final report

Enabling genetic improvement of reproduction in tropical beef cattle

Abstract

Reproduction rate is a key profit driver in many northern Australian production systems. Genetics is a tool that can increase performance, however difficulties in recording and later expression of the traits associated with female reproduction have meant little or no genetic progress. Genomic selection has emerged as powerful new tool in livestock breeding but has had little application in beef due to low numbers genotyped. This Project used intensive recording and genotyping to build genomic reference populations for three tropical beef breeds. This is enabling the application of genomic selection as a result of significant increases in the accuracy of the female reproduction EBV days to calving (DC) in all three tropical breeds, and increased numbers of young bulls with DC EBVs. This research sets the platform for northern Australia to select more effectively for improved female reproductive performance.

Executive summary

The Project has built significantly on the knowledge and outcomes from the Beef CRC and has enhanced and enabled the recent developments of genomic evaluations in BREEDPLAN and the evaluation of additional female reproduction traits. As a direct result of the outputs of this Project Brahmans were the first breed in Australia to implement the new single-step genomic BREEDPLAN evaluations.

These outcomes have been achieved through intensive recording of early-in-life female reproduction traits in maiden heifers and 1st calf-cows in Brahman, Santa Gertrudis and Droughtmaster cattle managed in large herds on research facilities in Queensland and the Northern Territory. Use of ovarian ultrasound scanning and recording of mating outcomes from natural mating has allowed accurate continual assessment of individual female reproductive performance on an annual basis under commercial management and production systems.

Recording has been undertaken on the progeny of highly relevant seedstock sires that were the influential or emerging sires from each of the breeds. Sires were included via artificial insemination and also large numbers of natural mates were used from leading seedstock herds. This sampling strategy helped to maximise the relevance of project outcomes directly back into existing breeding programs of these bull breeding herds. This will become increasingly important for benefits of genomic selection to be fully realised, where close relatedness to the reference population will increase resultant EBV accuracies.

Genotyping was undertaken on more than 5,600 animals using the latest DNA single nucleotide polymorphism (SNP) chip platforms in all Project animals as well as animals in leading performance recording industry herds, and existing high EBV accuracy sires across the three breeds. This genotyping has provided a big impact into single-step genomic evaluations and has also provided the ability of these breeds to access genomic breed composition assessment of individuals, as well as DNA diagnostic tests for poll/horn and the Pompe's disease.

The intensive phenotypic recording and SNP genotyping contributed to building the size of reference populations for the three largest tropical beef breeds. This is a crucial development in enabling the implementation of genomic selection, which will allow the northern beef industry to take advantage of the potential for increased rates of genetic progress being experienced in temperate beef breeds, and also being witnessed in dairy cattle breeding programs around the world.

Results from the intensive recording have confirmed the magnitude of the genetic differences for early female reproduction traits in tropical beef breeds in northern Australia, including now the Santa Gertrudis and Droughtmaster breeds.

Analyses have been undertaken for the first time on the performance and genomic profiles of the Northern Territory's Brahman selection lines. This long-term project has demonstrated that selection for reproduction has changed performance and this Project has examined some of the underlying component traits of early reproduction, as well as undertaking full genomic profiling of the herd.

The Project has developed genetic evaluations for existing traits not previously reported in these tropical breeds. The Project has provided the first genetic estimates for gestation length in tropical beef breeds and the first set of EBVs for Brahmans for the trait. Another important outcome of the Project is that it has enabled the development of a trial DC EBV for the Droughtmaster breed.

Genetic models and parameter estimates have been created using data on novel traits that were recorded in the Project including: cow mothering score, heifer navel score, hip height, teat and udder scores, body condition score and coat length scores. Genetic analyses of these traits

identified most of them to be moderately heritable, and in some cases, will lead to the development of new EBVs for industry.

The Project has provided the first estimates of the magnitude of genotype by environment interactions (GxE) in tropical production systems for a range of traits. These outcomes will help inform genetic evaluations on the likely impact of differences in the environment, and will be especially important as evaluations build towards across-breed capacity. At this stage, estimates for early growth traits and heifer age at puberty suggest little evidence for GxE, however more records are required to confirm possible GxE for cow body composition traits.

To help the northern industry increase the levels of recording the Project investigated alternative measures that may be easier or most cost effective to record. An indirect measure of birth weight using coronet circumference was recorded on several thousand calves at birth and at branding. Whilst the trait proved heritable it was deemed not suitable for genetic evaluation as an alternative to birth weight, however a weight taken at branding could be considered.

The Project has been pivotal in the growth of northern genetic evaluations through the addition of new traits, increased levels of genetic linkage and improved accuracy of several lowly recorded traits (e.g. birth weight and flight time). Project data and genotypes on all animals has been included or is in the process of being included in the genetic evaluations of the three breeds. Resultant BREEDPLAN EBVs, especially on high impact industry sires, are accessible to the public (for free) via the web.

The northern industry is now in an improved position as a result of the Project to genetically improve tropical beef breeds, and this can continue to be built into the future. Bull breeders can use the improvements available to increase rates of genetic progress with benefits that will flow directly to the commercial bull buyer.

The developments in single-step genomic evaluations provides an immediate value proposition for breeders to undertake genotyping in tropical breeds. The increased accuracy of economically important hard-to-measure traits provides the opportunity for more balanced selection decisions across traits, and immediately increases the utility of selection indexes for the north.

The Project structure and collaboration across organisations to conduct this research on large numbers of experimental animals provides a model for future research (e.g. in southern Australia). The Project has provided a blueprint to enable industry to build beyond the current design and possibly transition to a more direct ownership model allowing assessment of very latest genetics and mix of breeds to maintain and grow genomic reference populations for the northern beef industry. However this will require ongoing co-investment and the ability to secure suitable locations.

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Abbreviations and acronyms

ABRI   Agricultural Business Research Institute

AGBU   Animal Genetics and Breeding Unit

AI   artificial insemination

AP   heifer age at puberty

BCS   body condition score

BIN   Beef Information Nucleus

BP   Brian Pastures research facility, QLD

CL   corpus luteum

CRC   Beef Cooperative Research Centre

DAF   Queensland Department of Agriculture and Fisheries

DD   Douglas Daly research farm, Northern Territory

DGV   direct genomic value

EBV   estimated breeding value

GRM   genomic relationship matrix

GEBV   genomic estimated breeding value

GxE   genotype by environment interaction

h^2 direct genetic heritability estimate

h^2_m maternal heritability estimate

LAI   anoestrous interval in lactating cows

LSM   least squares mean

MDC   MLA Donor Company

MLA   Meat and Livestock Australia

r_g genetic correlation estimate

s.e.   standard error

SFF   Queensland Government Smart Futures Fund – Next Gen Project

SG   Spyglass research facility, QLD

SNP   single nucleotide polymorphism

std   standard deviation

Va   additive genetic variance

Ve   residual variance

Vm   maternal genetic variance

Vp   phenotypic variance

Ve   permanent environmental variance

1 Background

The following three Sections (i.e. Background, Project Objectives, and Methodology) and all sub-sections have been copied directly from the original proposal. From Section 4 (i.e. results) onwards is all new material.

1.1 Reproduction rates in Northern Australia

Reproduction rates in northern Australia are often low, accentuated by an extended post-partum anoestrous interval of *Bos indicus* cattle. Traditionally, genetics have played little role in improving reproduction due to difficulties in recording and a relatively slow selection response. However, published selection line experiments in Droughtmaster (e.g. Hetzel *et al.* 1989) and Brahman (Schatz *et al.* 2010) have shown that significant improvement in reproduction rates can be achieved. Recent research findings from the Beef CRC northern breeding projects (B.NBP.0363) have expanded this knowledge, providing opportunities to increase rates of genetic improvement for female reproduction through a greater understanding of the degree of genetic control on component traits in both females (Johnston *et al.* 2009 Johnston *et al.* 2014a) and males (Corbet *et al.* 2012). The CRC research has identified ways to capture this genetic variation through: 1) recording of early-in-life traits in females and young bulls; and 2) use of genomics (Hawken *et al.* 2012 and Zhang *et al.* 2013), thus providing the basis for a more effective selection strategy to improve reproduction rates in northern Australia (Barwick *et al.* 2014). These results demonstrate that compared to current practices, or lack there-of, the northern beef seedstock industry can greatly improve selection response in reproduction rates by focusing primarily on increasing the accuracy of selection and the selection intensity in bulls.

Currently, few northern seedstock producers record reproduction traits, principally due to the cost and a lack of demand and positive market signal from commercial herds. Consequently, few bulls are available with EBVs for reproduction. This, in turn, frustrates any demand from commercial producers. As the genetic technologies involved simply will not work until there are sufficient data to underpin EBVs and genomic tests, this market failure will likely continue without intervention, and the lack of genetic improvement for reproduction will therefore persist into the future. The proposed R&D represents the intervention required to overcome this market failure - a major investment in targeted measurement of reproductive phenotypes and genotypes across the major breeds, in collaboration with key seedstock producers.

This Project will use a combination of strategic phenotypic recording and single nucleotide polymorphism (SNP) genotyping to rapidly increase the number of bulls (and AI sires) with accurate reproduction EBVs for northern Australia. This will be undertaken for the three major northern breeds (Brahman, Droughtmaster and Santa Gertrudis) utilising a mix of industry and research station herds. The Project will generate female progeny on influential sires and also capitalise on existing phenotypic recording for female reproduction. These include: i) stud females in industry seedstock herds as part of the Smart Futures Fund (**SFF**) Project: Transformational Genomics and Beef Breeding Strategies - 2011003753; ii) ex Beef CRC females and their progeny recorded, since the end of the Beef CRC, at Queensland research facilities (Brian Pastures, Spyglass/Swans Lagoon and Belmont; and iii) Brahman females from the Northern Territory's Brahman Selection line at the Douglas Daly and Kidman Springs Research stations.

The project will generate data that will further our understanding of the genetics of reproduction, thus allowing improvements in trait definitions, use of correlated traits, better models and methods of genetic evaluation. Importantly, as modern genetic evaluations move towards the use of genomic

relationship matrices and single-step methodologies (Misztal *et al.* 2009) the data (and research) from this project will be pivotal in driving this new era of genetic evaluation in Australian beef cattle. The single-step procedure represents a seminal change in the evolution of the BREEDPLAN genetic evaluation system. Single-step allows simultaneous use of existing pedigree relationships (for the majority of animals) in conjunction with a genomic relationship matrix (**GRM**) of genotyped animals from high density SNP profiles (e.g. 10K or 50K). This simplifies, and is equivalent to, the use of genomic information currently using estimated genomic breeding values (GBV) derived from prediction equations. However the new procedure allows the evaluation to be continually updated as additional phenotypes and genotypes are added. Currently, the existing pedigree relationship matrix allows differences in phenotypic performance to be transmitted to relatives whereas the single-step (and GRM) will allow genetic differences between individuals to be influenced through their degree of genomic relationship. Therefore animals with large amounts of phenotypic information when genotyped will influence the EBVs and accuracies of any animal that is genotyped and genomically associated with the high accuracy individual. The project design will ensure that elite sires have their genetics available through the project industry herds thus allowing each of the breeds to provide the industry with young sale bulls with increased accuracy for reproduction traits. The project will put the northern breeding industry in a unique situation to take immediate advantage of this major change to the BREEDPLAN genetic evaluation system.

The project will create the opportunity for the breeds to more effectively undertake ongoing selection to improve reproduction and will provide the commercial industry with a source of improved genetics. The involvement and interaction with a core group of seedstock breeders will help disseminate the output of the project through their peers and clients thus stimulating and expanded base of recording.

2 Project objectives

2.1 General

Genotyping of industry bulls, research station females and key sires with the latest high density DNA SNP chips will add significantly to the genomic databases of these three breeds. The levels of phenotyping and genotyping will differ across the 3 breeds and is reflected in the project design. This is necessary given the history of CRC involvement by Brahman and differences the levels of industry recording of female reproduction traits across the breeds. The outcomes from the Project will greatly enhance the genetic evaluation of female reproduction in the 3 major tropical breeds through the combined use of phenotyping and genotyping on industry and research station herds. These will be used initially with existing prediction equations but will be of most value when implemented into the single-step procedures currently being developed in BREEDPLAN. The precision experimental design with respect to the generation of female reproduction data on pedigreed animals with described managements and basic information (e.g. accurate birth dates) will potentially have benefits beyond the existing objectives by providing a resource for the overlay of additional projects and to provide links to existing projects for additional value. Through the collaboration with industry the Project will enable commercial breeders to source improved genetics for reproduction.

In total, it is expected that up to 5,000 animals will be SNP genotyped and over 2,500 Project females will be recorded for high accuracy female reproduction traits. In addition, the design of the Brahman Beef Information Nucleus (BIN) project means that the recording of reproduction phenotypes in the young females (3 drops; N-1,100) should also add significantly to this Project. The existing females at the research stations represent a unique resource for conducting this experiment. Firstly, the Brahmans and Tropical Composites at Queensland Department of Agriculture and Fisheries (DAF) stations are ex-CRC cows and, with their daughters, are highly recorded for reproduction through the CRC, and post-CRC, and will provide additional female reproduction phenotypes in the first years of

the Project. The high accuracy older females are also valuable as a resource for conducting AI programs to progeny test new sires. The NT herd is also a unique resource with respect to reproduction in Brahmans. This herd has been selected for more than a decade for female reproductive performance and much of their outside genetics has been sourced from the largest recorder of DC in the Brahman breed. Therefore the genomic and phenotypic benchmarking of these genetics add significantly to the scope of the project. The project is designed to record female reproduction at a range of locations across three major tropical breeds. The design will ensure genetic linkage of breeds across locations (and to industry herds) generated through AI and the use of natural mating bulls. Brian Pastures research facility at Gayndah will run Santa Gertrudis, Brahman and Droughtmasters, while Spyglass Research Station at Charters Towers will run Droughtmasters and Brahmans. The Douglas Daly herd in the Northern Territory will provide additional Brahman data from the yearling mating component of the Selection line experiment. All herds are recorded on BREEDPLAN, so that all project animals will have EBVs and will allow benchmarking of their genetics against all other animals in the breed. Over time, genetic trends can be computed to monitor the genetic progress of the herds for all EBVs and $Indexes.

2.2 Objective 1 – Genotyping industry sires with high accuracy BREEDPLAN DC EBVs

This objective is to identify key sires based on several different criterion and genotyping them with 50K SNP platforms in each breed. Genotyping of these sires will immediately build the foundation for the effective implementation of single-step in each of the breeds for female reproduction and all other traits recorded on these sires. Genotypes from this project will be included in routine evaluation with new genomic procedures currently being developed as part of MLA Project B.BFG.0050.

2.3 Objective 2 – High accuracy phenotyping for female reproduction traits

The key to Objective 2 is the collection of large numbers of quality phenotypes (~3,000 females) for female reproduction traits, in particular recording specific early-in-life traits that have been shown to be moderately to highly heritable in the Beef CRC project. These data, coupled with genotypes on their sires, will add significantly to the genetic evaluations of these 3 breeds by increasing the number of animals with high accuracy female reproduction records. Collecting daughter reproduction records in current generation influential sires and future generation young bulls will increase their accuracy for female reproduction EBV as quickly as possible and then through single-step the benefits will flow to large numbers of animals in the breed.

2.4 Objective 3 – Validation and enhancement of genomic selection for female reproduction in tropical breeds

Existing groups of young females will be genotyped to demonstrate the predictiveness of current CRC genomic productions for age at puberty and first lactation anoestrous interval across the breeds as soon as the records become available in the first 12 months of the project. This will provide an early project results on application of genomic testing and the genotypes would be included immediately into BREEPLAN for Brahman (and possibility Santa) to increase accuracy of these females. The data from these females will also be added to the existing CRC database and used by the project to re-estimate the predictions equations to increase their accuracy thus benefiting industry genotyping through improved blending accuracy. The second part of this objective is to genotype the young male selection candidates in the industry herds. The genotyping will allow these bulls to have increase accuracies for female reproduction through the single-step and increased levels of phenotypic recording on female relatives. This will immediately increase effectiveness of selection/cull decisions of the co-operators. It will also serve as a demonstration of the genomic selection and also start of dissemination of improved genetics.

3   Methodology

3.1   Overall design

The intensive recording undertaken by the project will generate a critical mass of data allowing industry and thus creating an ongoing means to improve reproduction rates in northern Australia for the range of breeds and production systems. The project will increase the accuracy of selection for reproduction traits in the genetic evaluations of tropical breeds that was established in the Beef CRC.

The precision experimental design with respect to the generation of female reproduction data on pedigreed animals with described managements and basic information (e.g. accurate birth dates) will potentially have benefits beyond the existing objectives by providing a resource for the overlay of additional projects and to provide links to existing projects for additional value. The demonstration capacity the project in its ability to show both seedstock and commercial producers the opportunity that exists to improve reproduction through selection is be very valuable. Through the collaboration with industry the project will enable commercial breeders to source improved genetics for reproduction.

3.1.1 Genotyping industry sires

High accuracy days to calving (DC) EBV sires will be identified from the BREEDPLAN database and a DNA sample (likely semen straw) will be sourced. These sires will be genotyped with commercially available 50K SNP chips. It is estimated that between 250 and 300 sires will be identified and checking will be done to ensure they have not already been genotyped (e.g. as part of CRC Industry sires). For Brahman and Santa this selection will be based on EBVs where possible. However, for Droughtmasters, that currently don't have DC EBV in their BREEDPLAN evaluation, an equivalent number of high accuracy sires for available BREEDPLAN EBVs will be genotyped.

The project will genotype (50K) the sires of the heifers recorded for reproduction phenotypes as part of the SFF project and NT selection herd. Depending on the levels of recording achieved it is expected approximately 20-50 sires per herd will be genotyped for each of the 3 breeds (approx. 105 in total).

3.1.2 High accuracy phenotyping for female reproduction traits

Maiden heifers at the NT and QLD research stations will be intensively recorded using ovarian scanning, provided by commercial scanners, to determine heifer age at puberty. Approximately 2,500 animals (including heifers generated by the project in Objective 2.3) will be recorded for age at puberty and/or outcome from mating 1. All heifers will be naturally mated in large multi-sire contemporary groups. Accurate date of birth and parentage will be recorded on all subsequent calves. This will allow adjustment for age effects and give accurate records for subsequent reproductive outcomes (e.g. DC from mating 1). The number of Droughtmasters heifers included in the project is more than the other breeds due to current low numbers of records (research or industry). The frequency of ovarian scanning is an important consideration for the experimental protocols of the project. It is not feasible to scan at the frequency used in the Beef CRC (every 4-6 weeks). However, preliminary analyses conducted as part of this application development has established (using Beef CRC BRAH and TCOMP data) that the majority of the heritability of heifer age at puberty can be captured by doing 3-4 strategically timed ovarian scans per year.

First-calf cows at the NT and QLD research stations will be recorded using ovarian scanning to determine the time to return to cycling in lactating cows at their second annual mating season. Approximately 1,700 1st calf cows (including those generated by the project in Objective 2.3) will be recorded for lactation anoestrous interval (LAI) and/or outcome from mating 2. All these females will be naturally mated in large multi-sire contemporary groups. The actual numbers of females recorded for LAI (i.e. lactating 1st-calf cows) will be determined by reproductive rates achieved from the previous maiden mating.

Again, the frequency of ovarian scanning is an important consideration for the experimental protocols of the project, as it is not feasible to scan at the frequency used in the Beef CRC (every 6 weeks). However, preliminary analyses conducted as part of this application development has established that the majority of the heritability of lactation anoestrous interval (LAI) can be captured by doing 2-3 strategically timed scans per year. Foetal ageing will also be employed to increase the accuracy of determining LAI. All cows will be monitored for calving and accurate date of birth and parentage, allowing adjustment for age effects and giving accurate records for computing reproductive outcome traits from calving (e.g. days to calving mating 2) through to weaning (e.g. weaning rate mating 2). Up to 2 additional herds per breed will be selected by the project to provide increased phenotyping capacity and to allow strategic genotyping, particularly of well recorded sires in the Santa Gertrudis breed. The mix of phenotyping and genotyping will vary across breeds and herds due to current levels of recording female reproduction.

All available older cows at 2 research stations (and 2 co-operator Santa herds) will be used in artificial insemination programs to generate daughters on high genetic merit young sires and several highly influential sires (and to contribute to genetic link across sites). The number of sires used will depend on the number of available females at each location for AI in each breed. For Brahman and Santa there are currently 9 very high-use sires with a total of 1,955 and 1,846 progeny born in the last 4 years in each breed, respectively. Only 2 and 4 of these sires have DC accuracies greater than 50% in Brahman and Santa, respectively. Droughtmasters have 20 sires with more 2,560 progeny born in last 4 years but have no female reproduction EBV at this time. The aim of this part of the project will be to obtain semen from as many of these sires as possible and use in AI programs to generate approximately 10-15 daughters/sire. Genetic linkages with be established between this project and other previous northern breeding projects (*viz*: Beef CRC Northern Fertility project and Brahman Breed Society BIN). Linkages will also be generated within the project across locations (including the NT herd) and years.

The daughters generated will be intensively phenotyped to increase the accuracy of these sires for female reproduction traits as per recordings described above. An important added benefit of generating progeny of these sires at the research stations will be the head-to-head data of their daughters' performance which will add to the across-herd genetic linkage within a breed that is commonly lacking in tropical breeds due to lower levels of AI. The daughters and their sires will also be genotyped to provide critical data to drive genomic selection through the single-step methodology, and this will then flow through to large numbers of current generation animals in industry. At each of the research station herds a management strategy will occur using a combination of selection and culling practices. The genetics of the herd for reproduction will be monitored by the genetic trend that will be available through the respective BREEDPLAN evaluations over the life of the project, and beyond. Culling all non-pregnant females will occur and restricted mating periods applied. At this stage, the male calves generated at the research stations could be considered for additional research depending on availability of additional resources including land. At a minimum they will be taken through to weaning to get weaning performance data on their dams. They could be steered and grown out to collect additional records to increase the accuracy of their sires (and dams) for growth and carcase traits. Alternatively they could remain entire and recorded for male reproduction traits, thus adding to the accuracy of selection of young bulls and could be used as sires in the project herds. These various options have not been budgeted but will warrant further consideration when the level of male recording in the industry herds is known.

3.1.3 Validation and enhanced genomic selection

Use existing females to validate CRC genomic prediction equations. Females with existing reproduction phenotypes, and those recorded in the first 12-24 months of the project, will be genotyped with 10K. The reproduction phenotypes will include age at puberty (or mating 1 outcome) and lactation anoestrous interval (or mating 2 outcome of wet cows) for 2010, 2011, 2012 and 2013 drop heifers (plus N=850 + 1200 BIN animals from 30 sires). These will then be imputed up to 800K (background IP) and have the CRC prediction equations (background IP) applied to compute genomic estimated breeding values (GEBV). Regression analyses will be performed to estimate the prediction of phenotype on GEBV or (sire GEBV) and will require known fixed effects for female reproduction traits. This will determine the accuracy of the existing CRC prediction in the three breeds. Records for Santa may be supplemented by SFF data.

Use existing females to re-estimate CRC genomic prediction equations. The phenotypic and genotypic data will be combined with the existing CRC data to allow the re-estimation of the genomic prediction equations. This will require the project perform a genome-wide association analysis (GBLUP) and will result in upgraded equations. The new equations would be made available for blending of GEBVs into BREEDPLAN EBVs for Brahmans and, depending on the resultant accuracies, may be used for Santa and Droughtmasters.

Young bulls in SFF herds (and other co-operator herds recording female reproduction) that are retained as replacement sires or are available for sale (N=1,200) after 12 months of this project (2013 and 2014 drop) will be genotyped with 10K and submitted to BREEDPLAN to generate genomically enhanced EBVs. This will also allow elite young bulls to be identified and semen collected to use in objective 2.3. The genomically enhanced EBVs and improved accuracies on large numbers of young bulls will be a powerful demonstration to industry of the use of phenotyping and genotyping and will provide a critical mass to give bull buyers the opportunity to start improving reproduction through genetics. Other herds not part of the project could also genotype their young bulls and start to see the benefits as well.

4   Results

The project has successfully generated and recorded the projected numbers of animals in the original proposal, despite some very severe drought conditions in the early years of the Project. The intense recording of the reproduction traits has occurred with more than the targeted frequency, particularly for recording heifer age at puberty. Genotyping of Project and Industry cattle has occurred with a range of SNP microarrays (chips) including a new *Bos indicus*-specific research 80K chip that became available during the Project. The new 80K chip has greatly improved the quality of genotyping through increased accuracy of imputation and has therefore improved the ability to utilise data previously collect with different (usually lower) SNP density in historic data (e.g. Beef CRC). All other Project animals were genotyped using lower density products including Neogen GGP and more recently, the new Trop Beef 35K SNP chip. During the Project, DNA parentage assignment progressed from the microsatellite markers method to SNP-based assignment.

Serial ovarian scanning data was used to record the two new BREEDPLAN female reproduction traits and mating outcomes. These key traits were included in the standard BREEDPLAN runs. Large numbers of other BREEDPLAN traits were also fully recorded in the Project animals (males and females) and included: gestation length (AI calves only), birth weight, flight time, 200d weight, 400d weight, 600d weight, cow weight, heifer ultrasound scan rib fat, P8 fat, eye muscle area (EMA), and days to calving (DC, repeat records). Additional traits were recorded on Project generated steers as part of the Northern BINs (P.PSH.0774 and P.PSH.0743) and these include: 600d weight, ultrasound scan traits, carcase weight, carcase EMA, P8, rib, IMF and shear force, as well as some other non-BREEDPLAN traits.

Statistical models were required to analyse the Project data to account for experimental design effects and other non-genetic effects (e.g. age). Planning was required throughout the experiment to ensure the important effects could be partitioned, however in some instances they were intentionally confounded to simplify the design. It was important that technicians were trained to ensure same recording e.g. trait definitions (e.g. score, scales and time) to ensure data could be pooled across years and locations. Artificial Insemination (AI) and natural mate breeding programs were designed to ensure linkage across years and locations, and linkage across AI and natural mate sire groups. At a location, breeds were run together to allow the data to be pooled across breeds. During the Project there was no culling, drafting or splitting of the project animals, except in instances of very poor temperament or injury. Females were culled only if they failed to calve or wean a calf. In the AI program cows were assigned to AI sires to stratify lactation status, cow age group, and calf age. Sire of cow was also considered to avoid close inbreeding. AI programs were scheduled to ensure an overlapping of resultant calves with natural mate progeny. The Project relied on accurate birth dates to obtain precision reproduction records and to adjust for differences in animal ages. Sire parentage of all project animals was established by DNA assignment using a hair sample taken at birth. At birth each calf was double tagged to ensure correct identification and all animals were later individually number branded.

For all analyses, data was edited to remove any biological, experimental error-caused and statistical outliers. Initial statistical models for each trait were constructed to include the full suite of known fixed effects and first-order interactions. Terms were sequentially removed (P > 0.05) to yield the final model for each trait. The identified significant fixed effects were included in REML analyses using ASREML (Gilmour *et al.* 2009) or threshold analyses using THRGIBBS1F90 (Misztal *et al*. 2002) along with full pedigree (up to 3 generations, where available) to estimate variance/covariance components and heritabilities.

4.1   Project Genotyping

All Project animals were genotyped with high density SNP microarrays using hair or semen samples. Sires used to generate progeny in the Project (provided a DNA sample was available) and sires from industry herds were genotyped with a specific research *Bos indicus* 80K chip. All other Project animals were genotyped with Animal Genetics Laboratory (AGL)-supplied chips including the 30K Neogen GGP and more recently, the new 35K Trop Beef chip. Listed in Table 1 are the number of animals genotyped in the project.

Table 1. Numbers of animals genotyped in the Project

Class	Location	N
Project animals	DAF	3,950
	DD	1,218
Industry natural mate sires		101
DD sires		35
Brahman BIN sires		71
SSF and Industry herds sires		140
AI Project sires		89
Total		5,604

The genotypes from the 35K chip were used in the transition from microsatellite-based parentage to SNP-based assignment. New diagnostic DNA SNP tests were also provided for poll/horn (see Table 2) and Pompe's disease. All SNP genotypes were checked for quality and loaded into the genomics database, and from there they have been made available to AGBU's genomic pipeline for BREEDPLAN single-step evaluations. This has greatly boosted the numbers of genotyped animals for the three breeds and has increased the size of the breed reference population for estimated SNP frequencies used in single-step and genomically-determined breed composition, for example using principal component analysis of the 3 breeds and other foundation breeds. For Droughtmaster and Santa Gertrudis the SNP-based test allows individual assessment of breed composition of the foundation breeds in these two tropical composites, enabling differences in Brahman content to be quantified.

The selection of sires used in the Project was not based on poll status but an effort was made in the purchase of natural mate bulls to source those that were polled or scurred. This was done to reflect the trend in industry towards more polled genetics. However, AI sires were selected primarily on the criterion of merit and importance so the frequency of polled/horn across breeds in the Project is not a population estimate but simply a reflection of the actual sample of sires used in the Project.

Table 2. Poll/horn SNP genotype frequency in 2015-2018 born DAF animals

Breed	SNP genotype		
	PP	PH	HH
Brahman	15	199	864
Droughtmaster	206	613	318
Santa Gertrudis	22	112	153
total	243	924	1,335

Table 2 shows that 47% of the Project born animals were PP or PH and therefore phenotypically would be polled or scurred. A new SNP based Pompe's disease test was also available and within these cohorts a total of 55 animals have been identified as carriers. This primarily occurred through the use of a few (unknown) carrier sires. To prevent the increased frequency of the Pompe's in the herds care has been taken in recent years when purchasing sires and AI semen.

4.2 Genetic linkages established

It is important in any genetic evaluation that the environmental influences can be removed to allow accurate genetic comparison of animals across groups (e.g. across herds). This is enabled by the existence of genetic links between herds, known as linkage. This linkage is usually generated through the use of common sires (i.e. paternal ½ sib linkage) and generally requires the use of several sires in a breed and the recording of both male and female progeny (depending on the trait of interest). Outlined below are the various genetic linkages that were generated in the Project through designed matings. Additional linkages were also generated in the Project through the maternal pedigrees (across locations and also with the Brahman BIN and Beef CRC projects) because the base cow herds at both Brian Pastures and Spyglass consisted of large numbers of females that were originally Beef CRC cows or their daughters from Brian Pastures, Toorak, Swans Lagoon and Belmont.

4.2.1 Links within Project

Linkages were established across Brian Pastures and Spyglass locations for both Brahmans and Droughtmasters through the use of the same AI sires and also through the natural mate bulls that were used at both locations. In total 75 sires had progeny (N=2,796) recorded at both DAF locations, of those 68 sires had daughters (N=1,284) at both locations.

To ensure accurate comparisons across the Northern Territory (NT) Brahman herds and DAF Brahman herds direct linkages were established through the AI using three NT sires (N prog = 58) and an additional sire has progeny in the 2019-calf crop. In addition, Project used sires (N=4) which used in the AI programs for the Douglas Daly (DD) herd generating 53 progeny, and 2 additional sires were represented in the 2019-drop of Douglas Daly calves.

4.2.2 Links to other research projects

AI matings were undertaken in early years of the project in Brahmans to create direct sire progeny linkage to the Brahman Breed Society MDC-funded (**P.PSH.0559**) BIN project (6 sires and 71 progeny) and to the Beef CRC northern fertility project (**B.NBP.0363**) for 4 sires generating 68 progeny. As the project progressed other projects emerged and common sires were added to the battery of AI sires used in this project. This included establishing international linkages in Brahmans, to enable the development of global evaluations, through the use of US sires (N=4) as well as sires nominated to generate increased linkage with Southern Africa (N=4 Brahman sires and currently 59 progeny). Links were also established with the large MDC satellite Brahman project at Kaiuroo (**MLA P.PSH.0921**) through purchase of natural mate bulls and an AI sire, as well as a sample of project sires have been used in AI breeding programs at Kaiuroo.

Over the course of the Project we have witnessed an increased awareness of the unique genetic resource in the NT Brahman selection line experiment and those genetics are increasing in usage in Brahman seedstock herds. This is allowing these genetics to contribute to the wider Brahman population and also creates increased genetic linkage between the NT herd and other performance BREEDPLAN herds.

4.2.3 Links to Industry

Direct genetic links were established to Smart Futures Fund Next Gen Beef Breeding Strategies for the Northern Australian Beef Industry project (Burns *et al.* 2016). This occurred though the purchase of young natural mate bulls or semen, and in some cases, Project AI sires were also used back in those herds. These were leading performance herds and this linkage was critical to ensure the benefits from genomic evaluations flowed back through industry.

Project bulls also provided indirect across-herd linkage in seedstock herds by generating head-to-head comparisons in the DAF Project herds. By design, the sires selected were highly used (this will continue to increase over time) and currently have 19,232 progeny (excluding Project generated progeny) in seedstock herds. This not only increases industry linkage it ensures close relatedness of current and future industry animals to the genomic reference population. The genotyping of the high accuracy industry sires also creates genomic linkages within the breeds.

To further strengthen the experimental design for Santa Gertrudis an additional 32 high EBV accuracy BREEDPLAN recorded cows were purchased from the leading performance stud Rosevale in 2015. These females were relocated to Brian Pastures where they became part of the Project herd. The progeny performance data from these cows will greatly enhance the direct breed comparisons. To date (up to 2017 born calves) the cows have generated a total of 65 calves that have been recorded head-to-head with the Brian Pastures generated calves.

4.3 High accuracy recording of female reproduction phenotypes

The achievements of this Project have been underpinned by the intensive recording of female reproduction traits that occurred through the application of regular ovarian scanning of large numbers of Project females. An experienced team (N=4) of ultrasound scanners used the technology on Project females on a very regular basis to identify the presence of a *corpus luteum* (CL) on the ovaries. The CL is a structure that develops on the ovary after a follicle has been shed. It produces progesterone and maintains a pregnancy, however it regresses if a pregnancy does not occur and the reproductive cycle continues. Our technicians were able to identify this structure quickly allowing several hundred females to be scanned on a single day, and on a regular basis (i.e. every 4-6 weeks). The first occurrence of the CL in a heifer and in a lactating first calf-cow from regular scanning were used to construct two key female reproduction traits from this Project viz, heifer age at puberty and anoestrous interval, respectively.

All maiden heifers (first mated as 2-year olds) and lactating 1st calf cows were naturally mated for approximately 12 weeks in large single-breed multi-sire mating groups. Females that were not pregnant or lost the calf were culled. All bulls were Bull Breeding Soundness Evaluation examined prior to the mating period each year to ensure high quality semen and physical health. Accurate birth dates were obtained from daily inspection.

4.3.1 Numbers of animals in the Project

The project commenced in September of 2013 with the calving of the #14 cohorts. At this time at the DAF stations there were three existing year cohorts of females #11, #12 and #13s which had been managed together since birth to allow valid recording for reproduction traits. The Project generated the first AI calf crop (males and females) at the end of 2014 (i.e. #15s) and then three more year cohorts (#16, #17, #18's) with the weaning of the #18s in April/May 2018 representing the end of the project.

An important design feature was the generation of progeny of key industry sires that were influential or emerging to build the size of the reference population for the 3 breeds. There were 89 AI sires used in the project and generated a total of 2,537 Project recorded progeny (males and females). Natural mate sires (N=200) were used for mating of all maiden and 1st calf cows (and backup of AI programs). These bulls were purchased to be of value to the genomic reference populations of the three breeds through consideration of their (paternal) pedigree (i.e. by influential sires not represented in AI team) and/or from influential studs previously not included in the Project. The progeny of these matings were also fully recorded in contemporary groups head-to-head with AI-generated calves and therefore

these data are useful data to further build the size of the reference populations and also contribute data for the development of multi-breed EBVs.

Total numbers of animals at DAF are presented in Table 3, numbers of females were generally lower in the first half of the Project given the extreme drought conditions in 2014 and 2015. However, more favourable seasons in the last 2-3 years have increased pregnancy rates, especially in first rebreed cows, and total numbers have begun to build, allowing older cows to be culled for age. Numbers for the NT Douglas Daly herd are presented in a section below.

Table 3. Numbers of animals by cohort (i.e. location and year) at DAF locations.

	Year drop							
Location	11[#t]	12[t]	13[t]	14	15	16	17	18
Brian Pastures	100	115	125	249	349	389	334	350
Spyglass	262	128	190	464	496	600	508	581

includes 67 Belmont Research Station purchased heifers split between BP and SG

[t] females only

4.3.2 Heifer ovarian scanning

Ovarian scanning to determine heifer age at puberty was performed on all heifers in DAF herds and in the NT DD herd. The frequency of ovarian scanning at the DAF herds are presented in Table 4. At Brian Pastures the five cohorts were scanned on average 11 times (range 9-14) and an average total duration of 14 months (range 9-17) with an average scanning frequency of an event every 5.7 weeks (range 5.3-6.6). At Spyglass the five cohorts were scanned on average 13.6 times (range 9-22) and an average total duration of 20 months (range 13-31) with an average scanning frequency of an event every 6.4 weeks (range 5.6-7.4). Over the whole Project the cohorts were scanned on average 12 times, for a total average duration of 17 months, and an average scanning frequency of every 6.1 weeks.

Table 4. Number and frequency of ovarian scanning for heifer age at puberty at DAF Project herds

Location	Cohort	Number of scanning events	Total scanning duration (mths)	Average scanning frequency (wks)
Brian Pastures	13	11	17	6.6
	14	8	10	5.6
	15	13	16	5.3
	16	9	12	5.9
	17	14	17	5.3
	Av.	11.0	14	5.7
Spyglass	13	14	22	6.9
	14	22	31	6.2
	15	13	18	6.0
	16	10	13	5.6
	17	9	15	7.4
	Av.	13.6	20	6.4
overall		12.3	17	6.1

At DD a total of 788 Brahman heifers had an age at puberty phenotype constructed using a combination of ovarian scanning (for presence of a CL) and pregnant foetal age from yearling mating (see section 4.5.1 below).

For all analyses the data was edited to remove records from crossbred, freemartins, scanning abnormalities/deformities, and if the heifer died or was missing. The trait age at puberty (AP) was

constructed as the number of days between the heifer's birth date and date of the first observed CL. After editing a total of 1,671 records were available from DAF herds with number of records 786, 643 and 260 for Brahman, Droughtmaster and Santa Gertrudis, respectively. Numbers of records and raw means by cohort for AP are presented in Table 5.

Table 5. Numbers of records and raw statistics by location and cohort for heifer age at puberty (days) from Project DAF herds.

location	cohort	N	mean	std	min	max
Brian Pastures	BP13	125	684.1	104.1	489	893
	BP14	108	484.3	86.7	347	768
	BP15	147	622.4	139.7	391	1003
	BP16	169	536.1	89.1	390	784
	BP17	155	608.9	135.0	341	875
	ALL BP	704	588.5	131.5	341	1003
Spyglass	SG13	102	824.0	105.5	716	1185
	SG14	186	736.4	131.9	455	1106
	SG15	202	677.2	113.3	456	1101
	SG16	129	569.3	95.7	398	754
	SG16_BP[#]	125	546.0	99.7	395	756
	SG17	222	609.9	123.4	386	894
	All SG	966	657.2	143.3	386.0	1185

[#] Spyglass heifers born at BP when their mothers were relocated from Spyglass due to drought

The final fixed effect model for heifer AP from all DAF generated data included: breed, cohort, animal age, dam group, age x cohort and cow group x age. These effects were used to produce adjusted AP records and these were submitted to ABRI's northern multi-breed database for inclusion in subsequent BREEDPLAN evaluations for the three breeds. Univariate estimates of the variance components and heritability are presented in Table 8. The results are very similar in magnitude to the estimates for the Tropical Composite (TCOMP) breed from the Beef CRC (Johnston *et al.* 2009) and demonstrate that the frequency of scanning has generated high quality phenotypes and that Project cattle are exhibiting similar genetic variation to that estimated previously in TCOMP.

4.3.3 Lactating first calf-cow scanning

Ovarian scanning records were used to determine the time to return to cyclicity in lactating first-calf cows at DAF and NT sites. At DAF sites ovarian scanning commenced at the end of the calving period and coincided with the start of the annual mating period. Cows were scanned regularly up to weaning of their calf (see Table 6) and any acyclic cows at this time were continued to be scanned (approximately every 8 weeks) until a CL was observed. At Brian Pastures the five year cohorts were scanned on average 4.6 times (range 4-5) prior to weaning (over an approximate 20 week period) and with an average of 2.2 (1-3) scanning events post-weaning, for an average total of 6.8 scanning events per cohort. At Spyglass the five cohorts were scanned on average 4.2 times (range 4-5) prior to weaning (approx. 20 week period) and an average of 3.2 (2-5) scanning events post-weaning, for an average total of 7.4 scanning events per cohort.

Table 6. Number and frequency of ovarian scanning for lactating first-calf cows at DAF herds

Location	Cohort	Number of scans prior weaning	Number of scans post-wean	Total
Brian Pastures	11	4	3	7

	12	5	1	6
	13	4	3	7
	14	5	1	6
	15	5	3	8
	Av.	4.6	2.2	6.8
Spyglass	11	4	3	7
	12	4	5	9
	13	4	4	8
	14	4	2	6
	15	5	2	7
	Av.	4.2	3.2	7.4
overall		4.4	3.7	7.1

At the Douglas Daly herd the breeding system of mating females as yearlings and then retaining those that don't calve has made the construction of anoestrous interval traits quite complex. A full description and analyses is provided in Section 4.5.2 below.

Data from DAF herds were edited to remove the records on cows that calved out of period, dry cows, those having twins, cow died/missing, and calf deaths or were poddied. The trait anoestrous interval (LAI) was constructed for each lactating cow as the number of days from the commencement of mating (i.e. bull-in date) until her first observed ovulation. For non-pregnant cows first ovulation was the date of first observed CL, and for pregnant cows, the foetal age was used to estimate the date of first ovulation. After editing a total of 1,142 records were available from DAF herds with the number of records of 504, 490 and 140 for Brahman, Droughtmaster and Santa Gertrudis, respectively. Number of records by location and cohort are presented in Table 7.

Table 7. Numbers of records and raw statistics by location and cohort for Anoestrous Interval (days) in lactating 1ˢᵗ-calf cows (3-year olds) from Project DAF herds.

location	cohort	N	mean	std	min	max
Brian Pastures	BP11	53	57.2	52.1	7	190
	BP_BEL11[#]	27	31.3	30.5	0	160
	BP12	93	85.5	63.1	0	204
	BP13	95	58.9	66.8	0	309
	BP14	87	40.3	28.6	16	174
	BP15	111	47.0	62.5	0	330
	all BP	466	56.1	58.2	0	330
Spyglass	SG11	147	146.4	85.9	0	349
	SG_BEL11[#]	30	62.5	61.2	0	188
	SG12	68	121.7	102.0	8	360
	SG13	122	124.5	81.9	3	343
	SG14	144	33.0	42.5	0	261
	SG15	165	29.2	25.9	0	201
	all SG	676	83.5	84.4	0	360

[#]Cohort of Brahman heifers purchased from Belmont Research Station, Rockhampton

Fixed effects were recorded and used as independent variables in the development of statistical models. Data was pooled across locations, breeds and years and analysed in fixed effect models considering: sire breed, cohort, dam breed group, sex and age group of calf (at foot) and all first-order interactions. The recording of LAI did not commence until the start of the annual mating period and therefore fixed effects associated with the calf at foot were also modelled. The calf age-group term

was constructed to account for the age of the calf and also season (i.e. month) of birth on the anoestrous interval of its mother.

The final model for LAI from DAF generated data included: breed, cohort, calf sex and calf month and calf month x cohort. Fixed effect solutions were used to produce adjusted records and these were submitted to ABRI's northern multi-breed database for inclusion in BREEDPLAN evaluations. Univariate estimates of the variance components and heritability are presented in Table 8. The additive variance and heritability (h^2 = 0.22) is lower than the estimates from Beef CRC (Tropical Composites = 0.26, Brahman = 0.51) and most likely reflect the relatively high levels of early cyclicity and reduced LAI as a result of very good seasons experienced in the Project in the last few years, particularly at Spyglass.

Table 8. Variances and heritability estimates for heifer age at puberty and first-calf cow anoestrous interval from Project herds.

Trait	Va	Ve	Vp	h^2(se)
Heifer age at puberty (d)	5,688	5,050	10,738	0.53 (0.07)
Lactation anoestrous interval (d)	853	2,991	3,844	0.22 (0.07)

4.3.4 Mating outcomes – natural mates

All maiden and lactating first-calf cows were naturally mated in multi-sire groups for approximately 12 weeks. The start of mating date differed across locations to reflect seasonal differences. Cows were pregnancy tested and foetal aged and all non-pregnant females were culled. All females were monitored at calving on a daily basis to collect accurate date of birth, calving difficulties scores and calf deaths (plus other Project traits). Calves were branded (and castrated) at approximately four months of age and weaned at an average of 6 months. This data allowed the construction of several mating outcome traits for heifers and first-calf cows including: pregnancy rate, foetal age, calving rate, and DC and weaning rate. Days to calving records from these first two natural matings were submitted to BREEDPLAN databases for inclusion in the computation of the DC EBV.

Summary reproductive rates (and losses as a percentage of total females mated) are presented in Fig. 1 for maidens (N = 1,165) and 1st calf cows (N = 627) at the two DAF locations. On average maiden pregnancy rate was 87% with BP slightly higher on average than Spyglass and with a resultant calving rate of 84% and a 77% weaning rate, representing a calf loss (of those born) of 7.4%. For first calvers, the average pregnancy rate was 67% (again lower at Spyglass), the average calving and weaning rates were 66 and 60% respectively, with 8% calf losses to weaning.
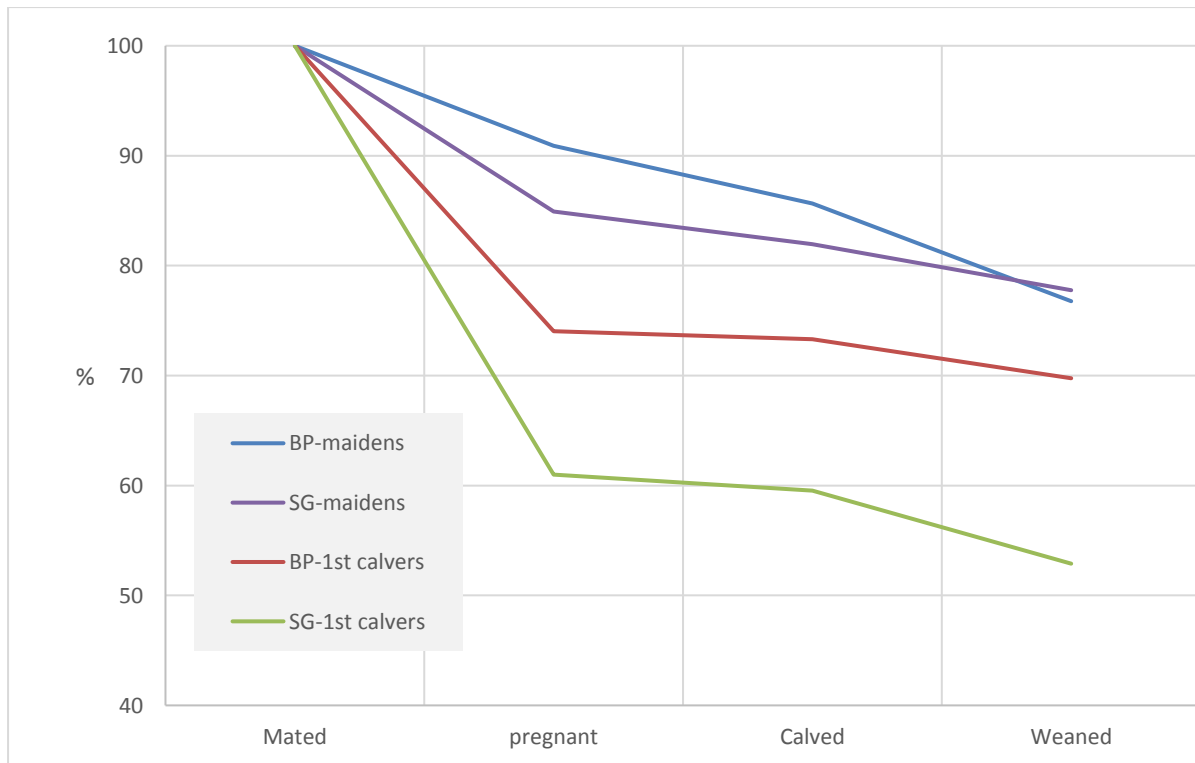
Fig. 1. Pregnancy, calving and weaning percentages (of total mated) for maiden heifers and 1st calf cows at Brian Pastures and Spyglass.

4.3.5 Mating outcomes – Artificial Insemination

All cows 4-years or older in the DAF herds each year were eligible to enter the Project's AI program. A modified 2-round fixed-time program was implemented to enable the introduction of outside genetics on key sires in the three breeds. During the Project the early years were extremely challenging where cow body condition scores were lower than ideal but the programs went ahead in an attempt to generate the experimental progeny and to maintain the Project design. AI sires were used across locations and across years in an attempt to generate approximately 30 progeny/sire. Over the Project the total number of cows inseminated was 2,744 with some inseminated twice in a given year and some cows had repeat records over years. From these cows 54.4% resulted in an AI calf born and 49.3% were weaned (or 9.3% calf losses of those born). The calving rate per straw of semen was 36%. There were no differences between Brian Pastures and Spyglass.

4.4 NT Brahman selection line traits

The Northern Territory (NT) Brahman Selection line experiment is a unique genetic resource that has been using a phenotypic selection index for male and female traits for more than 30 years (Schatz *et al.* 2011). The herd is fully BREEDPLAN recorded and has been submitting DC and scrotal circumference records for many years. The selection line responses and Brahman BREEDPLAN EBV genetic trends (not shown here) show that the herd has made significant genetic improvement in reproduction over the years. Therefore it was important to include the herd in this Project to obtain the genomic profiles on the herd and to use ovarian scanning to collect improved phenotypes for the early female reproduction traits on the breeding heifer component of the experiment that are run on the Douglas Daly (DD) research farm. The females at the DD herd are the yearling, 2- and 3-year old females of the Selection line. Some of the females are generated at Douglas however the majority of the weaner

heifers are generated at the other NT research herd at Victoria River Research Station (known as Kidman Springs) where all the mature cows from the experiment are run.

Heifers were ovarian scanned to identify the CL and foetal age (as at the DAF locations) however the intense wet season experienced during the summer mating period has restricted the ability to muster and record these traits regularly. Therefore, modifications were required in the construction of the traits to reflect the reduced levels of recording. The mating management of the herd also presents additional complexities in trait development/definitions. The herd is yearling mated with all heifers exposed to natural mate bulls at about 14 months of age. A proportion (av. = 38%) conceived at this yearling mating and are calved out and are then re-mated as lactating 2-year olds. Those heifers that fail to conceive as yearling, and are pubertal as 2-year old, are eligible to be AI mated, the remainder (i.e. not pubertal into mating as 2-year olds) are naturally mated. The age at puberty data is not greatly affected by this mating management regime but traits associated with lactation anoestrous interval are affected by parity and type of mating. This required modifications to trait definitions as detailed below.

4.4.1 Heifer age at puberty

Data extracts from DD cohorts from 2011 to 2018 yielded a total of 6,678 records on 1,343 animals and after editing to include those with a puberty scanning measurement recorded, leaving 6,122 records on 787 animals.

Age at puberty (AP) was defined as the age that a CL is observed or was based on pregnancy data given the heifers were exposed to yearling mating. AP based on pregnancy was calculated by the first pregnancy record per animal and the conception date was determined using the estimated foetal age of the pregnancy. The estimated age at conception date was then used as the AP record. The final AP trait was defined as the earliest age of either an observed CL or a pregnancy. All heifers continued to be evaluated through to their 2nd mating (as 2-year olds). Table 9 shows numbers of records per year cohort and the breakdown of AP by pregnancy records and observed CL and Fig. 12 provides a plot of the raw AP pooled across all cohorts.

Table 9. Description of data used to construct heifer AP records by cohort for DD herd

| Cohort	AP from a preg record				AP from CL record				AP from preg or CL record			
	N	age	min	max	N	age	min	max	N	age	min	max
DD11	62	646.4	412	1146	3	1349	1298	1377	62	646.4	412	1146
DD12	102	727.2	420	894	16	1194.4	894	1326	102	727.2	420	894
DD13	105	765.7	411	1159	72	761.0	464	1357	107	706.6	411	888
DD14	102	591.1	387	875	74	637.4	392	1230	108	551.7	387	827
DD15	99	598.8	384	1147	72	610.6	387	1049	101	520.6	384	813
DD16	146	643.0	401	883	124	691.8	373	1101	150	595.2	373	952
DD17	56	487.5	386	548	79	512.7	367	729	105	501.8	367	729
ALL	674	648.4	384	1159	441	671.0	367	1377	**735**	**604.0**	**367**	**1146**
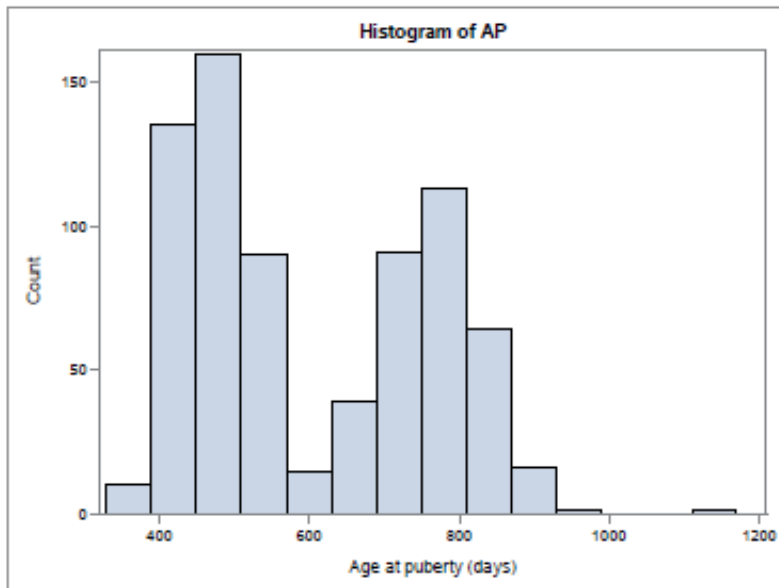
Fig. 12. Raw distribution of heifer age at puberty in Douglas Daly herd

A total of 735 heifer AP records were available for analysis after editing. Fixed effects models were developed from the full model that contained terms for cohort, birth month origin, age of dam class (aodc), and first-order interactions (*viz:* cohort x birth month, cohort x origin, cohort x aodc, birth month x origin, birth month x aodc, origin x aodc). The final model included significant terms for cohort and origin. Origin was used to define heifers born at DD or Kidman Springs.

Variance components for heifer AP were estimated using an animal model, results are presented in Table 10. Fitting a maternal genetic effect was not significant based on log-likelihood (LogL) ratio test. The size of the additive variance was similar to Johnston *et al.* (2009) however the heritability was lower reflecting the larger residual variance, indicating reduced precision in the measure that was likely due to the lower frequency of scanning and also the reliance of foetal aging to determine first observed CL.

Table 10. Variances and heritability estimates for heifer age at puberty in DD Brahmans

model	Va	Vm	Ve	Vp	h^2(se)	h^2m(se)	LogL
Animal	5,432	-	11,893	17,325	0.31 (0.08)	-	-3,860.03
Animal + maternal	5,013	662	11,684	17,360	0.29 (0.08)	0.04 (0.05)	-3,859.57

The records from DD for AP were then considered for pooling with AP data from DAF Project data and the Beef CRC (DAFCRC). Variance components for DAFCRC records animals and pooled with the DD data are presented in Table 11. Results showed that pooling the datasets had a significant effect on the variance component estimates. When further divided into just Brahman animals in the two populations the estimates were more similar. These records were then analysed in a bivariate analysis with the full multi-breed extract and again with Brahman only datasets. Similar variances were estimated with a genetic correlation of 0.90 (0.62) across datasets.

Table 11. Variances and heritability estimates for heifer age at puberty from 2 populations and from pooled datasets

Dataset	Va	Ve	Vp	h^2(se)
Douglas Daly (DD)	5,432	11,893	17,325	0.31 (0.08)
DAF + CRC (DAFCRC)	6,333	5,007	11,340	0.56 (0.04)
Pooled (DD + DAFCRC)	5,576	6,616	12,192	0.46 (0.04)

DAFCRC Brahman	5,607	5,779	11,386	0.49 (0.06)
Pooled Brahman (DD + DAFCRC)	4,816	7,987	12,803	0.38 (0.04)

Based on these variance and genetic correlation estimates, the decision was made to pool the datasets for AP and predict a joint set of AP EBVs. Fig. 13 plots AP EBVs for heifers with records and Fig. 14 for sires. The ability to make reliable genetic comparisons across the populations depends on the level of genetic linkage across the herds (i.e. DAF herds and DD) to allow direct comparison of EBVs. Currently there are only four sires with progeny (i.e. daughters) recorded for AP at DD and also at DAF (see Table 12) and these sires have AP EBVs spread across the range of EBVs.

Table 13 shows the average AP EBV of heifers with records from the joint evaluation for the two populations. On average the DD heifer has an AP EBV 21.7d younger than the Project and Beef CRC population. Fig. 15 and Fig. 16 plots the distribution of AP EBVs by location for all animals and sires, respectively. Again the plots show a lower mean EBV for AP from the DD herd, likely reflecting the selection that has occurred. This is further demonstrated in Table 14 showing Brahman sire EBVs from DD and the Project sires had a mean AP EBV difference of 41.8d.

Table 12. Common sires in DD and DAF herds with daughters with AP records

		Number of daughters	
Sire ident	AP EBV	DD	DAF
LAN4999MM	-136.0	3	33
TTS973273M	2.9	4	56
DRF15431M	-169.0	32	12
CBV10-7694M	41.0	7	26

Table 13. Average AP EBV (d) for Brahman females with a records

Dataset	N	AP EBV	std	range
Douglas Daly (DD)	781	-26.9	57.3	-169.7 to 136.3
DAFCRC	1,988	-5.2	49.4	-158.4 to 155.8
Pooled (DD+DAFCRC)	2,769	-11.3	52.6	-169.7 to 155.8
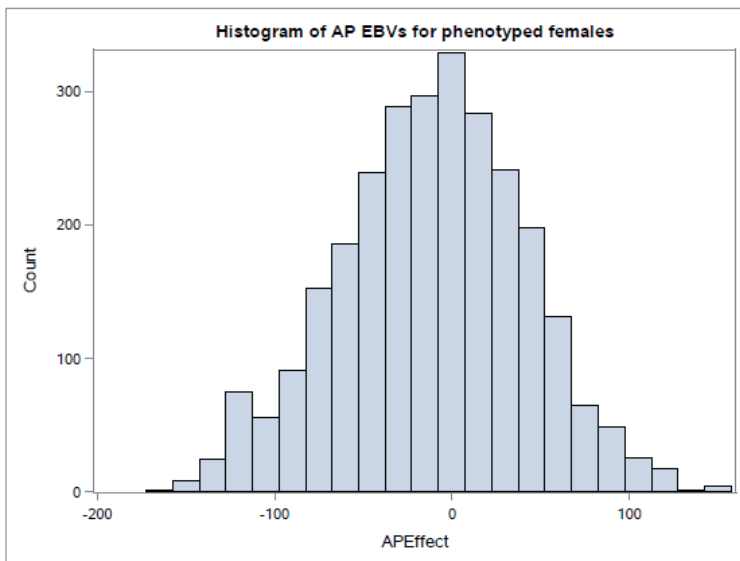
Fig. 13. Distribution of Brahman heifer AP EBVs for all animals with AP record in DD and DAFCRC datasets
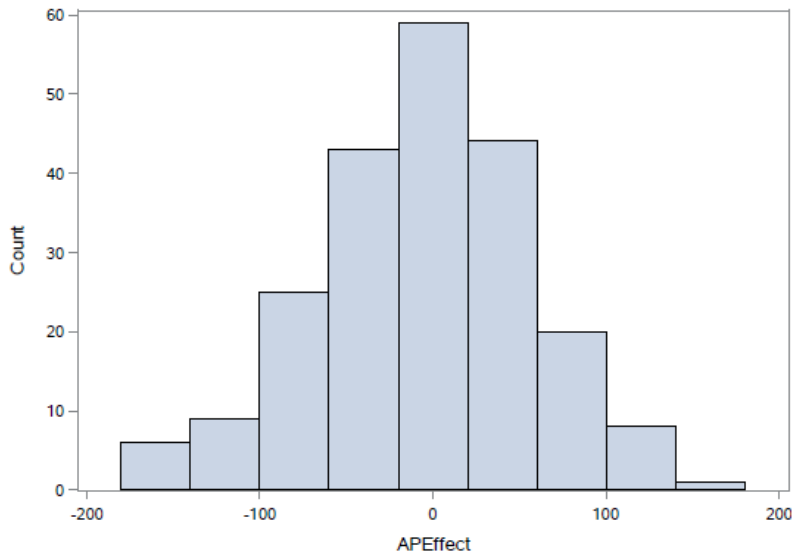
Fig. 14. Brahman sire AP EBV distribution pooled across pooled datasets (DD + DAFCRC)
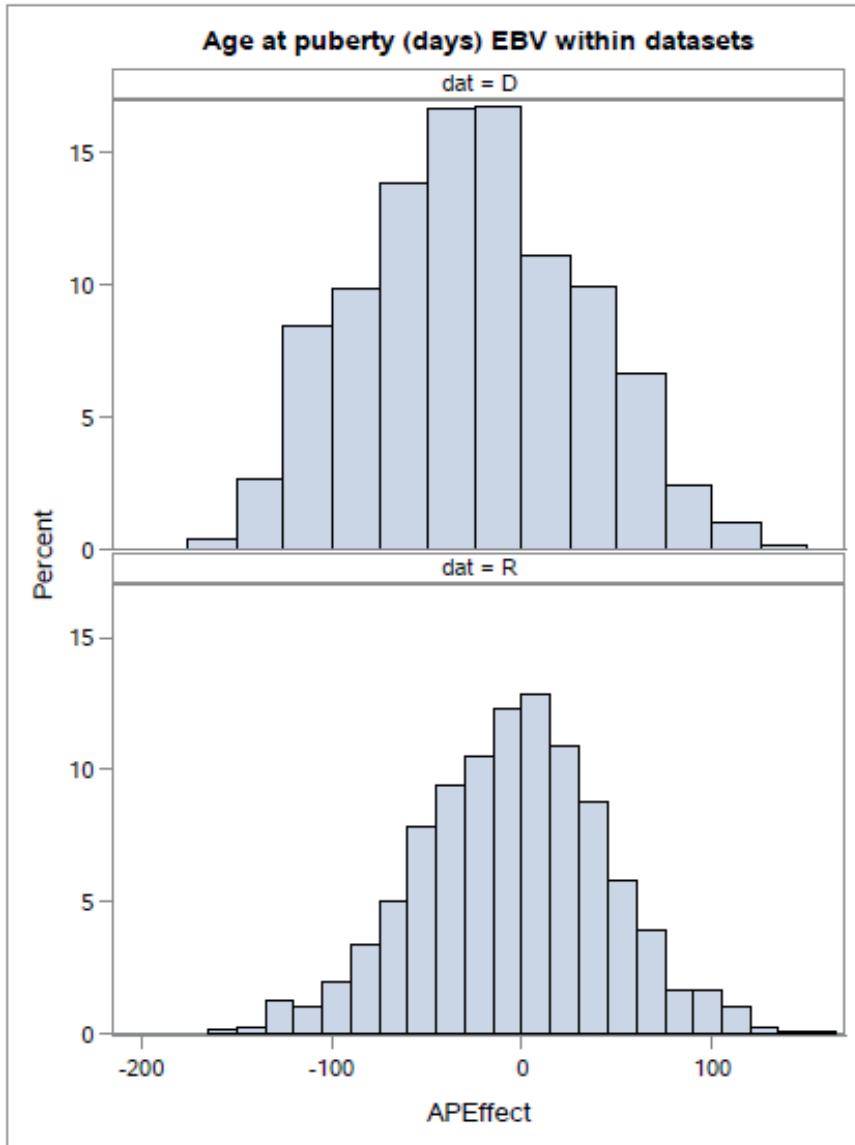
Fig. 15. Distribution of AP EBV by location all DAF animals (dat=R) and Douglas Daly (dat=D)

Table 14. Age at Puberty EBVs for Brahman sires with daughters with records from DD and DAF herds

Dataset	n	AP EBV	std	Range
All	215	-6.1	62.0	-173.3 to 155.6
DD (avg N dtr=9.9 (1 to 41)	72	-28.8	66.4	-173.3 to 120.9
DD ≥ 10 dtrs	29	-45.1	73.4	-173.3 to 118.5
DAF sires (avg N dtr=13.7 (1 to 57)	147	3.4	58.8	-169.1 to 155.6
DAF sires ≥ 10 dtrs	80	-3.3	69.1	-169.1 to 155.6
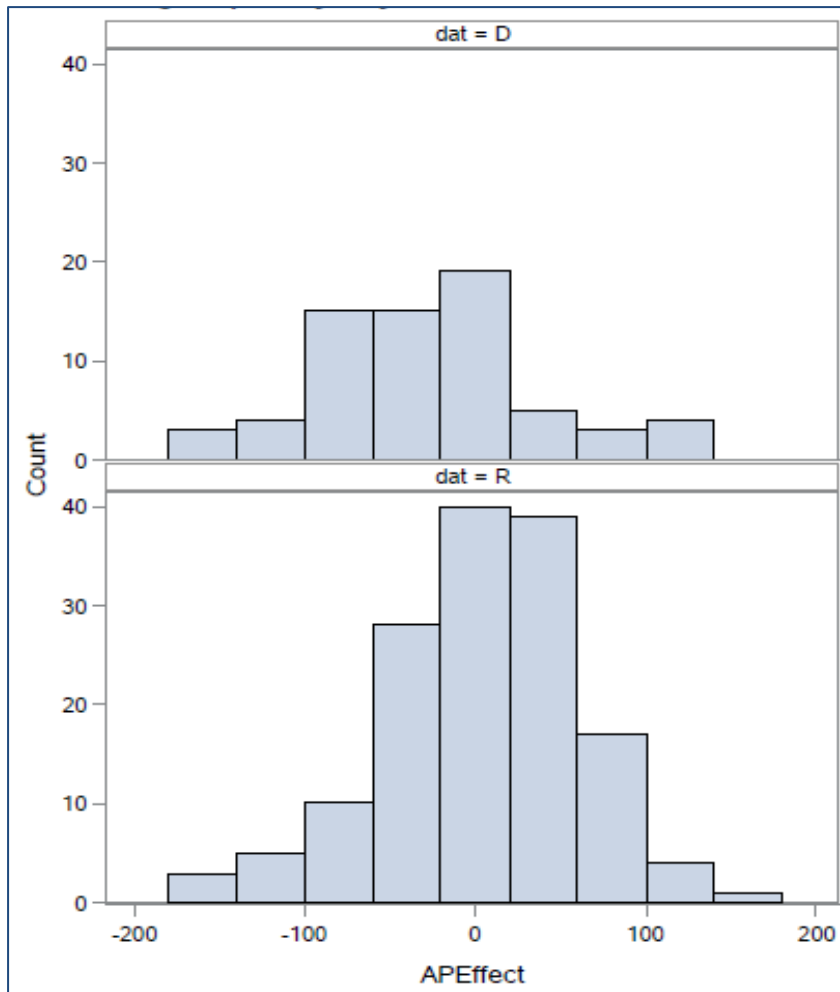
Fig. 16. Sire AP EBV distribution for DAF (dat=R) and Douglas Daly (dat=D) datasets

The results and the distribution of EBVs suggests the pooling of data appears to have produced sensible results but the relativity of the EBVs from DD and the rest of the Brahman data depends entirely on the across herd genetic linkage to correctly remove environmental effects and correctly align the genetic merit of the two populations. Therefore, it is important to continue to strengthen the genetic linkage to ensure unbiased comparison across herds. Given the parameters stated above, it is recommended that the 735 heifer AP edited records from DD can be submitted to BREEDPLAN for inclusion in the Brahman single-step genetic evaluation.

4.4.2 Mating outcomes and anoestrous interval

Ovarian scan records were extracted on a total of 786 females from 6 mating cohorts at DD. Data was merged with mating records and full calving details to allow the construction of phenotypes anoestrous interval for lactating females from natural mating. The data were edited to remove mating records on cows that had been in the AI program (irrespective if they conceived or not), cows that were dry (i.e. failed to wean a calf), and any cows that reared twins. This resulted in a total of 654 cows (in cohorts 11 to 16) that were available for analyses. The structure of the data and modelling of fixed effects was challenging given the mating design and cow culling management. The management of the DD herd included all heifers were exposed to natural mating at yearling age. Those that calved were re-mated using natural service as 2-year olds and were re-mated again as 3-year olds (AI or natural) even if they failed to get pregnant from the previous mating (as a lactating 2-year olds). Those heifers that failed to conceive as yearling and were known to be cycling were used in an AI program. If they conceived and calved they were re-mated as 3-year olds. Those heifers not eligible for the AI

program (i.e. not cycling at start of joining) were naturally mated. Any 2-year old that did not get pregnant as a yearling and failed to conceive as a 3-year old was culled.

On average yearling mating (Year 1) resulted in a 38% calving rate (range 15-51% across six cohorts). A total of 224 heifers had a valid calving, 21 calved but failed to wean and 409 failed to calve. For those heifers that calved from yearling mating (and had the opportunity to calve again) on average 77% calved again from their 2nd mating as 2-years old (range across five cohorts 60-81%) and of those a further 78% calved to their next mating (62-88% across four cohort) as lactating 3-year olds and these (i.e. 3 calves from 3 matings) represented only 17% of total cows (from the four cohorts with complete records).

For those heifers that did not calve at 2 years of age (i.e. failed yearling mating) and were naturally mated, on average 83% calved as 3-year olds. For this group of cows (plus those successful AI mated at 2 years) that were naturally mated, 59% calved again as 4-year olds. For all Year 2 matings, there were 261 with a valid calving, 84 did not calved, 11 that calved but failed to wean, 133 calving as a result of AI, 2 that had multiple births and 10 that were mated with AI but either did not calve or calved as a result of natural mating. For all Year 3 matings there were 226 with a valid calving, 158 that did not calved, 2 that calved but failed to wean, 11 calving as a result of AI and 1 that were mated with AI but either did not calve or calved as a result of natural mating.

The construction of the anoestrous interval for each cow required consideration the cow's age, parity, lactation status and mating type (i.e. natural versus AI). Ovarian scans for presence of a CL and or a foetal age from a successful pregnancy were used to estimate the date of recycling (or estimated conception date) in lactating cows after the commencement of the annual mating period. Lactation Anoestrous Interval (LAI) was computed as the difference from estimated cycling date and start of annual mating date from a natural mating. This trait computation differed from the DAF herds that were ovarian scanned more regularly, particularly during the mating period.

Table 15 provides a summary of the various record structures from each cohort for calculating the LAI record for each cow from first re-breed (as a 2-year old) for heifers that successfully calved from yearling mating. Any cow that failed to record a CL or a pregnancy was assigned a "penalty" cycling date (plus 2 cycles = 42 days) longer than the last valid LAI record. This included 18 cows that were assigned a penalty record for LAI of 332 days. These cows may have been still acyclic or simply missed being identified with a CL due to infrequent scanning. Fig. 17 plots the raw distribution of LAI records from rebreed as 2-year olds.

Table 15. Description of data used to construct lactation anoestrous interval for 2-year old cows by cohort at Douglas Daly.

Cohort	Number cows calved	Number cows weaning a calf	Number records from preg test	%	Number records from CL	%	Number cows with a resultant calf	%
DD11	33	29	29	100.0	0	0.0	25	75.8
DD12	22	21	15	71.4	6	28.6	15	68.2
DD13	16	15	10	66.7	5	33.3	10	62.5
DD14	41	33	26	78.8	7	21.2	32	78.0
DD15	48	48	32	66.7	16	33.3	30	62.5
DD16	61	57	25	43.9	32	56.1	-	-
All	221	203	137	67.5	66	32.5	112	70.0
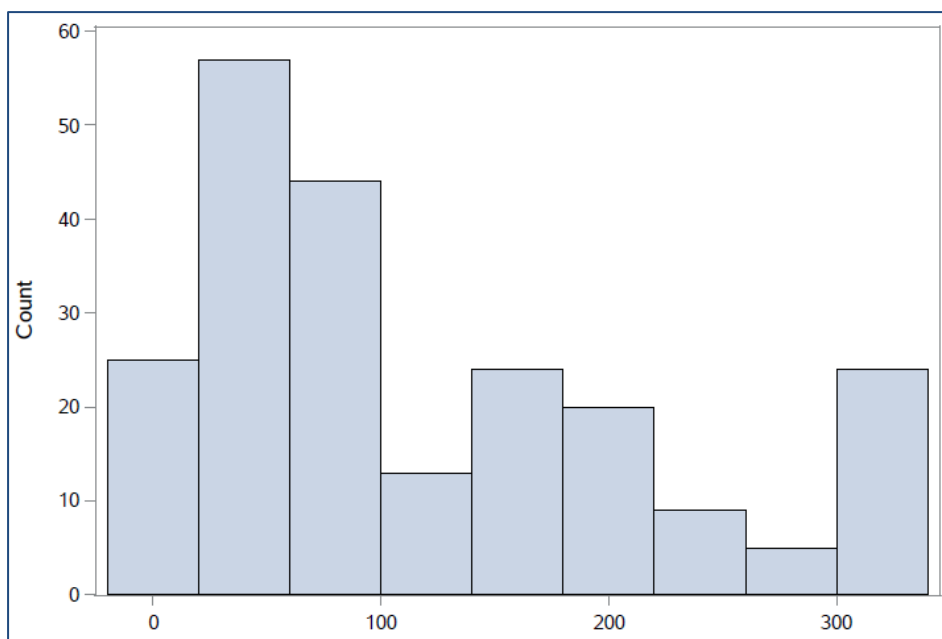
Fig. 17. Distribution of Lactation Anoestrous Interval from 2-year old cows in Douglas Daly herd.

Mating of lactating 3-year olds was a mix of cows on their second re-breed (i.e. with their 2nd calf at foot after a successful yearling mating) and those on their first re-breed. Table 16 provides a summary of the various record structures from each cohort for calculating the LAI record for each cow. Any cow that failed to record a CL or a pregnancy was assigned a "penalty" cycling date (plus 2 cycles = 42 days) longer than the last valid record and included a total of 50 cows that were assigned a penalty record for LAI of 226 days. Again, these may have been still acyclic or simply missed due to infrequent scanning. Fig. 18 plots the raw distribution of LAI records from 3-year olds. Table 17 is a subset of the total cows in Table 16 and provides a breakdown of the structure of the data for those cows on their 2nd re-breed only.

Table 16. Description of data used to construct lactation anoestrous interval for all 3-year old cows by cohort at Douglas Daly

Cohort	Number cows calved	Number cows weaning a calf	Number records from preg test	%	Number records from CL	%	Number cows with a resultant calf	%
DD11	33	30	29	96.7	1	3.3	28	84.8
DD12	61	57	47	82.5	10	17.5	35	57.4
DD13	62	38	32	84.2	6	15.8	45	72.6
DD14	60	43	42	97.7	1	2.3	37	61.7
DD15	45	43	41	95.3	2	4.7	-	-
DD16	-	-	-	-	-	-	-	-
All	261	211	191	90.5	20	9.5	145	67.1

Table 17. Description of data used to construct lactation anoestrous interval for 3-year old cows on their 2nd calf by cohort at Douglas Daly

Cohort	Number cows calved	Number cows weaning a calf	Number records from preg test	%	Number records from CL	%	Number cows with a resultant calf	%

DD11	26	22	22	100	0	0	22	84.6
DD12	17	15	12	80	3	20	12	70.6
DD13	10	5	5	100	0	0	9	90
DD14	37	25	25	100	0	0	27	73.0
DD15	35	29	28	96.6	1	3.4	-	-
DD16	-	-	-	-	-	-	-	-
All	123	96	92	95.8	4	4.2	70	78.8
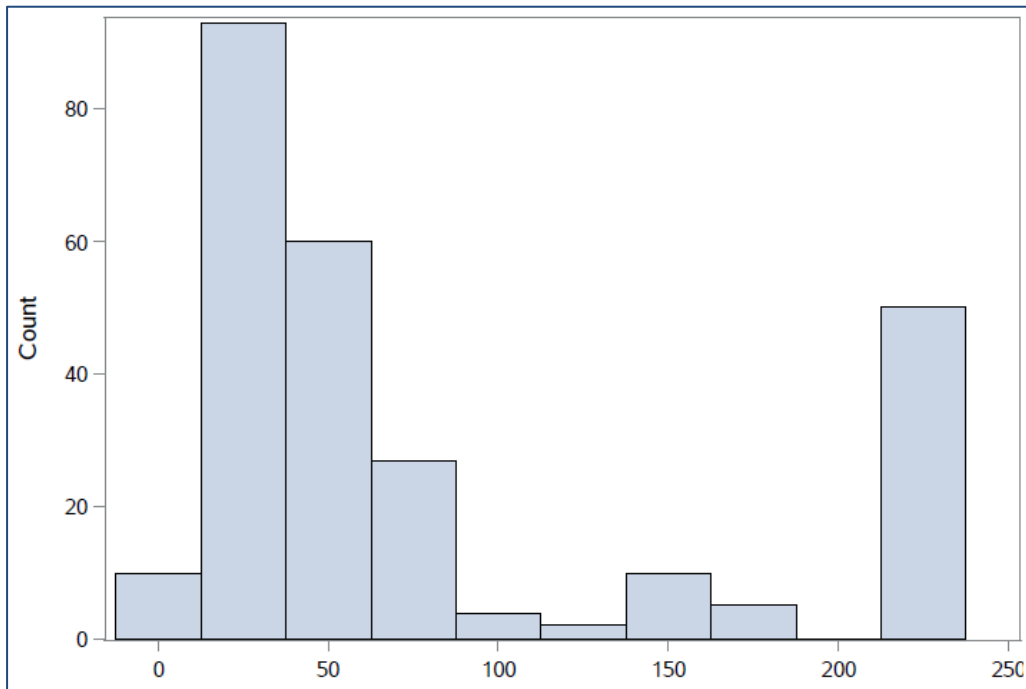
Fig. 18. Distribution of Anoestrous Interval in 3-year old cows in Douglas Daly herd

The LAI records statistics for rebreed as 2-year olds and for 3-year olds (by parity) are presented in Table 18. The mean LAI was longer in 2-year olds compared to 3-year olds, and LAI for those with their second calf at 3 years of age were shorter than those on their first re-breed.

Table 18. Raw statistics for lactation anoestrous interval in lactating 2- and 3-year old cows.

Age	parity	N LAI	Mean	std	min	max
2-year old	1	221	122.3	101.4	1.8	332
3-year old	1	138	98.2	83.1	1.8	226
	2	123	61.1	68.4	1.0	226
	both	261	80.7	78.6	1.0	226

The anoestrous records were pooled and were analysed in SAS with the full model including terms for: cow contemporary group (cow birth cohort and origin), cow birth month, sex of calf (at foot), calf birth month and cow calving history and all 1st order interactions. Sire of the cow was included as a random effect. The term for cow mating history was included to account for the different ages and parity of the cows and was based on the mating number (i.e. 1, 2) and the number of calves (i.e. 1 or 2). Therefore 3 levels (i.e. LA11, LA21, LA22) existed in the dataset and the term was included as a fixed effect. The final model included cow contemporary + calving history + calf birth month. Cow calving history was also used to split the records and consider them as separate traits.

Least squares means (LSM) for calving history were LA11=127 days, LA21=88 days and LA22=73 days showing longer return to cycling in the 2-year olds (yearling mated heifers) compared to 3-year olds, whereas the LAI for those previously calving as yearling was shorter than for those first calving at 3-years old. This was a further indication of the genetic superiority of those heifers getting pregnant as yearlings, as they displayed higher calving rates and shorter lactation anoestrous intervals. Calf birth month LSMs were 84 days for Oct born, 94 days for November and 110 days for December illustrating an age of calf effect and month of birth. Sire LSMs were generated for LA11 and LA22 analyses and sires with five or more daughters are plotted in Fig 19. Large differences exist between sires for LA11, and in the subset of sires also with daughters at LA22 suggesting some possible re-ranking, which indicate LAI is a different trait in the yearling females compared to in the 3-year olds. This will need to be confirmed with additional data and may warrant considering them as separate traits in a genetic analysis.
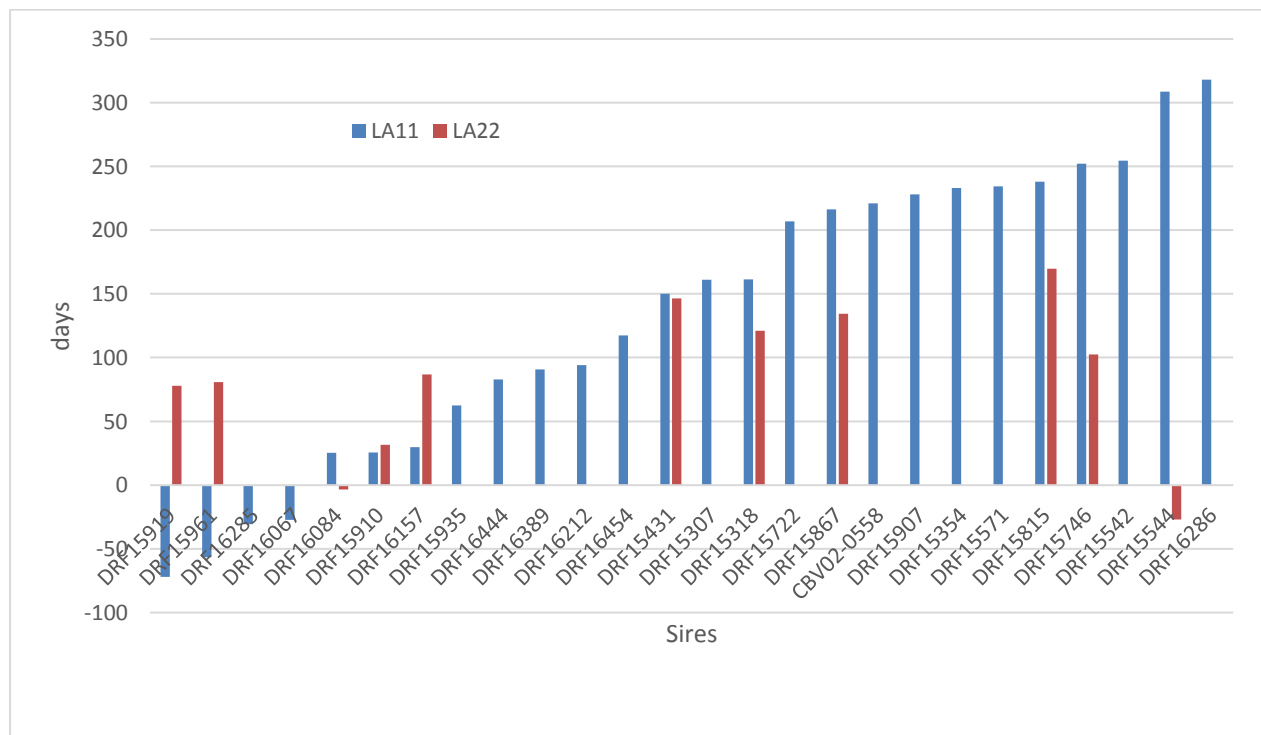
Fig 19. Brahman sire least squares means for Lactation Anoestrous Interval in 1st (LA11) and 2nd (LA22) calf daughters at the Douglas Daly herd.

Genetic parameter estimates for LAI were not obtained due to low numbers and there is a need to further separate the data based on cow calving history. Issues also existed with possible selection bias with records from the 2nd mating due to the use of AI as these programs occurred earlier than natural mating, and was only undertaken on cows showing a CL (and not pregnant). Records for LA22 are also censored for those yearlings mated that calve but fail to conceive at their 2nd mating. Therefore to account for the selection/censoring of the later records the analyses will need to run (when sufficient records are available in the future) in bivariate models treating LA11 and LA22 as separate traits. However, these preliminary data summaries and analyses show the likely genetic variation for these traits and possible genetic correlations with heifer age at puberty.

4.4.3 Data to BREEDPLAN

At this stage it is apparent that more several hundred more records will be required to correctly model LAI in this herd, but at this stage there is evidence of large differences in yearling conception rates and re-breed rates, and the successful combination of the two, yielding some unique genetics representing

less than 20% of the total data. Estimation of genetic correlation will assist in understanding how these reproduction genetics are associated with key production traits e.g. young animal weights and cow weight however will require several more years of data to generate datasets of sufficient size (i.e. more than 1,000) to obtain estimates with suitable standard errors. Therefore, based on the current data and results it is recommended that the heifer AP phenotypes from DD should be submitted to Brahman BREEDPLAN. However, at this stage the LAI data needs additional records and analyses before any recommendations on the suitability of the data can be made. As well as additional cohorts being recorded at DD, progression towards the utilisation of DD data in BREEDPLAN analyses would be increased if future data collection in this herd included more frequent scanning, including earlier foetal aging.

4.5 Gestation length

In tropical beef breeds very little data exists on gestation length, primarily due to the low levels of AI and lack of data captured in performance programs. Given the large number of AI-generated calves in the Project, and the accurate recording of birth dates, the computation of gestation length was undertaken. Earlier analyses of gestation length records generated in the first two years of the Project were published (Johnston and Grant 2017).

The data set used in this analysis had birth weight and weaning weight records for 4,320 calves born between 2014 and 2018 and gestation length records for 1,501 calves (AI only) born between 2015 and 2018. Records were edited to remove for multiple births, suspected premature births, incomplete information (sex, date of birth, sire or dam unknown, dam date of birth) or where matings resulted in a crossbred calf either as a result of an AI straw mix ups or cows in the wrong mating groups. The final dataset contained 1,469 gestation length records sired by 67 sires. The average sire family group was 21.9 progeny per sire and ranged from 3 to 49. After edits, 3,715 records remained for birth weight, of which 3,090 also had weaning weight recorded. Birth weight records were sired by 153 sires, with the average sire family group being 24.3 progeny per sire and ranging from 1 to 101. Raw data summaries for the three traits are presented in Appendix 2.

Initial statistical models for gestation length included the calf cohort (a concatenation of the AI herd, birth herd, Project herd and birth year), cow lactation status (wet or dry), calf sex (male or female), insemination round conceived (1st or 2nd), calf sire (N= 33 Brahman, 24 Droughtmaster and 10 Santa Gertrudis), cow group (a concatenation of cow Project herd, cow breed type, cow herd of origin and cow age group) and all first-order interactions. Cow was fitted as a random effect. In most cases the herd information in the calf cohort was the same. However, a bad season at Spyglass meant that some of the 2016 born Spyglass calves were mated at Spyglass but calved at Brian Pastures. The cows were then re-mated at Brian Pastures before cows and the 2016 born calves were transferred back to Spyglass, where the 2017 calves were subsequently born. There was also a confounding between the age of the cow and her breed type with Tropical Composite cows tending to be the older cows, therefore to account for cow age, the following three age groups were created; cows born 2001-2005, 2006-2009 and 2010-2013. The final model for gestation length included sire breed, sex, calf cohort, sire breed x calf cohort and sire breed x sex as fixed effects. Fixed effect models for birth weight and weaning weight also determined using the same procedures (not reported here).

Genetic parameters were estimated using univariate mixed linear animal models in ASReml (Gilmour *et al.* 2009) with data from the three sire breeds pooled into a single dataset. All these traits have maternal effects and these were partitioned (where possible) to estimate maternal heritabilities (h$_m^2$) and maternal permanent environmental variances (Vpe). However, maternal effects for gestation length were not able to be partitioned as the current data structure does not include females that were born as a result of AI that have progeny generate from AI matings. Therefore, only the maternal

permanent environment was included as an additional random effect for gestation length (see Tables 19 and 20). A series of bi-variate models were used to estimate the genetic and phenotypic correlations between gestation length, birth weight and weaning weight (Table 21).

Table 19. Variance components and heritability estimates for gestation length, birth and weaning in Brian Pastures-born animals

Trait	Va	Vm	Vpe	Ve	Vp	h^2 (se)	h_m^2 (se)
Gestation length (d)	18.6	-	5.6	6.4	30.6	0.61 (0.13)	0.18 (0.10)
Birth weight (kg)	12.0	1.2	1.6	8.8	23.5	0.51 (0.08)	0.05 (0.05)
Weaning weight (kg)	205.2	23.9	78.8	89.8	397.8	0.52 (0.11)	0.06 (0.07)

Table 20. Variance components and heritability estimates for gestation length, birth and weaning in Spyglass-born animals

Trait	Va	Vm	Vpe	Ve	Vp	h^2 (se)	h_m^2 (se)
Gestation length (d)	23.7	-	0.0	5.4	29.1	0.81 (0.10)	0
Birth weight (kg)	12.4	2.2	0.0	7.0	21.5	0.57 (0.06)	0.10 (0.03)
Weaning weight (kg)	179.9	52.0	28.2	127.1	387.3	0.46 (0.07)	0.13 (0.06)

Table 21. Genetic (above) and phenotypic (below) correlations between gestation length, birth and weaning weights.

Trait	GL	BWT	WWT
Gestation length (GL, d)	-	0.39 (0.09)	-0.02 (0.11)
Birth weight (BWT, kg)	0.29 (0.03)	-	0.73 (0.05)
Weaning weight (WWT, kg)	0.03 (0.04)	0.48 (0.02)	-

Gestation length showed considerable variation and was highly heritable. At Spyglass too few cows had repeat records to allow the partitioning of the maternal PE or maternal effect, and this has most likely contributed to the high heritability estimate. Gestation Length was positively moderately correlated with birth weight (r_g = 0.39) but was not genetically correlated with weaning weight. Jeyaruban *et al.* (2016) reported genetic correlations in Australian temperate beef breeds between gestation length and birth weight (direct effects) ranging from 0.15 to 0.45. Gestation length is of interest because of its possible association with calf losses. Dystocia was evident in the Project and calf losses have been recorded throughout, however no analyses have been performed to date. Bunter *et al.* (2014) showed that low birth weight was a significant risk factor for calf losses and these parameters suggest it could be associated with shorter gestation lengths.

4.6 *GxE* investigations

The experimental design included the ability to estimate genetic correlations across the DAF locations, and thereby quantify the existence of genotype by environment interactions (GxE). These estimates provide knowledge that will be important in the ongoing development of genetic evaluations, especially as they move towards combined across-breed evaluations. It is critical to understand whether genetics (i.e. breeds or animals within a breed) change in performance (and therefore re-rankings) as a result of differences in the environment (e.g. benign vs harsh).

To investigate the magnitude of possible GxE the Project records for the Brahman and Droughtmaster from Brian Pastures and Spyglass were used. At both locations all recording was performed using the same protocols and trait definitions, and the design of the annual mating programs ensured that large numbers of sires were used across locations. This included AI sires and as well as several natural mate sires that were used at one location and then relocated and used at the other. The Santa Gertrudis

breed was only present at one location therefore for all further analyses their records were removed from the Brian Pastures dataset.

A series of bivariate analyses were performed where the measure at Brian Pastures was treated as a different trait to the measure at Spyglass. This enabled the genetic correlation across environments to be estimated. Generally, correlations less than 0.80 are considered to be evidence of GxE and considerable re-ranking of sire progeny performance across environments is expected. Unfortunately for many traits the numbers of records after splitting were not large, so as expected, the genetic correlation estimates have large standard errors.

4.6.1 GxE - Gestation length, birth weight and weaning weight

Gestation length (GL), birth weight and weaning weight estimates of GxE are presented in Table 23. Models for analyses of GL were previously described and fixed effects and adjusted phenotypes for birth weight and weaning. For these traits there were maximum numbers of records available (i.e. all cohorts and both sexes) and as a result the genetic estimates have lower standard errors.

Table 23. Variance components and genetic correlations across locations (BP and SG) for gestation length (GL, d), birth weight (BWT, kg) and weaning weight (WWT, kg).

Trait	BP						SP						r_g(se)
	Va	Vm	Vpe	Vp	h^2 (se)	h_m^2 (se)	Va	Vm	Ve	Vp	h^2 (se)	h_m^2 (se)	
GL	18.6	-	5.6	30.6	0.61 (0.13)	0.18 (0.10)	23.7	-	5.4	29.1	0.81 (0.10)	-	0.98 (0.09)
BWT	12.0	1.2	1.6	23.5	0.51 (0.08)	0.05 (0.05)	12.4	2.2	7.0	21.5	0.57 (0.06)	0.10 (0.03)	1.02 (0.06)
WWT	205	24	79	398	0.52 (0.11)	0.06 (0.07)	180	52	127	387	0.46 (0.07)	0.13 (0.06)	0.99 (0.09)

For these three traits the variances and heritability estimates were similar across the locations. For all traits the genetic correlation estimates were not statistically different from unity suggesting no evidence of GxE for these early-life traits across these two locations.

4.6.2 GxE - Cow body composition traits into mating

The numbers of records for these analyses were reduced compared to the previous section because these traits are only recorded on the females. The numbers were further restricted due to a lower number of completed cohorts and also lower numbers of females available for measurement at mating 2 (determined by reproduction rates at mating 1). Analyses were undertaken for completeness of this report, but more records will be required before a scientific publication of the estimates could be considered. Therefore these results should be viewed with a degree of caution.

Traits included several measures of cow body composition including: cow weight, P8 fat depth, hip height (HH) and eye muscle area (EMA). For these analyses the measures taken at the start of mating as maiden heifers (i.e. into mating 1 as a non-lactation maiden heifer) and again start of mating as 1st calf cows (i.e. into 2nd mating as a 3-year old first-lactation cows). The records were split by location and considered as separate traits, numbers by trait and location are presented in Table 24.

Fixed effect models were constructed separately for each trait and mating time using full fixed effect models. Listed below are the final models used in bivariate analyses for each trait:

- EMA into 1st mating = sire breed + birth cohort + measurement age (l)

- EMA into 2nd mating = sire breed + birth cohort + calf birth month + calf age (l)
- WT into 1st mating = sire breed + birth cohort + measurement age (l)
- WT into 2nd mating = sire breed + birth cohort + calf birth month + calf age (l)
- P8 into 1st mating = sire breed + birth cohort + cow group (cohort) + birth month + cow group (cohort) x measurement age + measurement age (l)
- P8 into 2nd mating = sire breed + birth cohort + cow group (cohort) + calf birth month + birth month + calf Sex + cohort x calf birth month + cow group (cohort) x calf birth month + calf sex x birth month + measurement age (l) + calf age (l) + measurement age x calf age
- HH into 1st mating = sire breed + birth cohort + birth month + cow group (cohort) + measurement age (l) + measurement age x birth month
- HH into 2nd mating = sire breed + birth cohort + birth month + cow group (cohort) + calf birth month + measurement age (l) + birth cohort x calf birth month + cow group (cohort) x calf birth month.

Table 24. Variance component and genetic correlations across locations for cow weight (WT), eye muscle are (EMA), hip height (HH) and fat depth (P8) at 2nd mating measurement times (Brian Pastures – BP and Spyglass – SG).

| Trait | BP | | | | SG | | | | |
	N	Va	Vp	h²(se)	N	Va	Vp	h²(se)	r_g(se)
				Mating 1 (M1)					
EMA	329	10.9	31.3	0.35 (0.14)	715	13.2	35.7	0.37 (0.11)	0.62 (0.42)
WT	402	719	982	0.73 (0.14)	794	602	991	0.61 (0.10)	0.78 (0.13)
HH	400	8.9	13.7	0.65 (0.15)	792	11.9	16.5	0.72 (0.12)	0.71 (0.25)
P8	402	2.8	5.3	0.54 (0.16)	794	4.2	7.3	0.58 (0.11)	1.00*
				Mating 2 (M2)					
EMA	249	12.6	45.7	0.28 (0.18)	421	24.4	49.0	0.50 (0.17)	0.77 (0.55)
WT	302	960	1843	0.52 (0.17)	430	1351	1639	0.82 (0.12)	0.22 (0.41)
HH	313	6.9	13.4	0.52 (0.22)	431	7.2	14.7	0.49 (0.19)	*nc*
P8	316	2.1	4.0	0.53 (0.18)	432	3.9	5.8	0.67 (0.15)	0.35 (0.56)

* at bounds; nc convergence failed

Results in Table 24 show that all these cow body composition traits are moderately to highly heritable, although the low numbers of records at BP resulted in larger standard errors of the estimates. Generally, variances and heritabilities were larger at SG than BP and also for M2 reflecting more trait variance when cows are older and lactating (except for HH). However with the low numbers of records the standard errors on the genetic correlation estimates were very large but there is an indication that some may be less than one. Inspection of single-trait EBVs reveals some sires re-ranking based on plots of univariate EBVs. The numbers of M2 records were lower at Spyglass due to lower maiden heifer conception rates in early drought years, but with better recent seasons the number of records has increased substantially. At this stage the data structure at M2 has limited numbers of sires use across locations because it only includes daughters from Year 1 AI programs and there are only limited number of natural mates used across cohorts for these data.

From these very preliminary analyses of cow body composition traits there is no conclusive evidence of GxE with M1 and M2 correlations not being significantly different from 1, although at mating 2 when the cows are lactating for the first time there are indications the correlations may be less than 1. More records are needed to obtain more precise estimates, and if over time additional records are collected, it would be recommended to further split the analyses by breeds. This would allow any differences in the magnitude of GxE to be observed due to breed which may exist due to breed difference between mating 1 and mating 2 cow body composition traits (Wolcott *et al.* 2014).

4.6.3 GxE - Female reproduction traits

The female reproduction traits are of great interest regarding the occurrence of GxE. Like the previous blocks of cow traits the numbers of records are not sufficient at this time to yield definitive results. For these analyses the AP and LAI were used across locations. Fixed effects were as defined previously and results from bivariate estimates are presented in Table 25.

Table 25. Variance component and genetic correlations across locations (Brian Pastures – BP and Spyglass – SG) for heifer age at puberty (AP) and lactation anoestrous interval (LAI).

	BP				SG				
Trait	N	Va	Vp	h^2(se)	N	Va	Vp	h^2(se)	r_g(se)
AP	430	6,488	11,178	0.58 (0.11)	966	8,634	11,572	0.75 (0.08)	0.91 (0.13)
LAI	273	711	2,713	0.26 (0.13)	556	548	2,665	0.21 (0.11)	0.77 (0.80)

Variances and hertabilities were reasonably similar across locations and show that these early-in-life reproduction traits were moderate to highly heritable at both locations. For AP the genetic correlation was very high, however for LAI too few records existed. At this stage the results are suggesting little evidence for GxE for heifer age at puberty across the two locations, but analyses need to be re-run when more records become available beyond this Project, especially for LAI.

4.7   Across-breed EBV development

The experiment was designed to ensure that all breeds were managed and performance recorded together i.e. under the same conditions. However the mean breed performance cannot be used as a standalone breed comparison because the selection of sires was not done randomly within each breed. Instead the sires where selected based on merit and influence in the breed but they have known EBVs in their breed's BREEDPLAN evaluation. Therefore the head-to-head performance recording of their progeny provides a very powerful database to allow the alignment of the current BREEDPLAN evaluations for the three breeds and to yield across-breed EBVs, and ultimately, the development of a combined breed evaluation to generate northern across breed and multi-breed EBVs.

The key towards the development of multi-breed evaluations is that the performance data of the breeds run together is kept together. For this Project the data has not been submitted separately to each breeds' BREEDPLAN databases data but instead has been stored on ABRI's research multi-breed database - Northern (MBDN). This ensures the structure of the data is maintained with regard to trait management groups and pedigrees (in case of CRC TCOMP base cows). The database system has been designed at ABRI such that all animals on the MBDN have cross-reference identification numbers that allows each animal to be correctly identified back in its breed of origin. This allows for easy combining of a BREEDPLAN database for a given breed and the MBDN. The inclusion of all the data held on the MBDN (including the Project data from the three breeds + Beef CRC data) into a modified breed run (to build appropriate genetic groups) generates research EBVs on all animals including those from other breeds. Importantly, the EBVs are generated are using the variances and co-variances of that breed.

This is the first step in developing across-breed EBVs for northern Australian tropical beef breeds and this first evaluation has allowed the sires from the Project from the three breeds to be directly compared for the full range of BREEDPLAN traits. The next step is the development of a single northern across-breed evaluation, instead of the existing procedure of combining the MBDN with a particular breed to generate an evaluation with two or more breeds. For this to be achieved further development work will be required at ABRI and R&D will be required at AGBU to provide new software to

accommodate the combining of two or more breeds. It is also likely that a new full set of variance components will need to be estimated to reflect the (combined) population being evaluated.

4.8 Genetic analyses of novel traits

Over the course of the Project the opportunity existed to record additional measures as part of the routine recording. These included existing traits not currently recorded in tropical breeds and also completely novel. Given the number of records collected the data was often pooled across the three breeds and locations, for analyses where models were run with and without breed fitted. Fixed effect models were developed as previously described and final models for each trait (after removing non-significant interactions and main effects) are presented below.

Several of the traits were subjectively scored (see Appendix 1) and to analyse these correctly required modelling the categorical distribution of the trait (i.e. not a linear model). Threshold models, using THRGIBBS1F90, were used, but these methods generally require large amounts of records to obtain convergence and stable variance estimates. Given our relatively low numbers of records difficulties were often experienced with convergence so different groupings of the scores were trialled. In most cases a stable result was achieved but additional records (beyond this Project) will be needed to get definitive variances and heritability estimates. For those traits that were identified as being heritable, research Project sire EBVs have been generated and will be used to help determine if there is merit in further developing the EBV beyond this Project.

4.8.1 Coronet circumference and birth weight

Birth weight is emerging as an important trait in tropical beef production but the levels of recording are low. Research by overseas vets (using temperate crossbred animals) proposed coronet circumference as a proxy for birth weight. No research exists in tropical beef breeds so it was important to determine if this simple measure would it be suitable as a correlated trait for genetic evaluation of birth weight. More importantly, if the measure could be taken at branding (when most animals are first encountered) and could be shown to be correlated with birth weight then it would potentially provide large amounts of data for genetic evaluation. Therefore, coronet circumference was recorded in the branding cradle and a branding weight was also recorded.

Cows were inspected daily during the calving season by a team of highly experienced technicians. All new calves were caught and tagged, birth weights were recorded using hand-held spring scales and coronet circumference measured using the commercially available Calfscale® hoof tape developed in the US (see Fig. 21). At an average of 103 days of age the calves were branded (males castrated) and a branding live weight was recorded using digital scales. Coronet circumference was measured while the calf was constrained in the branding cradle using a standard dress makers tape as the hooves were too large for the commercial Calfscale® hoof tape. Approximately 74 days later the calves were weaned and a weaning live weight was also recorded.

Fig. 21. Measurement of coronet circumference. (Source http://rublecattleservices.com/calfscale.html)

Data on the birth weight of 4,320 calves were collected over the five-year period from 2014 to 2018. Records were removed if they were part of a multiple birth, calves were crossbreds, sex was unknown, date of birth was unknown or was estimated, the sire and/or dam was unknown, the dam's date of birth was unknown or the birth weight was less than 15.5 kg (suspected to be premature births). Parentage through DNA was used to determine sire. After basic edits, 3,715 animals remained in the dataset. These calves were sired by 153 sires with an average paternal half sibling family of 24 calves (ranging from 1 to 101 half siblings). Raw trait means are presented in Table 26 across the measurement times.

Table 26. Raw statistics for birth weight, coronet circumference and weight recorded at different stages (Birth, Branding, Weaning).

Measurement time	Trait	N	Mean	std	min	max
Birth	weight (kg)	3,715	33.4	5.5	18	53
	coronet circumference (cm)	1,943	16.5	1.1	13.5	20.0
Branding	weight (kg)	2,841	133.4	32.8	49.5	260
	coronet circumference (cm)	2,848	23.6	1.8	18.0	31.5
	age (days)	2,848	102.7	27.6	20.0	170.0
Weaning	weight (kg)	3,090	191.6	34.4	78.0	322.0
	age (days)	3,090	178.6	25.4	97.0	244.0

Coronet circumference measured at birth averaged 16.5 cm (ranging from 13.5 cm to 20 cm) and increased to 23.6 cm at branding age (ranging from 18.0 cm to 31.5 cm). Fig. 22 shows the phenotypic relationship between the observed birth weight and birth coronet circumference for each breed by sex combination. It can be seen in all breed and sex combinations that there was a positive relationship between the birth weight and birth coronet circumference with simple correlations of 0.66, 0.65 and 0.73 for Brahman, Droughtmaster and Santa Gertrudis calves, respectively. Although these correlations existed between the raw phenotypes, there was also large variation in the birth coronet circumference measures for any given birth weight. For example, among calves weighing between 30 and 35 kg at birth the range in coronet circumference records had a spread of 5 cm (14 to 19 cm), which was almost the same spread in coronet circumference measures observed for all birth weights. This suggests that more than the skeletal structure of calves is influencing the birth weight of calves.
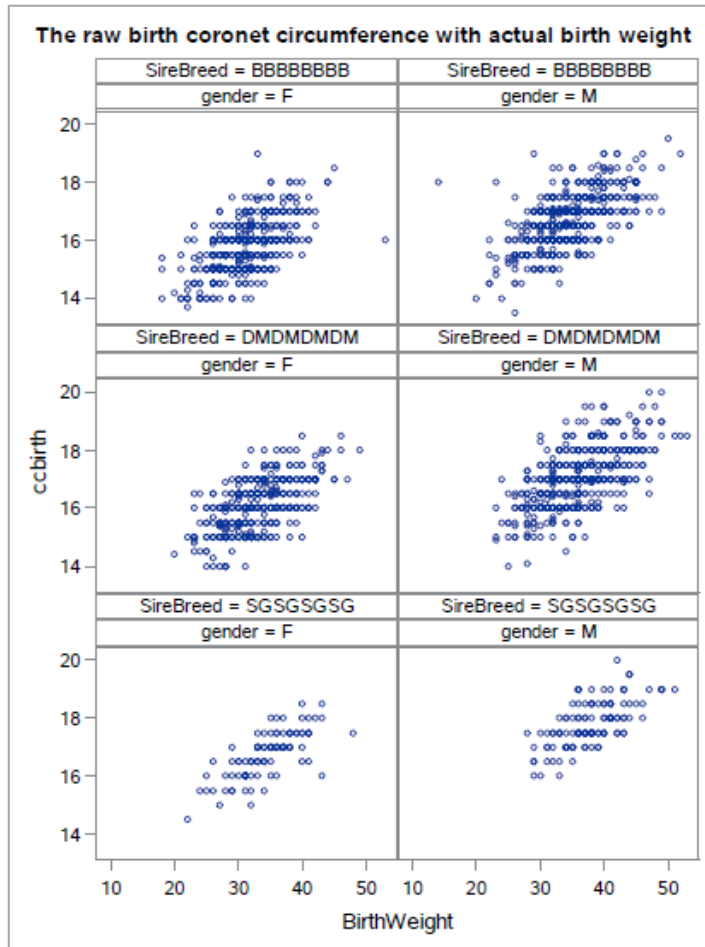
Fig. 22. Raw plots of the relationship between coronet circumference at birth and birth weight by breed (Brahman=BBBBBBBB Droughtmaster=DMDMDMDM and Santa Gertrudis=SGSGSGSG and gender (F=female nd M=Male)

For all traits, the initial statistical model included Project herd (Spyglass or Brian Pastures), birth cohort (herd and year of birth) nested within Project herd, calf sex (male or female), birth month, cow group (a concatenation of cow Project herd, cow breed type, cow herd of origin and cow age group) nested within Project herd and first-order interactions. The sire breed x herd interaction was also considered. For the analyses of coronet circumference and branding weight, the branding age was also fitted as a linear and quadratic covariate effect. For weaning weight, the initial model was the same and age at weaning was fitted as a linear and quadratic covariate effect.

For coronet circumference at birth significant fixed effects included were: Project herd, calf sex, birth cohort nested in Project herd, birth month, cow group nested in Project herd and sire breed. For branding coronet circumference additional significant interactions included: calf sex x birth month, sire breed x birth cohort nested in Project herd, sire breed x birth month and branding age fitted as a linear and quadratic covariate.

Table 27. Variance components and heritability estimates for weights and coronet circumference traits at different stages.

Trait	Va	Vm	Vpe	Ve	Vp	h^2 (se)	h_m^2 (se)
Birth weight (kg)	12.0	2.2	0.2	7.9	22.4	0.54 (0.06)	0.10 (0.04)
Birth Coronet Circ. (cm)	0.4	0.03	0.0	0.3	0.8	0.56 (0.10)	0.03 (0.04)
Branding weight (kg)	76.6	23.4	32.8	98.6	231.4	0.33 (0.06)	0.10 (0.04)

Branding Coronet Circ. (cm)	0.6	0.0	0.09	0.4	1.1	0.53 (0.07)	0.00 (0.04)
Weaning weight (kg)	184.7	46.2	43.9	118.2	392.9	0.47 (0.06)	0.12 (0.04)

Univariate analyses of each trait were performed using the fixed effects identified above and results presented in Table 27. All traits, including coronet circumference measured at birth and branding were moderately to highly heritable and all weight traits had small but significant maternal effects. These single trait analysis results showed coronet recording was repeatable, accurate and under a degree of genetic control. The low estimate of maternal effects for the coronet traits most likely reflects current data structure where few dams would have their own record and progenies with records.

Table 28. Genetic and phenotypic correlations# (se in brackets) between birth weight and coronet circumference measured at different stages

Trait	BWT	BCC	BrWT	BrCC	WWT
Birth weight (kg)		0.82 (0.04)	0.79 (0.05)	**0.59** (0.06)	0.73 (0.05)
Birth Coronet Circ.(cm)	0.66 (0.01)		0.64 (0.08)	0.82 (0.05)	0.65 (0.08)
Branding weight (kg)	0.52 (0.02)	0.37 (0.02)		0.83 (0.03)	0.99 (0.01)
Branding Coronet Circ. (cm)	0.42 (0.02)	0.51 (0.02)	0.64 (0.01)		0.87 (0.03)
Weaning weight (kg)	0.48 (0.02)	0.34 (0.02)	0.89 (0.01)	0.64 (0.01)	

#genetic correlations above diagonal; phenotypic below

To assess the utility of coronet recording genetic correlations were estimated across traits and measurement times and are presented in Table 28. Coronet circumference at birth was highly genetically correlated with birth weight (r_g = 0.82) but reduced (r_g = 0.59) when coronet circumference was measured at branding time. Coronet measured at birth could be used as a correlated trait in the genetic evaluation of birth weight but there is still the need to physically handle the calf at birth and therefore taking the weight would be the preferred measure. This may not be the case however if it could be shown that coronet circumference was a better predictor of dystocia or calf losses than birth weight, but this is unlikely.

Coronet circumference at branding offers the advantages that calves do not need to be handled at birth and it is relatively easily measured when the calves are constrained in the branding cradle. The measure at this time was estimated to be heritable and was only moderately genetic correlated with birth weight. However, the magnitude of the genetic correlation was smaller than the estimated correlation between birth weight and the weights taken at branding (r_g = 0.79) and at weaning (r_g = 0.73). Both weights are easy to collect, and weaning live weight is already part of the routine genetic evaluation. However, these weight traits require adjustment for calf age (i.e. requires date of birth known) and if this was not known (i.e. age removed from the model) then the correlation between branding coronet circumference and birth weight reduced significantly.

The conclusions from this study is that branding coronet circumference is not a useful predictor trait for the genetic evaluation of birth weight in the northern Australian cattle breeds. Branding or weaning weights could be used as genetically correlated traits for birth weight but these still rely on having a known date of birth.

4.8.2 Cow body condition scores

Body condition score (BCS) is not currently a standard BREEDPLAN trait but the Beef CRC showed that it is a heritable trait and is correlated with female reproductive performance (Wolcott *et al.* 2014). Given the focus of this study is improving reproduction by selection it was important that we continue to understand any consequences of that selection on cow body composition, in particular as it may relate to cow survival in northern Australia.

Body condition score was visually assessed using a 5 point scale (with + and – categories for each whole score) where 1 = poor to 5 = very fat (see Appendix 1, A). The Project females were recorded at Yearling (420 d), into first mating (779 d), at birth of first calf, and into 2nd mating (lactating) and birth of second calf. Given the trait distributions observed (i.e. the number of classes) the trait was considered as continuous (recoded 1 to 15) and was analysed using a linear animal model.

a)   **Yearling heifers:** All 2013 to2017-born heifers had a BCS recorded (with an average of 3.0, recorded at an average of age of 420 days and distribution of scores in Fig. 23.
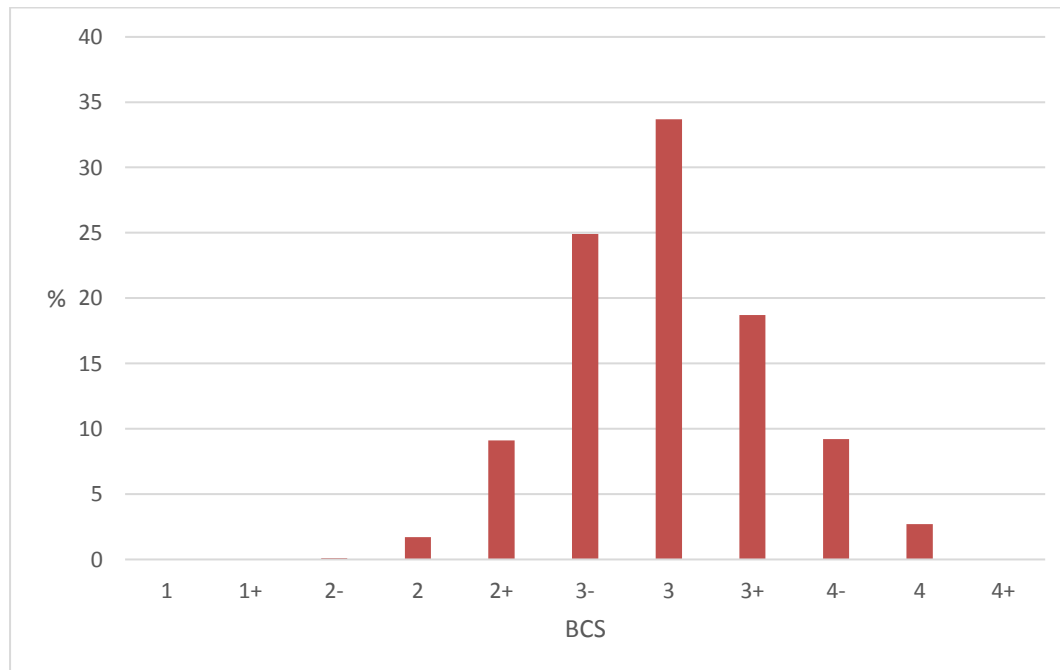

Fig. 23. Distribution of heifer body condition scores: Yearling stage (420 days) measure.

Final fixed effects models included sire breed, cohort, breed x cohort, age and age x cohort interaction. Listed in Table 29 is the variance components and heritability from different models of fitting random effects. Model 4 (not significantly different to more parameterised models) shows a heritability of 27% and this increases to 35% (model 5) if the breed term was removed from the model.

Table 29. Variance components and heritability estimates from different random effects models (1 to 5) for body condition scores of yearling (420 d) heifers

Model	Va	Vm	Vpe	Ve	Vp	h²(se)	LogL
1	0.011	0.003	0.000	0.038	0.052	0.21 (0.07)	1348.50
2	0.014	-	0.000	0.038	0.052	0.27 (0.08)	1347.56
3	0.011	0.003	-	0.038	0.052	0.21 (0.07)	1348.50
4	0.014	-	-	0.038	0.052	0.27 (0.07)	1347.56
5	0.019	-	-	0.035	0.054	0.35	

b)   **Into mating 1**. Body condition scores of the heifers at the commencement of first mating period for 2012 to 2016-born heifers. The average BCS was 3.1, at an average of age of 779 days (range 705 to 879 days) and distribution of scores are presented in Fig. 24. The final model included: sire breed + birth cohort + birth month + cow grp (birth cohort) + measurement age + measurement age x birth month. Interactions with sire breed and the other terms were tested and none were significant,

sire breed itself is not significant but was left in the model. With so few records and the interaction not being significant in other breeds the birth month x cohort interaction was not fitted.
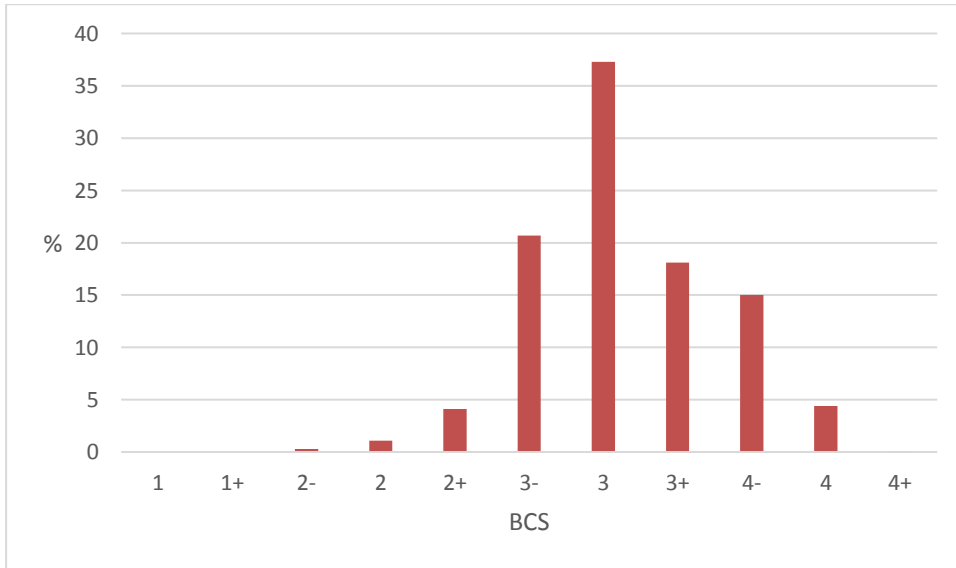

Fig. 24. Distribution of heifer body condition scores: Into 1st mating (as 2-year olds)

Table 30. Variance components and heritability estimates from different random effects models (1 to 5) for body condition scores of heifers into first mating (as 2-year olds)

Model	Va	Vm	Vpe	Ve	Vp	h^2(se)	LogL
1	0.024	0.000	0.003	0.064	0.091	0.26 (0.07)	836.572
2	0.024	-	0.003	0.064	0.091	0.26 (0.07)	836.572
3	0.026	0.000	-	0.065	0.091	0.29 (0.06)	836.296
4	0.026	-	-	0.065	0.091	0.29 (0.06)	836.296
5	0.026	-	-	0.065	0.091	0.29	

Variance components and models for BCS at into mating 1 are presented in Table 30. Model 4 provides the best fit to the data and while there were slight increases in variances compared to heifers the heritability was very similar at 29%, however the contribution of breed differences has reduced at this measurement stage.

c)   **First calving cows**: Cow BSC was scored at calf birth (within 24 hrs) which has been proposed as a new measure that might be associated with calf loss (i.e. low BCS). The 2012 to 2015-born females (N=870 females) with a 1st calf in the data were scored within a week of the birth of their calf. The average BCS was 3.2, at an average of age of 1,093 days and distribution of scores shown in Fig. 25.
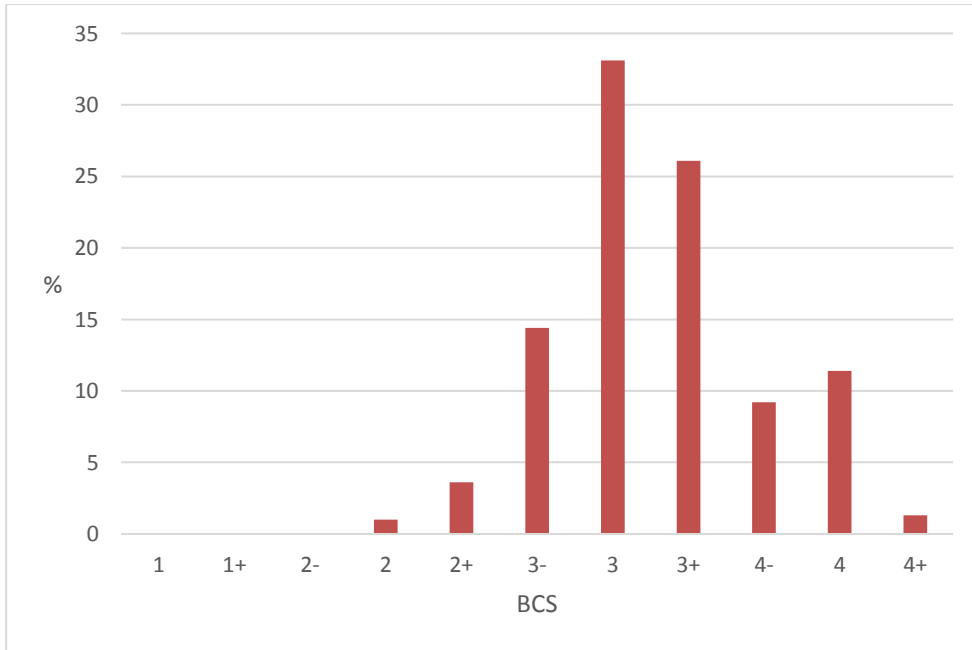
Fig. 25. Distribution of cow body condition scores: At birth of first calf (as 3-year olds)

The final model included: sire breed + birth cohort + birth month + cow group (birth cohort) + measurement age (l) + measurement age x birth month + measurement age x birth cohort. Interactions with sire breed and the other terms were tested and none was significant, sire breed was not significant.

Table 31. Variance components and heritability estimates from different random effects models (1 to 5) for body condition scores of cows at birth of first calf (as 3-year olds)

Model	Va	Vm	Vpe	Ve	Vp	h^2(se)	LogL
1	0.011	0.000	0.024	0.099	0.134	0.08 (0.08)	257.660
2	0.011	-	0.024	0.099	0.134	0.08 (0.08)	257.660
3	0.012	0.010	-	0.112	0.134	0.09 (0.09)	255.065
4	0.016	-	-	0.119	0.134	0.12 (0.09)	254.511
5	0.014	-	-	0.112	0.126	0.10	

Variance components (Table 31) for BCS scored at this measurement time has slightly lower additive but increased residual and a resultant heritability estimate of 12%. This lower heritability (i.e. increased residual) most likely reflects issues with defining an appropriate management group over the calving season that is likely to be changing and affecting cow BCS. There may also be issues with the scoring of the trait in the paddock not being so accurate. The trait at this stage is recorded by several scorers used within a location that may not be completely aligned on their scoring scales with some evidence of this in distribution of raw scores in Fig 24. Therefore this trait would need to be refined if it was to be suitable for a genetic evaluation, although it may be a suitable phenotypic measure to include in calf loss analyses.

d)   **Into 2nd mating**: BCS was scored on 2011 to 2015-born cows at the commencement of their mating as lactating cows. The average BCS was 2.6, at an average age of 1,148 days and Fig. 26 shows a very large range in BCS at this time.
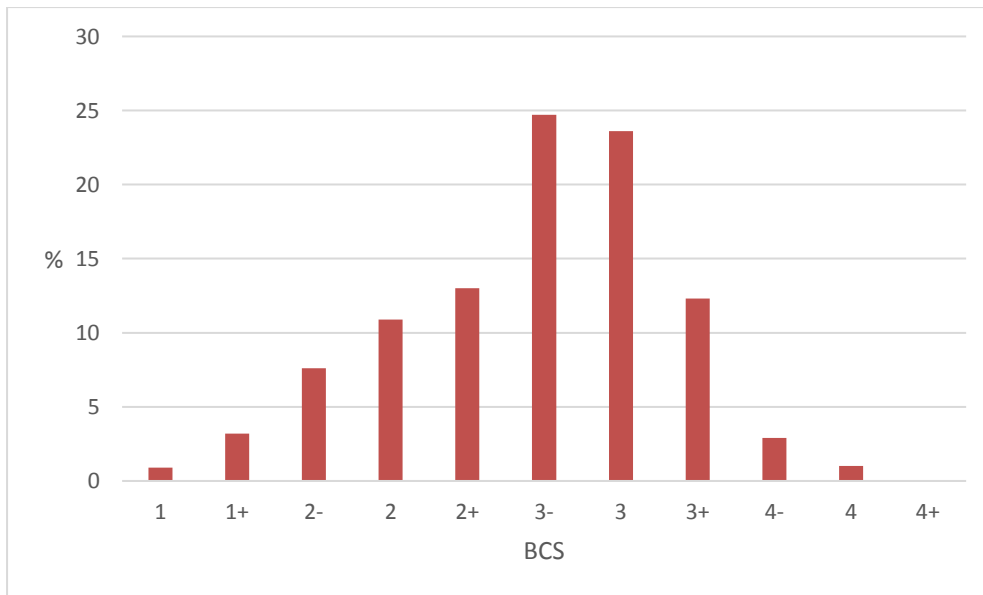
Fig. 26. Distribution of cow body condition scores: Into 2nd mating

For this measure the additional effects of the calf at foot (i.e. age and sex) on its mother's BCS had to be considered in the fixed effects models. The final model included: sire breed + birth cohort + cow group (cohort) + birth month + calf birth month + calf sex + measurement age (l) + calf age (l) + Cow group (cohort) x calf sex + cohort x calf sex + calf age x birth month + calf age x calf sex.

Interactions with sire breed and the other terms were tested and none was significant, including the effect for sire breed. With so few records for Santa Gertrudis and most of the interactions not being significant in other breeds meant that interactions were only fitted if they were significant also in another breed.

Table 32. Variance components and heritability estimates from different random effects models 1 to 5) for body condition scores of cows at into second mating

Model	Va	Vm	Vpe	Ve	Vp	h^2(se)	LogL
1	0.068	0.000	0.008	0.066	0.143	0.48 (0.11)	215.874
2	0.068	-	0.008	0.066	0.143	0.48 (0.11)	215.874
3	0.071	0.000	-	0.071	0.142	0.50 (0.11)	215.632
4	0.071	-	-	0.071	0.142	0.50 (0.11)	215.632
5	0.070	-	-	0.072	0.142	0.49	

Variance components (Table 32) for BCS recorded at this time has increased additive and phenotypic variances and a resultant heritability estimate of 50%. It also shows large genetic differences for these cow's BCS under the effects of lactation. The increase in the size of the additive variance and the resultant heritability compared to the measures taken 12 months earlier i.e. into mating 1 (Table 30) show possible differences due to increased age but most likely the effect of cow lactating for the first time and differences in BCS due to weight loss over the period from calving to commencement of mating.

e)   **At birth of 2nd calf**: the 2011 to 2014-born females (N = 466 females) with a 2nd calf measured within a week of the birth of the calf. The average BCS was 3.0, at an average age of 1,487 days. Distribution of scores (Fig. 27) shows variation (similar to other measures) but too few at this stage to do further analyses.
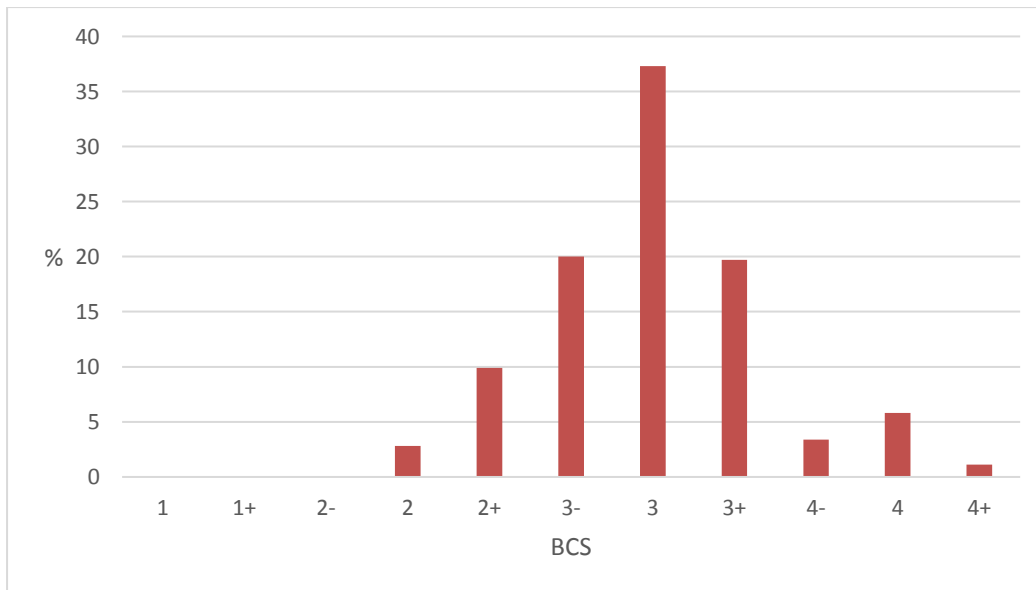
Fig. 27. Distribution of cow body condition scores: At birth of 2nd calf (as 4-year olds)

Genetic correlations were estimated between BCS across measurement times using a series of bivariate ASReml analysis. Genetic and phenotypic correlations were estimated from pair-wise combinations of the various measurement times (Table 33). Some difficulties occurred with convergence with later measures but in general variance components remained similar to their univariate estimates.

Table 33. Genetic correlations of cow body condition scores across different measurement times

	yearling	1st mating	1st calving	2nd mating
yearling		0.88	0.78	0.79
1st mating			0.71	0.83
1st calving				0.81
2nd mating				

The genetic correlation estimated between yearling BCS and into first mating BCS was high but the correlations were lower at later stages suggesting a possible re-ranking of genetics when the females were lactating. Moderate heritabilities, and the spread in sire EBVs will have important ramifications with regards to selecting for cow survival (i.e. genetics that able to maintain higher BCS under lactation) and there is a need to also quantify relationships with female reproduction traits.

4.8.3 Hip height

Hip height (HH) is an easy measure to record and several research projects has shown the trait to be highly heritable (e.g. Wolcott *et al.* 2014). Although not currently a BREEDPLAN trait, it does provide a direct measure of the physical frame of an animal and therefore may be useful in better describing cow size and feed requirements, in conjunction with cow weight and BCS. For this analyses the hip height measures at different stages were used: at yearling then 12 months later at start of 1st mating period and at start of 2nd mating period were used (see Table 34).

a) Yearling: 2013 to 2017-born heifers (N=1,509) had HH recorded at an average of 420 days. The HH ranged from 109 to 138 cm, with an average of 124cm.
b) Into first mating: 2012 to 2016-born heifers (N=1,520) had a HH recorded at an average age of 779 days. The average was 135 cm and ranged from 115 to 156 cm.

c) Into 2nd mating: 2011 to 2015-born heifers had a HH at start of second mating recorded at an average age of 1,150 days. The HH ranged from 128 to 162 cm, with an average of 140 cm.

Table 34. Raw statistics for female hip height measured at different times by breed

Measurement time	breed	N	mean	std	min	max
Yearling	All	1,509	123.7	4.6	109	138
	Brahman	666	124.8	4.8	111	138
	Droughtmaster	587	122.8	4.2	109	134
	Santa Gertrudis	256	122.9	4.2	109	133
Into 1st mating	All	1,520	135.3	5.9	115	156
	Brahman	683	135.3	5.6	118	156
	Droughtmaster	585	134.5	5.7	115	156
	Santa Gertrudis	252	137.2	6.6	122	156
Into 2nd mating	All	882	140.3	5.4	128	162
	Brahman	410	140.5	5.3	129	162
	Droughtmaster	334	139.6	5.2	128	155
	Santa Gertrudis	138	141.6	5.7	128	156

The final model for hip height at yearling was sire breed + birth cohort + cow group (cohort) + birth month + measurement age (l). No interaction terms were significant, including any with sire.

The final model for hip height at into first-mating was sire breed + birth cohort + birth month + cow group (cohort) + measurement age (l) + measurement age x birth month. Interactions with sire breed and the other terms were tested and none were significant, nor was sire breed.

The final model for hip height at into 2nd mating was sire breed + birth cohort + birth month + cow group (cohort) + calf birth month + measurement age (l) + birth cohort x calf birth month + cow group (cohort) x calf birth month.

Univariate analyses were performed in ASReml to estimate variance parameters. The above fixed effects models were fitted, with animal fitted as a random effect. Variance components and heritability estimates are presented in Table 35. In all three analyses the removal of the term for breed did not significantly change the estimated additive variance estimates or heritabilities.

Table 35. Variance components and heritability estimates for female hip height at different measurement times

Measurement time	Va	Ve	Vp	h^2(se)
Yearling	7.26	6.74	14.00	0.52 (0.08)
Into 1st mating	11.13	4.56	15.69	0.71 (0.08)
Into 2nd mating	7.38	6.82	14.20	0.52 (0.12)

Heritability estimates showed that the trait measured at all stages was highly heritable and estimates are in agreement with other studies (Wolcott *et al.* 2014) in tropical cattle. Project HH EBVs were predicted for Brahman sires and show a large spread, reflecting the high heritabilities for the traits. The EBVs were plotted against their BREEDPLAN EBVs for 600d weight (see Fig. 28) with a correlation 0.49 and 0.57 for yearling heifer and 1st mating, respectively. Although these relationships are positive the plots show that there is variation in hip height genetics at the same 600d EBV which will be related to frame size (and maturity pattern) differences. The ease of measurement and the high heritability estimates show this is a useful trait for genetic evaluation. More work is now required beyond this Project to establish if it would add value to the current cow weight EBV in BREEDPLAN.
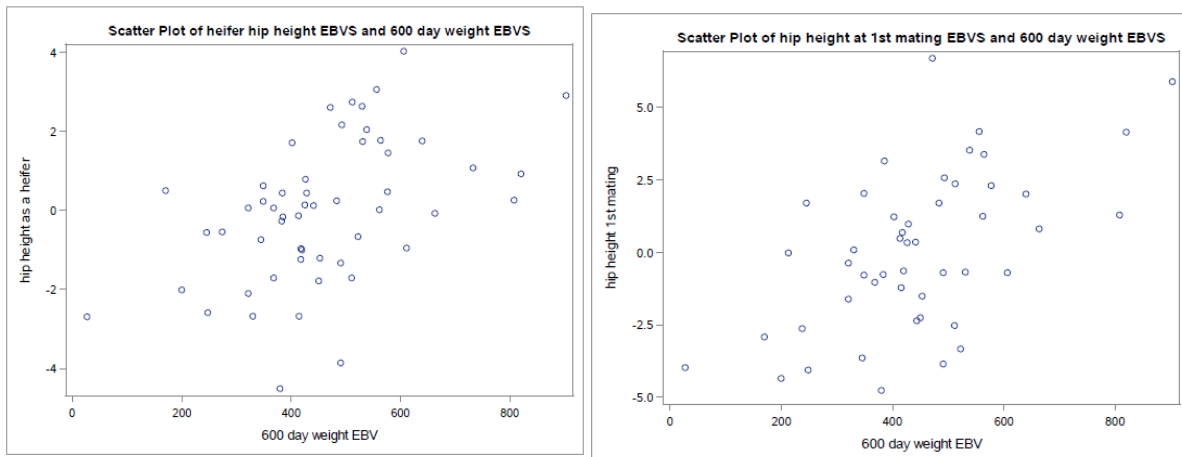
Fig. 28. Brahman sire hip height EBVs (at yearling and into 1st mating) and BREEDPLAN 600d WT EBV(x10).

4.8.4 Maternal behaviour scores

Maternal behaviour is of interest from a calf loss perspective given we experienced predation (e.g. dingoes) during the project and also because flight time (FT) EBVs are routinely produced and used by some breeders to improve temperament. Therefore, it was of interest to measure cow maternal behaviour to investigate if a simple scoring system could be implemented into the existing recording protocols, then establish if the trait was heritable, and ultimately to determine if it is related to FT and potentially establish associations with calf losses.

Cow mothering scores were recorded in the 2014-2018 cohorts for SG and BP in the 2011 to 2015-born females. Cows were scored at the birth recording of their calves on a scale: 1 = dam not present to 5 = cow very protective (see Appendix 1, B) i.e. low protectiveness to high protectiveness. Cows could have repeat records across years and a total of 2,154 records were available on 1,180 cows and the distribution of scores shown in Fig. 29.

Fig. 29. Distribution of mothering scores of cows at calving
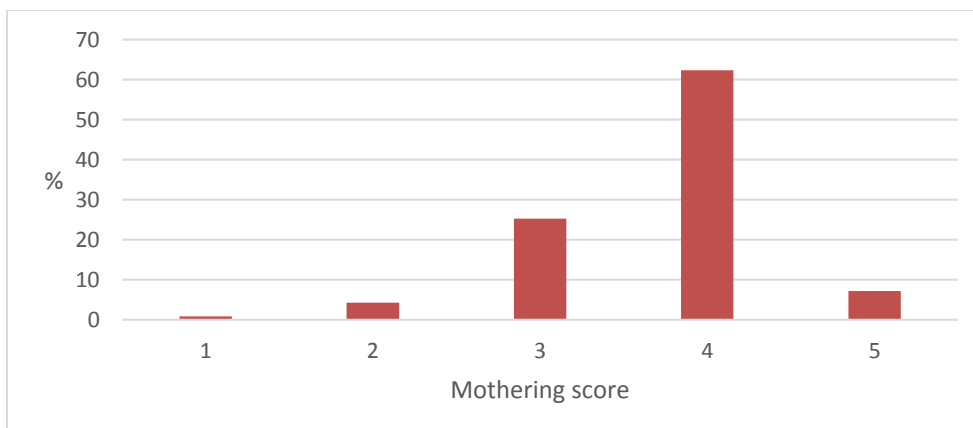
The final model for mothering score was sire breed + birth cohort + birth month + cow group (cohort) + cow age + birth cohort x birth month. Interaction with sire breed were tested but none were significant. A threshold model was used thrgibbs1f90. The above fixed effects were fitted, with cow fitted as a random effect as well as the repeatability for cow (see Table 36).

Table 36. Variance components and heritability estimates for various threshold models (1 to 4) for cow mothering score at birth

Model	N thresholds	Va	Vpe	Ve	h²	Threshold 3	Threshold 4	comment
1	1,2,3,4,5	0.54	0.06	0.99	0.34	3.73	5.54	Va range 0.25 to 0.98
2	1-2,3,4,5	0.39	0.10	0.88	0.28	3.69	-	Va range 0.22 to 0.64,
3	1-2,3,4-5	0.28	0.20	0.97	0.19	-	-	Va range 0.03 to 0.71
4	1-2,3-5	0.58	0.19	1.01	0.31	-	-	Va range 0.06 to 2.1

Fitting different numbers of thresholds affected the convergence behaviour of the analyses. Results for model 4 yielded a heritability of 0.31 on the underlying scale with the binary model, with a poor mothering (score 1&2) frequency of 0.51 resulted in a heritability of 0.20 on the transformed observed scale.

The results show the trait was heritable and so further analyses were undertaken to investigate the potential relationship between mothering score and flight time. This was done using BREEDPLAN flight time EBVs for 51 Project Brahman sires. The correlation between the mothering EBV and flight time EBV was 0.36, suggesting that it is a different trait, but the positive relationship suggests the genetics for higher flight times (calmer animals) tended to be those with genetics for higher mothering scores (more aggressive maternal behaviour). The graph below (Fig. 30) shows that sires with average mothering EBVs come from the whole range of flight time EBVs. However, it shows that the sires that produced the more aggressive daughters tended to be those with above average flight times. This indicates the two measures of temperament are different and suggest selection for improved flight time is not likely to have a correlated change in cow maternal behaviour.
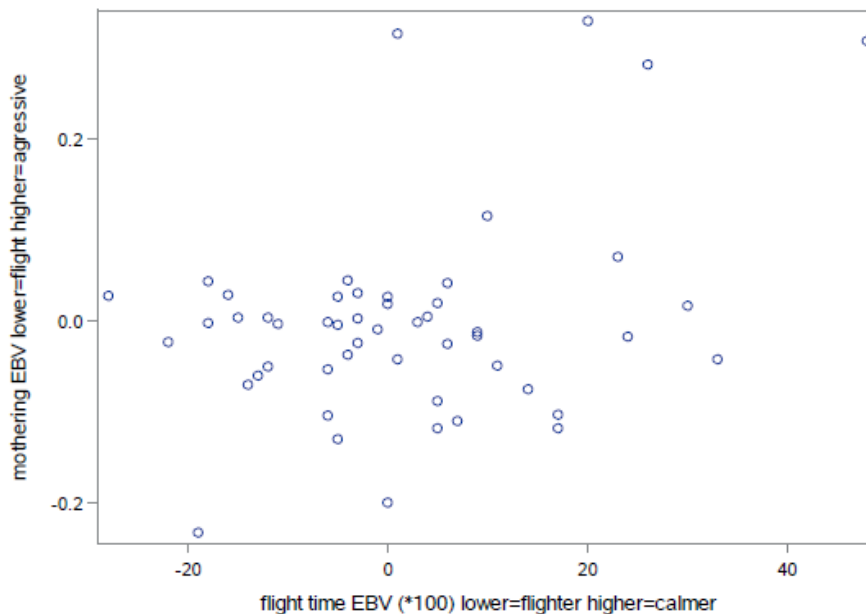
Fig. 30 Plot of mothering score EBV versus the flight time EBV for Brahman sires.

4.8.5 Teat and udder scores

Teat and udder size in tropical beef breeds have been shown in the Beef CRC (Bunter *et al.* 2013) to be heritable traits and teat size was associated with calf mortality. Teat and udder scores were recorded on 2011 to 2015-born cows for SG and BP herds (N=1,021) at the birth of their first calf (calving as 3-year olds). Teat and udder scores ranged from 1 to 5, with a higher score indicating larger teats and udders (See Appendix 1, C, D). Each teat was scored but only the highest single teat score was used in these analyses and distribution of scores are shown in Fig. 31 for scores taken at the birth

of their first calf. At this relatively young age the majority of scores for teats were 2 and 3 scores and udders 2, 3 and 4 scores.
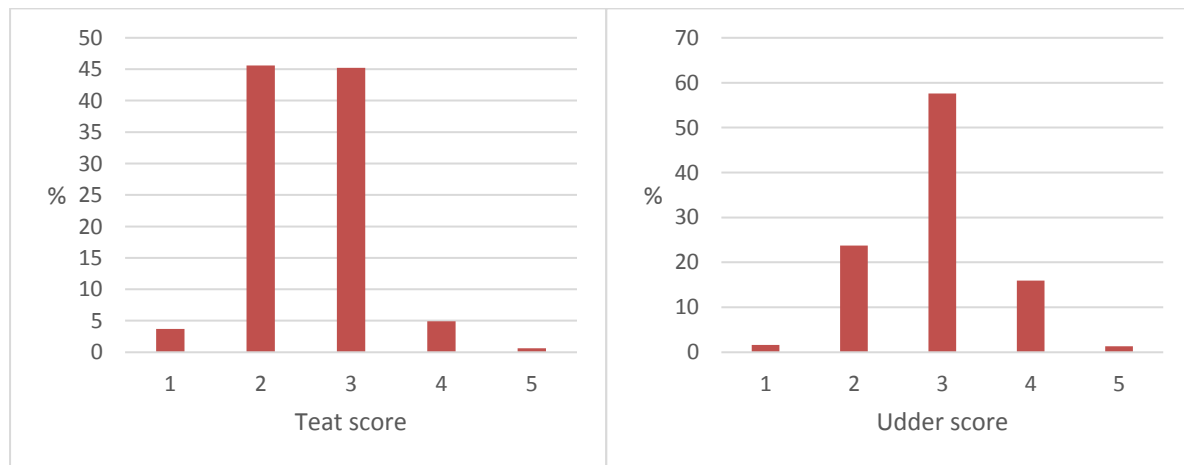

Fig. 31. Distribution of teat and udder scores in cows at birth of their first calf

Fixed effects models were developed for both teat and udder scores. The final model for teat score = sire breed + birth cohort + birth month + cow group (cohort) + measurement age. Note: calf effects were not significant. Interactions with sire breed and the other terms were tested and were not significant.

The final model for udder score = sire breed + birth cohort + calf birth month + calf sex + sire breed x birth cohort. Threshold models analyses with varying thresholds were attempted for teat (Table 37) and udder scores (Table 38) using Thrgibbs1f90 fitting the fixed effects above, with animal fitted as a random effect.

Table 37. Variance components and heritability estimates for various thresholds for cow teat score at birth of first calf

Model	N thresholds	Va	Ve	h^2	Threshold 3	Threshold 4	comment
1	1,2,3,4,5	0.60	0.84	0.41	3.26	5.25	Va max 1.39
2	1,2,3,4-5	0.78	0.86	0.47	3.59	-	Va max 1.73
3	1-2,3,4-5	0.49	0.84	0.35	-	-	Va max 1.89
4	1-2,3-5	0.83	1.03	0.43	-	-	Va max 3.57
5	1-3,4-5	25.12	0.87	0.88	-	-	Va max 250!

Analyses for teat score were somewhat unstable but the trait appears to be moderately heritable. The most stable model was the binary model (#4), with the residual variance close to one (which is expected for convergence) and a heritability estimate of 0.43 on the underlying scale. The lower threshold of teat score (score 1-2) frequency of 0.493 results in an observed heritability of 0.27 based on the binary model. However, grouping teat scores 3 with 4 and 5 scores is not logical because it is more likely that large teats (4 and 5) are important from a calf loss perspective (i.e. not small ones), so it is likely model 1 is a better model configuration and expressing an EBV based on the threshold above score 3.

Table 38. Variance components and heritability estimates for various thresholds for cow udder score at birth of first calf

Model	N thresholds	Va	Ve	h^2	Threshold 3	Threshold 4	comment
1	1,2,3,4,5	1.02	0.87	0.53	3.19	5.40	Va max 2.61
2	1,2,3,4-5	1.11	0.92	0.54	3.26	-	Va max 3.65
3	1-2,3,4-5	0.41	0.75	0.34	-	-	Va max 1.23
4	1-2,3-5	7.44	1.00	0.61	-	-	Va max 256!

For udder scores again convergence was difficult but the analyses indicate a heritable trait. Model 1 yielded an underlying heritability of 0.53, with smaller udder score (score 1-2) frequency of 0.25 resulting in an observed heritability of 0.29, however this assumes a binary model which not the case. Although not converged, model 1 or 2 appears the better fit.

Teat and udders were also scored at the birth of second calf for a total of 462 cows from 2011 to 2014-born females. Figure 32 shows the distribution of scores and there is an increase in numbers of 3 and 4 score teats and decrease in 2 score. However the distribution of udder scores were similar across the cow age groups. Too few records existed to perform any statistical analyses but the plots show the increase in scores across parities, with more 4 score and some 5 score teats. The frequency of scores 4 and 5 (i.e. bottle teats) is likely to increase as cows get older and future analyses will have more power to detect both genetic differences and correlations with other traits.
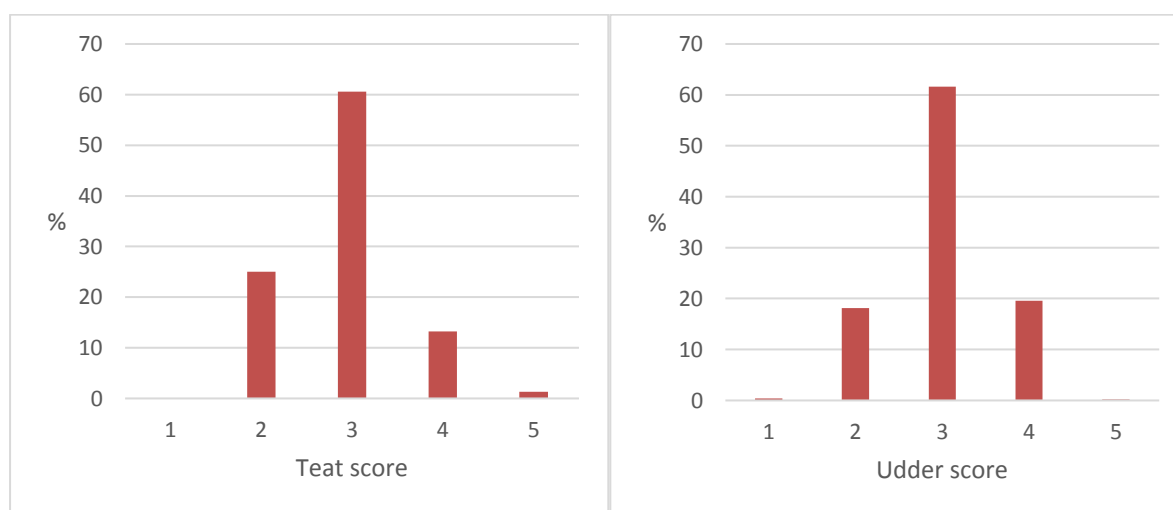

Fig. 32. Distribution of teat and udder scores in cows at birth of their 2nd calf

4.8.6 Calf vigour score at birth

Calf losses is a contributor to reduced reproductive outcomes in northern Australia as illustrated in Fig. 1. Anecdotal reports of "silly or dumb calf" syndrome exist in the northern beef industry so the Project instigated a simple scoring system at birth to score the "vigour" of the calf in an attempt to quantify the incidence of low/poor calf vigour at birth and determine if it was associated with calf losses. The scoring system was on a 5 point scale: 1 = extremely weak to 5 = extremely vigourous (see Appendix 1, E).

Vigour scores were recorded on 3,636 calves from the 2014-2018 cohorts from SG and BP. Calves were scored generally at birth and records taken later than one day of age were removed. The frequencies for the different scores are presented in Table 39 and show a very low incidence of scores 1 and 2 (less than 1%) across all three breeds, with 87% of the data being scores 3 or 4.

Table 39. Frequencies of calf vigour scores recorded at birth by breed.

Vigour score	All animals		Brahman		Droughtmaster		Santa Gertrudis	
	N	%	N	%	N	%	N	%
1	10	0.3	7	0.4	3	0.2	0	0
2	32	0.9	16	0.9	10	0.7	6	1.2
3	958	26.4	535	30.9	348	24.5	75	15.4
4	2,298	63.2	1,085	62.7	892	62.9	321	66.1
5	338	9.3	88	5.1	166	11.7	84	17.3
Total	3,636		1,731		1,419		486	

Fixed effects influencing the traits considered in the statistical model were: breed, cohort, cow group (defined the same as GL and BWT study, concatenation of herd, breed, origin and age) nested in location, birth month, calf sex, and all first-order interactions, sire of calf was included as a random effect. Birth weight was not included as an independent variable, although there is a link with those too small or very large being less vigorous, birth weight is a trait in itself and both traits could be fitted into an index for selection. The significant fixed effects identified were: breed, cohort, sex, birth month and cohort birth month. Given the categorical nature of the trait a threshold model (Thrgibbs1f90) was used to analyse the trait and included the fixed effects described above with animal and repeat records for dams fitted as random effects.

The genetic analysis did not converge despite reducing the number of threshold categories to 2. This could be because there are too few poor vigour calves recorded, or because the trait is not heritable. This most likely reflects issues with scoring the trait as the age of the calf when inspected will vary greatly and will influence the score given. Also the activity of the calf will differ depending on many factors that will not be standard across measurement times. In summary, the scoring did not provide evidence for the existence of "dumb" calf syndrome in these data and the incidence of poor vigour was very low (< 1%). Together these findings suggest that the current definition and recording protocols for calf vigour score is not a useful measure for genetic evaluation.

4.8.7 Coat length score

Adaptation to tropical environments is an important attribute in cattle raised in the sub-tropics and tropics. Coat length can be easily scored and was shown in the Beef CRC to be heritable and genetically related to both female reproduction and steers performance (Prayaga *et al.* 2009). Coat length scores were recorded on 3,439 animals from the 2014 to 2018-born cohorts for SG and BP herd using a 5 point scale 1 = extremely short to 7 = very woolly (see Appendix 1, F). Animals were scored at weaning with an average age of 156 days and distribution of score by breed are plotted in Fig. 33.
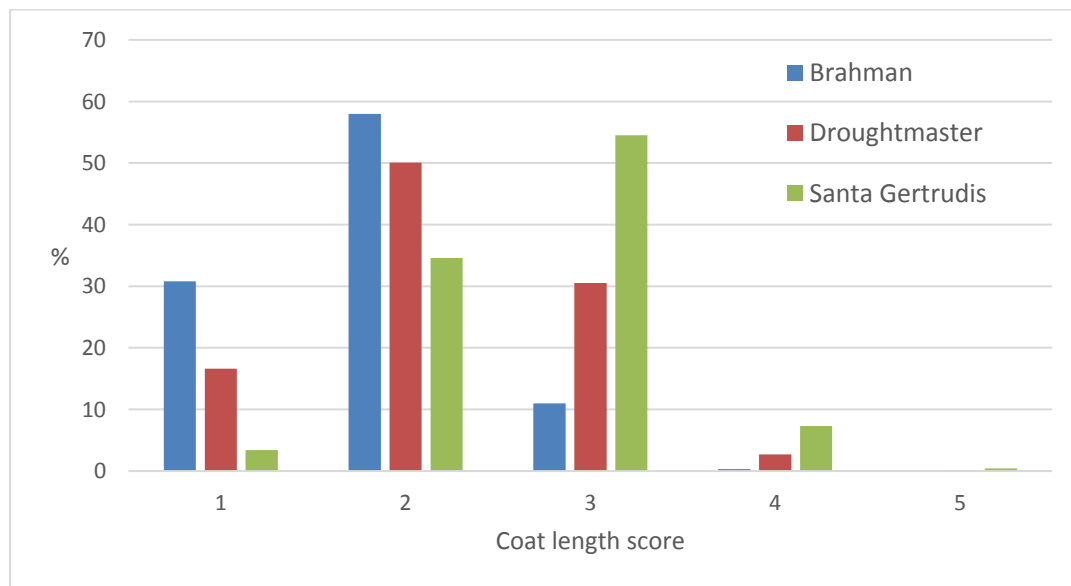

Fig. 33. Distribution of coat length score by breed

Fixed effects models were developed and the final fixed effect model for coat score included: sire breed + birth cohort + sex + cohort x sex + cohort x sire breed + measurement age (l&q) + measurement age x cohort. Interactions with sire breed and the other terms were tested and only

breed x cohort was significant. These significant fixed effects were included in threshold animal models using Thrgibbs1f90.

Table 40. Variance components and heritability estimates for various thresholds for calf coat length score at weaning

N thresholds	Va	Ve	h²	Threshold 3	Threshold 4	comment
1,2,3,4,5	0.39	0.71	0.35	2.56	5.12	Unstable variances
1,2,3,4-5	0.39	0.71	0.35	2.64	-	Unstable Ve
1,2,3-5	0.49	0.88	0.35	-	-	Relatively stable
1,2-5	5.34	0.99	0.61	-	-	Increase in Va

Results are presented in Table 40 for different thresholds and the models also struggled with convergence. Although it is not ideal with a Ve lower than 1, the 3 level threshold (sleek, normal, hairy) model appears to be the most stable with an underlying heritability of 0.35, with a sleek (score 1) frequency of 0.207 results in an observed heritability of 0.17 (assuming binary). Further, when the model was re-run but without sire breed effects the estimated parameters were Va = 2.02, Ve = 0.88, h² = 0.68, however the additive variance was not very stable over increasing number of iterations. These results suggest coat length score is heritable and there is a large breed effect and may be evidence of a single gene segregating for this trait.

4.8.8 Heifer navel scores

Pendulous sheaths in males is an attribute of many tropically adapted breeds. In some breeds (and by some breeders) a large, more pendulous sheath is seen as unfavourable in bulls because of links to increased levels of bull breakdown. However, the sheath size is also viewed as an indicator of adaption i.e. increased skin area. Previous research showed navel size in heifers is heritable (Prayaga *et al.* 2009) and a related measure that can be scored on females (Porto-Neto *et al.* 2014). Navel scores were recorded in the 2014 to 2016-born heifer cohorts at SG and BP herd females and were scored on simple 1 to 5 scale (1= tight to 5= very large/pendulous, Appendix 1,G). The frequencies for the different scores is shown below in Fig. 34 below by breed. In total there were 1,031 females scored at the commencement of first mating period (i.e. at bull-in) at an average age of 813 days.
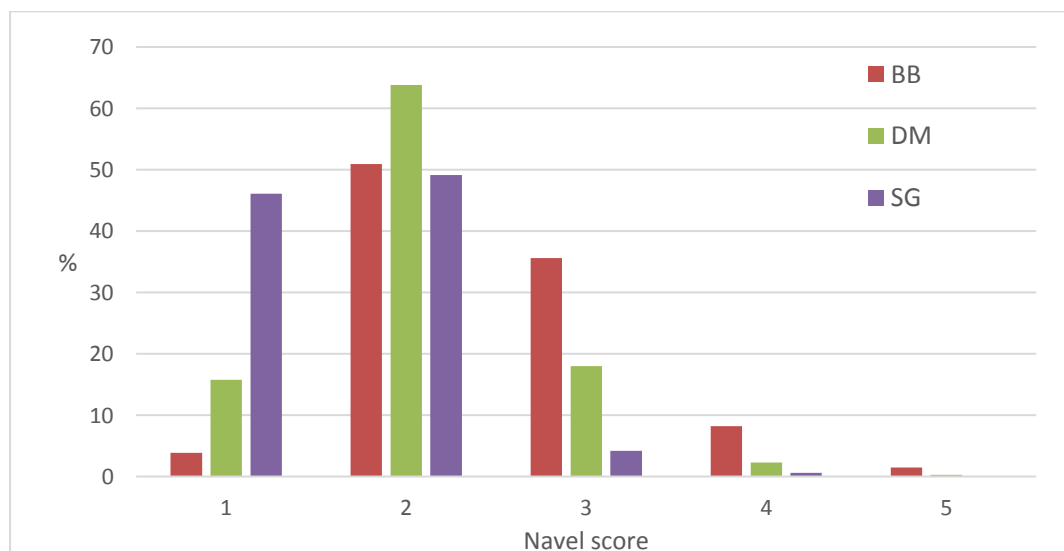
Fig. 34. Distribution of heifer navel score by breed

Analysis of navel considered the standard set of fixed effects previously described. The final model included significant fixed effects for sire breed, heifer cohort and age. Given the categorical nature of the trait a threshold model was used to estimate the heritability using Thrgibbs1f90. The above fixed effects were fitted, with animal fitted as a random effect and results in Table 41.

Table 41. Variance components and heritability estimates for various thresholds for heifer navel score

Model	N thresholds	Va	Ve	h^2	Threshold 3	Threshold 4	comments
1	1,2,3,4,5	2.99	0.79	0.45	3.21	5.50	Unstable Va
2	1,2,3,4-5	0.53	0.78	0.39	2.94	-	Va goes to 1.70
3	1-2,3,4-5	1.48	0.96	0.31	-	-	Unstable Va
4	1-2,3-5	0.42	1.01	0.27	-	-	Va goes to 2.4

Different models were used based on various grouping of scores and fitting of thresholds. Model 4 resulted in an estimated heritability on the underlying scale of 0.27, with an observed frequency of score 3 or higher being frequency of 29% of the data. Transformed onto the observed scale this yielded a heritability of 15%. Further, when the analysis was rerun with the breed effect removed the heritability estimate increased to 80% reflecting a very large breed effect on the trait. These analyses confirmed that navel scored trait is heritable and EBVs could be produced that would assist in breeding for navel (and sheath size), however modelling the categorical nature of the trait will require more data to allow the effective application of threshold models.

4.9 Other Project outcomes

4.9.1 Pompe's disease discovery

During the Project the routine SNP genotyping identified the presence of potential carriers of Pompe's disease in some of our Project animals. This lead to a separate clinical study that identified the existence of the Pompe's disease in the Droughtmaster breed. This work was subsequently published (Lyons *et al.* 2017) and has had a direct impact on the industry resulting in increased awareness of the occurrence of this common disease in cattle. Several Droughtmaster breeders are now routinely testing for the disease, particularly in sires and AI semen.

4.9.2 New "TropBeef" SNP chip

The Project was one of the first clients to use the new GeneSeek Genomics Profiler - Indicus test, known locally as the GGP-TropBeef developed by Neogen. SNP profiles from the new chip were processed on large numbers of Project animals and immediately revealed an issue with the chip with regard to the lack of a common set of SNPs. These sub-set of common SNPs are fundamental to the combining (and comparison) of SNP genotypes across different SNP genotyping platforms. This issue was communicated and discussed with the supplier and as a result the chip is in the process of being modified. As a consequence the use of this chip in the BREEDPLAN genomic pipeline currently requires an additional imputation step at AGBU to allow the genotypes from this chip to be included in single-step evaluations e.g. for Brahmans.

4.9.3 Improved AI program protocols

Over the five years of the Project a total of 4,100 artificial inseminations were performed at the two DAF sites. Cows were artificially inseminated using a modified 2-round FTAI program, where cows that failed to conceive to the 1st round were inseminated a second time 30 days later. All details at each AI program were recorded. The data was analysed from the first two years of the Project to help inform the management of subsequent AI programs (reported Project Milestone #8). Conclusions from those preliminary analyses are listed below:

- Semen quality had a direct impact on conception rates of individual sires. It is important to check the semen morphology (e.g. percent normal sperm) and post-thaw motility. The checks need to be done ideally for each batch of AI straws, especially for semen processed more than five years ago
- avoid if possible low BCS Composite cows
- avoid using older Brahman cows
- remove cows with history of AI ease score of 3 (i.e. can't get through the cervix)
- if AI ease score=3 at first round don't re-synchronise for 2nd round
- cut-off prior calving dates (i.e. minimum calf age) are suitable and including additional late calving cows at Round 2 is beneficial to the overall AI calving rates.
- timing of the insemination of Composite cows could occur slightly earlier by either starting ½hr earlier or during first hour bring Composite cows, but it doesn't warrant doing a complete breed draft.
- avoid having too many cows in a single program to prevent total AI time of greater than four hours (or may need to start earlier if a bigger group or use more than one AI technician)
- conception rates of dry cows were lower than lactating cow and may warrant an alteration to the synchronization protocols
- the synchronization protocols for use in tropical composite breeds could benefit from research into modifying the program to better suit this genotype
- need to DNA sire verify if using natural mate back-up bulls unless waiting more than 3-4 weeks to put bulls in due to variation observed in gestation length

Since these analyses were performed there has been another 3 years of data collected and therefore re-analyses should be re-done to check outcomes and refine recommendations. The results will be very useful to assist the northern industry to increase conceptions rates from AI.

4.10 Contributions to other research projects

Over the course of the Project collaborations have been made with other research projects. Primarily this has involved making the Project animals (and sometimes base data) available for these studies provided the overlay project has no impact on the existing project. The extension of this Project will continue to support collaborations and is likely the existing data will be a key resource in the future e.g. independent dataset for validating genomic predictions/products as they are developed from the Northern Genomics Project.

4.10.1 Northern Steer BIN

The largest associated project is the MDC Northern Steer BIN project (**P.PSH.0743** and **P.PSH.0744**) that purchased eight cohorts of steers generated by this Project. This has allowed the continued measurement of these steers for post-weaning growth, feedlot and pasture finishing performance, carcase and meat quality assessments. As part of that project it has also established links to the ALMTEC project of live animal assessment and improved carcase measurements (e.g. DEXA). A small number of carcases from each of the three breeds were used in MSA eating trials. Prior to slaughter

the steers have been ultrasound scanned and this has included a measure of scan IMF%. These records, along with the chemically-determined IMF% recorded in the lab will be used to re-assess the utility of live animal scanning of IMF% as a genetic indicator of carcase. Currently the trait is turned off in Brahman BREEDPLAN but these data could be used by AGBU to determine if that can change.

Data collected from the Northern Steer BIN will assist in building the genomic reference populations of the breeds for important carcase and meat quality traits. The data will improve the EBV accuracies of the sires in the Project, and will be important in the development of multi-breed EBVs for these traits. The data will add significant numbers of records on abattoir and meat quality traits and will allow the re-estimation of genetic correlations between these traits and female reproduction traits (i.e. on their ½-sisters). Finally, the new measures being recorded on these steers will add data to the system that over time will allow the potential development of new BREEDPLAN carcase and meat quality EBVs.

4.10.2 Calf loss/Colostrum studies

Cows at Spyglass site have been involved in DAF-funded studies regarding calf losses. The first was a small pilot study on calf hydration that was a part of a UQ Master's thesis of Mr. Jarud Muller (title: *Dehydration as a risk factor for calf mortality in northern Australia*). Calves were recorded for early growth rate in a subset of the #14 Spyglass calves. A second project commenced in 2018 and recorded additional measures on the #19 Spyglass calves at birth (i.e. at time of calf birth catching) and again at 2 weeks of age. The main measure of interest in this new study is the colostrum production of the cows and its association with calf survival and early growth.

4.10.3 AGBU MLA Project (L.GEN.1704)

The phenotypic data and SNP genotypes from the Project have been pivotal in the recent developments of BREEDPLAN as part of the beef component of the AGBU/MLA project. The development of single-step genetic evaluation in BREEDPLAN has relied heavily on reference population datasets, which this Project data has contributed to, to assist with the development of the statistical methodologies and changes required to the BREEDPLAN code, especially in designing the genomic pipeline for processing the raw genotypes through to the construction of a GRM. Brahman data from this Project was used extensively in the development and testing phase, with Brahman the first breed to implement single-step with the release of BREEDPLAN single-step genomic evaluation in April of 2017.

The phenotypic data collected in this Project has allowed the development of the two new female reproduction traits (AP and LAI) and these are pivotal in the improvement of EBV accuracies from the new single-step evaluations. The large amount of phenotypic data will also be very valuable in the re-estimation of variance and covariance components for the majority of the BREEDPLAN traits in the three breeds. The female reproduction data will also be pivotal in the proposed work plan of the project to re-define the trait definitions and modelling of female reproduction traits. Finally, the SNP genotypic data from the Project has added significantly to the size of SNP reference sets for breeds used in the genomic breed composition diagnostics in the existing genomics pipeline.

The data provides a very powerful database for the development of northern across-breed EBVs at AGBU and the data (and its structure) will provide ABRI with a working dataset for their database development and delivery systems for multi-breed evaluation. Additional research will be required to allow the building multi-breed GRMs for combined breed single-step evaluations, and the data from this Project will be invaluable in that further research.

4.10.4 AGBU Poll/Horn Project (MLA L.GEN.1803)

SNP genotypes generated in the Project on recent cohorts for Poll/Horn (Celtic and Friesian alleles) has been used in this project to compare to the CRC microsatellite DNA test. Accurate phenotypes were also recorded and used in conjunction with the genotypes to do part of this research.

5 Discussion

The Project has clearly delivered on its aim to build the genomic reference populations of the three most prominent tropical breeds to enable enhanced capacity for beef producers in northern Australia to improve female reproduction rates as well as other economically important traits. The Project has directly resulted in the increase in EBV accuracies for each of the three breeds across an increased number of animals in each breed. These advantages will continue to yield ongoing benefits for selection decisions for many years. This Project builds on results from Beef CRC and quantifies the benefits from single-step genomic evaluations.

5.1 Meeting of project Objectives

5.1.1 Genotyping industry sires with high accuracy BREEDPLAN days to calving EBVs

ACHIEVED: A total of 420 industry sires were SNP genotyped and this data has been used to build the genomic reference populations for the breeds. The genotypes are also available for SNP parentage of future progeny from industry and the DNA diagnostic tests for polled/horn and Pompe's disease can also be used by industry in making breeding decisions. Industry sire genotyping was important feature of the Project particularly for the Santa Gertrudis breed to enable them to build their reference population. The 53 sires genotyped in the Project had high accuracy DC EBVs which equates cumulatively to approximately 4,600 daughters with industry recorded DC records. The increase in Brahman reference population though the Project with high DC EBV accuracy has been achieved by genotyping a combination of ABBA BIN sires, Industry herd sires and DD sires. All genotypic data are stored on a purpose built Project database (see Appendix 11.3).

5.1.2 High accuracy phenotyping for female reproduction traits

ACHIEVED – The number of females recorded for age at puberty and lactation anoestrous interval was very close to the proposed number across all sites. The total number of records, after data editing, was 2,452 for heifer age at puberty and 1,501 lactation anoestrous interval records. The frequency of ovarian scanning achieved to record these female reproduction traits was also more than projected and resulted in very high precision phenotypes. All phenotypic data generated in the project at DAF and DD are stored on a purpose built Project database (see Appendix 11.3).

5.1.3 Validation and enhancement of genomic selection for female reproduction in tropical breeds

ACHIEVED – Throughout the Project the use of DGVs and genomic prediction became completely redundant with the move world-wide to single-step genomic evaluations. In the initial years of the Project assessment of the predictability of DGV was reported for Brahmans (Milestone Report 4: section 4e) and Santa Gertrudis (Milestone Report 5: section 5g). These results confirmed DGV did explain additive variance and that the phenotypic data being collected as part of this Project was sufficiently accurate to allow differences to be determined. However this technology was replaced with single-step genomic evaluations and all the phenotypic and genotypic data from

the Project has added significantly to the genetic evaluations of the three breeds for reproduction but also a large amount of other difficult to measure traits. The Project also planned to genotype young industry animals but with the delays in implementation of single-step evaluations in the BREEDPLAN tropical breed this was not undertaken (Milestone Report 5). Instead to demonstrate the value of single-step, and to add further to the reference population, the #17 and %18 drops Project animals were genotyped (N=1,907) with new 35K chip.

5.2   Enhanced genetic evaluations for the three breeds

The Project deliverables in terms of enhanced genetic evaluations have differed across the three breeds and reflects their histories of CRC involvement and levels of industry performance recording. All the breeds have directly benefited from the phenotypic recording from the Project that has added significant numbers of records across the full range of traits, including female reproduction. These include the development of two new female reproduction EBV to be included in the standard northern breed BREEDPLAN analyses that have been a direct result of this Project. The inclusion of the phenotypic data has lifted sire accuracies across almost all traits and have provided additional genetic linkage to strengthen the across-herd comparison in the whole analysis. The genotypic data has increased the size of the genomic reference population of each of the three breeds.

Brahmans have built on previous Beef CRC and Brahman BIN research projects and are now delivering a powerful set of female reproduction EBVs (possibly the most comprehensive anywhere in the world). The amounts of phenotyping and genotyping have enabled the introduction of single-step genomic evaluations and is providing enhanced evaluation across the diversity of genetics and studs that exist in the breed.

Santa Gertrudis was the smallest breed in the Project. The results show the Project data is having benefits, but the breed definitely requires additional intensive recording to build their genomic reference population before the benefits of genomic selection will be more apparent. Also in the early years of the Project the Santa Gertrudis animals were generated from base Beef CRC Tropical Composite cows: whilst this benefited the overall experimental design it has restricted the number of these females being currently eligible for the construction of the genomic relationship matrix for the single-step. In future as new methodology is implemented to allow multi-breed construction of a GRM these records will be included and will further boost the size of the reference population coming from recording done in this Project.

The Droughtmaster breed is relatively new to performance recording and the Project has spring-boarded them into a new and exciting position of genetic evaluation. The development of a DC EBV is a critical development for the breed but requires additional genotyping to capitalise on single-step capacities. The phenotypic data provides a core dataset for their evaluation and will be pivotal in re-estimation of variance components in the future.

5.3   Industry engagement

Over 90 studs have their genetics represented in the Project and this has provided powerful direct ownership of the Project outcomes by industry. Over the five years the Project has received high levels of media coverage including features in MLA Feedback Magazine, Queensland Country Life, BEEF CENTRAL, SBTS and TBTS newsletters, local newspapers, and overseas exposure in the USA, South Africa, Namibia and Uruguay. The Project has also had features on the MLA website, NTDPI and DAF website, FutureBeef, commercial company websites and numerous breeder websites.

The Project has hosted field days and herd visits including AgForce executives, Stock & station agents, Research station producer advisory committees, QLD Minister for Agriculture and DAF's Director-General of Agriculture, and MLA RBC regional chairs.

Levels of industry engagement and interest in the Project have been very high. The Project was featured at two MLA Beefup forums (Spyglass and Kidman Springs) attracting a combined total of over 300 producers and industry professionals. Participants were presented with the latest Project results and live animal displays demonstrating the Project design and differences in female reproduction traits and EBVs.

5.3.1 Major presentations

- Banana Station Brahman BIN field day, March 2016

- Project cooperating breeders workshops, Rockhampton, July 2015 & July 2016

- Brahman World Congress, Rockhampton, May 2016

- Brian Pastures Breeder Information day, March 2017

- Spyglass industry advisory committee field day, June 2017

- AAABG Conference, Townsville, July 2017

- Douglas Daly Producer information day, Aug 2017

- Beef 2018, Rockhampton, May 2018

- AgForce Brian Pastures Forum , June, 2018

- Kidman Springs MLA Beefup Forum, August 2018

- Spyglass MLA Beefup Forum September 2018

- The three breed Society boards and technical committees (annually)

- Various producer groups and international visitors

5.4 Extension messages

The extension messages from this Project build on years of work to get BREEDPLAN EBVs adopted in both the seedstock and commercial sectors of the northern beef Industry. The Project has demonstrated the magnitude of genetic differences that exist in these breeds for female reproduction traits and the outcomes of the Project provide improved genetic evaluations to greatly increase the ability (and confidence) of producers to select for increased reproduction.

All breeds should encourage their members to submit days to calving data and this especially is now the case for Droughtmasters. Breeders may also consider implementing ovarian scanning to record AP and LAI traits in their herds to greatly increase their EBV accuracies and rate of genetic progress. Consultation is also required regarding future genotyping strategies to maximise the benefits from single-step evaluations for individual breeds and breeders, including determining the most suitable sires to include in any future mating in maintaining their reference populations. Commercial breeders can now consider using genomic selection when sourcing replacement bulls and could also consider genotyping existing sires (without EBVs) to obtain single-step EBVs to determine estimated genetic merit.

AGBU is working with the MLA genetics extension team, TBTS and the northern breeds to incorporate and strengthen these key Project messages and outcomes into extension and training programs.

6   Conclusions/recommendations

6.1   General Conclusions

The Project has been very successful at meeting its objectives and delivering real change to the northern beef industry. The Project has demonstrated the value of collaboration in achieving the levels of recording that no one organisation would have been able to achieve. Given the large investment in generating the reference populations the establishment of a drought contingency fund was very important to ensure the delivery of outcomes and should be considered in future funding of long-term breeding projects.

The Project has built capacity to assist industry in the future delivering large benefits for genetic improvement of female reproduction but also measuring the full range of economically important traits which value adds to the investment. There is the opportunity for steers generated in future reproduction-focused projects to be retained and recorded as they are a valuable resource for other off-farm or hard-to-measure traits (e.g. feed intake, abattoir carcase and meat quality traits). Additional data on steers will also benefit the estimation of correlations between steers traits and the female recorded traits.

There is an immediate need to ensure Santa and Droughtmaster evaluations are transitioned to BREEDPLAN single-step evaluation as soon as practical to see the full benefit of this Project. However efforts are also required to continue to grow the sizes of the reference populations, especially for difficult to measure high economic value traits on the most current genetics and for additional tropical breeds. Currently, genetic parameters (i.e. trait heritability estimates) have been estimated using pooled breed datasets but have fitted a breed term in the statistical models to remove breed effects. Ideally, genetic evaluations use breed-specific heritability estimates when sufficient numbers of records exist, therefore over time (i.e. beyond this Project) the aim would be to re-estimate all the genetic variances and heritabilities to ensure the evaluations are using the most appropriate set of parameters for the prediction of EBVs and accuracies. It will also be important to re- estimate all genetic correlations to ensure effective indirect selection and to further understand any possible antagonisms of reproduction traits with other key traits.

The opportunity exists to develop new traits of economic importance for northern Australia (e.g. bottle teats). Many of these novel traits are simple scores that would be easy to implement in industry however statistically they are more difficult to analyse and currently require more data to get stability in the estimation of genetic parameters. The evidence from this study is that many of these new traits are heritable and could be developed further to produce EBVs to allow selection for improved teats and udders, coat scores, and navels. The Project has also demonstrated the value of doing additional research using the resource herds generated. The ability to overlay research projects provides opportunities for trialling new technologies (often not possible in industry) as we need to keep discovering cheaper or easier measures for use in genetic evaluations in northern Australia.

6.1.1 Practical application

The northern beef industry now has greatly enhanced capability to select for and genetically improve female reproduction. The increased accuracy of EBVs and increased numbers of young animals with available EBVs will provide both bull breeders and bull buyers with the opportunity to source superior genetics, especially for female reproduction. The capacity to use genomics in the single-step genetic evaluations provides a powerful and unique situation where any animal in a breed can be DNA-

sampled, included in the evaluation and receive a full set of EBVs, to then be used when making selection decisions.

6.1.2 Development and adoption activities

The data and enhancements of BREEDPLAN will ensure the northern beef industry benefits from this Project. The project provides a model for other regions (e.g. the south) and other breeds on development of reference populations, trait recording and industry collaboration. Workshops for contributing breeders should be considered (beyond this Project) to update them on the final results of the Project and their genetics, this will ensure end-users are fully briefed, so that they can apply the knowledge in their breeding programs and provide quality advice to their commercial clients.

On-site demonstrations have proved a powerful medium for getting the Project messages out and has generated practice change back in seedstock and commercial herds as evident with sire selection and bull purchases. It is recommended that the extension for the application of across-breed EBVs as they develop in the future is managed in a similar way through on-site demonstrations and workshops. There is opportunity to develop a comprehensive program of engagement with seedstock breeders, commercial producers, service providers, agents, vets etc to drive the adoption and use of genetic technologies.

As Santa Gertrudis and Droughtmaster breeds transition to single-step BREEDPLAN evaluations they will benefit from additional industry genotyping to build their numbers of genotyped animals. One of the most beneficial ways would be to sample current high accuracy sires (and cows), particularly those with DC records that have not been genotyped. Further development of the Droughtmaster genetic evaluation would benefit with the implementation of the DC EBV and the development of BreedObject Indexes as both would allow greater accuracy of selection and improved herd profitability. The Brahman breed should include gestation EBVs in their routine evaluations to allow this trait to be routinely evaluated and may assist in avoiding calving difficulties and calf losses.

For effective use of genomic data the new Trop-beef Chip upgrade needs to be completed to ensure its utility is realised, especially when it is able to be packaged to provide genetic test for polled genotype and Pompe's disease. Commercialisation of a genomic-based breed composition test should proceed for tropical breeds but care is needed in its application to ensure it in not misused/misunderstood as to its use/limitation in predicting genetic differences in performance within a breed.

The primary goal of this project was to generate accurate genomic reference data for the breeds involved, to enable earlier and more accurate selection in young animals than is possible solely relying on industry data. The project co-investment has been substantial, but the cost effectiveness is also high given the increases in genomic accuracy for a large number of traits important in breeding objectives of tropically-adapted cattle.

The intensity and trait coverage of the recording reported here is unlikely to be replicated in industry herds, and accordingly an industry priority should be the development of co-funding models for ongoing maintenance of intensive high quality recording. Given that the benefits from a genomic reference population are shared among bull breeders, commercial producers and others in industry value chains, there is a strong case for a mechanism that includes contributions from across the sectors.

7   Key messages

- Performance recording is a powerful tool to determine genetic differences. Intensive high quality recording from well-designed programs can generate increased accuracy across many traits simultaneously, and more precise estimates of genetic parameters than are possible from field data.

- The availability of genotyping and the increased accuracy of EBVs for young animals, especially for reproduction traits will enable breeders to increase the rates of genetic progress for improved reproductive performance in tropical beef breeds.

- Female reproduction traits, especially component traits measured earlier-in-life, have moderate to high heritabilities and can be used to improve the accuracy of selection and genetic progress towards improving reproductive performance.

- Good phenotypic recording when coupled with high density SNP genotyping can be used to grow reference populations and consequently drive increased rates of genetic improvement with new genomic selection genetic evaluations.

- There is scope for significant increase in the adoption of EBVs in northern Australia breeding programs, particularly via use of genotyping for single-step genetic analyses, exploiting the growing genomic reference populations.

- Commercial breeders will benefit from gains made in the seedstock sector and can also directly use the technology to assist in bull buying to ensure better match of genetic to markets and to individual production systems, especially for female reproduction.

- Use of appropriately designed across-breed data, such as this project, can assist both within-breed and the development of across-breed evaluations

- Direct industry involvement within projects of this sort can provide greater encouragement for industry to adopt the use of genetic tools and technologies for productively improvements

- The Project provides a strong dataset for very comprehensive analysis and selection for the whole maternal productivity complex (fertility, growth, carcase, survival, behaviour)

- Given the scale – in time, numbers of animals, numbers of environments and years – at which intensive recording needs to be maintained for effective genomic selection, mechanisms need to be considered for long-term and large-scale recording.

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11 Appendices

11.1 Appendix 1 - Scoring scales used in the Project

A) Body condition score (with +/- each score)
- 1 = poor
- 2 = backward
- 3 = moderate
- 4 = prime
- 5 = fat

B) Mothering score
- 1 = dam not present but returns
- 2 = dam runs away
- 3 = dam pays attention at distance
- 4 = dam remains close
- 5 = very protective, aggressive

C) Teat score
- 1 = very small
- 2 = small
- 3 = normal
- 4 = large
- 5 = very large (bulbous)

D) Udder score
- 1 = very small
- 2 = small
- 3 = normal
- 4 = large
- 5 = very large

E) Calf vigour score
- 1 = extremely weak
- 2 = weak
- 3 = healthy
- 4 = vigourous
- 5 = extremely vigourous

F) Coat length score
- 1 = extremely short (slick)
- 2 = very short
- 3 = short hair
- 4 = medium hair
- 5 = long hair
- 6 = woolly (not used)
- 7 = very woolly (not used)

G) Heifer navel score
- 1 = tight
- 2 = small
- 3 = moderate
- 4 = large
- 5 = very large

11.2 Appendix 2 – Gestation length evaluation

Table A3.1: Summary statistics of the raw gestation length, birth weight and weaning weight of Brahman, Droughtmaster and Santa Gertrudis sired calves born 2014-2018.

Trait	Data subset	Overall	Sire breed			Project herds	
			Brahman	Droughtmaster	Santa Gertrudis	Brian Pastures	Spyglass
Gestation length (days)	N	1,469	699	592	178	633	836
	Mean	289.5	291.6	288.4	284.9	288.6	290.2
	Standard deviation	6.0	5.5	5.7	5.4	6.1	5.8
	Minimum	271	276	272	271	271	272
	Maximum	312	310	312	298	310	312
	N sires	67	34	24	9	57	56
	Mean prog/sire	21.9	20.6	24.7	19.8	11.1	14.9
	Range prog/sire	3 - 49	5 - 48	8 - 49	3 - 33	1 - 35	1 - 44
Birth weight (kg)	N	3715	1814	1345	556	1541	2174
	Mean	33.4	32.3	34.0	35.8	34.3	32.8
	Standard deviation	5.5	5.1	5.5	5.4	5.5	5.4
	Minimum	18	18	18	19	18	18
	Maximum	53	52	53	53	53	52
	N sires	153	69	58	26	97	119
	Mean prog/sire	24.3	26.3	23.2	21.4	15.9	18.3
	Range prog/sire	1 - 101	1 - 79	1 - 101	1 - 86	1 - 86	1 - 63
Weaning weight (kg)	N	3,090	1,515	1,157	418	1,123	1,964
	Mean	191.6	185.5	193.0	210.1	206.7	183.0
	Standard deviation	34.3	31.7	35.1	34.5	33.8	31.6
	Minimum	78	78	91	109	109	78
	Maximum	322	283	322	310	310	322

11.3 Appendix 3 – Project data storage

1. **Phenotypes:** Phenotypic data recorded in the Project is stored on a custom-built *Postgres* database on a server at AGBU and backed up on multiple locations off-site. Data is stored on an individual animal basis and contains all identifications (e.g. project, breed society, DNA sample), experimental design variables (e.g. location, date of birth, sex, cohort), pedigree, progeny and trait blocks. Summary total of total numbers of record by trait block:

   i.   Live animal records (weights, scans, measures, scores, etc) = 245,889

   ii. Ovarian records (scans, preg test, etc) = 40,370

   iii. Natural mating records = 7,116

   iv. AI mating records = 4,741

   v.   Multi-sire natural mating groups = 268

2. **Pedigrees:** Individual pedigree data is stored for the mating and paddock records (e.g. mothering dam) and DNA parentage (sire and dam) using microsatellites, and more recently SNP-based.

3. **Genomics:** Genomic data is held on a custom-built *file* based database on server at AGBU (backed up off-site). It contains SNP profiles. Results for DNA polled/horn and Pompes test are held in phenotypic database.

4. **BREEDPLAN extracts**. Throughout the Project regular data extracts from the data for the full suite of BREEDPLAN traits recorded were send to ABRI's northern multi-breed research database for use in the Brahman and Santa Gertrudis evaluations. Project genomic data has been used in the monthly construction of the Brahman G matrix for inclusion in the single-step evaluations.