 200d weight maternal (WWM), 600d weight (FW), cow weight (MCW), bull ultrasound rib fat (BRF), P8 fat (BP8), eye muscle area (BEMA), intramuscular fat percent (BIMF), heifer ultrasound rib fat (HRF), P8 fat (HP8), eye muscle area (HEMA), intramuscular fat percent (HIM), days to calving (DTC), abattoir carcass weight (CWT), rib fat (CRF), P8 fat (CP8), eye muscle area (CEA), intramuscular fat (CIM), retail beef yield (CMY), shear force (SHF), scrotal circumference (ScS), heifer age at puberty (AP), flight time (FT) and percent normal sperm (PNS), heifer age at puberty (AP), lactation anoestrous interval (LAI)

The changes observed in the EBV accuracies in this subset of animals is presented in Fig. 5 and shows the inclusion of the project data increased the accuracy of all trait EBVs. Results showed relatively large increases in average accuracies were observed for gestation length of 8 units (18% increase), days to calving of 10 units (23% increase), heifer age at puberty of 18 units (48% increase) and lactation anoestrous interval of 15 unit (48% increase). The average accuracy of this subset when the project data was included for the days to calving EBV was 52.5%. The increased accuracies reflects the large amount of recording of those traits in the project. However, for traits not recorded (e.g. scrotal size, retail beef yield) they showed only slight increased changes in accuracies, generated from correlated traits.

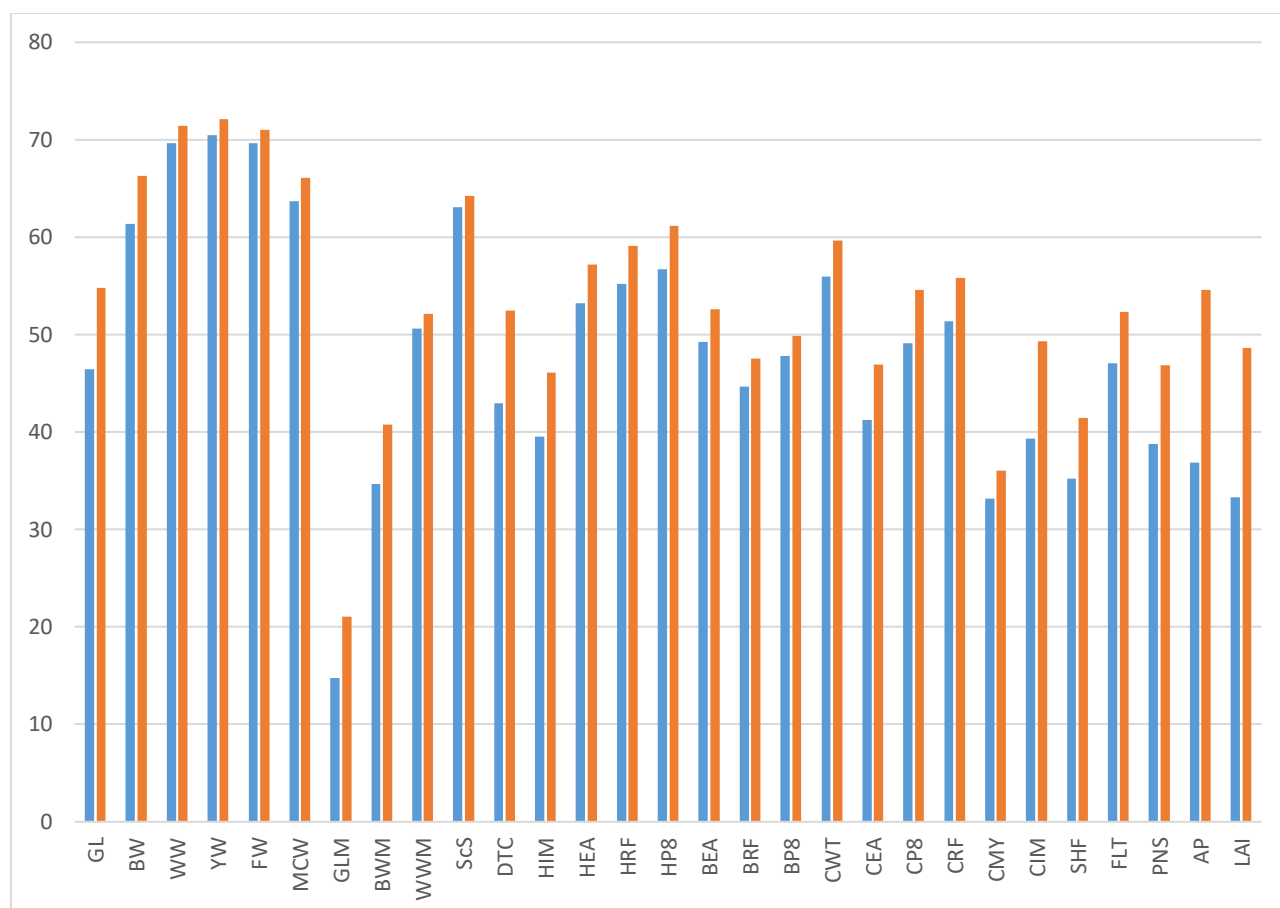


Figure 5. Brahman single-step EBV accuracies for genotyped (N=61,938) non-Repronomics animals without (blue) and with (orange) inclusion of project data in Brahman BREEDPLAN analyses (see Table 18 for trait descriptions)

- b) **Droughtmaster.** Droughtmaster was the breed with the smallest number of animals genotyped (total in GRM=10,245) but were also a large breed in the project. For the subset of genotyped non-project Droughtmaster animals (N=5,519) the changes in mean EBV (Table 19) were very slight but the change in EBV standard deviation were large for many traits, especially for those recorded in this project. Fig. 6 shows the large impact of the project data on most trait accuracies. For example, birth weight showed a 13.3 unit accuracy increase (36% increase), days to calving 13.8 units (56% increase) and heifer age at puberty 28 units (1175% increase). Clearly, the results for Droughtmaster show the project data has been pivotal on the implementation and outcomes achieved from single-step BREEDPLAN for this breed.

Table 19: Droughtmaster single-step EBVs for genotyped non-project animals (N=5,519) without (NO) and with (WITH) inclusion of project animals in BREEDPLAN analyses

EBV*	NO project data				WITH project data			
	mean	std	min	max	mean	std	min	max
GL	-0.08	0.31	-2	2.9	-0.2	1.00	-4.5	5.2
BW	0.10	0.82	-5.5	3.8	-0.09	1.25	-5.8	6
WW	12.68	5.02	-12.4	34.8	11.68	5.52	-8.6	39.6
YW	19.37	7.39	-17.3	55	18.58	7.78	-16.4	53
FW	26.77	12.52	-32.3	86	25.76	13.02	-30.2	80.8
MCW	25.27	13.94	-70.4	88.3	26.06	16.32	-68.6	92.9
GLM	-0.02	0.06	-0.5	0.3	-0.11	0.2	-0.7	1.9
BWM	-0.08	0.26	-2.4	1.9	-0.18	0.41	-3.6	2.7
WWM	5.25	2.12	-3.5	15.7	4.95	2.3	-5.7	14.4
ScS	1.37	0.66	-1.6	4.8	1.33	0.72	-1.2	4.7
DTC	0.62	2.29	-20.7	12.4	0.26	3.44	-18.2	12.7
HIM	0.04	0.22	-0.7	1.5	0.02	0.26	-0.7	1.6
HEA	1.04	1.85	-5.5	11.8	0.82	2.15	-6	12.1
HRF	0.01	0.22	-0.7	1.7	-0.02	0.3	-1	2
HP8	0.04	0.37	-1.4	2.6	0.01	0.55	-1.8	2.7
BIM	0.00	0.12	-0.4	0.7	0.00	0.13	-0.4	0.8
BEA	0.70	1.3	-4.3	7.4	0.58	1.51	-4.2	7.9
BRF	0.01	0.16	-0.6	1.0	-0.01	0.21	-0.7	1.2
BP8	0.00	0.3	-1.3	2.1	-0.03	0.39	-1.3	2.1
CWT	14.98	6.72	-29.8	44.8	14.5	6.54	-23.9	40.9
CEA	1.03	1.02	-2.7	6.1	0.94	1.52	-3.6	7
CP8	-0.08	0.67	-3.5	4.5	-0.17	0.94	-3.4	4.2
CRF	-0.06	0.57	-2.7	3.8	-0.14	0.76	-2.8	3.7
CMY	0.59	0.33	-1.3	2.5	0.64	0.43	-1.4	2.7
CIM	-0.03	0.2	-0.7	1.5	-0.05	0.26	-0.9	1.9
SHF	0.01	0.06	-0.64	0.6	0.01	0.14	-0.5	0.69
FLT	-0.01	0.03	-0.25	0.2	0.00	0.07	-0.37	0.3
AP	-1.32	9.3	-144.2	106.2	0.53	25.84	-139.4	125.4
LAI	-1.4	6.22	-90.9	70.5	-4.02	12.95	-76.8	66.2

* see Table 18 for trait descriptions

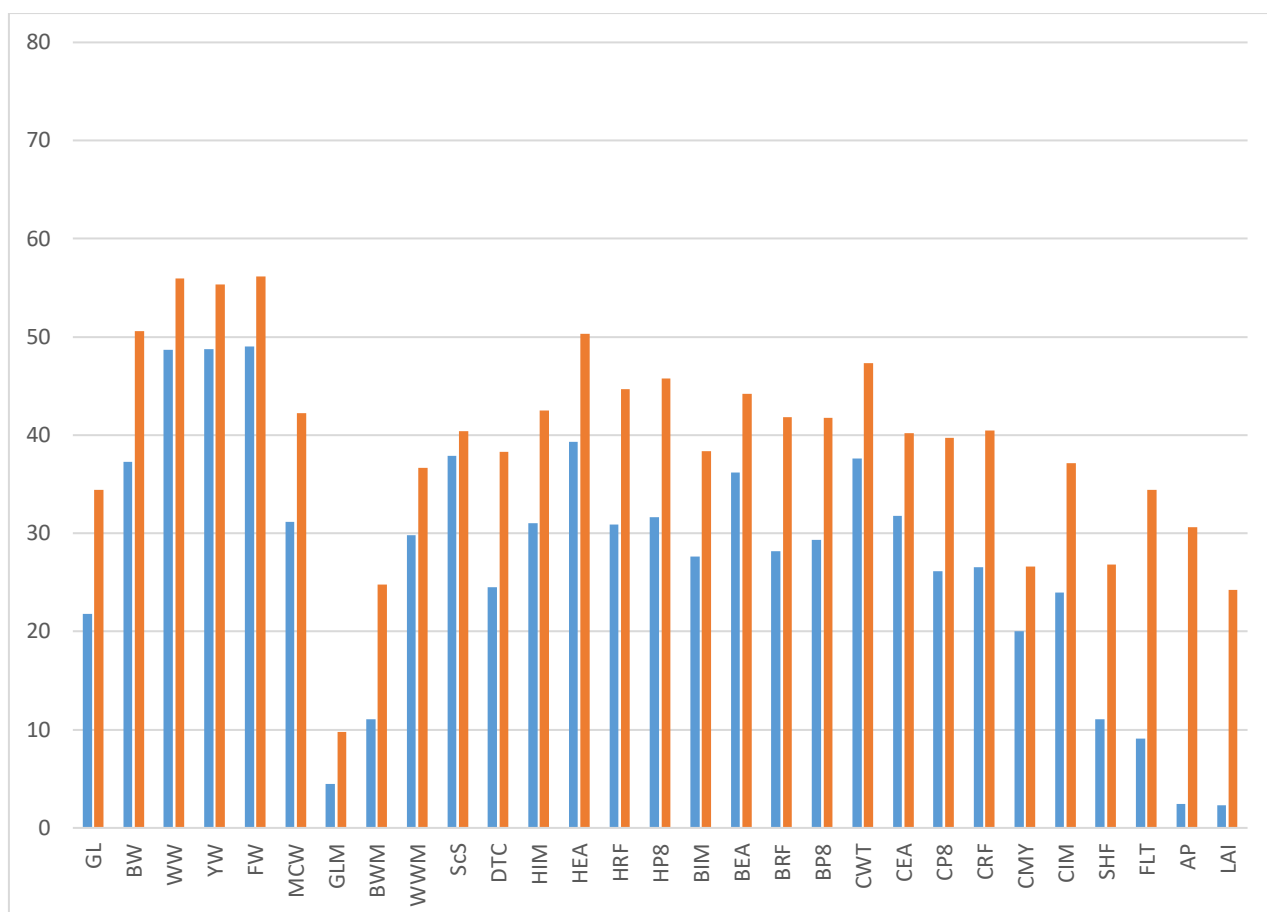


Figure 6. Droughtmaster single-step EBV accuracies for genotyped (N=5,519) non-project animals without (blue) and with (orange) inclusion of project data in Droughtmaster BREEDPLAN analyses (see Table 18 for trait descriptions)

- c) **Santa Gertrudis.** Santa Gertrudis was the breed with the smallest number of animals in this project, and had relatively larger numbers of animals genotyped in industry compared to other breeds. The analyses showed for non-Repronomics genotyped animals (10,267) the changes in mean EBV (Table 20) and standard deviations were only very slight. Trait accuracies in Fig. 7 shows some small to modest impacts of the project (between 3-8 accuracy units) for example, gestation length had a 4.0 unit accuracy increase (11% increase), days to calving 2.8 units (5.4% increase) however larger increases were observed for heifer age at puberty 7.5 units (31 % increase) and lactation anoestrous interval 3.7 units (13% increase). Figure 7 shows the average EBV accuracies of this group of animals were already relatively high across most traits and this is likely to be due to the herds genotyping were herds that were also good performance recorders. Thus the impact of the project data on these animal's EBVs was expected to be only small. Overall the impact of the project data on the Santa single-step evaluation was small to modest, and reflects the small size of the current reference.

Table 20: Santa Gertrudis single-step EBVs for genotyped non-project animals (N=10,267) without (NO) and with (WITH) inclusion of project animals in BREEDPLAN analyses

EBV	NO project data				WITH project data			
	mean	std	min	max	mean	std	min	max
GL	-0.23	0.87	-6.4	3.1	-0.39	1.07	-6.8	4.3
BW	1.65	1.42	-4	7.7	1.51	1.57	-5.1	7.5
WW	13.59	6.69	-12.6	40	12.58	6.75	-12	38.2
YW	20.45	9.63	-18.8	59	19.66	9.60	-15.7	54.3
FW	28.79	13.64	-25.6	76.1	27.22	13.64	-23	74.3
MCW	37.86	22	-66.5	123.1	35.91	22.33	-69.7	122
GLM	-0.04	0.24	-0.9	0.8	-0.08	0.3	-1.3	1.1
BWM	-0.12	0.36	-1.5	1.8	-0.12	0.43	-2.1	2.1
WWM	0.49	2.78	-14.5	11.2	0.01	2.92	-15.9	10.6
ScS	1.21	0.99	-3.1	4.9	1.12	1.00	-3.7	5.1
DTC	-3.51	6.94	-29.2	26.6	-2.94	6.58	-27.2	25.7
HIM	0.29	0.43	-1.3	1.9	0.27	0.43	-1.3	1.9
HEA	3.1	2.13	-4.6	11.6	2.84	2.21	-5.4	11.3
HRF	0.33	0.4	-1.2	2.3	0.29	0.4	-1.2	2.3
HP8	0.81	0.71	-2.3	4.1	0.75	0.73	-2.4	4.4
BIM	0.13	0.29	-0.8	1.3	0.13	0.29	-0.9	1.3
BEA	3.58	2.36	-6	12.9	3.32	2.41	-6.9	13.3
BRF	0.12	0.25	-0.8	1.2	0.11	0.25	-0.8	1.3
BP8	0.52	0.5	-1.6	2.7	0.5	0.51	-1.6	3
CWT	12.39	6.62	-22.4	35.6	11.44	6.83	-23.3	35.8
CEA	2.46	1.43	-3.2	8.5	2.38	1.53	-5.3	11.1
CP8	0.17	1.18	-4	6.5	0.25	1.25	-4.5	6.7
CRF	0.54	0.96	-3	5.5	0.54	0.99	-3.1	5.6
CMY	0.72	0.61	-1.7	3.1	0.67	0.65	-1.8	3.5
CIM	0.14	0.35	-1.2	1.5	0.14	0.36	-1.2	1.5
SHF	0.1	0.11	-0.41	0.53	0.1	0.15	-0.65	1.1
FLT	0.07	0.17	-0.62	0.78	0.07	0.17	-0.58	0.78
PNS	1	3.72	-18	14.5	0.95	3.93	-17.9	14.2
AP	-24.08	37.74	-168.4	130.6	-19.47	36.32	-154.7	153.8
LA	-23.47	32.74	-148.7	110.7	-20.04	30.31	-130.1	101.6

* see Table 18 for trait descriptions

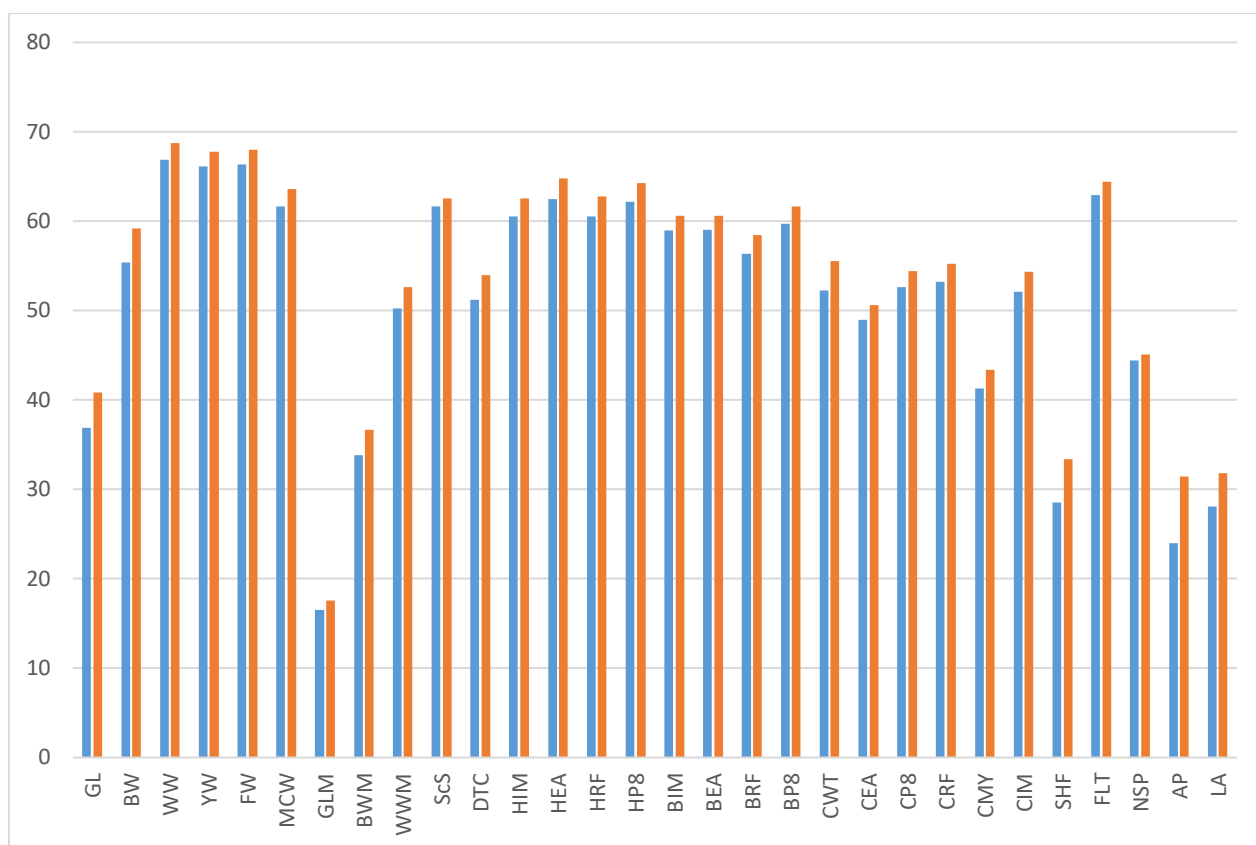


Figure 7. Santa Gertrudis single-step EBV accuracies for genotyped (N=10,267) non-project animals without (blue) and with (orange) inclusion of project data in Santa Gertrudis BREEDPLAN analyses (see Table 18 for trait descriptions)

4.3.2 Impact of single-step genomic evaluations

Data from this project has been pivotal in the implementation of BREEDPLAN single-step evaluations of the three breeds (as demonstrated in section 4.3.1). To further examine the benefits of the inclusion of genomics in the evaluations of each breed a series of analyses were performed (in conjunction with MLA project L.GEN.2204) to quantify the benefits of single-step evaluations compared to previous pedigree-based evaluations. Results were prepared for an invited AAABG paper and industry presentation (Johnston *et al.* 2023). LR forward-validation procedures (Legarra and Reverter 2018) were used to compare population statistics for single-step versus convention pedigree evaluations. Results for Brahman and Santa Gertrudis are presented in Appendix 9.3.1 and show the improvements in population accuracies averaged across all traits in the evaluation as 13% and 5% for Brahman and Santa Gertrudis, respectively. Critically, the improvement in the days to calving EBV was 24% and 12%, respectively. These results show the impact that genomics is having in the single-step evaluations of the two breeds, and highlights the opportunity that exists to further increase accuracies (and spread in EBVs) through building the size of the reference populations for these breeds. The results do not include Droughtmasters because at the time these analyses were done they had not yet implemented single-step BREEDPLAN.

4.3.3 Industry uptake

In most modern livestock breeding programs, genetic improvement is generated in the nucleus sector and genetically superior animals are then multiplied through commercial tiers of the industry. This model exists in the Australian beef industry with bull/seedstock breeders undertaking selection and their genetics are disseminated to the commercial sector, generally through the sale of young 1-3 year old bulls. In the north of

Australia this structure often includes an additional bull-multiplier tier. For the beef industry to make genetic progress it relies on the ability to predict the genetic merit of selection candidates, and the rate of genetic progress is linear to the accuracy and the generation interval. Therefore the key to the beef industry making genetic improvement is increasing the accuracy of the EBVs of all selection candidates, many of which in the north are effectively zero because they don't have EBVs, especially if herds are breeding their own bulls.

This project and the advent of single-step evaluations is assisting the adoption of genetic evaluation resulting in more bulls evaluated with increased EBV accuracies (as shown in the previous section). This was clearly evident in the recently completed bull selling season across the north. The national sale of Brahman (the Rockhampton Brahman Week Sale) catalogued 828 bulls and of those all but three bulls (99.6%) were presented with the female reproduction days to calving EBV and with the full suite of other EBVs. The majority of these sale bulls had genomics-only generated EBVs. This is a resounding success and reflects the outputs of this project and the efforts of the management of Australian Brahman Breeders' Association and their members. Likewise, the Droughtmaster National sale catalogued a total of 453 bulls and of these 193 (43%) had a days to calving EBV. Whilst this seems relatively low, it is quite impressive given all previous years the percentage was zero. On the back of this project along with the industry adoption of genotyping and single-step, the Droughtmaster bull buyers had access to this critical female reproduction EBV for the first time, and again the vast majority were bulls with genomics-only generated EBVs. The availability of single-step BREEDPLAN is enabling more bulls at younger ages with higher accuracies and this was also being observed in the Santa Gertrudis breed.

4.3.4 Scientific publications

- Campbell J. Johnston, D. J. (2022) Genetics of heifer puberty and growth in tropically adapted beef breeds In: Proceeding of the 34th Biennial Conference of Australian Association of Animal Sciences, Cairns, Queensland 5-7 July, pp. lxiii-lxiii
- Grant T. and Johnston, D. J. (2022). Poll genotype or phenotype are not associated with growth performance in tropical beef breeds. Proceeding of the 34th Biennial Conference of Australian Association of Animal Sciences, Cairns, Queensland 5-7 July, pp. lxxvi
- Hubbard K., J. Campbell, T. Grant, D. Johnston, K. Moore (2023) The effect of nitrogen use efficiency on productivity in tropical beef. In proceeding North Australia Beef Research Council Conference. 6: 59
- Johnston D. J., Dayman, M., Grant, T. P., Hubbard, K., Goodwin, K., Doughty, A. K. and Cook, J. A. (2023) Remote sensor collars measure age at puberty in tropical beef heifers in northern Australia, pp. 246
- Moore K. L., Johnston D. J., Grant T. P. (2023) An investigation into potential genetic predictors of birth weight in tropically adapted beef cattle in northern Australia. *Animal Production Science* 63, 1105-1112.
- Moore K. L, D.J. Johnston, and Tim Grant (2025a) Myostatin alleles are segregating in Australian Droughtmaster and Santa Gertrudis populations but not in Brahman. *Proc. Assoc. Advmt. Anim. Breed. Genet.* 25: (submitted)
- Moore K. L, D. J. Johnston and T. P. Grant (2025b) Gestation length is highly heritable and could indirectly reduce birth weight without impacting the weaning weight of Australian tropically adapted *Bos indicus* beef cattle. *Proc. Assoc. Advmt. Anim. Breed. Genet.* 25: (submitted)

4.3.5 Presentations and media

Over the five years of the project there have been many presentations and media coverage including conferences, breed societies (boards, tech committees, delegates meetings, forums, annual conferences) producer days, workshops, and seminars. The project has had coverage in rural newspapers, Beef Central, breeder's websites, podcasts and regional radio. The most important presentations are listed below:

- Cloncurry Genetics Muster 2021.
- Invited US Beef Improvement Federation presentation 2021.
- Southern Multi-breed Project presentation - Grafton field day 2021.
- Beef2021 – Project participant’s workshop.
- Repronomics field day and Project cattle demonstrations, Gayndah 2022.
- Droughtmaster board presentation and Project cattle display, Spyglass 2023.
- BEEF 2024 - Property tour.
- BEEF 2024 – Presentation beef cattle seminar series.

4.4 Improved genetic evaluation and adoption

The primary aim of the project was to improve the genetic evaluation of the three most numerically popular tropical beef breeds in northern Australia, and in doing so, drive increased adoption of BREEDPLAN EBVs by providing accurate description of genetic merit to create opportunities for increased rates of genetic gain in key profit driver traits. This has been achieved by increasing the size of the reference population in these breeds and the inclusion of these data into the routine single-step BREEDPLAN evaluations, thus increasing the EBV accuracies particularly of genomics-only animals.

4.4.1 Single-step & numbers genotyped

This project has benefited each of the three breeds by enabling their evaluation to transition to single-step BREEDPLAN (Johnston *et al.* 2017). During the course of this project both Santa Gertrudis and Droughtmaster transitioned their BREEDPLAN genetic evaluation to genomic single-step, whereas Brahman went to single-step during the previous phase of project in 2017. As shown in section 4.3 the phenotypic data and SNP genotypes from this project have been critical to these developments. Fig. 8 below shows the steady growth in the number of animals per year genotyped and entering the Santa Gertrudis and Droughtmaster single-step BREEDPLAN evaluations.

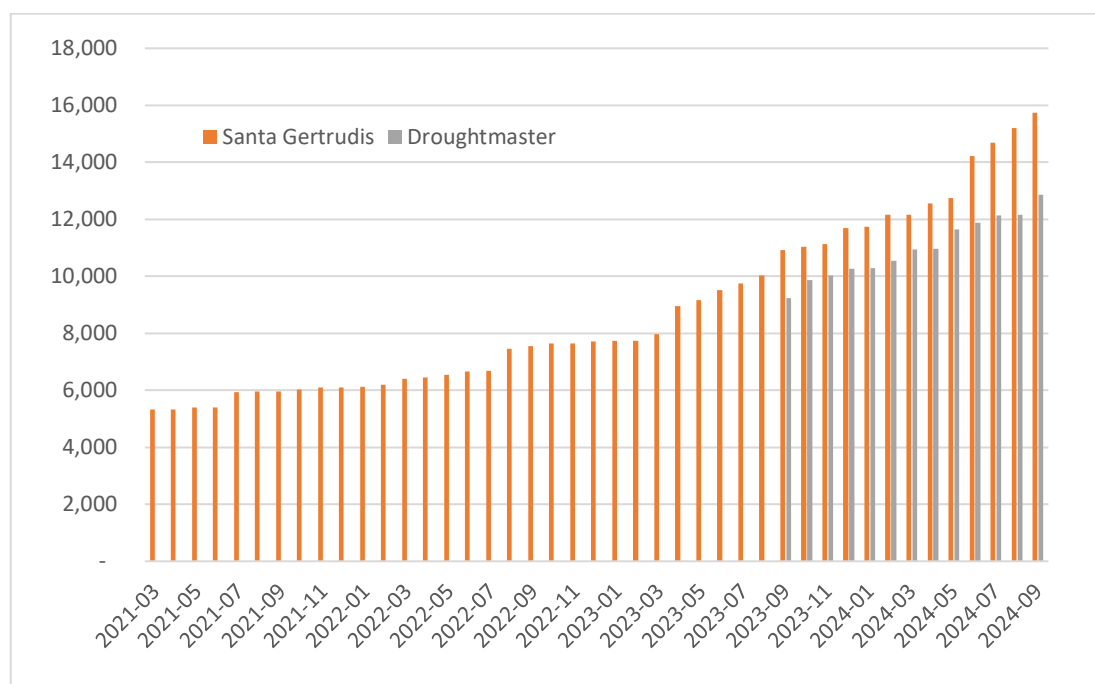


Figure 8. Cumulative numbers animals genotyped in Droughtmaster and Santa Gertrudis single-step evaluations during the period of this project

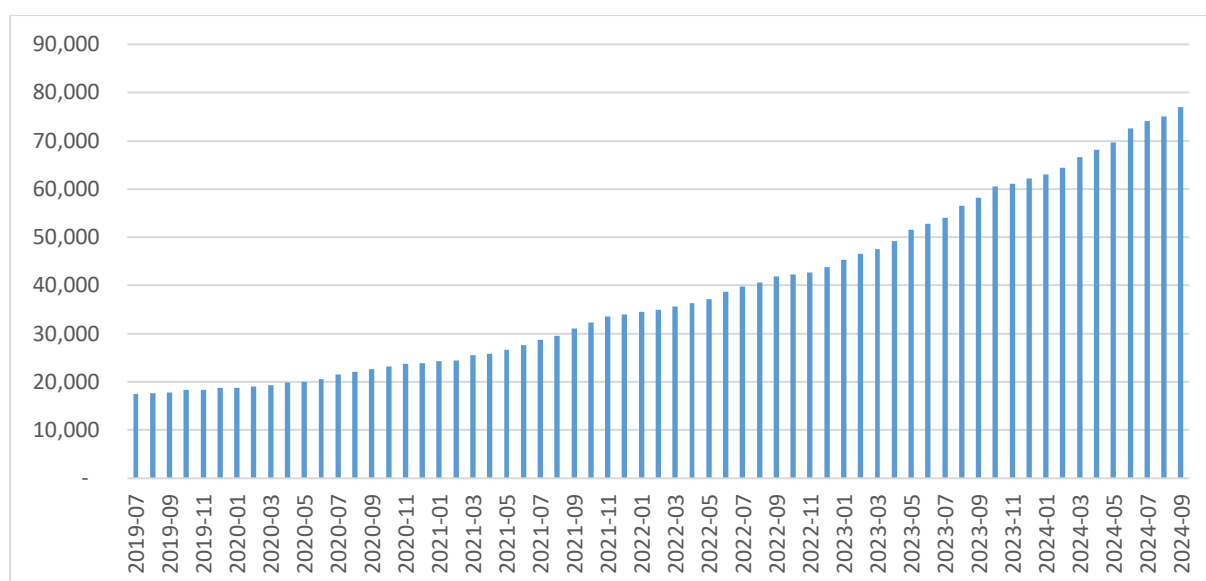


Figure 9. Cumulative numbers animals genotyped in Brahman single-step evaluations during period of this project

Brahmans commenced single-step BREEDPLAN in 2017 and Fig. 9 shows that during the period of this current project the amount of SNP genotypes going into their evaluation has grown exponentially. These plots provides a direct metric for the adoption of SNP genotyping by industry and the increased use of the genomic BREEDPLAN. However, the value proposition for further (increase rates) genotyping relies on the inherent value placed on EBV accuracies generated from each of the single-step evaluations.

The large amount of genotyping undertaken by this project represents an increasingly large sample of the breeds' current genetics. This data will also be benefiting the single-step evaluation by providing additional SNP data to allow the re-estimation of each breed's genomic profile that will better define genomically the population (as part of MLA L.GEN.2204 genomic pipeline).

4.4.2 Improved BREEDPLAN EBVs

- a) **Data and linkage.** This project has led to improved BREEDPLAN EBVs directly as a result of the large volumes of project phenotypic data across the range of traits submitted into each breed's evaluation. This has been critical data for several EBVs that have recently been included in the routine evaluations of the three breeds, including gestation length, birth weight, flight time, shear force and, critical for Droughtmaster, the addition of the days to calving EBV. The project data also provides head-to-head comparisons of genetics from large numbers of studs for each breed. This generates direct genetic linkage across herds that benefits the whole evaluation in its ability to accurately partition non-genetic effects, thus allowing more robust comparison of genetics across herds.

The project recording also directly benefits the EBVs of all the sires used in the project. The breadth of recording on large numbers of progeny have resulted in increased accuracy across the full range of EBVs for some very influential sires in each breed. Fig. 10 shows the webpage listing all Brahman Repronomics sires. This is easy for breeders to access and shows the large number of bulls used, their EBV, their accuracies and \$Indexes.

Brahman Animal Listing

REPRONOMICS PROJECT - LIST ONLY NOT FOR SALE

[Search/Sort Catalogue](#)
[Home](#) [Animal Enquiry](#) [EBV Enquiry](#) [Mating Predictor](#) [Member Enquiry](#) [Sale Catalogues](#) [Semen Catalogues](#) [Download Files](#) [Online Registrations](#)

October 2024 Brahman BREEDPLAN																			
Name/ID	Gestation Length (days)	Birth Wt. (kg)	200 Day Wt. (kg)	400 Day Wt. (kg)	600 Day Wt. (kg)	Mat. Corr. Wt. (kg)	Milk (kg)	Scrotal Size (cm)	Days to Calving (days)	Carcass Wt. (kg)	Eye Muscle Area (sq.cm)	Rib Fat (mm)	Rump Fat (mm)	Retail Beef Yield (%)	DME (%)	Percent Normal Sperm (%)	Flight Time (secs)	Shear Force (kg)	Central Production Index (\$)
CBV 11-9090 TOM BONUS (H)	-1.0 52%	+6.6 88%	+44 88%	+57 88%	+95 90%	+126 87%	+5 83%	+5.0 80%	-13.2 78%	+49 83%	-0.6 75%	-1.6 74%	-1.1 79%	+0.9 55%	0.0 68%	+1.2 41%	+0.01 80%	-0.48 74%	+\$ 129
LANCERFIELD M 2708/M (AD) (H)	-0.7 53%	+8.6 89%	+43 87%	+54 87%	+85 89%	+115 87%	+1 78%	-0.8 57%	+9.6 79%	+42 78%	+7.0 67%	-2.8 68%	-2.9 79%	+1.6 46%	-0.7 60%	-1.3 25%	+0.11 85%	-0.17 71%	+\$ 56
HAZELTON B SIR ANGELO 1895 (ET) (H) 	+0.7 78%	+9.2 86%	+45 88%	+50 90%	+79 92%	+95 86%	-3 61%	+0.4 59%	+7.7 77%	+44 86%	+1.4 81%	-2.4 82%	-2.5 86%	+1.1 50%	-0.9 76%	+2.1 30%	+0.29 87%	-0.34 80%	+\$ 49
FBC BECKER 191/1 (H) 	+2.5 77%	+7.6 89%	+38 94%	+58 94%	+78 94%	+98 90%	+1 87%	-1.1 62%	+4.3 80%	+35 88%	+5.3 78%	+0.2 80%	+0.1 85%	+0.8 56%	-0.4 74%	-0.3 26%	0.00 87%	+0.39 79%	+\$ 58
ROCKLEY LP ETHERIDGE (IVF) (PS) 	-1.0 85%	+4.8 91%	+36 91%	+56 92%	+73 93%	+103 91%	-3 76%	+1.8 78%	-0.7 82%	+43 87%	-1.1 82%	-1.9 82%	-4.6 87%	+1.4 54%	-0.5 76%	+0.4 43%	+0.32 89%	-0.29 82%	+\$ 77
MUAN A BRUTUS 7370 (PS) 	-0.8 33%	+5.5 51%	+35 56%	+54 55%	+72 57%	+88 52%	-1 37%	+0.3 44%	+3.8 42%	+41 47%	+4.4 41%	-1.6 40%	-1.1 49%	+1.4 26%	-0.3 35%	- -	-0.07 46%	+0.05 41%	+\$ 65
FBC GARTH MANSO 537/1 (H) 	+1.6 86%	+7.0 92%	+36 93%	+47 94%	+70 95%	+95 92%	-3 79%	-1.2 64%	+16.0 84%	+42 88%	+3.5 84%	-3.3 81%	-5.0 86%	+1.7 56%	-0.8 76%	-1.1 29%	-0.09 89%	+0.31 82%	+\$ 28
KENROL DARBOCCA 2761 (PP) 	+2.6 86%	+9.1 91%	+40 88%	+56 89%	+69 89%	+106 79%	0 41%	+0.5 51%	+7.7 46%	+42 70%	+5.2 52%	-3.1 52%	-5.2 69%	+1.2 35%	-0.3 42%	-3.1 25%	-0.05 86%	-0.43 60%	+\$ 30

Figure 10. BREEDPLAN webpage that lists Brahman sires used in Repronomics (source: <https://abri.une.edu.au/online/cgi-bin/>)

b) Genetic parameter estimation. The project data has been pivotal in increasing the precision and scope of routine genetic parameter re-estimation that occurs periodically for each breed as part of MLA L.GEN.2204. The volume, structure and the breadth of trait recording in the project directly benefits the genetic evaluation by providing more accurate genetic parameter estimates that underpin the BREEDPLAN evaluations. In conjunction with the data from Northern Steer BIN project this provides unique data on ½ sib steers that allows the estimation of genetic correlations between female traits (especially reproduction traits) and steer traits (i.e. carcass and meat quality) that are critical in breeding objectives that values both female and steer traits.

c) New reproduction module. The current and previous project have been important in the development of a BREEDPLAN reproduction module as part of MLA L.GEN.2204. The knowledge of the reproduction traits and the large volume of structured data from this project has helped inform the design of this new module, including trait definitions, required fixed effects and trait configurations. It is likely new EBVs published for northern BREEDPLAN breeds will be the same definition and data presented in this report (e.g. heifer age at puberty).

Research undertaken around modelling and estimation of variance components for percent normal sperm from the NT herd to account for censoring on yearling scrotal culling/no sample will also benefit the BREEDPLAN evaluation. Issues of potential data quality identified with crush-side assessments also highlights need for data scrutiny from industry with emphasis on the importance of lab assessment of sperm morphology.

d) BREEDPLAN multi-breed EBVs. The project data has been used as the model dataset for the first research into the development of BREEDPLAN multi-breed EBVs as part of MLA L.GEN.2204. This project design, management and levels of recording and genotyping makes it ideal for this task. The genetics used are highly represented in each breed's evaluations and the head-to-head management of breeds maintained through the whole project is key to the development of a multi-breed evaluation. This is further boosted by the availability of full genomics data allowing the application of the metafounder groups methodology (Legarra *et al.* 2015). Again, the research is benefiting from the Santa Gertrudis and Droughtmasters being composite breeds of Brahman and their SNP profiles revealing shared genomics that will not be captured by pedigree.

4.4.3 GxE investigation

Fundamental to any national genetic evaluation is the ability to account for non-genetic effects and to compare animals across years and herds, this is achieved by removing environmental effects by having genetic linkage across herds. There is an underlying assumption when establishing a genetic evaluation for a given trait that an animal's genetic expression, while influenced by the prevailing environment, does not display re-ranking of individuals (or breeds) across environments. If it does, then the trait is experiencing what is termed a genotype by environment interaction (GxE) and if not modelled precisely, the records from each environment should be treated as a different trait. This would complicate the genetic evaluation system and make genetic selection much more complex.

The experimental design of this project through the extensive use of common genetics across locations allowed the estimation of the magnitude of GxE interactions. Of the sires listed in Appendix 9.1.1 of the Brahman and Droughtmaster sires a total of 43 AI sires and 16 natural mate sires were used across locations, and this number of sire is larger in the full dataset (i.e. when the previous Phase of the project is considered). Santa Gertrudis were not considered for these analyses because they were only used at the Brian Pastures location.

The magnitude of a GxE interaction can be estimated by treating the trait at each location as a separate trait and estimating the genetic correlation between traits. If that correlation is close to unity then there is no evidence of GxE, however if it less than one then the trait is displaying GxE, and if the correlation is below 0.80 there can be significant re-ranking of sires for the trait across locations.

4.4.3.1 GxE for birth and weaning traits

Data from birth weight (BW), gestation length (GL) and weaning weight (WW) from this project and Phase 1 were analysed to investigate the occurrence of GxE for these traits by considering the data from each location as a separate traits. That is, the data from Brian Pastures was treated as a different trait to Spyglass. There were lower numbers of records for gestation length because records were only generated from calves born from AI.

Least squares means for location are presented in Table 21 and show no significant location effect for GL but calves were significantly heavier for both birth weight and weaning weight from Brian Pastures compared to Spyglass.

Table 21: Location least squares means (LSM) and standard errors (SE) for gestation length, birth weight and weaning weight for Brahman and Droughtmaster calves born 2014-2022

Trait	variable	Location*	
		Brian Pastures	Spyglass
Gestation length (days)	N	604	1,424
	LSM	289.7 ^a	289.9 ^a
	SE	0.26	0.19
Birth weight (kg)	N	1,965	4,010
	LSM	35.2 ^a	32.9 ^b
	SE	0.21	0.18
Weaning weight (kg)	N	1,688	3,637
	LSM	194.8 ^a	187.8 ^b
	SE	2.72	1.90

Subscripts within project herd represent LSMs significantly different based on 95% confidence intervals.

*Santa Gertrudis data removed because only present at Brian Pastures

(Adapted Table 2 Moore *et al.* 2025b)

Full genetic modelling of each trait was undertaken using various pooled datasets and models. All results for the three traits are in Appendix 9.4.1. All three traits were estimated to be moderately to highly heritable with significant maternal effect for all traits. The genetic analyses were re-run splitting the location into separate traits and dropping the Santa Gertrudis data. Results are presented in Table 22 and show similar variances and heritabilities across locations and genetic correlations close to unity. These analyses show no evidence of GxE for these traits and resultant EBVs for sires would not exhibit re-ranking i.e. the genetically superior sires at Brian Pastures would be genetically superior at Spyglass.

Table 22: Variance component, heritabilities and genetic correlation estimates across Brian Pastures and Spyglass (standard errors in brackets) for gestation length (GL, days), birth weight (BWT, kg) and weaning weight (WWT, kg) of Brahman and Droughtmaster

	Brian Pastures				Spyglass				
	V _A	V _M	h ²	h _m ²	V _A	V _M	h _d ²	h _m ²	r _g
GL	25.4		0.89 (0.09)		22.2		0.77 (0.06)		0.98 (0.05)
BWT	14.6	3.5	0.59 (0.07)	0.14 (0.04)	12.7	2.5	0.56 (0.05)	0.11 (0.03)	0.99 (0.05)
WWT	167.2	69.9	0.44 (0.08)	0.18 (0.06)	164.8	56.5	0.41 (0.05)	0.14 (0.04)	0.87 (0.09)

V_A = additive genetic variance; V_M = maternal genetic variance; V_{pe} = permanent environment variance; V_E = residual variance; V_p = phenotypic variance; h_d² = direct heritability; h_m² = maternal heritability; r_g = genetic correlation for direct effect.

(Adapted Table 5 Moore *et al.* 2025b)

4.4.3.2 GxE for female reproduction traits

A series of analyses were undertaken using the project data for heifer age at puberty and lactation anoestrous interval in first-calf cows. Lower numbers of records were available from Brian Pastures because Santa Gertrudis records have been removed (for these analyses only) because the breed was not used across locations. Results are presented in Table 23 and show for both traits, the additive variances and heritabilities were higher at Spyglass, reflecting greater trait expression in the tougher environment. Also, removing the breed term from the model used in genetic parameter estimation increased the heritability estimates, showing breed differences were contributing to the genetic variation of these two reproduction traits. The genetic correlations estimated across locations were not significantly different from unity, indicating no evidence of GxE for these two traits. This is a very unique set of results, and provides evidence that existing genetic evaluations that pool records across environments is sound, however differences in variances could require further consideration.

Table 23. Genetic parameter estimates for reproductive traits treated as different traits across locations and genetic correlations to estimate genotype by environment interactions (GxE).

Trait	Location	N	model*	V_A	h^2 (se)	r_g (se)
AP	BP	856	+ breed	3,572	0.32 (0.07)	0.93 (0.15)
	SG	1840	+ breed	6,507	0.55 (0.05)	
	BP	856	no breed	5,213	0.44 (0.07)	0.94 (0.11)
	SG	1840	no breed	7,455	0.61 (0.05)	
LAI	BP	735	+ breed	1,035	0.22 (0.08)	0.81 (0.25)
	SG	1518	+ breed	2,464	0.44 (0.06)	
	BP	735	no breed	1,179	0.25 (0.08)	0.87 (0.22)
	SG	1518	no breed	2,621	0.46 (0.06)	

* analyses performed with and without the breed term (viz: Brahman, Droughtmaster) included in the genetic model

5 Conclusions

The project has successfully built and delivered effective genomic selection in northern Australia. The building of the reference populations of the three most numerically popular breeds has increased the number of young sale bulls with BREEDPLAN EBVs, thus increasing adoption of genetics in the north. The project has produced the first set of across-breed research EBVs for a large number of traits and represents a seminal development for the north capturing both the between and within breed variation in a single EBV. Listed below are key findings from the project.

5.1 Key findings

- Recording and genotyping of relevant animals in a breed has been key to building an effective genomic reference population that drives increased BREEDPLAN EBV accuracies in young sale bulls.
- The magnitude of the increase in EBV accuracies from genomics was dependent on size of the reference and the heritability of the trait.
- Genomic reference populations increases the number of young bulls available with EBVs.
- New traits create an opportunity to select additional traits influencing profit, and the recording of them in the reference populations allows delivery via genomics.
- Calf losses continues to be a significant issue for northern Australia. Many factors were involved (many unknown) but dystocia was the single largest identifiable cause identified. And this can be addressed through breeding with the opportunities to now improve through genomic selection resulting from the large amount of recording of birth weight and gestation length in the reference populations.
- Seedstock/bull breeders are clearly adopting genomic testing and the profiles are being included in BREEDPLAN genomic evaluations at an increasing rate.
- Management of the breeds in the project has allowed the estimation of breed differences and are captured in a single-set of across-breed research EBVs. However, for most traits the within breed genetic variation is as large, or larger than the estimated breed differences, and this represents an opportunity to improve breeds with selection.
- Basic recording increases EBV accuracy.
- There was no evidence of GxE for several traits investigated and this supports the existing genetic evaluation's position of combining data and predicting breeding values across a diversity of herds and environments.

- DNA test for polled/horn showed good agreement with polled, horn and scur phenotypes, however although polled is dominant the occurrence of scurs in PH genotype animals presents a further challenge to reduce dehorning.
- At least two variants of the double-muscling gene were shown to be segregating in the Droughtmaster and Santa Gertrudis breeds. This creates both an opportunity and challenge for future breeding programs.

5.2 Benefits to industry

The main benefits to the industry has been the increased numbers of animals (in particular young bulls) in northern Australia with EBVs available, especially for the key profit driver female reproduction traits. The project enhances the ability of commercial producers to buy genetics that are better suited to their productions systems (and markets) and now have the ability to make those comparisons across breed for those sires used in this project. With increased accuracies from genomic-only generated EBVs commercial producers have the opportunity to genetically benchmark their herds and make more informed decisions on the purchase of herd-improving sires.

Critically, the seedstock industry has increased capacity to make faster rates of genetic gain, through increased accuracy (and spread) in EBVs, and across a broader suite of traits driving profitability, especially the key traits of female reproduction. Multi-breed EBVs allows both between and within breed genetic difference to be captured in a single EBV. This will allow commercial breeders to compare the genetic merit of animals directly across breeds. New traits add the ability to include additional traits that affect profitability now, and into future breeding programs.

6 Future research and recommendations

- Continue to increase the size of reference for key traits to increase accuracy, allowing greater industry confidence in genomics-only EBVs.
- Build future reference populations using sampling of latest influential genetics.
- Use the data to develop BREEDPLAN across-breed genetic evaluations for the three breeds, including investigations into the estimation of appropriate genetic parameters for pooled breed populations.
- Expand the number of breeds evaluated head-to-head to build greater multi-breed capacity.
- Investigate the genetics of scurs to allow gene(s) to be selected against, which will reduce the incidence of dehorning.
- Research how to appropriately include the myostatin genotype into the genetic parameter estimation and genetic evaluation of traits influenced by the condition.
- Continue to research new traits, with the understanding that it is essential to record all other key traits in the same population to allow the estimation of correlated effects and to facilitate the critical step of adding new traits to existing selection indexes.
- Develop economic values for new traits to allow inclusion in selection indexes.
- Investigate cheaper genotyping strategies and technologies.
- Conduct across-breed research EBV demonstration field days.

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9 Appendix

9.1 Sires used in this project

9.1.1 DAF AI and natural mate sires used to generate progeny born in this project by sire breed

BRAHMAN	DROUGHTMASTER	SANTA GERTRUDIS
2AM TAIT 4906M (PS)	ALDINGA KILO 145 (P) D5	BULLAMAKINKA K476 (P)
AJC ERNIE (AI) (PS)	ALDINGA KITBAG 108 (S) D5	CARDONA TRAVELER T141 (PS)
ALC 12-0065 POLL DESIRE (PS)	ALMAFI ILLUMINATE (HP) D5	CREE FERRERO M176 (P)
ALC 19-3426 (ET) (PS) (COM)	BILLABONG HENDRIX 8546 (PP) D5	CREE MANTUAN M230 (P)
ALC 19-3474 (H) (COM)	BREFFNI IMPACT 2ND (ET) (P) (AI) D5	DANGARFIELD X-ECUTIONER (P)
BARDIA AMBASSADOR (ET) (PS)	BRYVONLEA JBH ULTAN (P) D5	DUNLOP TESCO P550 (PS)
BIZZY PRIOR P4 (AI) (H)	BRYVONLEA QUARTZ (S) D5	EIDSVOLD STATION G362 (P)
BLACKDOWN 15/16724 (PS) (COM)	CASHMERE RANGER (P) D4	GREENUP LANCELOT Q196 (PP)
BOOGALGOPAL CASUAL GLANCE (PS)	CLONLARA 16050 (PP)	GYRANDA L680 (PS)
BRAHROCK COOPER 6965 (IVF) (H)	CLONLARA 17253 (P) D5	GYRANDA LORAX L794 (PP)
BRAHROCK NEPTUNE 5689 (IVF) (PS)	CLONLARA 2113 (P) D4	GYRANDA R430 (P)
CARINYA M BOLIVIA (IVF) (PS)	CLONLARA 2130 (P) D3	JAMALLY QUENTIN Q6 (P)
CARINYA SERRATELLI (AI) (PS)	COMANCHE 4479 (P) D5	ROSEVALE JACKAROO J566 (P)
CLUKAN T KODY MANSO 1331 (H)	DALMALLY JOSHUA (PP) D5	ROSEVALE KING K88
DDRF 16024 (AI) (H) (COM)	FAIRHAVEN JIMBORELLA (P) D4	ROSEVALE MAVERICK M102 (P)
DDRF 16454 (H) (COM)	GARTHOWEN XBOW 2 (PP) D5	ROWANLEA ATOMIC A02 (P)
DOONSIDE CAPPALLO 2525 (AI) (PP)	GLENAVON TORNADO (P) D5	ROWANLEA MAGUIRE M70 (P)
EL JA J MALLORY MANSO (AI) (H)	GLENLANDS D BASE OVER APEX	ROWANLEA SAMARAI S60 (P)
EL MARIAH 1262 (PS)	GLENLANDS D UNCONFIRMED (P) D5	WACO N96 (P)
ELANORA PARK TRIDENT (PS)	GLENLANDS D WATCHMAN (HP) D5	WACO Q20 (IVF) (P)
ELMO PICASSO 1023/7 (PP)	GLENLANDS J CREWMAN (PH) D5	WACO S60 (P)
ELROSE BENTLEY 9484 (H)	HAMADRA ICEMAN (PP) D4	WARENDA SAHARA (P)
ELROSE BRUNO 13536 (H)	HAMADRA JERRY (P) D5	WATASANTA MILKY BAR KID 2264 (P)
FAIRY SPRINGS CAPITALIST 6179 (PP)	HAZELWOOD CRONK (PH) D5	WAVE HILL JAGER J14 (PS)
FBC GARTH MANSO 537/1 (H)	HEITIKI G49 (P) D5	YARRABEE JETT 175 (PS)
FBC HANK MANSO 556/2 (PS)	HEITIKI HANRAHAN (PP) D5	YARRAWONGA N466 (P)
FBC REYNOLDS MANSO 887/1 (PS)	HIGH COUNTRY JONAS (PP) D4	YARRAWONGA Q436 (PS)
FERN HILLS S MONARCH 2071 (ET) (H)	IANBRAE JUNIOR (ET) (PH) (AI) D5	YARRAWONGA WAGER (ET)(P)
FIVE STAR 190001 (PS) (COM)	IVANHOE FORCE (P) D5	
HAZELTON KINGSTON 5485 (PS)	LISGAR 13135 (P)	
JOMANDA JARRETT 1089 (AI) (PS)	LISGAR 18152 (P)	
KAIUROO 167703 (AI) (H)	LISGAR FRAZER (P) D5	
KAIUROO FAIRPLAY 167619 (AI) (PS)	LOCARNO MILWAUKEE (P) D5	
KAIUROO POTENTE 147250 (H)	LYNSEY PARK VERNON (PP) D4	
KANDOONA 13448 (ET) (H)	MEDWAY CHARITABLE (HP) D5	
KANDOONA BUTLEER (ET) (H)	MUNGALLA KINGSWOOD (HP) D4	
KANDOONA HAMILTON (PS)	NEEDMOR ELROY (S) D5	
KENROL DARROCCA 2761 (PP)	NEEDMOR INGLIS (HP) D5	
KENROL EUMUNDI MANSO 2788 (H)	OASIS A THURSTON (P) (AI) D5	

LANCEFIELD S MCNEIL (PS)	OASIS LAMONT (P) D5
MR KALLION 1352 (IMP US) (H) (COM)	RONDEL VONZIPPER (HP) D5
MT CALLAN REWARD 168/17 (PS)	RSVP QUICKDRAW (PP) (AI) D5
MT CALLAN VAUTIN 43/21 (PS)	SC BLINKY BILL 5883 (PP) D4
NBS KINGSTON TOWN 390-0 (ET) (PS)	SC GLENCOE (P) D4
NCC JUSTIFIED (H)	SEYMOUR R JIGSAW (IVF) (P) (AI) D5
NICNEIL SUGAR DADDY (IVF) (H)	STRATHFIELD DON (P) D5
NIOKA PABLO (PP)	TRUE BLUE J NIXON (HP) D5
NK STEEL (PS)	TRUVALLE BODE (S) D5
OOLINE SINBAD (H)	VALERA VALE 15128 (P) D4
PALMAL AMOS 7972 (PS)	VITWOOD X TRAVAGANT 4209 (PP) D5
PALMVALE PATCHES 4047 (PS)	WAJATRYN INDUSTRY (P) D5
PALMVALE QUAMBY 4139 (PS)	YARALLA APOLLO (P) D5
PBF AUSTIN MANSO 866/7 (ET) (H)	YARALLA TROWBRIDGE (P) D5
POLLED PATHFINDER 24 (IMP US) (PS)	
RAGLAN MR MARBURG 2956 (H)	
RELDARAH DAMIEN (ET) (PS)	
ROCKLEY LP ETHERIDGE (IVF) (PS)	
ROXBOROUGH MR 2787 (H)	
SOMERTON DORIEMUS (ET) (H)	
TARRAMBA A PALMIRO 3093 (PS)	
TIMBREL SIR BRODIE 921 (PS)	
TOKEN JINGLE 674/7 (PP)	
WHITAKER MR ARIATT 3204 (IVF) (H)	
WILARANDY LEON 8028 (PP)	
Y3K BILLIONAIRE 9002 (PP)	
YENDA FLYNN 690 (PS)	
YOMAN 2158/3 (H)	

BEEFMASTER	ANGUS	HEREFORD
LOGAN (H)	ALUMY CREEK PRIME QUARTER	ELITE 4110 E212
BRAVADO (H)	RENNYLEA H708	ELITE K124 R216 (P)
CF UNICO (H)	RENNYLEA L519	ELITE TRUST K215
DOCE DOCE	RENNYLEA P987	JARRAH FORTUNE Q236
ESCALADES	BOORAGUL REVENUE M4	WIRRUNA FLETCHER F214
L BAR HABANERO	DANCE COMRADE Q73	WIRRUNA LEAP FORWARD L95
FRENZEL 3112	BOWMONT KING K306	WIRRUNA PAPA P149
SUMMIT 5306	LAWSONS ROCKY R4010	TALBALBA CHISEL Q010
D'ANGELO	TE MANIA FORGO F893	TYCOLAH SERGEANT Q117
L BAR TEJAS	TE MANIA JOE J963	
L BAR MOMENTUM	TE MANIA NEON N1387	
LYSSY MAVERICK	TE MANIA NOLAN N1423	
	TE MANIA PESO P888	

9.2 NT DPI across-breed research EBVs

9.2.1 Male reproduction trait research EBVs for NT DPI Brahman (BRAH) and NT TCOMP (TC) sires (if F_PNS accuracy > 60%)

socid	breed	F_PNS EBV (%)	acc	Y_PNS EBV (%)	acc	Y_SS EBV (cm)	acc	F_SS EBV (cm)	acc
DRF16285M	BRAH	27.3	0.61	18.3	0.77	4.0	0.89	3.3	0.89
DRF50623M	BRAH	25.1	0.72	9.6	0.77	3.4	0.88	2.4	0.88
DRF50650M	BRAH	24.0	0.71	14.6	0.75	4.1	0.87	4.4	0.88
DRF51008M	BRAH	23.3	0.64	15.5	0.55	3.1	0.81	2.5	0.84
DRF16764M	BRAH	22.5	0.69	24.2	0.77	4.4	0.91	3.2	0.90
DRF50633M	BRAH	21.5	0.77	17.3	0.79	4.4	0.90	3.7	0.90
DRF50303M	BRAH	20.7	0.65	11.2	0.73	3.4	0.86	3.7	0.86
DRF16444M	BRAH	20.2	0.69	10.9	0.73	2.4	0.90	2.2	0.90
DRF50654M	BRAH	19.9	0.65	8.7	0.66	4.1	0.82	4.5	0.84
DRF16084M	BRAH	19.7	0.69	20.5	0.78	3.2	0.90	2.1	0.90
DRF16454M	BRAH	19.2	0.76	12.4	0.81	2.0	0.93	1.0	0.93
DRF16389M	BRAH	19.0	0.60	3.4	0.75	2.4	0.88	2.3	0.88
DRF50803M	BRAH	18.8	0.60	13.3	0.66	2.7	0.78	1.9	0.78
DRF50614M	BRAH	18.0	0.73	4.5	0.77	2.4	0.88	2.7	0.89
DRF31274M	BRAH	17.6	0.60	23.4	0.67	3.9	0.78	2.9	0.78
DRF50957M	TCOMP	17.4	0.67	9.4	0.56	3.3	0.82	3.0	0.86
DRF16891M	BRAH	16.9	0.66	12.3	0.75	2.6	0.85	1.9	0.85
DRF50466M	BRAH	16.5	0.63	14.9	0.67	2.3	0.85	1.6	0.85
DRF16483M	BRAH	16.5	0.67	21.2	0.73	3.7	0.91	3.1	0.90
DRF50337M	BRAH	15.8	0.69	17.3	0.75	5.1	0.86	4.5	0.86
DRF30902M	TC	15.6	0.73	23.5	0.79	5.1	0.89	4.3	0.88
DRF15919M	BRAH	15.5	0.61	9.6	0.76	1.6	0.89	0.5	0.88
DRF50323M	BRAH	15.3	0.65	15.3	0.74	0.9	0.86	0.0	0.86
DRF30109M	TC	15.3	0.62	20.9	0.75	3.0	0.88	1.6	0.87
DRF31785M	TC	14.6	0.62	16.0	0.65	2.2	0.80	1.0	0.81
DRF16735M	BRAH	14.5	0.78	1.8	0.78	2.1	0.92	3.1	0.92
DRF51146M	BRAH	13.8	0.68	8.5	0.62	1.0	0.83	1.4	0.85
DRF30729M	TC	13.7	0.69	11.0	0.75	1.4	0.85	0.0	0.85
DRF51597M	BRAH	13.5	0.60	7.3	0.67	2.1	0.79	1.5	0.78
DRF31780M	TC	12.8	0.61	17.9	0.67	2.5	0.80	1.5	0.81
DRF31626M	TC	12.6	0.67	22.5	0.67	4.1	0.84	2.8	0.86
DRF31257M	TC	11.7	0.65	13.2	0.73	3.5	0.83	3.3	0.83
DRF6636M	TC	11.5	0.61	21.7	0.78	2.8	0.89	2.3	0.86
DRF31588M	TC	11.3	0.63	16.9	0.66	2.9	0.81	1.7	0.83
DRF31688M	TC	11.2	0.70	19.1	0.68	2.1	0.84	1.1	0.86
DRF30111M	TC	10.9	0.72	17.0	0.82	3.4	0.91	2.5	0.91
DRF16493M	BRAH	10.8	0.69	13.8	0.77	2.4	0.92	1.9	0.91
DRF31678M	TC	10.1	0.63	12.1	0.61	2.5	0.78	2.4	0.82
DRF30626M	TC	9.6	0.65	18.1	0.76	2.5	0.86	1.0	0.86
DRF30891M	TC	9.5	0.74	18.0	0.80	2.3	0.90	1.1	0.89
DRF18239M	TC	9.4	0.64	19.0	0.78	2.6	0.89	1.5	0.89

DRF30917M	TC	8.9	0.72	8.2	0.79	2.6	0.89	2.1	0.88
DRF30158M	TC	8.8	0.68	13.3	0.79	2.4	0.88	1.9	0.87
DRF31372M	TC	8.7	0.66	25.6	0.72	3.9	0.83	2.3	0.83
DRF16157M	BRAH	8.5	0.67	-2.7	0.76	1.3	0.92	2.8	0.92
DRF51180M	BRAH	8.4	0.61	8.5	0.67	2.1	0.79	1.3	0.79
DRF16286M	BRAH	8.3	0.61	2.5	0.75	1.9	0.89	3.8	0.89
DRF31140M	TC	8.3	0.67	18.5	0.76	2.5	0.86	2.7	0.85
DRF17785M	TC	8.0	0.67	14.6	0.81	1.4	0.92	0.2	0.91
DRF30913M	TC	7.8	0.70	12.0	0.77	1.6	0.88	0.2	0.87
DRF50915M	BRAH	7.7	0.60	1.3	0.62	0.5	0.78	-0.2	0.78
DRF50394M	BRAH	7.7	0.69	10.3	0.77	3.1	0.88	4.2	0.88
DRF31651M	TC	6.9	0.61	14.9	0.48	2.5	0.76	1.5	0.82
DRF30642M	TC	6.4	0.72	15.9	0.81	1.9	0.90	2.2	0.89
DRF15431M	BRAH	6.4	0.66	-1.5	0.74	1.2	0.91	2.1	0.91
DRF17987M	TC	6.4	0.65	15.4	0.78	2.0	0.91	1.6	0.90
DRF30714M	TC	6.4	0.65	11.7	0.76	1.5	0.88	0.9	0.85
DRF50355M	BRAH	6.4	0.66	3.2	0.74	0.2	0.86	0.4	0.86
DRF30043M	TC	6.3	0.72	15.7	0.83	2.2	0.93	0.8	0.92
DRF17661M	TC	6.0	0.63	21.5	0.79	2.6	0.92	2.0	0.90
DRF51194M	BRAH	5.9	0.61	16.6	0.67	2.1	0.79	1.5	0.78
DRF50207M	BRAH	5.7	0.70	0.4	0.75	0.3	0.89	1.3	0.88
DRF18168M	TC	5.3	0.61	13.1	0.76	1.6	0.90	0.9	0.88
DRF30393M	TC	5.0	0.72	14.0	0.79	2.3	0.88	1.8	0.88
DRF31466M	TC	4.9	0.63	19.5	0.62	3.2	0.81	2.1	0.83
DRF51566M	BRAH	4.2	0.60	6.0	0.66	1.0	0.78	0.5	0.78
DRF16698M	BRAH	3.6	0.66	9.4	0.74	2.1	0.86	2.1	0.86
DRF18447M	TC	3.4	0.63	17.6	0.74	1.9	0.88	0.9	0.87
DRF16861M	BRAH	3.2	0.76	7.3	0.80	1.4	0.91	0.5	0.91
DRF30675M	TC	3.1	0.70	17.7	0.75	2.5	0.85	1.3	0.85
DRF18335M	TC	3.0	0.60	16.8	0.74	2.3	0.90	1.8	0.90
DRF17522M	TC	2.9	0.61	11.4	0.78	0.5	0.91	0.1	0.90
DRF51635M	BRAH	2.6	0.60	7.5	0.66	1.7	0.78	1.3	0.78
DRF16450M	BRAH	1.5	0.66	5.7	0.73	2.8	0.89	2.8	0.89
DRF50147M	BRAH	1.4	0.70	-0.8	0.76	0.7	0.87	0.2	0.87
DRF30080M	TC	0.7	0.61	9.3	0.73	0.4	0.86	1.1	0.86
DRF31044M	TC	0.6	0.70	16.8	0.78	3.1	0.87	1.7	0.87
DRF50343M	BRAH	-1.2	0.71	-1.6	0.78	0.6	0.89	1.2	0.88
DRF31522M	TC	-3.8	0.66	12.7	0.66	1.3	0.83	1.5	0.85
DRF16727M	BRAH	-4.1	0.61	0.2	0.66	1.0	0.84	0.5	0.84
DRF51575M	BRAH	-4.3	0.60	4.4	0.67	-0.4	0.78	-1.4	0.78

Highlighted are project link Brahman sires to DAF herds

9.2.2 Heifer age at puberty (days) research EBVs for NTDPI Brahman (BB) and NT TCOMP (TC) sires

Society id	breed	AP EBV (d)	acc
DRF16764M	BB	-103.0	0.69
DRF50623M	BB	-100.9	0.83
DRF16861M	BB	-100.0	0.84
DRF50337M	BB	-90.3	0.80
DRF50982M	BB	-84.6	0.55
DRF30567M	TC	-82.2	0.64
DRF30111M	TC	-81.3	0.80
DRF50650M	BB	-79.6	0.81
DRF30955M	TC	-78.8	0.65
DRF50151AM	BB	-76.8	0.67
DRF30724M	TC	-75.2	0.64
DRF31126M	TC	-72.0	0.65
DRF31537M	TC	-70.8	0.73
DRF31506M	TC	-69.2	0.63
DRF16891M	BB	-67.0	0.65
DRF51388M	BB	-64.9	0.51
CBV10-N7668M	BB	-63.4	0.63
DRF51682M	BB	-62.2	0.59
DRF50466M	BB	-61.8	0.69
DRF31372M	TC	-61.1	0.76
DRF30675M	TC	-59.6	0.75
DRF30860M	TC	-59.0	0.70
DRF31978M	TC	-55.9	0.51
DRF16454M	BB	-54.8	0.84
DRF50397M	BB	-54.4	0.45
DRF51246M	BB	-53.7	0.58
DRF30902M	TC	-53.1	0.84
DRF30393M	TC	-51.4	0.84
DRF31466M	TC	-51.2	0.71
DRF51280M	BB	-49.8	0.57
DRF30913M	TC	-49.2	0.70
DRF51403M	BB	-48.8	0.57
DRF50958M	BB	-46.1	0.71
DRF16804M	BB	-45.8	0.52
DRF31825M	TC	-45.8	0.57
DRF50957M	BB	-44.6	0.77
DRF51744M	BB	-44.5	0.54
DRF31496M	TC	-43.7	0.55
DRF31688M	TC	-43.0	0.80
DRF30626M	TC	-42.4	0.70
DRF31044M	TC	-42.1	0.79
DRF51289M	BB	-41.9	0.57
DRF51294M	BB	-41.2	0.74
DRF51122M	BB	-40.8	0.64

DRF30772M	TC	-39.5	0.59
DRF51008M	BB	-38.2	0.73
DRF31086M	TC	-37.9	0.44
DRF16493M	BB	-37.0	0.73
DRF31257M	TC	-36.7	0.76
DRF50654M	BB	-33.7	0.73
DRF51398M	BB	-33.4	0.72
DRF31518M	TC	-32.9	0.62
DRF50633M	BB	-32.3	0.85
DRF50355M	BB	-31.7	0.64
DRF30134M	TC	-31.0	0.52
DRF32245M	TC	-30.9	0.65
DRF16918M	BB	-28.0	0.65
DRF31840M	TC	-25.8	0.51
DRF16869M	BB	-24.8	0.61
DRF31678M	TC	-24.7	0.83
DRF31785M	TC	-24.6	0.66
DRF30917M	TC	-21.2	0.86
DRF31757M	TC	-20.3	0.51
DRF30937M	TC	-19.9	0.47
DRF51742M	BB	-18.5	0.57
DRF51272M	BB	-18.4	0.71
DRF16483M	BB	-18.2	0.71
DRF31995M	TC	-18.2	0.64
DRF31034M	TC	-18.1	0.63
DRF31588M	TC	-17.6	0.75
DRF31651M	TC	-17.6	0.72
DRF31960M	TC	-16.8	0.57
DRF16876M	BB	-15.7	0.70
DRF30815M	TC	-15.0	0.61
DRF31642M	TC	-14.3	0.53
DRF31513M	TC	-12.4	0.73
DRF30714M	TC	-11.3	0.70
DRF31255M	TC	-11.1	0.46
DRF31819M	TC	-11.1	0.50
DRF51256M	BB	-10.4	0.67
DRF16444M	BB	-8.4	0.77
DRF31831M	TC	-7.4	0.57
DRF16956M	BB	-6.4	0.46
DRF16994M	BB	-4.8	0.62
DRF31339M	TC	-3.4	0.71
DRF50803M	BB	-2.4	0.64
DRF50986M	BB	-2.3	0.70
DRF51139M	BB	-2.2	0.52
DRF30158M	TC	-1.8	0.75
DRF31626M	TC	-1.3	0.77
DRF32013M	TC	-0.9	0.62
DRF30461M	TC	1.7	0.73

DRF51015M	BB	1.8	0.54
LAN4999MM	BB	2.8	0.48
DRF30891M	TC	3.6	0.85
DRF31843M	TC	3.7	0.81
DRF50187M	BB	3.7	0.40
DRF16846M	BB	5.6	0.58
DRF30697M	TC	7.7	0.53
DRF30798M	TC	8.1	0.56
DRF30729M	TC	9.7	0.72
CBE070192M	BB	10.1	0.61
DRF50814M	BB	17.0	0.55
DRF50154M	BB	17.7	0.50
DRF50323M	BB	21.3	0.67
DRF30146M	TC	22.9	0.60
CBV10-7694M	BB	24.4	0.56
DRF30946M	TC	24.8	0.74
DRF50614M	BB	25.4	0.83
DRF31274M	TC	25.6	0.63
DRF31818M	TC	28.8	0.79
DRF16701M	BB	32.4	0.58
DRF30080M	TC	35.1	0.64
DRF16735M	BB	35.2	0.86
DRF51270M	BB	35.7	0.72
DRF51146M	BB	35.8	0.69
DRF31780M	TC	37.9	0.75
DRF30109M	TC	40.4	0.60
DRF50303M	BB	43.7	0.73
DRF31522M	TC	45.6	0.75
DRF16450M	BB	46.7	0.69
DRF51096M	BB	50.5	0.68
DRF50394M	BB	51.4	0.84
DRF50147M	BB	60.3	0.80
DRF51265M	BB	62.2	0.59
KAI147250M	BB	64.0	0.50
DRF16698M	BB	69.4	0.71
DRF50207M	BB	72.9	0.75
DRF16727M	BB	79.4	0.64
DRF16800M	BB	85.1	0.63
DRF31524M	TC	86.8	0.50
DRF31140M	TC	123.0	0.69
DRF50343M	BB	152.8	0.79
DRF30642M	TC	173.2	0.83

Highlighted are project link Brahman sires to DAF herds

9.3 Validation Results

9.3.1 Population accuracy estimates for genotyped validation animals from pedigree (PED) and single-step (S-S) BREEDPLAN EBVs for Brahman and Santa Gertrudis*

EBV [^]	Brahman		Santa Gertrudis	
	PED	S-S	PED	S-S
BW	0.79	0.99	0.33	0.38
WW	0.54	0.70	0.37	0.41
YW	0.43	0.57	0.41	0.45
FW	0.46	0.61	0.41	0.46
MCW	0.42	0.64	0.50	0.53
BEM	0.41	0.49	0.43	0.52
HEM	0.39	0.48	0.50	0.58
BIM	.	.	0.34	0.39
HIM	.	.	0.33	0.39
BP8	0.35	0.49	0.44	0.51
HP8	0.43	0.55	0.38	0.47
BRF	0.34	0.48	0.45	0.52
HRF	0.50	0.61	0.38	0.47
CWT	0.35	0.43	0.33	0.37
CIM	0.40	0.46	0.31	0.34
CP8	0.35	0.47	0.35	0.38
CRF	0.37	0.43	0.38	0.41
SHF	0.36	0.42	0.28	0.32
DTC	0.36	0.60	0.55	0.67
AP	0.41	0.47		
PNS	0.21	0.26	0.26	0.29
SC	0.59	0.76	0.40	0.46
GL	0.32	0.33	0.24	0.25
FT	0.41	0.46	0.51	0.57

* Adapted Table 1 Johnston *et al.* (2023)

[^] see Table 18 for trait descriptions

9.4 Birth weight, gestation length and weaning weight

9.4.1 Univariate variance component and heritability estimates (standard errors in bracket) for gestation length (days), birth weight (kg) and weaning weight (kg) of tropical beef breeds

Trait	V _A	V _M	V _{pe}	V _E	V _P	log	h _d ²	h _m ²
Pooled breeds (breed fitted in model)								
Gestation length	20.2	1.1	0.0	6.8	28.1	-4846.98	0.72 (0.08)	0.04 (0.03)
Gestation length	20.2	1.1		6.8	28.1	-4846.98	0.72 (0.08)	0.04 (0.03)
Gestation length*	22.4			6.0	28.4	-4847.71	0.79 (0.05)	
Birth weight	11.6	1.8	0.5	8.3	22.2	-2255.94	0.52 (0.04)	0.08 (0.02)
Birth weight*	11.4	2.3		8.5	22.2	-2257.09	0.52 (0.04)	0.10 (0.02)
Birth weight	14.6			8.0	22.6	-2286.22	0.65 (0.03)	
Weaning weight*	156.1	60.3	44.9	132.3	393.5	-647.18	0.40 (0.04)	0.15 (0.03)
Weaning weight	146.3	114.7		144.5	405.5	-663.09	0.36 (0.04)	0.28 (0.02)
Weaning weight	287.2			126.0	413.2	-794.72	0.70 (0.03)	
Pooled breeds (breed excluded from model)								
Gestation length	25.9	0.2	0.0	4.1	30.1	-4870.36	0.86 (0.07)	0.01 (0.03)
Gestation length	25.8	0.2		4.1	30.1	-4870.36	0.86 (0.07)	0.01 (0.03)
Gestation length*	26.1			4.0	30.1	-4870.38	0.87 (0.05)	
Birth weight	12.2	2.1	0.6	8.1	23.1	-2472.39	0.53 (0.04)	0.09 (0.02)
Birth weight*	12.0	2.7		8.4	23.1	-2473.96	0.52 (0.04)	0.12 (0.02)
Birth weight	15.4			7.9	23.4	-2512.24	0.66 (0.03)	
Weaning weight *	194.9	65.2	41.7	126.1	427.9	-1202.51	0.46 (0.04)	0.15 (0.03)
Weaning weight	185.0	115.2		138.2	438.4	-1215.96	0.42 (0.04)	0.26 (0.02)
Weaning weight	304.4			133.8	438.2	-1353.13	0.69 (0.03)	
Brahman								
Gestation length	22.5			4.5	26.9		0.83 (0.07)	
Birth weight	11.5	2.5		6.2	20.1		0.57 (0.05)	0.12 (0.03)
Weaning weight	142.5	49.0	25.1	119.8	336.3		0.42 (0.06)	0.15 (0.04)
Droughtmaster								
Gestation length	24.0			7.5	31.5		0.76 (0.09)	
Birth weight	12.3	2.2		9.9	24.3		0.51 (0.06)	0.09 (0.03)
Weaning weight	158.7	67.4	55.5	156.7	438.4		0.36 (0.06)	0.15 (0.04)
Santa Gertrudis								
Gestation length	21.0			7.0	28.0		0.75 (0.14)	
Birth weight	9.2	1.4		12.1	22.7		0.40 (0.09)	0.06 (0.04)
Weaning weight	187.5	77.2	75.2	116.6	456.5		0.41 (0.11)	0.17 (0.08)

V_A = additive genetic variance; V_M = maternal genetic variance; V_{pe} = permanent environment variance; V_E = residual variance; V_P = phenotypic variance; h_d² = direct heritability; h_m² = maternal heritability;

* indicates the most parsimonious model after testing random effects for significance using log-likelihood ratio test; within breed models were the most parsimonious pooled breed model

(Adapted Table 3 Moore *et al.* 2025b)