Final report

Coordination of Beef Reference Population Projects

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Prepared by: Kirsty Moore, David Johnston, Jim Cook, Christian Girard, Sam Walkom and Phillip Gurman
Animal Genetics and Breeding Unit, University of New England

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Abstract

Genomic selection can increase selection response, especially for hard-to-measure, sex-limited traits, and those traits expressed later in life. Reference populations directly impact the benefits obtained from genomic selection, but the cost of developing and maintaining them is not insignificant.

This project has provided evidence-based guidance on where future investment in reference populations is required and has undertaken research to enable more effective reference populations.

Descriptions of the current status of beef reference populations found that for hard-to-measure traits, reference populations still required additional investment to enable genomic selection to benefit the whole breed. An empirical-based method for predicting the accuracy of genomic predictions was shown to predict accuracy better than current theoretical approaches. Several tools were developed that will assist in designing reference populations and determining the potential increase in EBV accuracy from genotyping individual animals. The impact of poor phenotype quality in the reference was determined to affect the prediction accuracy for those herds that submitted phenotypes identified as being of poor quality. In addition to genomic selection, reference populations provide a powerful resource for investigating novel phenotypes and the potential development of new EBVs. Immune competence traits were shown to be heritable with variation in northern beef breeds, while data from sensor technologies recording pasture feed intake were found unsuitable for genetic evaluation. Myostatin mutations were shown to be segregating in northern beef breeds.

Executive summary

Background

Including genomics in genetic evaluations can increase EBV accuracy and selection response, especially for hard-to-measure, sex-limited traits and traits expressed later in life. Single-step GBLUP has been implemented into Australian BREEDPLAN genetic evaluations (Johnston et al. 2018). The potential benefits of genomic selection are directly impacted by the structure of the reference population, including its size, trait heritability, effective population size, relatedness amongst the reference animals, and relatedness to selection candidates. A reference population of phenotyped and genotyped animals is required for each breed implementing single-step genetic evaluations. Developing and maintaining reference populations and the associated recording is not insignificant. As future reference population funding models are explored, knowledge of the current state of beef genetic reference populations is essential to prioritise resources. Furthermore, researching methods for determining genomic prediction accuracy and relatedness to the genomic reference can help to better understand how to maximise the return on investment in Australian beef reference populations. In addition to facilitating industry genetic gain, reference populations are ideal platforms for investigating potential new traits for genetic evaluation. This project added value to the existing investment in reference populations by assisting the organisations in data analysis that helped build better reference populations, provided knowledge to improve management and genetic evaluations, evaluated new technologies, and developed new EBVs for novel traits.

Objectives

This project aimed to support and add value to reference populations and undertake research in reference population design. This research had four core objectives.

- Descriptions of current and historical reference populations
- Provide reference population design support to current reference populations
- Data analysis to add value to current reference populations
- Undertake research related to the design of reference populations

Methodology

Australian beef reference population data (Angus, Hereford, Repronomics / Northern BIN: Brahman, Droughtmaster and Santa Gertrudis, Southern Multi-breed: Angus, Brahman, Charolais, Hereford, Shorthorn and Wagyu, and Wagyu) were used to undertake several studies to describe their structure and effectiveness. An empirical method to predict genomic accuracy was applied, and the methodology was extended to cover a wide range of applications in the beef industry. Numerator relationship matrices were used to develop a method to describe the linkage of Australian beef reference populations to wider breed populations. Variance components were estimated for novel traits using ASReml fitting animal or sire models. The PROC MIXED procedure in SAS calculated least squares means that were used to describe the impact of fixed effects on carcase and reproduction traits, and quantify the impact of having one copy of a myostatin mutation. A genome-wide association study for reproduction traits was undertaken using the “SNPSnappy” module of WOMBAT.

Results/key findings

- Descriptions of Australian beef genomic reference populations were compiled to capture the reference population design and summarise the data generated. This information will allow future investment in reference populations to be targeted for maximum benefit and better leverage existing reference populations for genetic improvement.
- An SQL database was created to capture an inventory of the animals and data collected as part of reference population projects. The database captures information on the project design and the information collected on reference animals.
- Genomic prediction accuracy is directly related to how the genotyped selection candidate is related to the genomic reference. A relatedness to reference metric was developed to describe how two groups of animals were related. This method had many applications, including assessing how animals and/or herds were related to reference populations and identifying sires to include in reference populations.
- The relatedness to reference metric was used to assess how animals in the wider breed populations were related to trait-specific reference populations. The results showed that for hard-to-measure traits (i.e. abattoir carcase traits, female reproduction traits and mature cow weight), most of the breed reference populations still required additional investment to ensure the full benefits of genomic selection for the whole breed.
- The relatedness to reference metric was used to describe and compare the relatedness of the Southern Multi-Breed reference population to a whole breed. The study confirmed that the foundation cows and sires used in the Southern Multi-Breed Project were highly related to the breed population. Therefore, the reference data collected will benefit within-breed genomic selection programs.
- The longevity of the Angus reference population was explored using the relatedness to reference metric. Angus Sire Benchmarking Program cohort data collected on animals born between 2011 and 2021 were used. As relatedness between Angus Sire Benchmarking Program cohorts and subsequently used industry sires declined, there was a corresponding fall in accuracy gains from the Angus Sire Benchmarking Program phenotypes.
- A new empirical-based method for predicting genomic predictions was applied and was shown to better predict accuracy than current theoretical approaches. The predicted accuracy of genomic predictions was calculated based on current Angus, Brahman, Hereford, and Santa Gertrudis reference populations. Analysis showed that the benefit of the empirical method was an improved estimate of the effective number of chromosome segments, which is an important factor in genomic accuracy.
- Applying the empirical-based method for predicting the accuracy of genomic predictions was limited to existing reference populations. Therefore, the method was extended to allow its application to a wider range of scenarios.
- Using the extended empirical-based method for accuracy prediction, two tools were developed to predict genomic accuracy when designing future reference populations and determining the potential benefit of genotyping individual animals. The accuracy prediction tools are available by license from MLA for within-breed.

- The impact of poor phenotype quality of reference animals on genomic selection was limited to those herds recording the phenotypes that were considered poor quality and did not impact herds that recorded phenotypes classified as medium or high quality or genomic-only breeding values.
- In addition to genetic improvement, the management decisions of producers also impact phenotypic performance and profitability. The following management strategies were identified to improve phenotypic performance and profitability for carcase and fertility traits:
    - Managing the age spread of a cohort – If the age spread is large, the spread of carcase weight within a cohort will be greater, and profitability will be impacted due to animals being slaughtered before meeting market specs or being kept longer, incurring additional costs. An age spread in the cohort that was too large was also shown to impact the number of pubertal heifers at the start of mating and the time it took for a cow to start cycling after weaning a calf.
    - Season of birth – Analysis showed that calves born late in the calving season were more likely to have delayed puberty, resulting in fewer heifers being pubertal at the start of mating. Furthermore, heifers that calve late in the season were also shown to take longer to cycle again after the calf was weaned.
    - Body weight and growth – Managing the live weight of heifers affected whether or not the heifers were pubertal at the start of mating. In tropical beef breeds, it was shown that for 85% of heifers to be pubertal at the start of mating, the average weight should be 221 kg as yearlings and 353 kg at the start of mating. Body weight and composition at the start of the 2nd mating period affected the lactation anoestrus interval.
    - Puberty status at mating – Heifers that were pubertal at the start of mating were more likely to have cycled again when the calf was weaned.
    - Tailoring management decisions in response to annual seasonal effects – Annual seasonal effects were shown to impact carcase weight, age at puberty and lactation anoestrus interval. Tailoring management decisions in response to annual seasonal changes may help mitigate the effect of the season.
    - Culling older cows – calves of older (10+ year old) cows were shown to be lighter at slaughter.
- The myostatin mutations (double-muscling) NT821 and F94L were shown to segregate in Droughtmaster and Santa Gertrudis. NT821 had the biggest impact on production traits, with heterozygote animals being heavier and more muscular, improved tenderness and leaner, but had delayed puberty age, increased days to calving, and an indication of higher incidence of calving-related deaths.
- Immune competence traits (cell- and antibody-mediated immune response) were found to be heritable, with variation indicating that selection is possible for these traits in northern beef breeds. However, more needs to be understood about the impacts of these traits on economically important traits before they can be effectively used in breeding programs.
- New sensor technology was trialled and results analysed. Sensor data from eGrazor collars classified behaviours of tropically adapted beef breeds at pasture that aligned with literature

reports, but showed no relationship with feedlot feed intake. Sensor data from Ceres ear tags was inconsistent across trials, and no beneficial outcomes could be made at this stage.

- The relationship between carcase traits currently not included in BREEDPLAN evaluations (viz. the cooking loss and meat colour a*, b* and l* of the longissimus dorsi muscle, MSA hump height, MSA Ossification and MSA index) and BREEDPLAN traits for female reproduction, weaning weight, carcase weight and shear force was estimated. Estimated variance components indicate that the non-BREEDPLAN carcase traits were heritable and could be included in genetic evaluations. There were no strong unfavourable correlated responses with the BREEDPLAN reproduction, growth and carcase traits. Shear force was moderately to strongly correlated with cooking loss and the three meat colour traits. Ossification was estimated to be moderately correlated with age at puberty and growth traits, and further research could investigate if there is merit in developing an ossification breeding value to describe the physiological development of animals.
- Analyses showed that animals with higher Brahman content had higher hump heights, lower MSA index, decreased hot carcase weight, hot P8 fat depth, MSA EMA, MSA rib fat at 12/13th rib, intramuscular fat percentage, MSA USDA Ossification, Longissimus dorsi a* colour, Longissimus dorsi b* colour, MSA Loin Temperature and MSA Marbling score and increased shear force, Longissimus dorsi cooking loss and Longissimus dorsi L* colour. These results showed that as Brahman content increased, the meat eating quality decreased. This study did not consider if the reduction in meat eating quality observed as Brahman content increased, aligned with the hump height adjustment applied to the MSA index.
- Principal component analysis of Brahman, Droughtmaster and Santa Gertrudis breeds showed that the Brahman and Droughtmaster genetics represented in the Repronomics project represented the genotyped Brahman and Droughtmaster industry animals. Santa Gertrudis animals in the Repronomics project did not represent the full range of genotyped Santa Gertrudis industry animals, with the PCA plot showing that Repronomics genotypes were only present in the lower half of the plot for Santa Gertrudis.
- Genome-wide association studies found several significant SNPs for heifer age at puberty and birth weight of Brahman and Droughtmaster animals. The significant SNPs for heifer age at puberty were in regions close to significant regions reported previously in the literature for tropical beef and dairy breeds.
- Multi-breed project EBVs for novel traits recorded at different times (as a heifer, into mating one, and into mating two) were developed for tropically adapted breeds.
- A preliminary analysis of Wagyu feed efficiency records estimated moderate heritability. Variation was observed for preliminary EBVs of 29 sires with progeny recorded for net feed intake.

Benefits to industry

The main benefit to the industry arising from this research was the development of evidence-based guidance on where future investment in genomic reference populations is required. Descriptions of the current effectiveness of beef reference populations and the development of improved accuracy tools and linkage metrics will allow more effective reference populations to be designed. This will help inform investment decisions and ultimately improve the genetic gain and profitability of the beef

industry. Investigations into the genetic evaluation of novel traits (e.g. immune competence) provide the beef industry with opportunities to incorporate these traits into their breeding programs. Research outcomes from this project will also benefit the industry by providing information to help producers manage known environmental effects to maximise carcase and female reproduction performance. Knowledge of the frequency and effects of myostatin mutations in the beef populations will help the northern industry manage this genetic effect, especially if there are both beneficial and detrimental effects on economically important traits.

Future research and recommendations

This project has shown that beef reference populations for hard-to-measure traits (i.e. abattoir carcase traits, female reproduction traits) and mature cow weight require further investment to reach an adequate size and ensure adequate relationships of reference animals to the wider beef populations. Given the limited resources available for investment, investing in reference populations that achieve multiple aims would be advantageous. Beef reference populations should also be recording a full range of traits to allow accurate genetic relationships to be estimated. Critically, as industry moves to a multi-breed genetic evaluation framework, the reference populations of the future should be designed to include several breeds and managed to ensure phenotypes are recorded in the same contemporary groups. The selection of animals to include in reference populations should focus on identifying animals unrelated to current reference animals but with strong relationships to current animals in the genetic evaluation. To assist in the maintenance of reference populations, the relatedness between reference animals and current animals in the genetic evaluation should be monitored to maintain the benefits of genomic selection.

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1. Background

Including genomics in genetic evaluations can increase selection response, especially for traits that are hard to measure, are sex-limited, or expressed later in life (Meuwissen et al. 2001). Single-step GBLUP has been implemented into Australian BREEDPLAN genetic evaluations (Johnston et al. 2018). The potential benefits of genomic selection are directly impacted by the structure of the reference population, including its size, trait heritability, effective population size, relatedness amongst the reference animals, and relatedness to selection candidates (Goddard and Hayes, 2009; Pszczola et al. 2012). As the relationship between the reference and selection population increases, smaller reference population sizes are required to achieve the same level of accuracy (Lee et al. 2017). Therefore, when designing reference data projects, multiple design principles must be balanced to maximise the value of the collected data. Furthermore, once a reference population has been established, ongoing maintenance is required, with new genetics contributing to the references so that recently born animals are related to the reference population.

A reference population of phenotyped and genotyped animals is required for each breed implementing single-step genetic evaluations. Developing and maintaining reference populations and the associated genotyping and recording are not insignificant. The industry challenge is how to invest in reference populations to obtain maximum accuracy for genomic prediction for the lowest investment, particularly given the large number of breeds that exist. The solution is relatively simple in some industries, such as the dairy industry or pig and poultry breeding. In dairy, genotyping bulls with high prior accuracy can establish the reference, and thereafter, the main challenge is to collect enough data on hard-to-measure traits. Approaches to achieving this in an ongoing way are still being developed in the dairy industry, but the situation is simplified by the smaller number of breeds, very highly related populations, and relatively high levels of recording (although structured investment in collecting sufficient records for fertility and disease traits is still developing). In pigs, well-structured breeding nuclei and large litter sizes make collecting reference data on selection candidates easier at a minimum cost. In Australia, by contrast, there is a large number of commercially relevant breeds and composite populations for beef cattle. Furthermore, genetic selection decisions are predominantly undertaken within individual seedstock herds, whereas genetic improvement decisions are dominated by AI and breeding companies for dairy, pigs, and poultry. To assist the development of beef genomic prediction, the industry has co-invested in the development of reference populations, initially via R&D projects in the Beef CRC (although this investment pre-dated genomic selection) and several Beef Information Nucleus (BIN) programs, supported via the MLA Donor Company program. In recent years, key multi-breed reference populations for northern Australia and southern Australia have operated. These populations have collected large reference data sets that include hard-to-measure traits, have enabled new breeds to implement single-step genomic evaluations, and will be critical for developing multi-breed genetic evaluations.

Current beef reference populations have been generated by several research projects and are run by breed societies or research organisations, with MLA often a co-investor. These projects and any future phenotyping and genotyping activities constitute the genomic reference portfolio for the industry, and the structure of this portfolio (breeds, sires sampled and traits recorded) determines the return on investment possible for the industry via accelerated genetic progress. The investment in reference populations has been considerable, and assuming future funding models are likely to change, there is

a significant optimisation challenge with recording and genotyping costs, particularly for the hard-to-measure traits. With limited funding, investing in collecting phenotypes and genotypes may not be a priority for traits routinely recorded on-farm, as the reference population can be built organically. Therefore, investment should focus on collecting phenotypes and genotypes for hard-to-measure traits that are difficult to record on-farm. Furthermore, to maximise the value of reference populations for hard-to-measure traits, it will be important to ensure that the animals recorded and genotyped are highly related to the current animals in the wider breeds, and are themselves diversely related.

As future reference population funding models are explored, knowledge of the current state of the beef genetic reference populations is essential. A large part of this project considered the current reference population designs and how they meet the requirement to generate accurate genomic predictions and genetic links to the wider breed populations that will use genomic selection to generate genetic gains. Furthermore, the research areas of genomic prediction accuracy and relatedness to reference are considered to better understand how we can maximise the return on investment in Australian beef reference populations. New methodologies to describe and assess relatedness to reference will be developed, and improved empirical-based accuracy predictions applied to assist in the design of future reference data projects. These new tools will enable a better assessment of the impact of current reference populations and ensure that future investment into references will maximise the investment benefit.

In addition to facilitating industry genetic gain, reference populations are ideal platforms for investigating potential new traits for genetic evaluation. This project will add value to the existing investment in reference populations by assisting the organisations in data analysis. These data analyses will vary and depend on the needs of each reference population, but they will include evaluating phenotypes generated by new technologies and undertaking research that will increase the understanding of hard-to-measure traits.

2. Objectives

Australian BREEDPLAN genetic evaluations use single-step methodology and rely on suitable reference populations to generate increased EBV accuracies. Several breeds have generated reference populations through projects initiated by breed societies or research organisations. Reference population design is critical and impacts the potential benefit of genomic evaluations. This project aimed to support and add value to the generated reference populations and undertake research in reference population design.

Objective 1 – Descriptions of current and historical reference populations

This objective was to review the reference populations and summarise their design and data collected. An SQL database was created to collate an inventory of the animals and data generated (but not the actual phenotypes) from reference populations.

Objective 2 – Provide reference population design support to current reference populations

This objective was to provide project design support to the organisations running reference population projects, and varied according to the individual needs of the reference population project.

Objective 3 – Data analysis to add value to current reference populations

This objective was to analyse data generated from reference data and add value to the reference population projects. These analyses vary and involve genetic parameter estimation, the evaluation of potential new phenotypes for genetic evaluation, the impact of fixed effects on phenotypes and animal value, and genome-wide association studies.

Objective 4 – Undertake research related to the design of reference populations

This objective was to research the design of reference populations to maximise the benefit of genomic selection. Methods for determining linkage to reference data, empirical estimates of accuracy after genotyping animals and the impact of phenotype quality on the prediction accuracy of genomic selection are considered.

3. Methodology and Results for Objectives 1 and 2

3.1 Descriptions of current and historical reference populations

Descriptions of each Australian beef genomic reference population were compiled to capture the reference population design and summarise the data generated. Appendix 9.1 includes descriptions of current reference populations that include Angus, Brahman, Charolais, Droughtmaster, Hereford, Santa Gertrudis, Shorthorn, and Wagyu animals. In addition, several historic reference populations were also described. Information was sourced from project final reports and communication with the organisations running reference populations. The information on the breeds, project duration and size, the project design (herds, sires and cows involved) and animal management, the traits and genotypes recorded, where the project data is stored, and who the current project contact is collated.

An SQL database was created to capture an inventory of the animals and data (not actual phenotypes) collected as part of projects. The database captured information on the project design and the information collected on reference animals. The information collected was as follows;

Project design – Project name, responsible organisation and organisation contact, breeds involved, project start and end dates and the planned number of cohorts and animals.

Basic animal information – The project that the animal belonged to, animal identification, sex, herd, year of birth, breed, AI or not, genotype information (is the animal genotyped and at what density), sire and paternal grandsire and what traits (Y/N) were recorded for the animal.

3.2 Design support to Australian beef genomic reference populations

Support was provided to organisations running reference population projects in several ways.

- Chairing the Southern Multi-Breed technical committee, which provided input into the overall project design and assisted with managing the data flow into an SQL project database and the ABRI Southern Multi-Breed database.
- Assistance with sire selections for the Angus, Hereford and Southern Multi-Breed projects using information obtained from linkage metrics developed as part of this project.
- Provided advice about genetic evaluations and reference population design to ensure the information from reference data projects could be best utilised.
- Assistance in preparing project proposals for the collection of reference population data.
- Assistance in data analysis and preparation of final and milestone reports.
- Developing genotyping strategies to help strengthen reference populations and maximise the value of genotyping investments.
- Allocation of reference population animals for add-on projects to ensure that the integrity of the reference population was maintained whilst maximising the value of data collected from both projects.
- Assistance in reviewing carcase data collected in the Northern BIN project.

4. Methodology and Results for Objective 3

A large number of statistical analyses were undertaken to explore new traits for genetic evaluation, including the development and analysis of fixed effects and how the management of these aspects can maximise performance. Genome-wide association studies (GWAS) were undertaken to discover any significant Single Nucleotide Polymorphisms (SNPs) of large effect on female reproduction and other traits and assess the impact of Myostatin mutations in northern beef breeds. The following sections of this report detail these analyses.

4.1 Wagyu Net Feed Intake

Net Feed Intake (NFI) for Wagyu animals was recorded as part of MLA-funded project P.PSH.0848, "Wagyu Net Feed Intake data collection and analysis." This project's analysis was to estimate preliminary genetic parameters and determine whether the dataset was suitable for inclusion in routine genetic evaluation and forming a genomic reference population for the hard-to-measure trait, NFI.

Twelve cohorts of feed intake data were collected at the Kerwee feedlot between 2017 and 2019. Contemporary groups were defined as animals in the same feed intake test, born in the same season (Autumn or Spring) at the same birth herd and with the same breed content (50, 75 or 100% Wagyu). Records were removed for animals that were not BREEDPLAN recorded (n=68), had less than 50% Wagyu content (n=2), were not steers (n=14), had unknown date of birth (n=298), date of birth was an outlier compared to contemporaries (n=4), or contemporary group contained fewer than five animals (n=25). After edits, 572 animals remained in the analysis. For most animals, the dam was unknown. ASReml (Gilmour et al. 2021) and a sire model were used to estimate Wagyu NFI variance components with the contemporary group fitted as a fixed class effect and age as a linear covariate. A three-generation pedigree was constructed. ASReml sire solutions for 29 sires with five or more progeny recorded for NFI were reported (Figure 4.1.1).

Moderate to strong heritability (h^2=0.43±0.22) was estimated for Wagyu NFI. However, the standard errors were large, and estimates varied depending on the subset of data (e.g., pure or cross-bred animals) included. More NFI records are required before variance components suitable for genetic evaluation can be estimated. The NFI dataset was collected on commercial animals; information about the dam was unknown, the date of birth was, in some cases, restricted to the season of birth, and there was evidence of harvesting in the dataset, therefore, more stringent data collection protocols will improve the genetic parameter estimates and suitability for genomic reference populations. Preliminary research EBVs for 29 sires with five or more progeny recorded for NFI showed variation in the genetic merit across the sires, with a 0.8 kg/day difference in the EBV between the least and most feed-efficient sire. This study concluded that the current dataset is too small to estimate robust variance components, especially as the dataset was collected on commercial animals with less stringent data collection protocols. More Wagyu NFI data is being collected to build the dataset and allow variance components to be re-estimated and NFI included in Wagyu genetic evaluations.

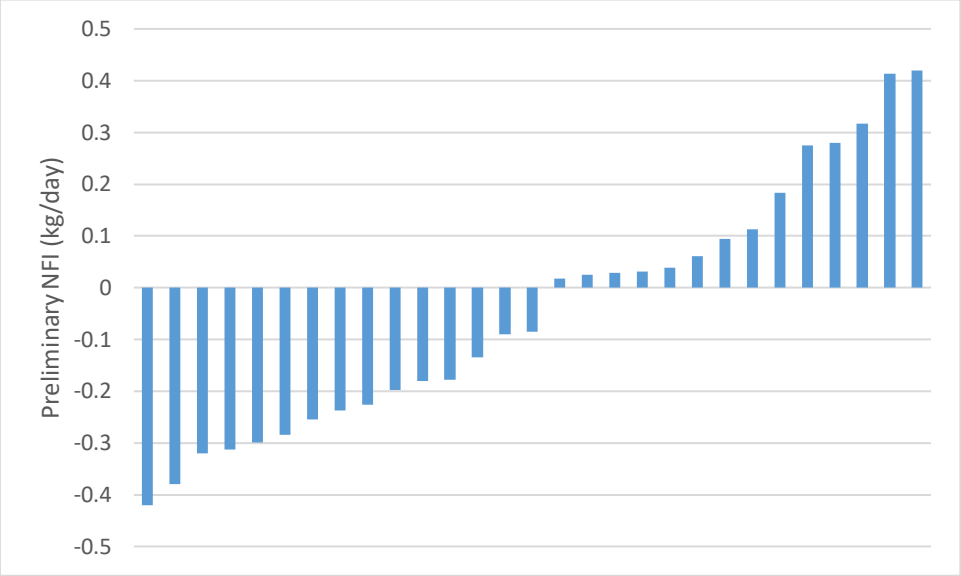


Figure 4.1.1: Preliminary research NFI EBVs for 29 sires with five or more progeny recorded for NFI

4.2 Variance component estimation and Repronomics EBVs for non-BREEDPLAN traits

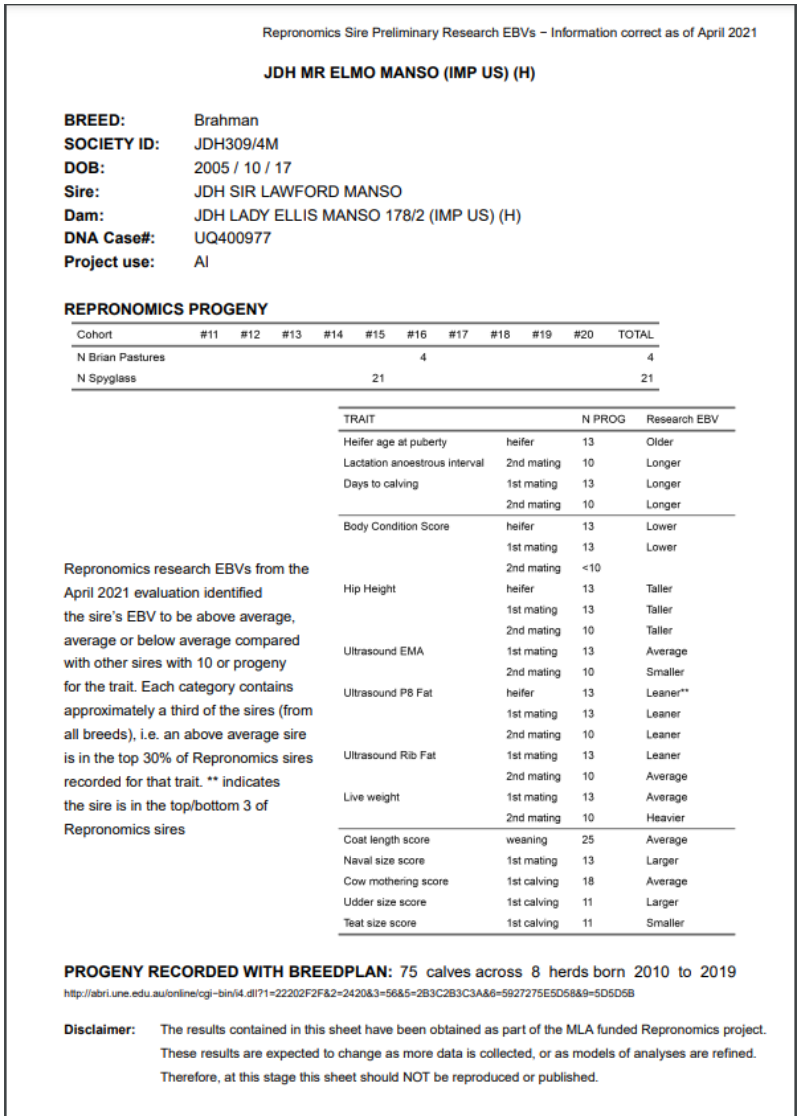
A large number of novel traits were recorded in the Repronomics reference population, and this project assisted the Repronomics reference project in undertaking variance component estimation and producing project multi-breed (Brahman, Droughtmaster, and Santa Gertrudis) EBVs for non-BREEDPLAN traits. In total, traits were considered at different times: as a heifer, into mating one, and into mating two. The impact of the breed effects was also considered, with breed fitted or not fitted, and in some traits, no breed differences were observed, while in other traits, there were differences in variance estimates due to breed. Where there were large breed effects and when the breed was not fitted in the model, the additive variance was generally inflated with inflated heritability estimates. The complete methods and results of this work were fully reported in the final report of the MLA-funded project P.PSH.1221, "Building and delivering effective genomic selection for northern Australia cattle". Table 4.2.1 below provides a summary of the estimated variance components.

Information sheets for each project sire were produced detailing basic information about the sire, its use in the project, and the preliminary research EBVs. An example of these sheets is shown below in Figure 4.2.1.

Table 4.2.1: Additive variances and heritability estimates for all new traits with (+ breed) and without (- breed) a breed term fitted in the model. (Source: Table 9, Johnston et al. 2024)

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

* on the underlying scale



Repronomics Sire Preliminary Research EBVs – Information correct as of April 2021

JDH MR ELMO MANSO (IMP US) (H)

BREED: Brahman
SOCIETY ID: JDH309/4M
DOB: 2005 / 10 / 17
Sire: JDH SIR LAWFORD MANSO
Dam: JDH LADY ELLIS MANSO 178/2 (IMP US) (H)
DNA Case#: UQ400977
Project use: AI

REPRONOMICS PROGENY

Cohort	#11	#12	#13	#14	#15	#16	#17	#18	#19	#20	TOTAL
N Brian Pastures						4					4
N Spyglass					21						21

Repronomics research EBVs from the April 2021 evaluation identified the sire's EBV to be above average, average or below average compared with other sires with 10 or progeny for the trait. Each category contains approximately a third of the sires (from all breeds), i.e. an above average sire is in the top 30% of Repronomics sires recorded for that trait. ** indicates the sire is in the top/bottom 3 of Repronomics sires

TRAIT		N PROG	Research EBV
Heifer age at puberty	heifer	13	Older
Lactation anoestrous interval	2nd mating	10	Longer
Days to calving	1st mating	13	Longer
	2nd mating	10	Longer
Body Condition Score	heifer	13	Lower
	1st mating	13	Lower
	2nd mating	<10	
Hip Height	heifer	13	Taller
	1st mating	13	Taller
	2nd mating	10	Taller
Ultrasound EMA	1st mating	13	Average
	2nd mating	10	Smaller
Ultrasound P8 Fat	heifer	13	Leaner**
	1st mating	13	Leaner
	2nd mating	10	Leaner
Ultrasound Rib Fat	1st mating	13	Leaner
	2nd mating	10	Average
Live weight	1st mating	13	Average
	2nd mating	10	Heavier
Coat length score	weaning	25	Average
Naval size score	1st mating	13	Larger
Cow mothering score	1st calving	18	Average
Udder size score	1st calving	11	Larger
Teat size score	1st calving	11	Smaller

PROGENY RECORDED WITH BREEDPLAN: 75 calves across 8 herds born 2010 to 2019

http://abri.une.edu.au/online/cgi-bin/i4.dll?1=22202F2F&2=2420&3=56&5=2B3C2B3C3A&6=5927275E5D58&9=5D5D6B

Disclaimer: The results contained in this sheet have been obtained as part of the MLA funded Repronomics project. These results are expected to change as more data is collected, or as models of analyses are refined. Therefore, at this stage this sheet should NOT be reproduced or published.

Figure 4.2.1: Example summary sheet for project sires presenting preliminary research EBVs

4.3 Analysis of fixed effects impacting carcase traits

Cattle producers aim to produce a carcase with many attributes (i.e. yield, fat content, eating quality) in their production system. However, the primary determination of the carcase sale price in the majority of instances is carcase weight. The sale price, in conjunction with management costs, determines the enterprise's profitability. Genetic selection using EBVs is an effective way to improve carcase weights. However, knowing and quantifying the magnitude of fixed effects impacting carcase weight may provide a mechanism for producers to increase profitability. These analyses used Northern BIN data (MLA projects P.PSH.0743, P.PSH.0774, P.PSH.2131 and P.PSH.2132, including Brahman, Droughtmaster and Santa Gertrudis), to determine which fixed effects significantly impacted the carcase weight and how this may be used to influence management decisions.

Data was recorded at two sites (Brian Pastures and Spyglass), and a summary of the raw data is shown in Table 4.3.1. Six data cohorts (2015-2021) were recorded at Brian Pastures for all three breeds, and

nine cohorts (2013-2021) were recorded at Spyglass for Brahman and Droughtmaster breeds. The average breed raw carcase weight ranged from 310.7kg (Brahman at Brian Pastures) and 334.8kg (Santa Gertrudis at Brian Pastures), and animals were aged at approximately 840 days at Brian Pastures and 900 days at Spyglass.

Table 4.3.1: Summary of raw carcase weight and animal age from within-breed datasets of tropically adapted beef breeds

		Carcase weight (kg)				Animal age (days)			
	N	**mean**	**std**	**min**	**max**	**mean**	**std**	**min**	**max**
Brian Pastures									
Brahman	312	310.7	28.2	220.5	395.9	842.3	81.0	629	975
Droughtmaster	258	323.1	31.4	234.4	417.7	836.4	91.9	619	967
Santa Gertrudis	346	334.8	34.3	226.5	441.1	840.3	92.8	621	965
Spyglass									
Brahman	956	315.3	32.8	187.9	426.4	902.0	53.7	774	1036
Droughtmaster	862	326.7	33.3	215.5	443.0	899.7	50.7	781	1020

The fixed effects considered within each breed were the cohort (herd and year), twin status (single or twin), dam age (years), and cow origin group (defined as site, dam breed type (composite or purebred), and origin herd) nested within the cohort as fixed class effects. The age at slaughter was considered a linear and quadratic fixed covariate. All first-order interactions were considered. The sire was fitted as a random effect.

The final significant models for carcase weight were as follows, and the least squares means for the significant fixed effects are reported;

Brahman – cohort + cow origin group (cohort) + measurement age
Droughtmaster – cohort + dam age + measurement age
Santa Gertrudis – cohort + cow origin group (cohort) + measurement age

Slaughter age: Regression coefficients indicate that for every day older the steer was at slaughter, the carcase weight increased by 0.38, 0.36 and 0.41kg, respectively, for Brahman, Droughtmaster and Santa Gertrudis. At 0.36 kg/day and an average 12-week maximum spread in age (within a cohort), that equates to a 30kg difference in carcase weight between the youngest and oldest animal.

Given the importance of age on carcase weight, managing the age spread of a cohort is an important management decision that will impact the carcase weight at slaughter. This may not be important for herds, which stagger the slaughter of animals as they reach market weight (i.e., harvest the older animals). However, for herds that need to slaughter animals as one group (i.e., due to transport costs or other logistics) or who wish to contribute carcase phenotypes for genetic evaluation, the age profile of the cohort must be managed. Too large an age spread will mean that the slaughter of older animals will be delayed until the younger animals reach the target weight. Older animals may also be heavier than the target weight, thus obtaining a higher sale price or penalty for overweight, but there will also be extra costs (i.e. feed costs) for keeping animals longer. When feed is plentiful, the impact on profit may be small or negligible. However, when feed is sparser or animals are fed grain, this extra time may impact the overall profitability of the older animals. Alternatively, cattle can be sent for slaughter before reaching the target weight; this will not incur extra costs but will reduce the sales price and

profitability. Producers can manage the age spread of a cohort by controlling the mating period of cows at mating.

Cohort (herd and year): The cohort effect captures the environmental effects. Table 4.3.2 summarises the least squares means for each breed, and Figure 4.3.1 plots the average cohort least squares means for carcase weight. The cohort in this data is the herd location and year of birth. A location effect was observed for Brahman and Droughtmaster, with cattle at Brian Pastures having an average least squares means approximately 20kg higher than Spyglass. After the initial decision about the location of a herd, there are limited management interventions to mitigate against the effects of the location.

The other cohort component is the year, which captures annual seasonal effects. A wide variation in carcase weights across years was reported at each breed and location – Droughtmaster showed an 86kg spread of carcase weights across Spyglass cohorts, and Santa Gertrudis showed a 109kg spread of carcase weights across Brian Pastures cohorts. This variation in cohort carcase weights can greatly impact the sale price obtained. The large variation across cohorts suggests that environmental factors play a role in the final carcase weight of animals. Producers cannot influence the seasonal conditions, but management practices should be reactive according to the season.

Table 4.3.2: Summary of carcase weight least squares means by cohort from within-breed datasets of tropically adapted beef breeds*

	Brahman	Droughtmaster	Santa Gertrudis
		Brian Pastures cohorts	
min	279.80	291.02	267.93
max	376.77	377.72	376.62
avg	323.43	342.77	333.35
std	32.28	29.85	36.45
range	96.97	86.70	108.69
		Spyglass cohorts	
min	259.63	272.55	
max	350.23	358.11	
avg	305.83	321.39	
std	31.10	30.03	
range	90.60	85.56	

* Estimates are not directly comparable across breeds as they have been estimated from different models and datasets

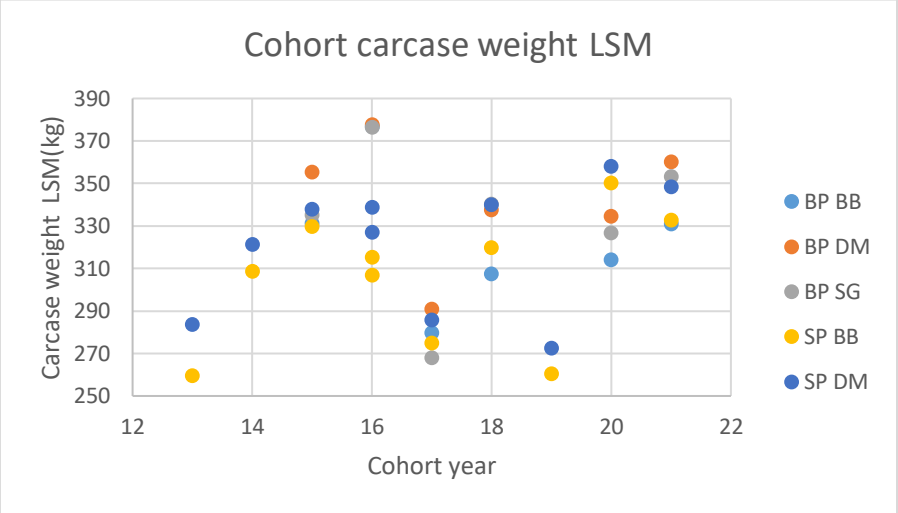


Figure 4.3.1: Summary of carcase weight least squares means by cohort from within-breed datasets of tropically adapted beef breeds*

* Estimates are not directly comparable across breeds as they have been estimated from different models and datasets

Effect of the cow: The cow origin group was significant for Brahman and Santa Gertrudis, with dam age significant for Droughtmaster (Table 4.3.3). Although the dam age was not significant for two breeds, the cow origin group was confounded with the dam's year of birth, and thus, dam age was captured in the cow origin term.

Table 4.3.3: Carcase weight least squares means by dam age for the Droughtmaster breed

	Droughtmaster		
Dam age (yrs)	**N**	**Carcase weight**	**SE**
3	350	326.8	2.0
4	203	327.8	2.3
5	127	329.1	2.5
6	106	330.2	2.8
7	82	332.7	3.1
8	74	332.9	3.2
9	55	333.7	3.7
10	123	322.1	2.6

Although significant from the ANOVA, the 95% confidence intervals did not show significance between the different levels of dam age for Droughtmaster. Droughtmaster cows ten years or older had progeny approximately 12kg lighter than 9-year-old cows. The reduction in performance for the older cows in the herd can be managed via a cow culling strategy. Three- and four-year-old cows also had calves approximately 2 kg and 1kg lighter than the progeny of 5-year-old cows, respectively. It was more difficult to interpret the least squares means for the cow origin group for the other two breeds. No systematic patterns were observed for cow origin groups.

Summary

This study showed that producers would benefit if they managed the age structure of calves in a cohort, managed cattle appropriately based on the current annual seasonal conditions, and culled older cows as required. Breed, location, and the impact of young dams were also found to have an effect, but with few mitigation options.

4.4 Analysis of fixed effects impacting female reproduction traits

Reproduction is a key component of the profitability of a production system. If cows fail to produce a live calf, the cow is a cost to the system with no income generated. Ovarian scans can determine when a heifer has reached puberty and when a cow has re-cycled after their first calf. Cow body composition into the 2nd mating also influences the ability of a cow to produce a 2nd calf in the subsequent year. These traits are heritable, and genetic selection using EBVs can improve reproduction. In addition, it may be possible to manage/change non-genetic (fixed) effects to improve reproduction. Female reproduction traits from the Repronomics reference population (MLA projects B.NBP.0759 and P.PSH.1221) were used to consider the impact of fixed effects on female reproduction.

Data was recorded at two sites (Brian Pastures and Spyglass), and a summary of the raw data is shown in Table 4.4.1. Nine data cohorts (2013-2021) were recorded for age at puberty at Brian Pastures for all three breeds, and ten cohorts (2013-2021) were recorded at Spyglass for Brahman and Droughtmaster breeds. The average age at puberty ranged from 531.5 days (Santa Gertrudis at Brian Pastures to 716.3 days (Brahman at Spyglass). Nine data cohorts (2011-2019) were recorded for lactation anoestrus interval at Brian Pastures for all three breeds, and eleven cohorts (2011-2019) were recorded at Spyglass for Brahman and Droughtmaster breeds. The average lactation anoestrus interval ranged from 65.6 days (Droughtmaster at Brian Pastures) to 92.3 days (Brahman at Spyglass).

Table 4.4.1: Summary of raw reproduction data from within-breed datasets of tropically adapted beef breeds

	Age at puberty (days)					Lactation anoestrus interval (days)				
	N	**mean**	**std**	**min**	**max**	**N**	**mean**	**std**	**min**	**max**
Brian Pastures										
Brahman	464	634.2	126.5	393	1003	361	77.4	77.6	0	338
Droughtmaster	392	553.3	118.5	373	859	287	65.6	68.1	0	330
Santa Gertrudis	477	531.5	112.3	334	1015	322	67.4	68.2	0	309
Spyglass										
Brahman	977	716.3	130.4	395	1219	658	92.3	89.4	0	324
Droughtmaster	859	619.1	139.6	386	1185	684	79.0	84.3	0	360

Heifer Age at Puberty

Analysis of the Repronomics data showed that, on average, only 6.4% of heifers would have been pubertal at the start of the mating period if mated as yearlings, and this increased to 33.8% pubertal by the end of a 12-week mating period. At the beginning of the mating period, when the heifers were two years old (when the heifers were mated for the first time), on average, 89.9% of heifers had achieved puberty.

Four age-at-puberty traits were considered;

1. The actual age (days) at puberty (agecl)
2. Pubertal at the start of yearling mating (0=no, 1=yes) (puby)
3. Pubertal at the end of yearling mating (0=no, 1=yes) (pubyom)
4. Pubertal at the start of 2-year-old mating (0=no, 1=yes) (pubIM)

The fixed effects considered within each breed were the cohort (herd and year), twin status (single or twin), birth season (defined as 30-day slices from the start of the cohort calving), cow age group (foundation base cows were grouped into old, medium, young groups and project born females were grouped by birth year), and cow origin group (defined as dam breed type (composite or purebred), and origin herd) nested within the cohort as fixed class effects. All first-order interactions were considered. The sire was fitted as a random effect. The final significant models for age at puberty are shown in Table 4.4.2.

Table 4.4.2: The significant fixed effects for age at puberty traits for within-breed datasets of Northern beef cattle

Trait\Effect	Cohort	Birth season	Cow age	Twin	Cow origin (Cohort)	Cohort x Birth season	Birth season x Cow age	Birth season x Cow origin (Cohort)
Brahman								
Agecl	x	x	x	x		x	x	
Puby	x	x			x			
Pubyom	x	x	x		x			
pubIM	x	x	x			x	x	
Droughtmaster								
Agecl	x	x	x	x				
Puby	x	x	x					
Pubyom	x	x	x	x				
pubIM	x	x	x			x	x	
Santa Gertrudis								
Agecl	x	x	x		x			
Puby	x	x	x			x	x	
Pubyom	x	x			x			
pubIM	x	x	x		x	x	x	x

Cohort (herd and year): The cohort effect captures the environmental impacts. Table 4.4.3 summarises the least squares means for cohort within each breed (account for all other fixed effects), and Figure 4.4.1 shows the cohort's least squares means for each puberty trait. The cohort in this data is the herd location and year of birth. Cohort least squares means showed that heifers at Brian Pastures reached puberty earlier than those at Spyglass. For Brahman, heifers at Brian Pastures reached puberty 75 days earlier, with 9% more heifers pubertal at mating. For Droughtmaster, heifers at Brian Pastures reached puberty 80 days earlier, with 6% more heifers pubertal at mating. Spyglass calves showed more variation in average age at puberty at mating than Brian Pastures. The yearling traits showed more variation at Brian Pastures, likely due to heifers reaching puberty earlier than Spyglass.

After the initial decision about the location of a herd, there are limited management interventions to mitigate against the effects of the location. Within location and breed, there was considerable variation across years in the average age at puberty. The difference between the best and worst years was 183 days (Brahmans at Brian Pastures) to 319 days (Droughtmaster at Spyglass), or when expressed as pubertal or not at mating, the difference between best and worst ranged from 8.8% (Santa Gertrudis at Brian Pastures) to 70.8% (Brahman at Spyglass). Producers cannot influence the annual seasonal conditions, but management practices should be reactive according to the season. In a poor season, without intervention, many heifers will not be pubertal at mating, impacting profitability.

Table 4.4.3: Summary of age at puberty least squares means by cohort from within-breed datasets* of tropically adapted beef breeds

	Brian Pastures cohorts					Spyglass cohorts				
Trait#	**min**	**max**	**avg**	**std**	**range**	**min**	**max**	**avg**	**std**	**range**
					Brahman					
Puby	-2.2	21.0	**3.3**	7.3	23.2	-1.7	4.2	**0.3**	2.0	5.9
Pubom	13.7	65.5	**32.7**	16.8	51.8	-7.2	25.5	**8.5**	11.5	32.7
pubIM	72.7	100.1	**92.1**	8.6	27.4	33.8	104.6	**83.2**	22.5	70.8
Agecl	596.8	779.9	**676.1**	64.3	183.1	626.7	884.4	**750.6**	91.6	257.7
					Droughtmaster					
Puby	-3.6	35.2	**9.5**	14.4	38.7	-5.9	14.3	**1.9**	6.6	20.1
Pubom	-12.5	66.1	**35.4**	25.2	78.6	-41.0	40.6	**9.1**	27.5	81.6
pubIM	86.4	97.2	**90.5**	3.5	10.8	54.5	92.7	**84.4**	12.0	38.3
Agecl	529.9	776.6	**623.7**	73.0	246.8	589.6	908.7	**703.9**	104.3	319.1
					Santa Gertrudis					
Puby	-14.9	45.5	**7.9**	23.1	60.4					
Pubom	-0.2	80.3	**50.1**	26.6	80.4					
pubIM	86.8	95.6	**90.9**	3.1	8.8					
Agecl	507.7	753.7	**611.4**	75.8	246.0					

Age at puberty trait definitions - The actual age (days) at puberty (agecl) - Pubertal at the start of yearling mating (0=no, 1=yes) (puby) - Pubertal at the end of yearling mating (0=no, 1=yes) (pubyom) -Pubertal at the start of 2-year-old mating (0=no, 1=yes) (pubIM); *Least squares means for puby, pubyom and pubIM are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets

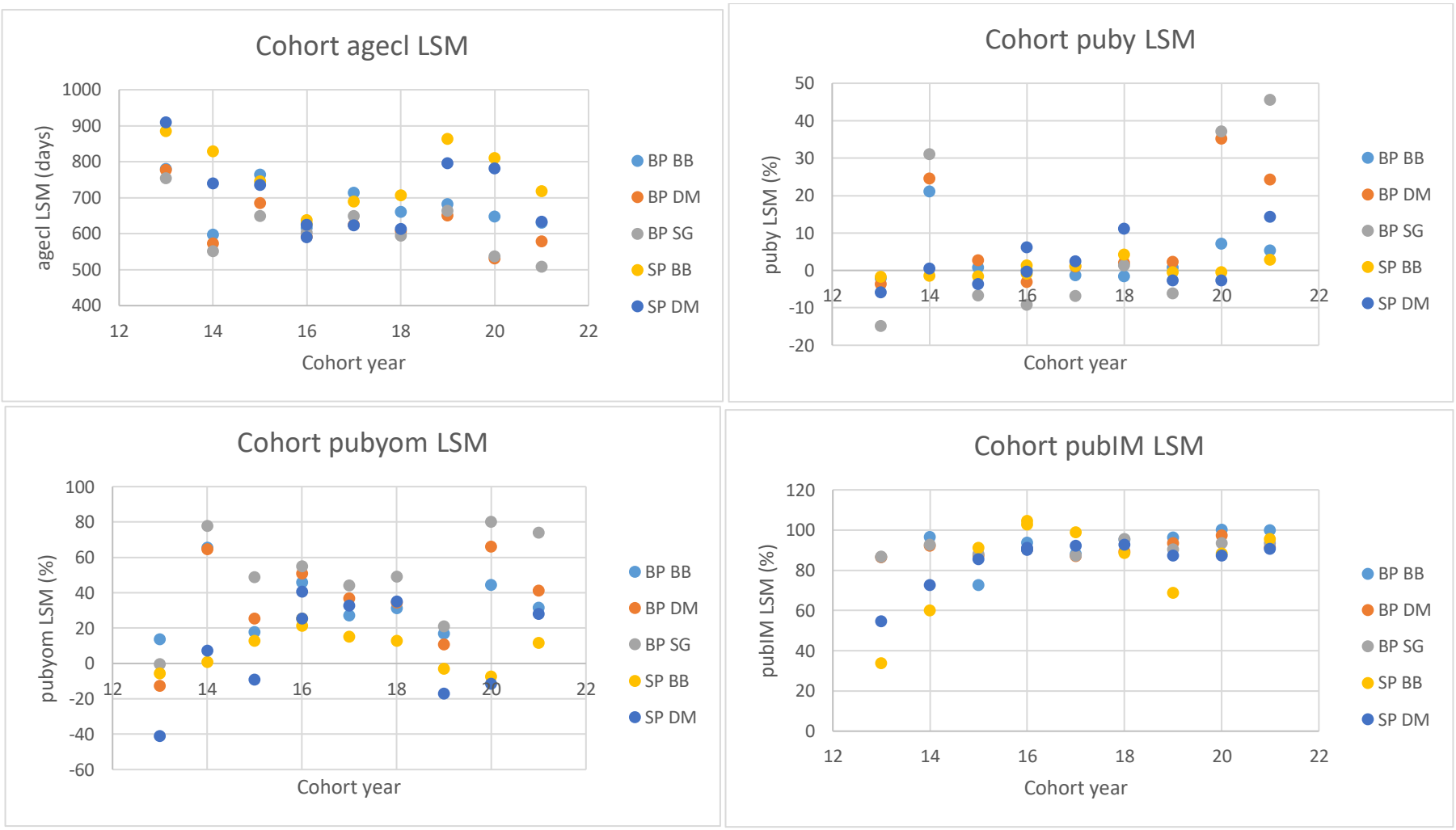


Figure 4.4.1: Summary of age at puberty least squares means by cohort from within-breed datasets* of tropically adapted beef breeds

Age at puberty trait definitions - The actual age (days) at puberty (agecl) - Pubertal at the start of yearling mating (0=no, 1=yes) (puby) - Pubertal at the end of yearling mating (0=no, 1=yes) (pubyom) -Pubertal at the start of 2-year-old mating (0=no, 1=yes) (pubIM) *Least squares means for puby, pubyom and pubIM are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets

Season of birth: Table 4.4.4 shows the least squares means for puberty traits for the season of birth, defined as 30-day slices of the calving period. A small number of Brahmans were born much earlier in the calving period. These calves were born to a group of base cows mated elsewhere before being transferred to the Brian Pastures herd to be used as base cows for the project. Calves born in the 2nd calving month will be considered the early calving group. Least squares means show that calves born earlier in the season tend to reach puberty earlier. Comparing heifers born in the 2nd and 4th calving months showed a 33, 57, and 36-day difference in the actual age that puberty was obtained for Brahman, Droughtmaster, and Santa Gertrudis, respectively, and this equated with 13%, 8%, and 3% fewer heifers being pubertal at the start of mating.

To increase the percentage of the herd being pubertal at the start of mating, producers should manage and avoid a large spread in the calving period, in particular, to avoid late calving. If the spread is too large, there will be an increase in the number of heifers not pubertal at mating. Attention should also be paid to the heifers born later in the season, and appropriate management (i.e. ensuring adequate nutrition) should be undertaken to minimise the number of late-born heifers that are not pubertal at mating.

Table 4.4.4: Summary of age at puberty least squares means by season of birth from within-breed datasets* of tropically adapted beef breeds

Month	**1**		**2**		**3**		**4**		**5**	
Trait#	**LSM**	**SE**	**LSM**	**SE**	**LSM**	**SE**	**LSM**	**SE**	**LSM**	**SE**
Brahman N	**35**		**409**		**604**		**340**		**53**	
Puby	1^{a}	3	5^{a}	1	3^{a}	1	0^{a}	1	0^{a}	2
Pubom	47^{a}	8	27^{b}	3	15^{bc}	3	7^{c}	3	4^{c}	5
pubIM	128^{a}	7	89^{b}	2	85^{bc}	2	76^{cd}	3	59^{d}	5
Agecl	612.37^{a}	30.63	714.06^{b}	19.88	723.79^{b}	19.76	746.84^{b}	20.41	779.48^{b}	24.97
Droughtmaster N			**456**		**483**		**268**		**44**	
Puby			14^{a}	1	6^{b}	1	1^{b}	2	1^{b}	4
Pubom			47^{a}	8	29^{ab}	8	11^{b}	8	0^{b}	10
pubIM			95^{a}	1	93^{a}	1	87^{b}	2	73^{c}	4
Agecl			621.39^{a}	20.32	646.92^{ab}	20.52	678.36^{ab}	21.49	717.07^{b}	26.45
Santa Gertrudis N			**177**		**190**		**99**		**11**	
Puby			23^{a}	4	12^{ab}	4	5^{ab}	5	-8^{b}	10
Pubom			72^{a}	5	59^{ab}	4	44^{bc}	5	26^{c}	13
pubIM			94^{a}	3	92^{a}	3	91^{a}	4	87^{a}	6
Agecl			580.88^{a}	18.42	584.49^{a}	18.54	616.49^{a}	20.72	663.66^{a}	32.54

^ subscripts define significant differences based on the 95% confidence interval; # Age at puberty trait definitions - The actual age (days) at puberty (agecl) - Pubertal at the start of yearling mating (0=no, 1=yes) (puby) - Pubertal at the end of yearling mating (0=no, 1=yes) (pubyom) -Pubertal at the start of 2-year-old mating (0=no, 1=yes) (pubIM); *Least squares means for puby, pubyom and pubIM are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets

Twin: There were very few twins in the dataset, but from the limited data, heifers that were twins were later to reach puberty by approximately 90 days. Management cannot influence whether an animal is a twin, but management interventions may be required to help twins reach puberty earlier.

Table 4.4.5: Summary of age at puberty least squares means by single or twin from within-breed datasets* of tropically adapted beef breeds

	Single			Twin		
	N	**LSM**	**SE**	**N**	**LSM**	**SE**
Brahman - agecl	1433	668.4[a]	9.5	8	762.2[b]	37.4
Droughtmaster - agecl	1244	619.3[a]	7.9	7	712.6[b]	39.4
Droughtmaster - pubyom	1244	37[a]	3	7	7[a]	15

^ subscripts define significant differences based on the 95% confidence interval; # Age at puberty trait definitions - The actual age (days) at puberty (agecl) - Pubertal at the end of yearling mating (0=no, 1=yes) (pubyom) *Least squares means for pubyom are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets

Effect of the cow: The cow age group was considered, but no clear trends were apparent in the least squares means, and the 95% confidence interval tended not to be significant across levels of cow age. The cow breed was significant for some breeds and trait combinations. The cow breed term encompasses the cows' herd of origin and breed type. No systematic patterns were observed from the cow breed least squares means.

Body weight: To investigate the impact of body weight, the fixed-effect models from above were fitted and included additional covariates (fit separately) for weaning weight, weight as a yearling, weight into 1st mating, or weight at puberty. Body weights were considered linear and quadratic terms, and regression coefficient solutions are presented in Table 4.4.6. Weaning, yearly and into mating weights are all recorded on an age-constant basis, and increased weights were associated with decreased age at puberty. Body weight at puberty was not recorded on an age-constant basis, and regression coefficients indicated that heavier animals were later to reach puberty. However, this is likely due to the relationship between age and weight, with heavier animals being older, regardless of puberty status. This demonstrates that when using body weight to help manage age at puberty, it is important that the weights are recorded at an age-constant time point, which requires a known date of birth to adjust for age differences.

The least squares means from within-breed analysis for age at puberty, proportion pubertal at mating and body weight as a yearling or into mating were plotted for each breed and cohort combination. Despite a small quadratic effect being significant for weight into mating, Figure 4.4.2 shows that the relationship was essentially linear, with heavier average weight cohorts associated with earlier average cohort age at puberty. The trend line indicates that to be pubertal by 750 days of age (start of mating), a cohort needs to be, on average, 350kg. A quadratic relationship between weight and proportion pubertal was observed, with the increase in the proportional pubertal at mating greatest as the weight increases, and then plateaus off once a certain weight has been obtained. For a cohort to have 85% of heifers pubertal, the weight entering into mating (at 750 days) needed to be, on average, 353 kg. If the target were 90% or 94% (the top of the trend line), the cohort's average weight would need to be 372kg and 413 kg, respectively.

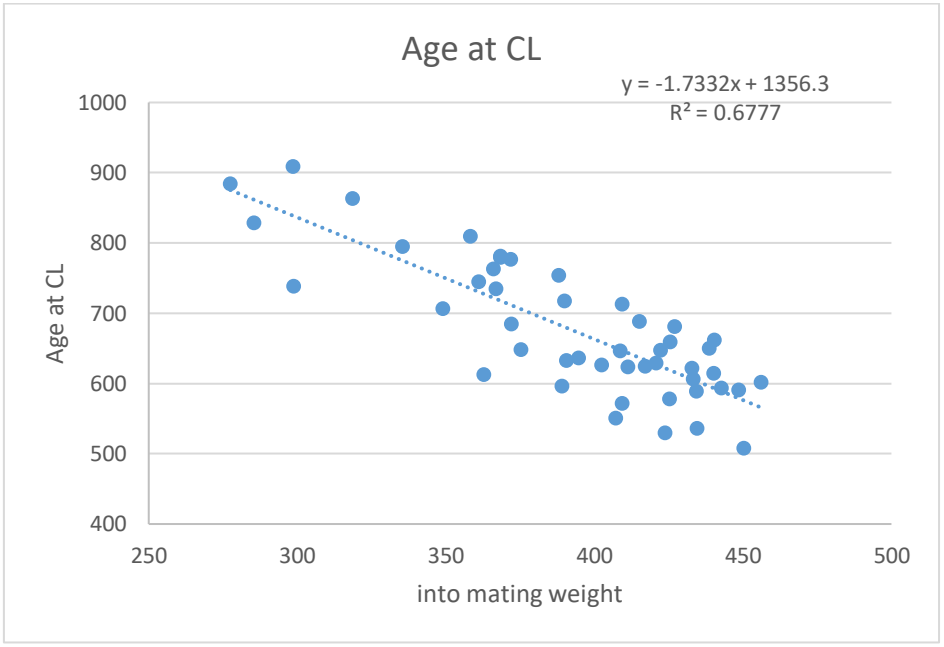
Similar relationships are observed with other body weight measures. However, the R^2 for the proportion of the cohort pubertal into mating was lower when the body weight was measured earlier in life. Figure 4.4.3 plots the body weight of a yearling. The trend line indicates that to be pubertal by 750 days of age, a heifer needs to be, on average, 216kg as a yearling. A quadratic relationship between weight and proportion pubertal was observed, with the increase in the proportion pubertal at mating greatest as the weight increases, and then plateaus off once a certain weight has been

obtained. For a cohort to have 85% of heifers pubertal, the cohort weight at one year of age needed to be, on average, 221 kg. If the target were 90% or 94% (the top of the trend line), the cohort's average weight would need to be 238kg and 271 kg, respectively.

Table 4.4.6: Summary of the age at puberty regression coefficients for body weight from within-breed datasets* of tropically adapted beef breeds

	agecl		puby		pubyom		pubIM	
weight	**Linear**	**Quadratic**	**Linear**	**Quadratic**	**Linear**	**Quadratic**	**Linear**	**Quadratic**
Brahman								
weaning	-0.92				0.1		0.2	
yearling	-1.10				0.1		0.8	-0.001
Into mating	-3.68	0.004					1.1	-0.001
At puberty	1.53		-0.6	0.0007	-2.1	0.002	0.7	-0.001
Droughtmaster								
weaning	-0.97		0.1		0.4		0.7	-0.002
yearling	-3.11	0.004	0.1		0.4		1.1	-0.002
Into mating	-4.37	0.005	0.04		0.2		1.4	-0.002
At puberty	1.56		-0.9	0.001	-1.8	0.002	0.6	-0.001
Santa Gertrudis								
weaning	-0.53		0.2		0.2			
yearling	-0.70		0.1		0.3			
Into mating					0.2			
At puberty	-0.83	0.003	-1.3	0.0015			1.1	-0.002

Age at puberty trait definitions - The actual age (days) at puberty (agecl) - Pubertal at the start of yearling mating (0=no, 1=yes) (puby) - Pubertal at the end of yearling mating (0=no, 1=yes) (pubyom) -Pubertal at the start of 2-year-old mating (0=no, 1=yes) (pubIM); *Regression coefficients for puby, pubyom and pubyIM are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets



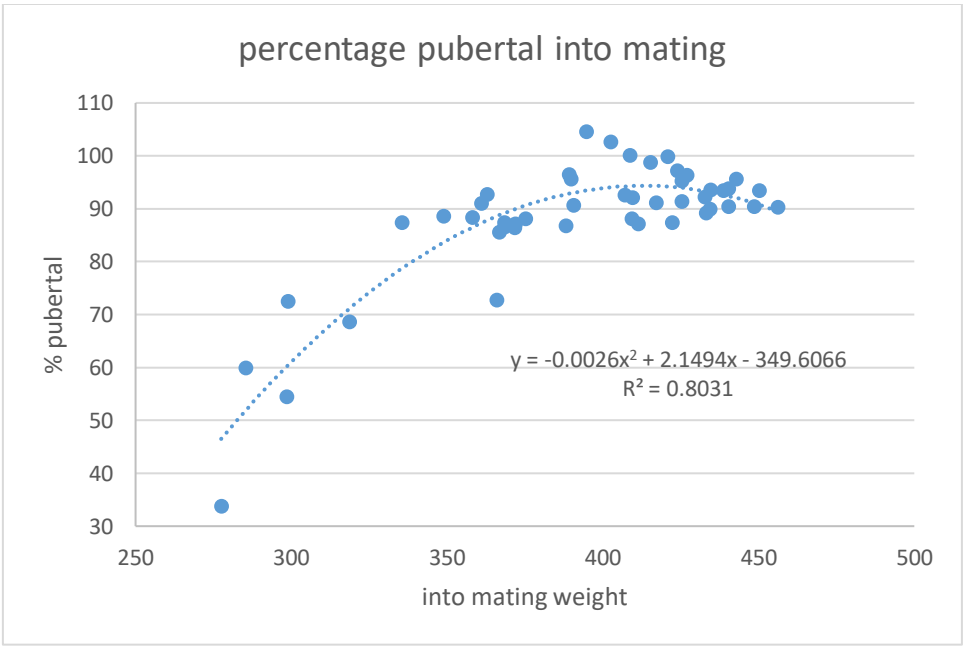
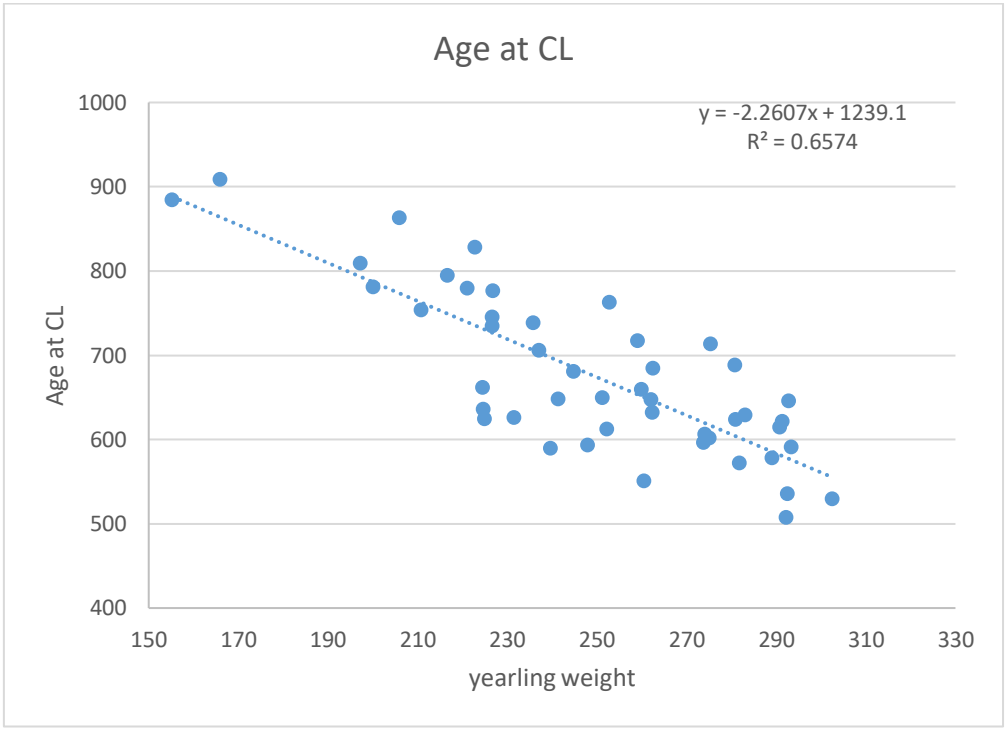


Figure 4.4.2: The relationship between age at puberty traits and body weight into mating based on within-breed cohort least squares means*

*Least squares means for pubyIM are multiplied by 100



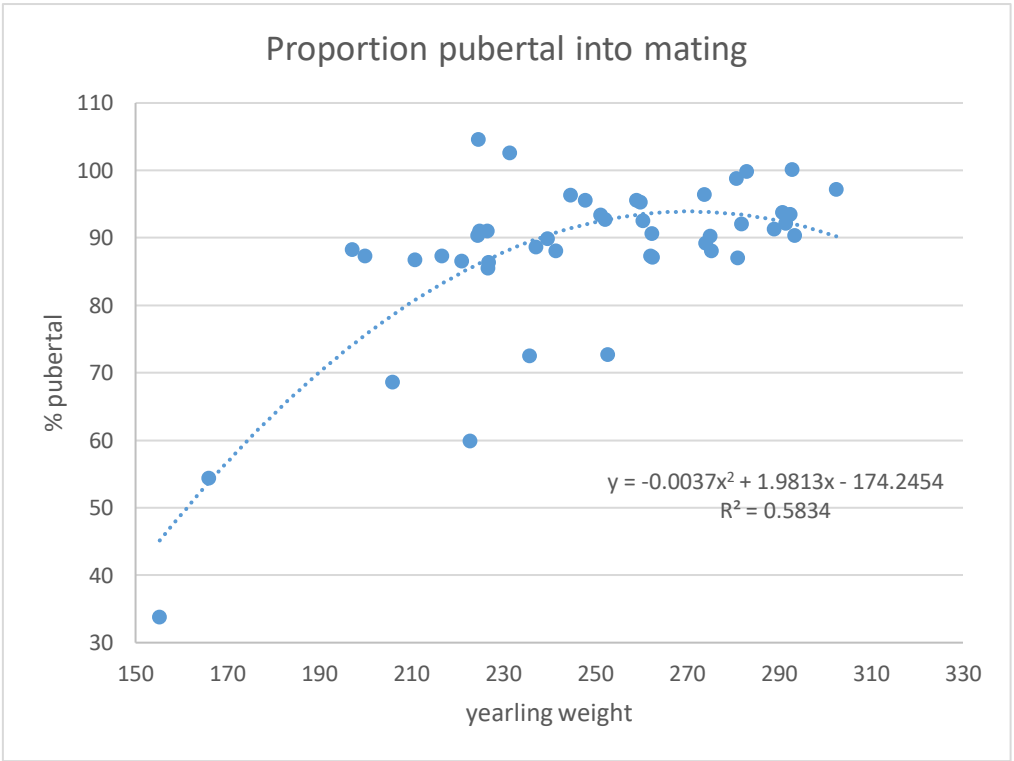


Figure 4.4.3: The relationship between age at puberty traits and yearling body weight based on within-breed cohort least squares means *

*Least squares means for pubyIM are multiplied by 100

Lactation anoestrus interval

Analysis of the Repronomics data showed that 74.4% of cows had recommenced cycling by weaning. The ability to cycle again and reconceive after calving is a critical point in the reproduction of cows. This is especially the case for the 2nd rebreed when the cow is not yet mature and still growing while rearing her first calf and is expected to conceive her 2nd calf. Measurement of lactation anoestrus interval commenced at the start of mating, and cows were regularly ovarian scanned during the mating period until a corpus luteum (CL) was recorded.

Two lactation anoestrus interval traits were considered;

1. The actual number of days from the start of mating that it took for the cow cycle (LAI)
2. Cycling prior to when the calf was weaned (0=no, 1=yes) (cycbw)

The fixed effects considered within each breed were the cohort (LAIcohort: herd and year), sex of the calf at foot (csex: male or female), the season of birth for the calf at foot (calfmon: defined as 30-day slices from the start of the cohort calving) and cow breed type (dam type: composite or purebred) as fixed class effects. All first-order interactions were considered. The sire was fitted as a random effect. The final significant models for lactation anoestrus interval are shown in Table 4.4.7.

Table 4.4.7: The significant fixed effects for lactation anoestrus interval traits for within-breed datasets of Northern beef cattle

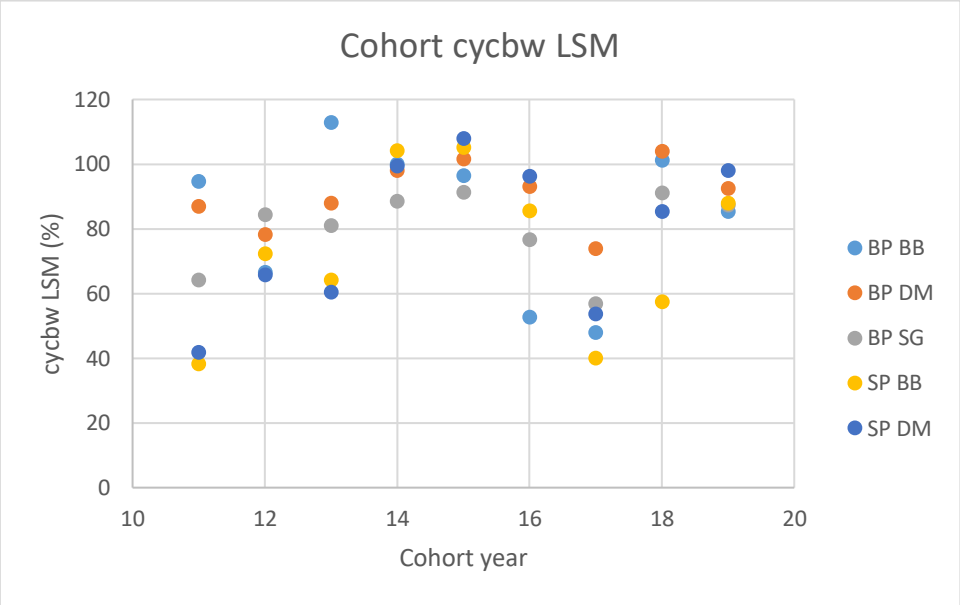
Trait\Effect	Cohort	csex	calfmon	damtype	Cohort x calmon	calfmon x damtype
			Brahman			
LAI	x	x	x		x	
cycbw	x		x		x	
			Droughtmaster			
LAI	x		x			
cycbw	x		x	x	x	x
			Santa Gertrudis			
LAI	x		x	x		x
cycbw	x		x	x		x

Lactation anoestrus interval trait definitions - The actual number of days from the start of mating that it took for the cow cycle (LAI) - Cycling when the calf was weaned (0=no, 1=yes) (cycbw)

Cohort (herd and year): The cohort effect captures the environmental impacts. Table 4.4.8 summarises the least squares means for the cohort within each breed. Figure 4.4.4 shows the cohort least squares means for the two LAI traits. The cohort in this data is the herd location and year of birth. Brahman and Droughtmaster cows at Brian Pastures cycled approximately 17 days earlier than cows at Spyglass, with 11% more cows cycling when their calves were weaned. The variation in cohort least squares means of Brahman cows was similar at both sites, but for Droughtmaster, cows at Spyglass showed larger variation than at Brian Pastures.

After the initial decision about the location of a herd, there are limited management interventions to mitigate against the effects of the location. Within location and breed, there was considerable variation across years in the average lactational anoestrus interval. Producers cannot influence the seasonal conditions, but management practices should be reactive according to the season. In a poor season, without intervention, more cows will not be cycling when weaning their calf, and this may reduce the number of subsequent calves born, or if they do conceive, the calves may be born later in

the season, and this will delay the calf's age at puberty. The difference between the best and worst years was 67 days (Droughtmaster at Brian Pastures) to 133 days (Brahman at Spyglass), or when expressed as cycling or not at weaning, the difference between best and worst ranged from 30% (Droughtmaster at Brian Pastures) to 67% (Brahman at Spyglass).



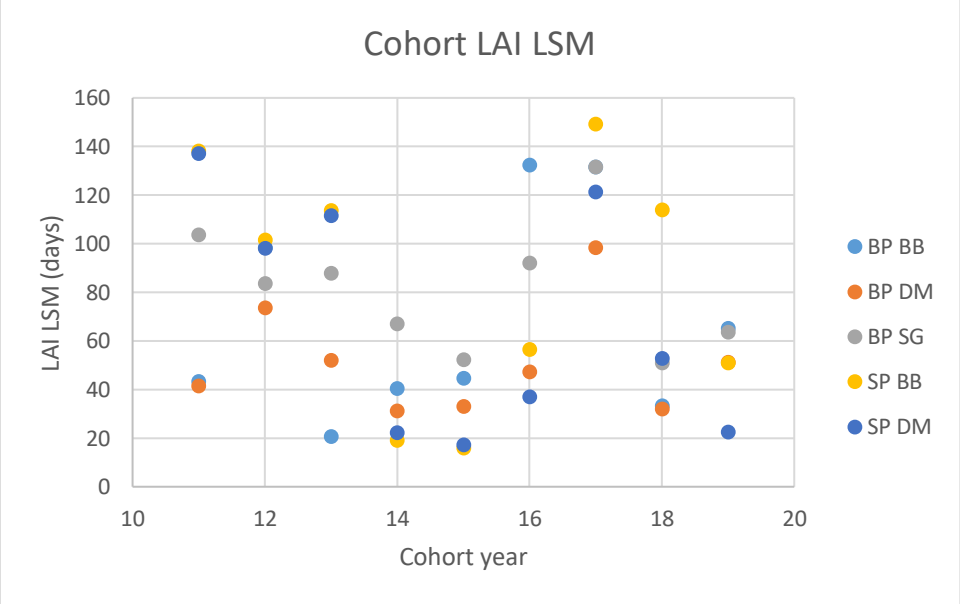


Figure 4.4.4: Summary of lactation anoestrus interval least squares means by cohort from within-breed* datasets of tropically adapted beef breeds

Lactation anoestrus interval trait definitions - The actual number of days from the start of mating that it took for the cow cycle (LAI) - Cycling when the calf was weaned (0=no, 1=yes) (cycbw)*Least squares means for cycbw are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets

Table 4.4.8: Summary of lactation anoestrus interval least squares means by cohort from within-breed datasets* of tropically adapted beef breeds

	Brian Pastures cohorts					Spyglass cohorts				
	min	**max**	**avg**	**std**	**range**	**min**	**max**	**avg**	**std**	**range**
Brahman										
LAI	20.6	132.2	**67.7**	42.6	111.6	15.7	149.2	**84.3**	49.9	133.4
cycbw	48	113	**84**	23	65	38	105	**73**	25	67
Droughtmaster										
LAI	31.2	98.2	**51.1**	22.1	67.0	17.1	137.1	**68.8**	47.9	120.0
cycbw	74	104	**91**	10	30	42	108	**79**	24	66
Santa Gertrudis										
LAI	51.0	131.6	**81.4**	26.2	80.6					
cycbw	57	91	**80**	12	35					

Lactation anoestrus interval trait definitions - The actual number of days from the start of mating that it took for the cow cycle (LAI) - Cycling when the calf was weaned (0=no, 1=yes) (cycbw)*Least squares means for cycbw are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets

Dam breed: The dam breed was only significant for Santa Gertrudis, with cows from a composite dam cycling approximately 40 days earlier than cows from a purebred dam. This was also evident with 18% more cows with composite dams cycling at calf weaning than cows with purebred dams. While significant for Droughtmaster, the least squares means are similar, possibly due to a significant dam breed x calf season of birth effect. After the initial choice of breed, there are no management interventions to mitigate against breed differences. But the breed might dictate management decisions.

Table 4.4.9: lactation anoestrus interval least squares means by dam breed type from within-breed datasets* of tropically adapted beef breeds

Dam breed type	**composite**			**pure**		
	N	**LSM**	**SE**	**N**	**LSM**	**SE**
Santa Gertrudis - LAI	157	62.9^{a}	8.4	165	99.8^{b}	9.3
Droughtmaster - cycbw	103	86^{a}	6	868	84^{a}	4
Santa Gertrudis - cycbw	157	89^{a}	4	165	71^{b}	5

^ subscripts define significant differences based on the 95% confidence interval significance; # Lactation anoestrus interval trait definitions - The actual number of days from the start of mating that it took for the cow cycle (LAI) - Cycling when the calf was weaned (0=no, 1=yes) (cycbw) *Least squares means for cycbw are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets

Calf Season of Birth: Table 4.4.10 shows the least squares means for lactation anoestrus interval traits for the calf season of birth, defined as 30-day slices of the calving period. A few Brahmans were born much earlier in the calving period (birth months 1 and 2). These calves were born to a group of base cows mated elsewhere before being transferred to the Brian Pastures herd as base cows for the project. Calves born in the 3rd calving month will be considered the early calving group, while those born in the 5th calving month are considered the later-born calves. These least squares means show that cows that calved earlier in the season cycled sooner and were more likely to be cycling by the time the calf at foot was weaned.

Comparing months 3 and 5 (a 2-month spread) showed a difference of 6% (Droughtmaster) to 20% (Santa Gertrudis) in the percentage of cows cycling at mating and a difference of 14 (Droughtmaster) to 51 (Santa Gertrudis) days difference for LAI. To increase the percentage of the herd cycling at

weaning, producers should manage and avoid a large spread in the calving period, mainly to prevent late calving. If the spread is too large, the number of cows not cycling at weaning will increase.

Table 4.4.10: Summary of lactation anoestrus interval least squares means by calf at foot sex from within-breed datasets* of tropically adapted beef breeds

Birth Month for calf at foot	1		2		3		4		5	
	LSM	SE	LSM	SE	LSM	SE	LSM	SE	LSM	SE
Brahman										
N	**19**		**21**		**423**		**418**		**138**	
LAI	21.86[a]	37.36	74.71[a]	25.49	84.69[a]	5.25	88.01[a]	5.41	106.46[a]	7.21
cycbw	116[b]	21	74[ab]	14	71[ab]	3	69[a]	3	60[a]	4
Droughtmaster										
N			**12**		**462**		**355**		**142**	
LAI			17.09[b]	20.69	67.00[a]	4.18	74.51[a]	4.59	81.16[a]	6.39
cycbw			106[b]	11	81[ab]	3	77[ab]	3	75[a]	4
Santa Gertrudis										
N					**218**		**76**		**28**	
LAI					60.58[b]	5.98	71.62[ab]	8.31	111.86[a]	12.34
cycbw					89[b]	3	83[ab]	4	69[a]	6

^ subscripts define significant differences based on the 95% confidence interval significance; # Lactation anoestrus interval trait definitions - The actual number of days from the start of mating that it took for the cow cycle (LAI) - Cycling when the calf was weaned (0=no, 1=yes) (cycbw) *Least squares means for cycbw are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets

Pubertal or not at the start of mating: To investigate the impact of being pubertal or not at the start of mating, the fixed-effect models from above were fitted and also included (fitted separately) the puberty status at the start of mating (0 = not pubertal / 1 = pubertal) and the age at puberty (days). Table 4.4.11 shows the least squares means and regression coefficients describing the impact of puberty status on the lactation anoestrus interval in the 2nd parity. Heifers that reached puberty earlier also cycled earlier in the 2nd parity. Of Brahman and Droughtmaster cows that were pubertal at the beginning of their first mating, approximately 10% more were cycling again at the weaning of their calf and were cycling about 30 and 38 days earlier than their contemporaries, which were not pubertal at the start of mating. The regression coefficients show that for every month that puberty was delayed, it was between 4.86 (Droughtmaster) and 6.39 (Santa Gertrudis) days longer to cycle again after calving. Managing heifers' puberty is important, as it has continued knock-on effects on cycling for their second mating.

Table 4.4.11: Summary of lactation anoestrus interval least squares means and regression coefficients for age of puberty for cows that were pubertal or not at the start of mating from within-breed datasets* of tropically adapted beef breeds

	Pubertal or not at the start of mating				Regression coefficient for age at puberty	
	Not pubertal		Pubertal		days	month
			Brahman			
cycbw	62[a]	4	72[a]	3	-0.10	-2.97
LAI	113.25[a]	8.16	83.42[b]	4.84	0.2086	6.2580
			Droughtmaster			
cycbw	74[a]	9	88[a]	7	-0.07	-2.16
LAI	95.37[a]	16.36	57.14[a]	11.40	0.1620	4.8600
			Santa Gertrudis			
cycbw					-0.0010	-2.97
LAI					0.2130	6.3900

^ subscripts define significant differences based on the 95% confidence interval significance; # Lactation anoestrus interval trait definitions - The actual number of days from the start of mating that it took for the cow cycle (LAI) - Cycling when the calf was weaned (0=no, 1=yes) (cycbw) *Least squares means for cycbw are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets

Body weight and composition at the start of mating 2: To investigate the impact of the cow's body composition at the start of the 2nd mating, the fixed effect models from above were fitted with adding, separately as covariates, body weight, body condition score, hip height, eye muscle area, P8 fat and rib fat at the start of the 2nd mating. All body composition traits were considered linear and quadratic and tested for significance ($P<0.05$).

The body condition score was significant for all breeds except for the quadratic effect for Brahman. The linear effect for Brahman indicated that for every increase of 1 body condition score, there was an increase of 20% of animals cycling at the weaning of their calf and a decrease of 43 days in the time taken to cycle again post-calving. Droughtmaster and Santa Gertrudis showed a quadratic relationship with body condition scores 3-4 being where the most animals were cycling at weaning and the shortest number of days to cycle post-calving.

A very similar trend was observed for EMA and the two fat traits. An increase in EMA and subcutaneous fat was associated with improved fertility until the EMA became larger than 55-70 cm^2, P8 fat became larger than 9 mm, or Rib fat became larger than 5-6mm, when fertility declined, and cows took longer to cycle post-calving.

Hip height was not associated with any lactation anoestrus interval trait.

Figures 4.4.5 to 4.4.8 show these relationships for the data ranges represented in the dataset.

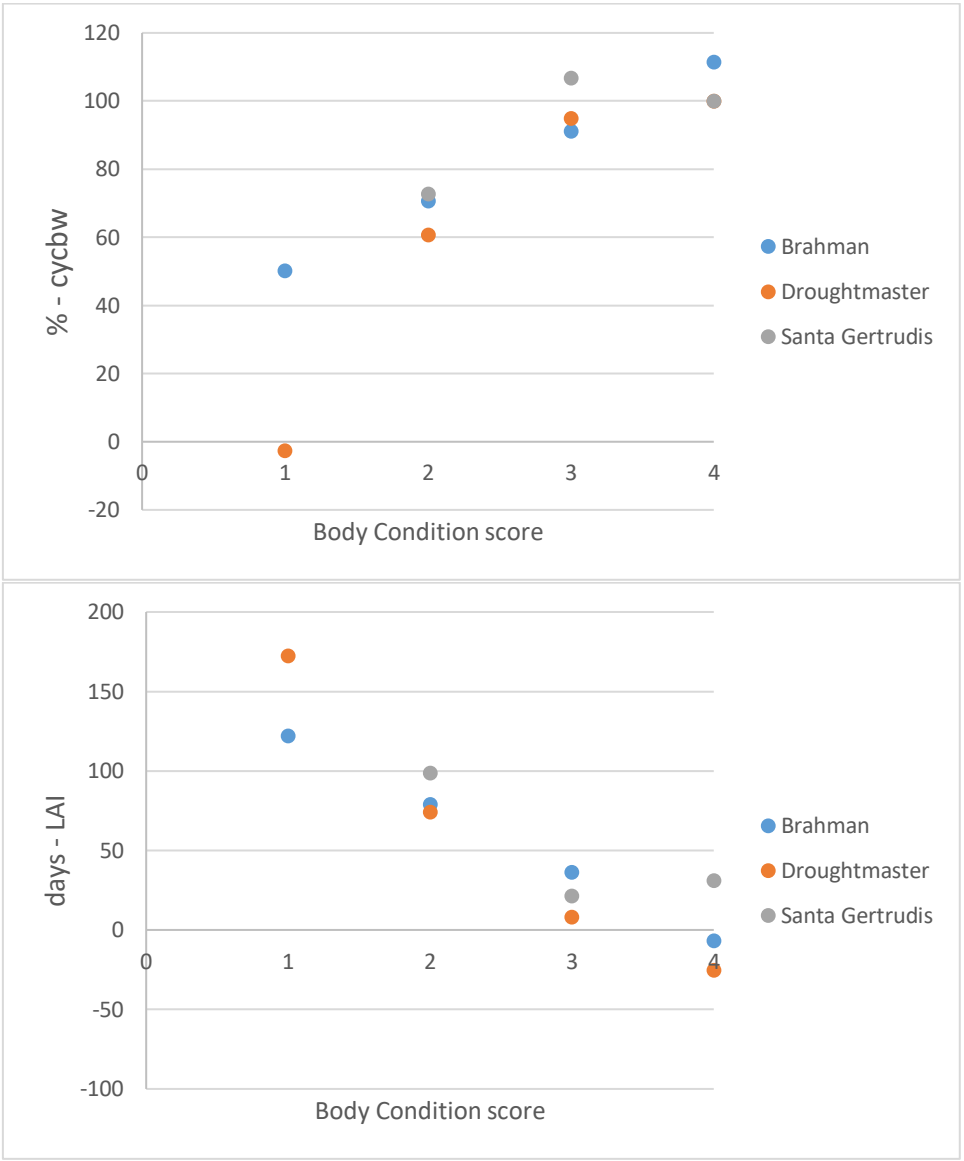


Figure 4.4.5: The within-breed relationship between lactation anoestrus interval traits and body condition scores

Lactation anoestrus interval trait definitions - The actual number of days from the start of mating that it took for the cow cycle (LAI) - Cycling when the calf was weaned (0=no, 1=yes) (cycbw) *Regression coefficients for cycbw are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets

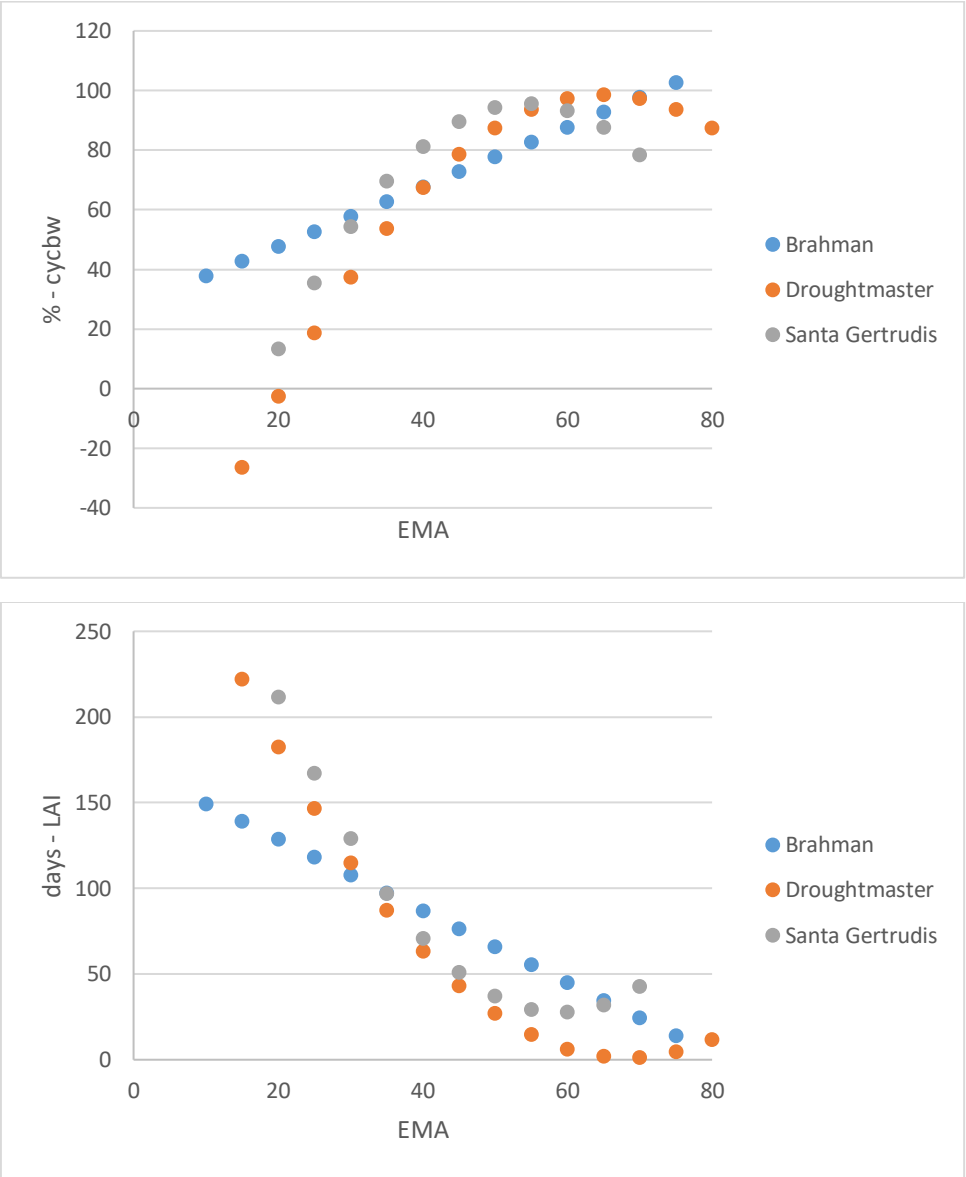
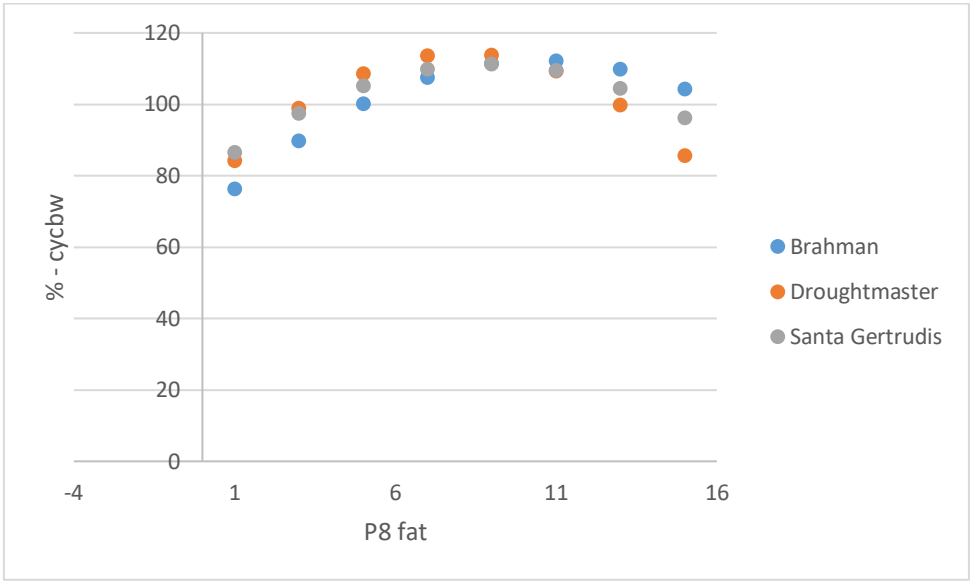


Figure 4.4.6: The within-breed relationship between lactation anoestrus interval traits and Eye muscle area (EMA)

Lactation anoestrus interval trait definitions - The actual number of days from the start of mating that it took for the cow cycle (LAI) - Cycling when the calf was weaned (0=no, 1=yes) (cycbw) *Regression coefficients for cycbw are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets



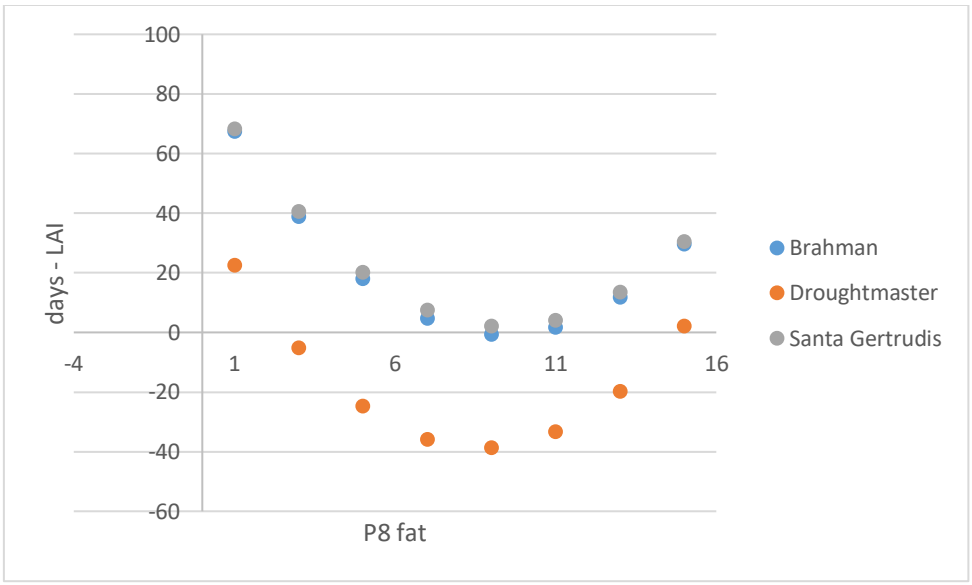


Figure 4.4.7: The within-breed relationship between lactation anoestrus interval traits and P8 fat

Lactation anoestrus interval trait definitions - The actual number of days from the start of mating that it took for the cow cycle (LAI) - Cycling when the calf was weaned (0=no, 1=yes) (cycbw) *Regression coefficients for cycbw are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets

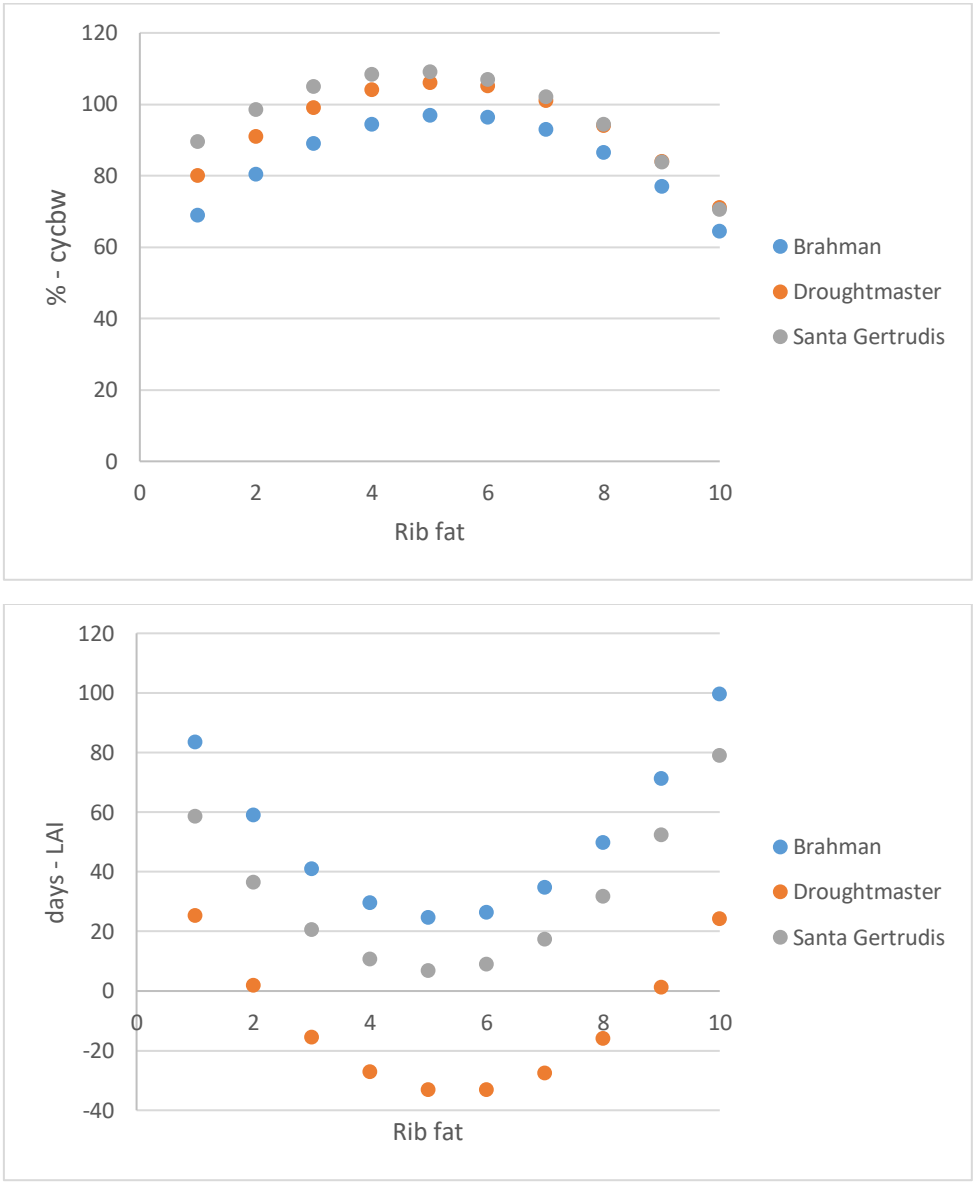
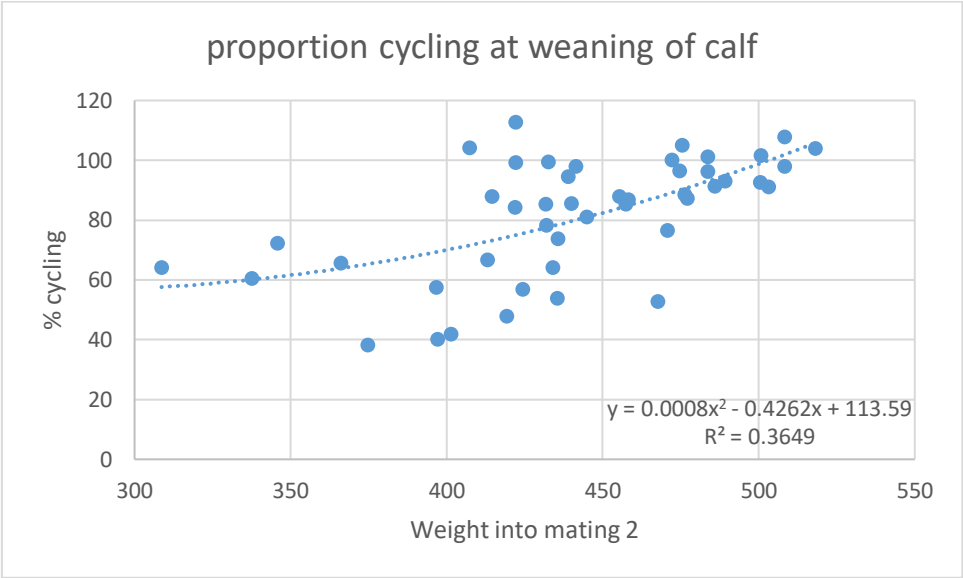


Figure 4.4.8: The within-breed relationship between lactation anoestrus interval traits and RIB fat
Lactation anoestrus interval trait definitions - The actual number of days from the start of mating that it took for the cow cycle (LAI) - Cycling when the calf was weaned (0=no, 1=yes) (cycbw) *Regression coefficients for cycbw are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets

Body weight was also associated with the ability to cycle post-calving. Plotting the least squares means for each breed and cohort combination for the lactation anoestrus interval traits and live weight into mating 2 (Figure 4.4.9) showed that cohorts with higher body weight at the start of mating tended to have a higher proportion of cows cycling when their calves were born and took fewer days to cycle again after the commencement of mating. Although this relationship is evident, variation across cohorts was observed.



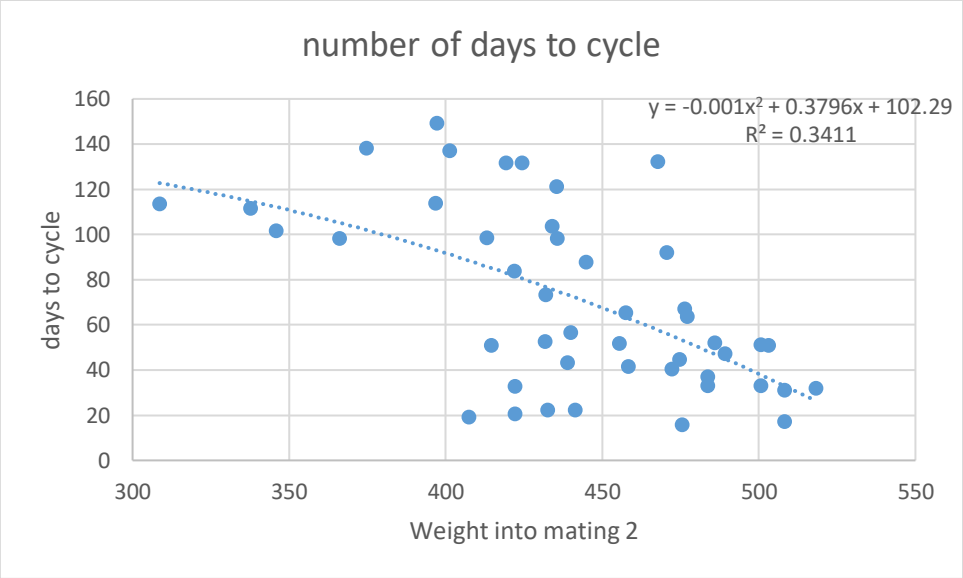


Figure 4.4.9: Least squares means for breed and cohort for lactation anoestrus interval traits and body weight into mating

Lactation anoestrus interval trait definitions - The actual number of days from the start of mating that it took for the cow cycle (LAI) - Cycling when the calf was weaned (0=no, 1=yes) (cycbw) *Regression coefficients for cycbw are multiplied by 100 and estimates are not directly comparable across breeds as they have been estimated from different models and datasets

Summary

The study showed that age at puberty was impacted by the management of heifer body weight, the length of the calving period and seasonal impacts, and these are all aspects that a producer can manage for improved puberty outcomes. Breed and location also impacted the age at puberty, but limited mitigation strategies are available for these aspects. Lactation anoestrus intervals were affected by the management of cow body weight and composition, the length of the calving period, the correct management of heifers to obtain puberty and seasonal impacts, and these are all aspects that a producer can manage for improved recycling outcomes. Breed, location, and calf sex also impact lactation anoestrus interval, but few management mitigations are possible.

4.5 Genome-wide association study for reproduction traits

BREEDPLAN genotypes and phenotypes were available for 61,044, 9,806, and 11,119 animals for Brahman, Droughtmaster and Santa Gertrudis, respectively. This included all Repronomics animals that were genotyped in these three breeds. After QC and imputation (Connors *et al*. 2017), the number of SNPs in the analysis for each breed was 55,000, 58,912 and 59,574.

Principal Component Analysis (PCA)

Based only on genomic animals, PCA was undertaken for each breed, and the first two principal components accounted for the largest variation explaining the population structure (Figure 4.5.1), but the amount explained differed across breeds.

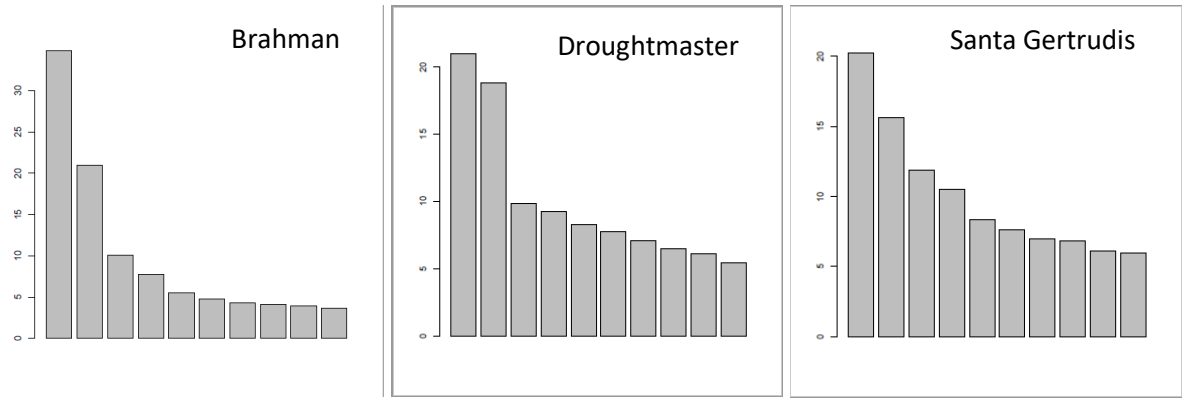


Figure 4.5.1: Percentage of variation explained by each principal component

No evidence of structure was observed for each of the breeds as a whole, and when highlighting the herd, if they were a Repronomics animal, year of birth and sex (Figure 4.5.2 – 4.5.6). Figure 4.5.4 shows that Repronomics animals represented the range of genotyped animals for Brahman and Droughtmaster. For Santa Gertrudis, the Repronomics animals were only represented in the cluster's lower portion.

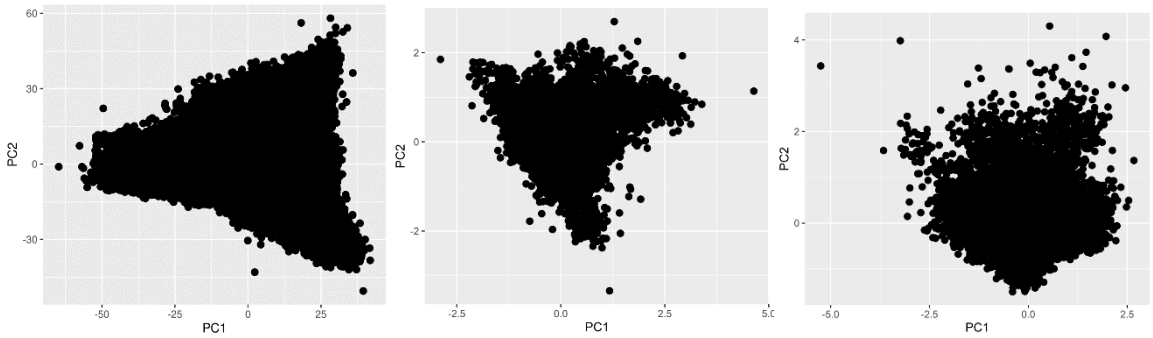


Figure 4.5.2: Principal component analysis for the first two components for Brahman, Droughtmaster and Santa Gertrudis (left to right)

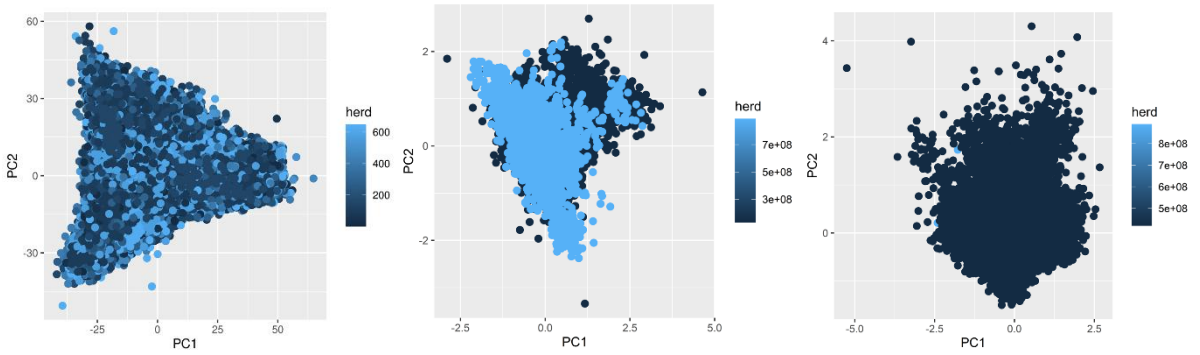


Figure 4.5.3: Principal component analysis for the first two components for Brahman, Droughtmaster and Santa Gertrudis with herds coloured (left to right)

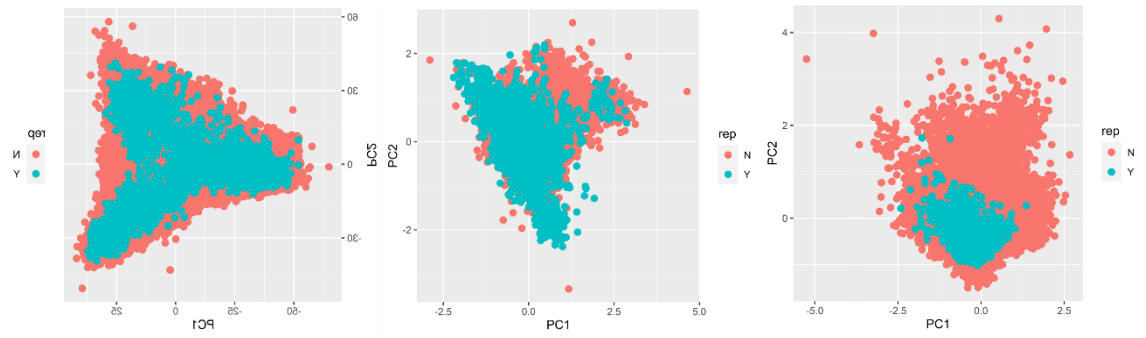


Figure 4.5.4: Principal component analysis for the first two components for Brahman, Droughtmaster and Santa Gertrudis with Repronomics herds coloured (left to right)

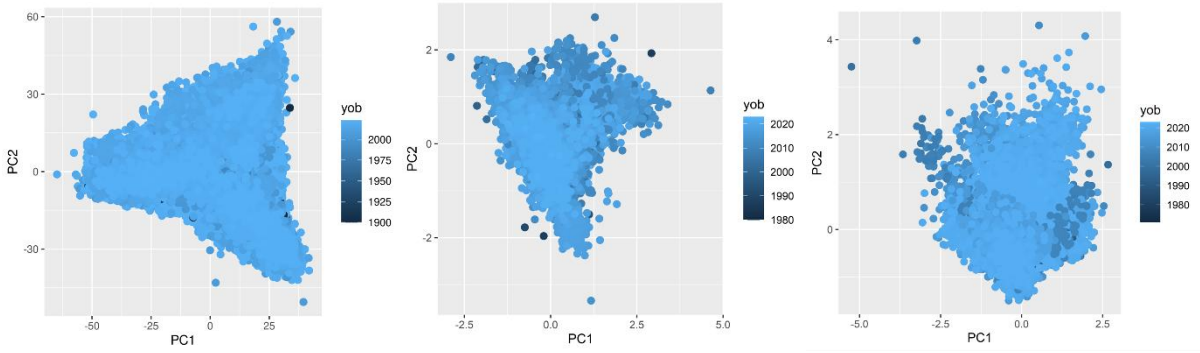


Figure 4.5.5: Principal component analysis for the first two components for Brahman, Droughtmaster and Santa Gertrudis with year of birth coloured (left to right)

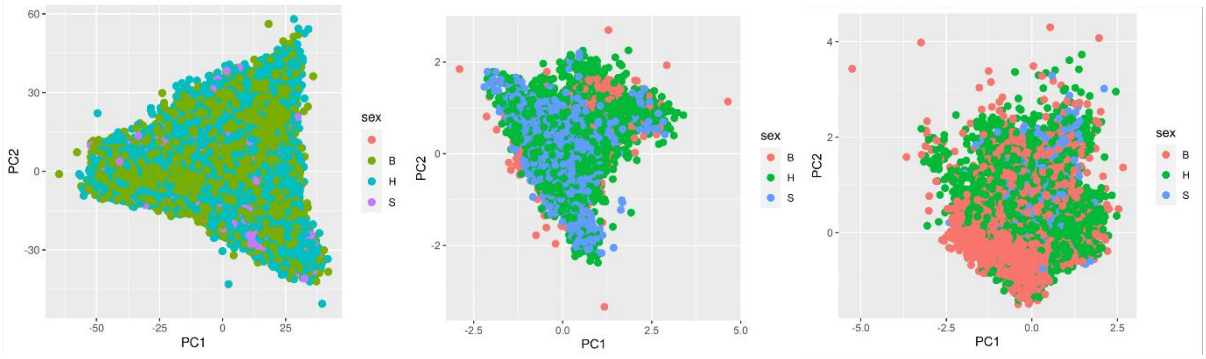


Figure 4.5.6: Principal component analysis for the first two components for Brahman, Droughtmaster and Santa Gertrudis with sex coloured (left to right)

Genome-wide association studies

Genome-wide association studies (GWAS) were performed using Repronomics data from Brahman and Droughtmaster for five reproduction traits (age at puberty, lactation anoestrus interval, birth weight, gestation length, and first parity days to calving). Phenotypes were pre-adjusted for age effects, and contemporary groups were extracted from within-breed BREEDPLAN data files. Table 4.5.1 outlines the number of Repronomics animals and total animals within the breed, with phenotypes and genotypes for each trait. The number of records was low for Santa Gertrudis due to the influence of tropical composite base dams and the subsequent reduction in the number of genotypes that met the relatedness to reference criteria. Therefore, GWAS was not undertaken for Santa Gertrudis. The "SNPSnappy" module of WOMBAT was used to undertake the GWAS, with genetic parameters obtained from the Brahman BREEDPLAN evaluation, and these parameters were also used for Droughtmaster. R packages were used to produce the Manhattan plots. However, due to rounding the P values to 6 decimal places in the WOMBAT output, the Manhattan plots do not show the peaks of SNPs significantly above the Bonferroni significance level. However, the -log10(p) values from WOMBAT utilise the unrounded P values and are correct. The SNP map was based on the ARS-UCS1.2 assembly, and the ensemble website was used to identify nearby genes.

Table 4.5.1: Number of Repronomics and total (in brackets) animals with phenotype and genotype for each of the traits considered

BREEDPLAN traits	Brahman	Droughtmaster
AP	1,411 (2,969)	1,137 (1,189)
LAI	861 (1,851)	747 (792)
BWT	3,596 (7,752)	2,935 (3,115)
GL	1,377 (2,288)	922 (971)
DTC (1st calf)	1,272 (5,575)	1,006 (1,106)

Summary of results: The Bonferroni correction accounted for multiple testing; the threshold values for genome-wide significance were 6.04 and 6.07 for Brahman and Droughtmaster, respectively. Generally, no genome-wide significant SNPs were identified. The three exceptions were age at puberty in Brahman and birth weight in Brahman and Droughtmaster. Table 4.5.2 summarises the maximum log10(p) values obtained from Wombat.

Table 4.5.2: Summary of female reproduction GWAS results for Brahman and Droughtmaster populations

	Brahman				Droughtmaster			
Traits	**N recs**	**Max Vg[#]**	**Max -log10(p)**	**significant regions (N SNPS)[*]**	**N recs**	**Max Vg[#]**	**Max -log10(p)**	**significant regions (N SNPS)[*]**
AP	2,969	0.17	15.65	Chr14 (101)	1,189	0.04	5.26	0
LAI	1,851	0.03	3.14	0	792	0.03	1.87	0
BWT	7,752	0.41	15.65	Chr5 (5) Chr6 (102) Chr7 (1) Chr8 (1) Chr13 (2) Chr14 (180) Chr16 (1) Chr21 (33) Chr25 (1)	3,115	0.03	6.39	Chr15 (1)
GL	2,288	0.03	4.77	0	971	0.03	5.26	0
DTC (1st calf)	5,575	0.03	5.45	0	1,106	0.03	4.67	0

[#] Maximum SNP genetic variance expressed as % of the total variance explained by all SNPs ($2pq\alpha^2/sum(2pq\ \alpha^2)*100$);
[*] Significance at genome-wide significance level

Significant regions for Brahman heifer age at puberty

All SNPs (n=101) above the genome-wide significance threshold were from chromosome 14. These SNPs were located from 15,125,634bp to 32,181,234bp, with the 20 SNPs at the top of the peak ranging from 20,574,088bp to 26,459,339bp. Many genes exist in this 5.89Mb region, as seen in Figure 4.5.7.

The top 3 SNPs (highlighted in yellow in Table 9.2.1 in Appendix 9.2) were located at 20,574,088bp, 21,096,233bp, and 24,825,146bp and had a minor allele frequency of 0.44-0.48 and an absolute SNP effect estimate of 26.5 to 27.9 days. The first of these SNPs was in the SNTG1 gene (14:20,398,321-20,699,673bp), the second SNP was located close to two genes, PCMTD1 (14:21,013,842-21,062,048bp) and ST18 (14:21,160,085-21,250,282bp) and the third SNP was located in the NSMAF gene (14:24,765,312-24,830,983bp).

Stephen et al. (2023) reported GWAS results from NZ Holstein-Friesian cattle for age at puberty and found regions on Chromosomes 5, 14, 6, 1 and 11 (in decreasing importance). The location on chromosome 14 ranged between 24,482,969bp and 25,731,992bp (UMD 3.1 map). This was the same region that was detected in the current Brahman dataset. The following is text from Stephen et al. (2023) suggesting that the gene in this region may be PLAG1. In the ARS-UCD 1.2 assembly used in this work, the PLAG1 gene was located at 14:23,330,541-23,375,751.

"The region on chromosome 14 had the second highest WPPA of 0.93 in our GWAS using the PS population and harbours 16 candidate genes. The PLAG1 gene is located at 25,007,291 bp - 25,009,296 bp, which is approximately 6 kb from the highest effect SNP within this window. The PLAG1 gene is well documented to affect stature and BW in cattle (Karim et al., 2011; Littlejohn et al., 2012; Fink et al., 2017), and has previously been reported to share an association with variation in the fertility traits 'age of first calving' and 'age of first corpus luteum' (Fortes et al., 2016). Given the association between

AGEP and stature, it seems likely that the PLAG1 gene was driving the association between this genomic window and our AGEP4 phenotypes in the PS data set."

This study also observed peaks on chromosomes 5, 6 and 15 (Figure 4.5.11). These peaks were not significant at the genome level (after Bonferroni correction) but were for the chromosome-specific threshold. The region most significant in chromosome 5 differed from those reported by Stephen et al. (2023). Hawken et al. (2012) also found a region on chromosome 14 associated with Brahman age at puberty, with their top 32 SNPs between 21.95Mb and 28.4Mb (based on the UMD3 assembly). They also noted that this region covered many annotated genes.

Significant regions for Brahman birth weight

SNPs from 9 chromosomes showed across-genome significance. There were 11 significant SNPs located on six chromosomes (Chr 5, 7, 8, 13, 16, and 25). On Chromosome 6, 102 significant SNPs were located between 16,963,160bp and 48,836,508bp. The top 20 SNPs in this peak were located between 29,293,834bp and 42,554,396bp. Figure 4.5.8 shows how many genes are in this 13.26Mb region.

The top 4 chromosome 6 SNPs (highlighted in yellow in Table 9.2.2 in Appendix 9.2) were located at 29,682,908bp, 32,801,223bp, 36,999,602bp and 37,672,865bp and had a minor allele frequency of 0.25-0.47 and had an absolute SNP effect estimate of 0.31 to 0.70 kgs. The gene closest to the first SNP was BMPR1B (6:29,373,117-29,593,444). There were no genes close to the second SNP, but there were several genes (SPP1, MEPE, IBSP, LAP3, MED28 and FAM184B) located near the third SNP but not in the 200,000bp window around the actual SNP. The gene closest to the fourth SNP was LCORL (6:37,380,296-37,557,106).

On Chromosome 14, 180 significant SNPs were located between 9,618,157bp and 51,573,048bp. The top 20 SNPs in this peak were located between 15,367,052bp and 38,822,904bp. Figure 4.5.9 shows many genes in this 23.46Mb region.

The top 3 chromosome 14 SNPs (highlighted in yellow in Table 9.2.2 in Appendix 9.2) were located at 27,771,064bp, 29,589,249bp and 30,323,253bp and had a minor allele frequency of 0.26-0.44 and had an absolute SNP effect estimate of 0.60 to 0.67 kgs. This region overlaps with the region identified for age at puberty, but the SNPs at the top of the peak were located further along the chromosome compared with the SNPs for age at puberty. The first SNP was located within the gene NKAIN3 (14:27,737,786-27,998,050), the second SNP was close to the gene CYP7B1 (14:29,199,622-29,460,150), and the third SNP was close to the gene DNAJC5B (14:30,355,171-30,448,182).

On Chromosome 21, 33 significant SNPs were located between 454,528 bp and 10,068,286 bp. The top 20 SNPs in this peak were located between 454,528 bp and 7,844,296 bp. Figure 4.5.10 shows that many genes are in this 7.39Mb region.

The top chromosome 21 SNP (highlighted in yellow in Table 9.2.2 in Appendix 9.2) was located at 1,196,735bp, had a minor allele frequency of 0.12, and had an absolute SNP effect estimate of 0.93 kg. This SNP was located close to the MAGEL2 gene (21:1,205,086-1,208,637).

None of these significant SNPs had the very high genetic variance reported in Table 4.5.2. Those SNPs with the highest variance were all associated with locations that were not significant (-log10(p))=0 and located on chromosomes 6 and 14.

Although several significant regions existed, they involve many genes and overlap with regions reported in the literature. Therefore, isolating a small number of genes from this study was difficult.

Weerasinghe et al. (2021) found regions on Chromosomes 5, 6, 7 and 20 associated with birth weight in Australian temperate beef breeds. After Bonferroni correction and multivariate regression, only five SNPs remained on Chromosome 6 near 39Mb (UMD3.1 assembly), which is in the large range detected in this study. They report that this SNP accounted for 11% of the genetic variance. The SNPs in this study accounted for 3.96% of the additive genetic variance.

Saatchi et al. (2014) also reported regions on Chromosome 6 associated with birth weight. Utsunomiya et al. (2013) reported a region on Chromosome 14 in Nellore cattle with the most significant SNP (14:25,376,827) accounting for 4.6% of the variance of birth weight EBVs.

Significant regions for Droughtmaster birth weight

Only one SNP was above the genome-wide significance threshold. This SNP was on chromosome 15 and was not the same as any in the Brahman dataset.

Table 4.5.3: Across genome Significant SNPs for Droughtmaster Birth weight

name	chrom	location	fp	estimate	serror	-log10(P)	gvarpc
hapmap32097-bta-150519	15	55523000	0.452	0.462	0.091	6.385	0.033

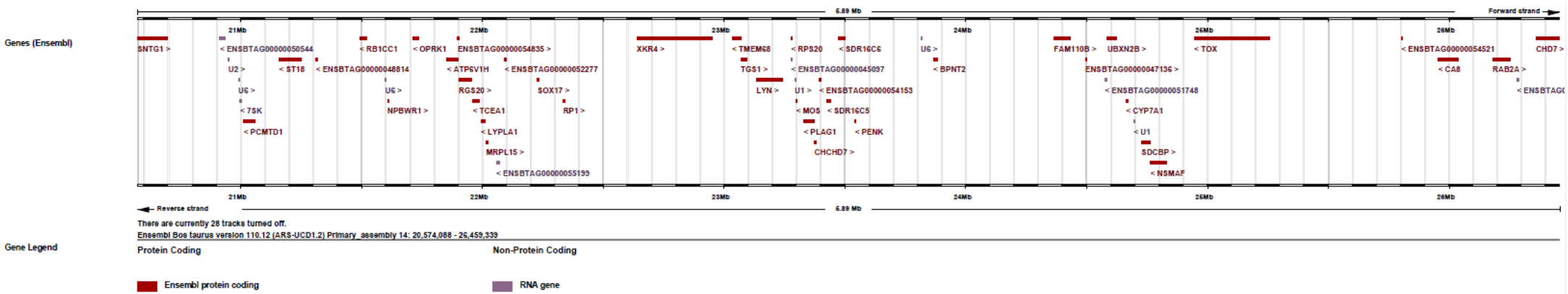


Figure 4.5.7: Genes present in the region with significant SNPs from a GWAS for Brahman age at puberty

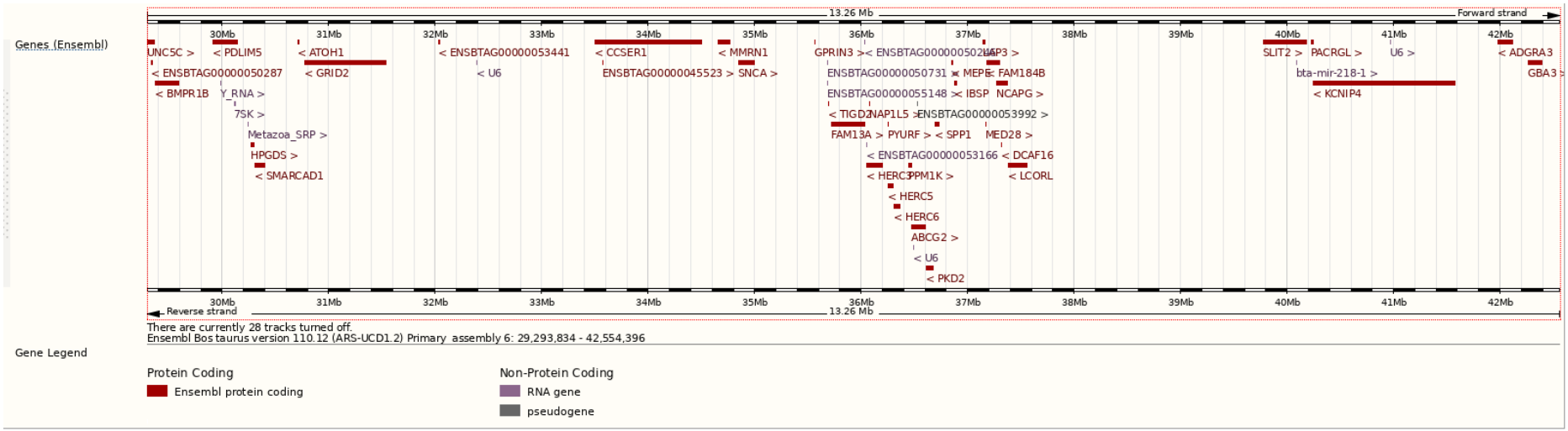


Figure 4.5.8: Genes present in the region with significant SNPs from a GWAS for Brahman birth weight

Figure 4.5.9: Genes present in the region with significant SNPs from a GWAS for Brahman birth weight

Figure 4.5.10: Genes present in the region with significant SNPs from a GWAS for Brahman birth weight

Total genetic variance and Manhattan plots of significance

Figures 4.5.11 to 4.5.15 present the genome-wide results for the percent of total SNP genetic variance and Manhattan plots of significance for Brahman and Droughtmaster for each of the female reproduction traits considered.

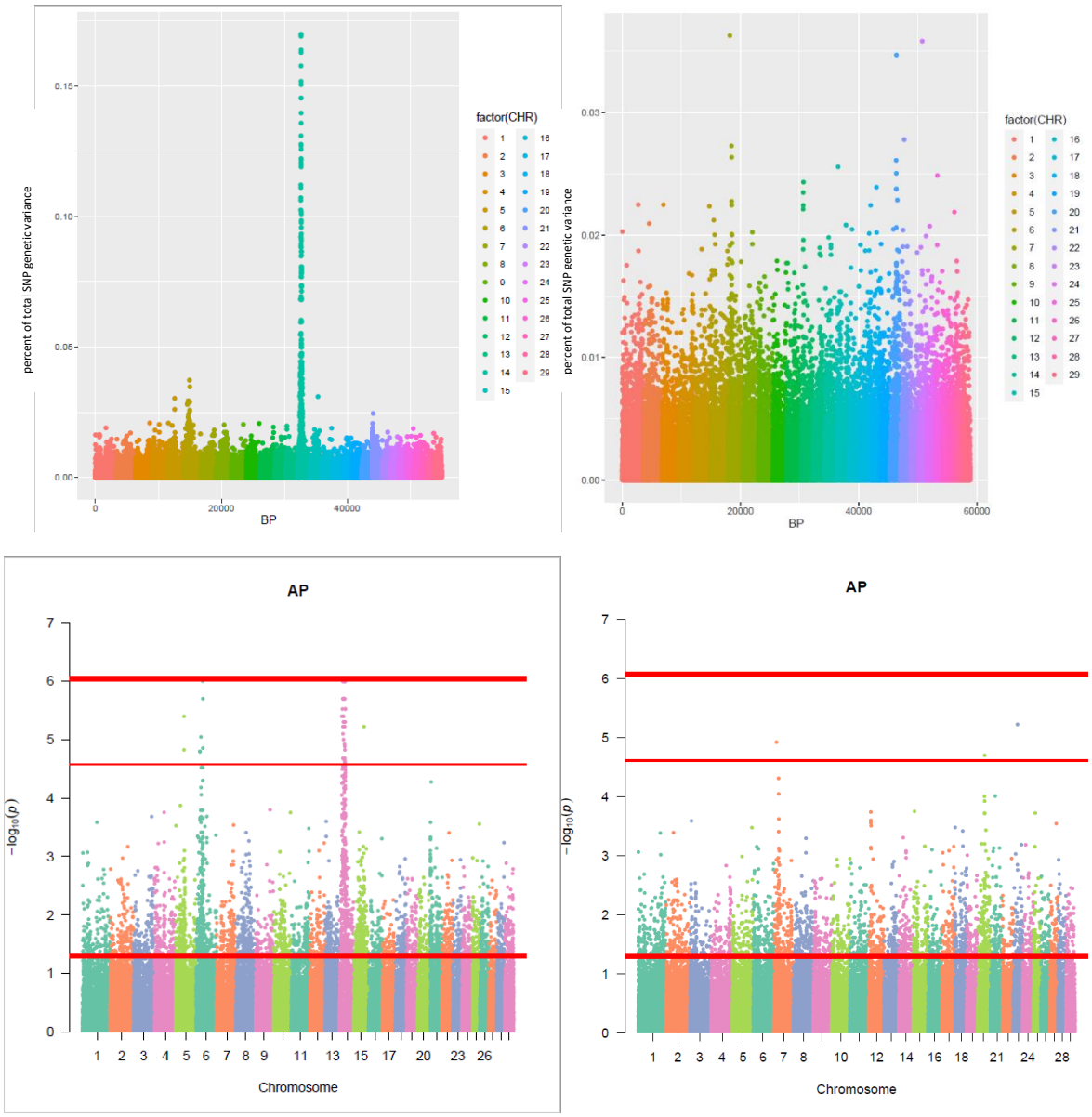


Figure 4.5.11: The percent of total SNP genetic variance (top row) and Manhattan plot (bottom row) for age at puberty for Brahman (left) and Droughtmaster (right)

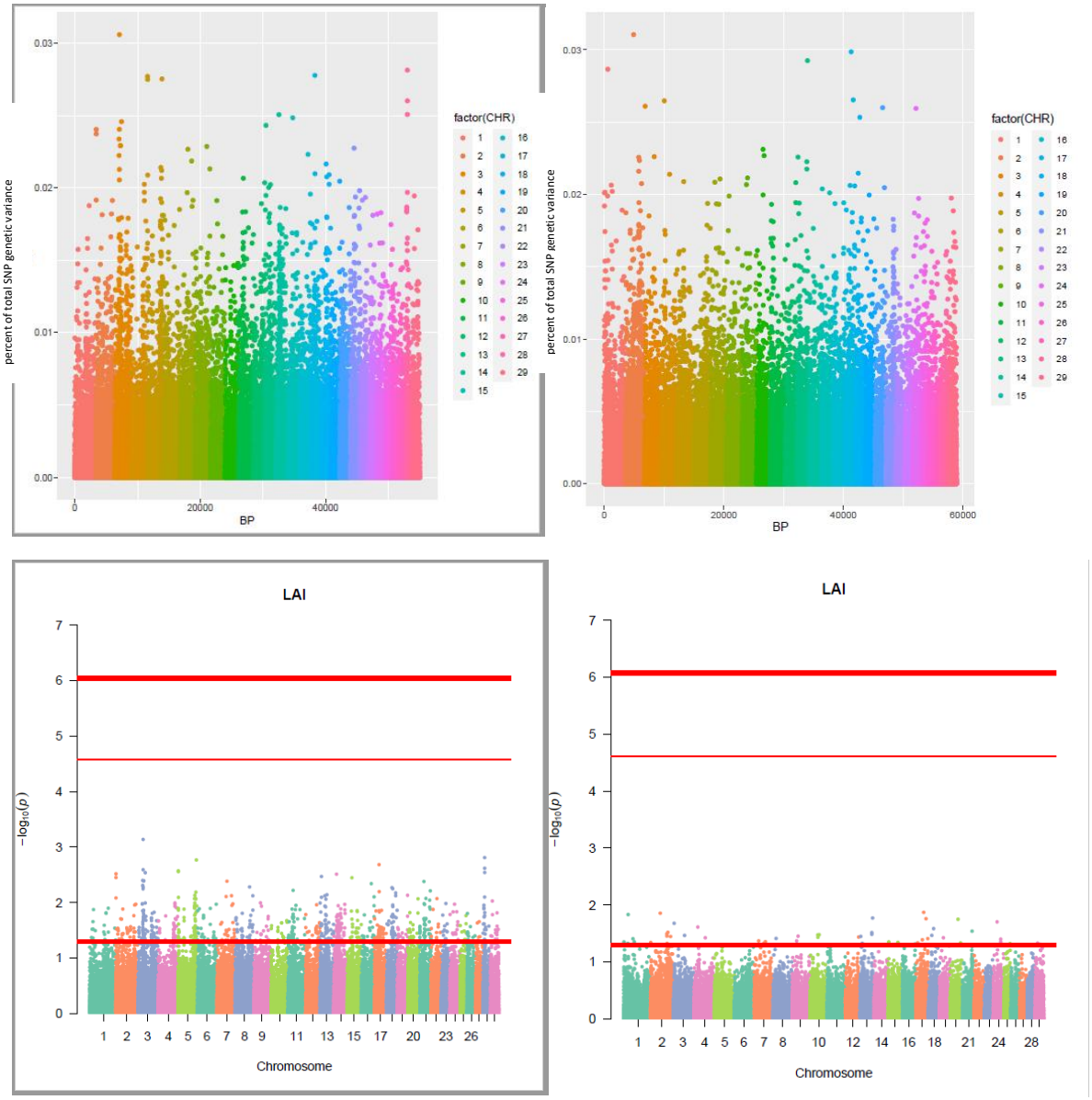


Figure 4.5.12: The percent of total SNP genetic variance (top row) and Manhattan plot (bottom row) for lactation anoestrus interval for Brahman (left) and Droughtmaster (right)

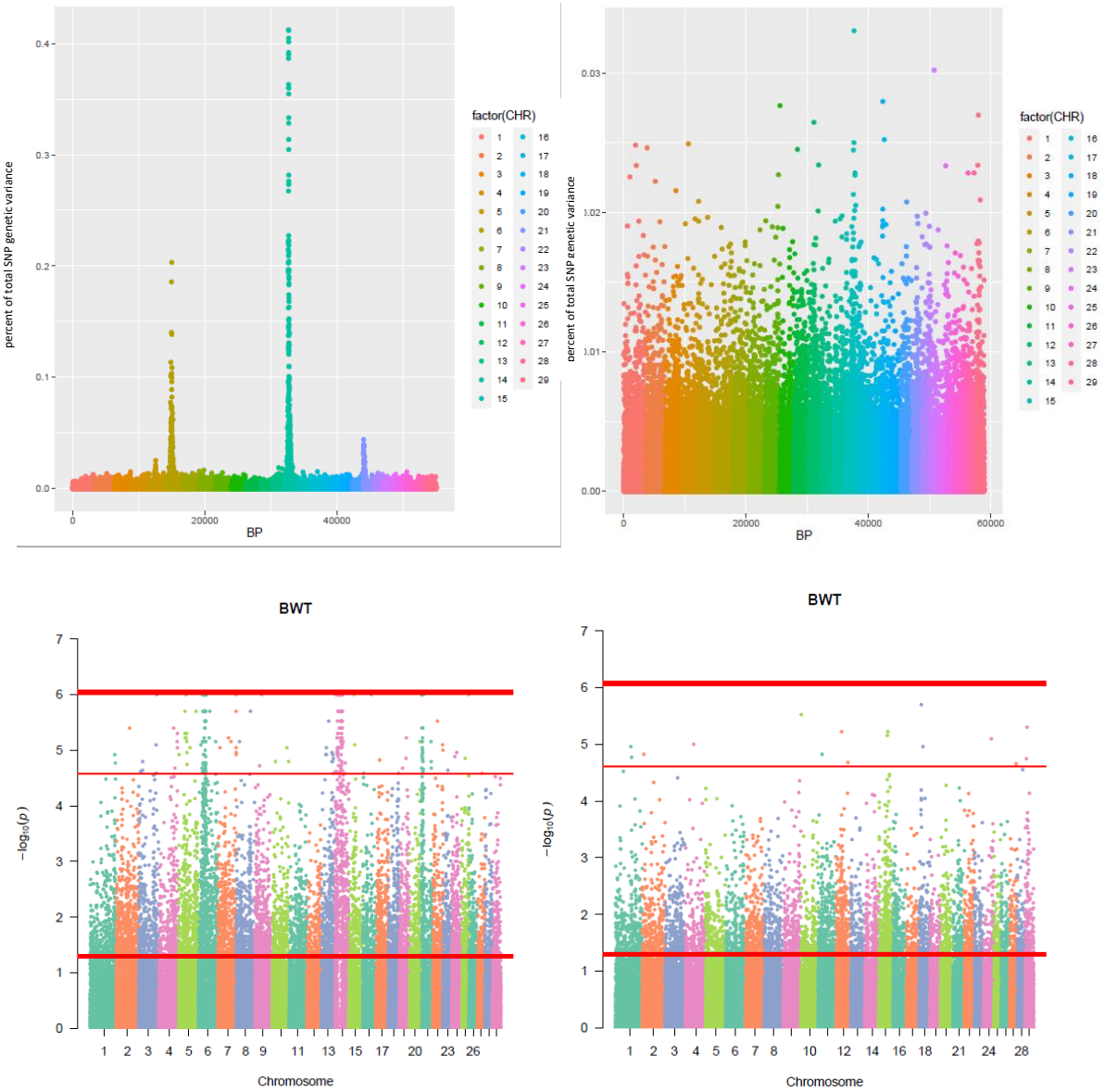


Figure 4.5.13: The percent of total SNP genetic variance (top row) and Manhattan plot (bottom row) for birth weight for Brahman (left) and Droughtmaster (right)

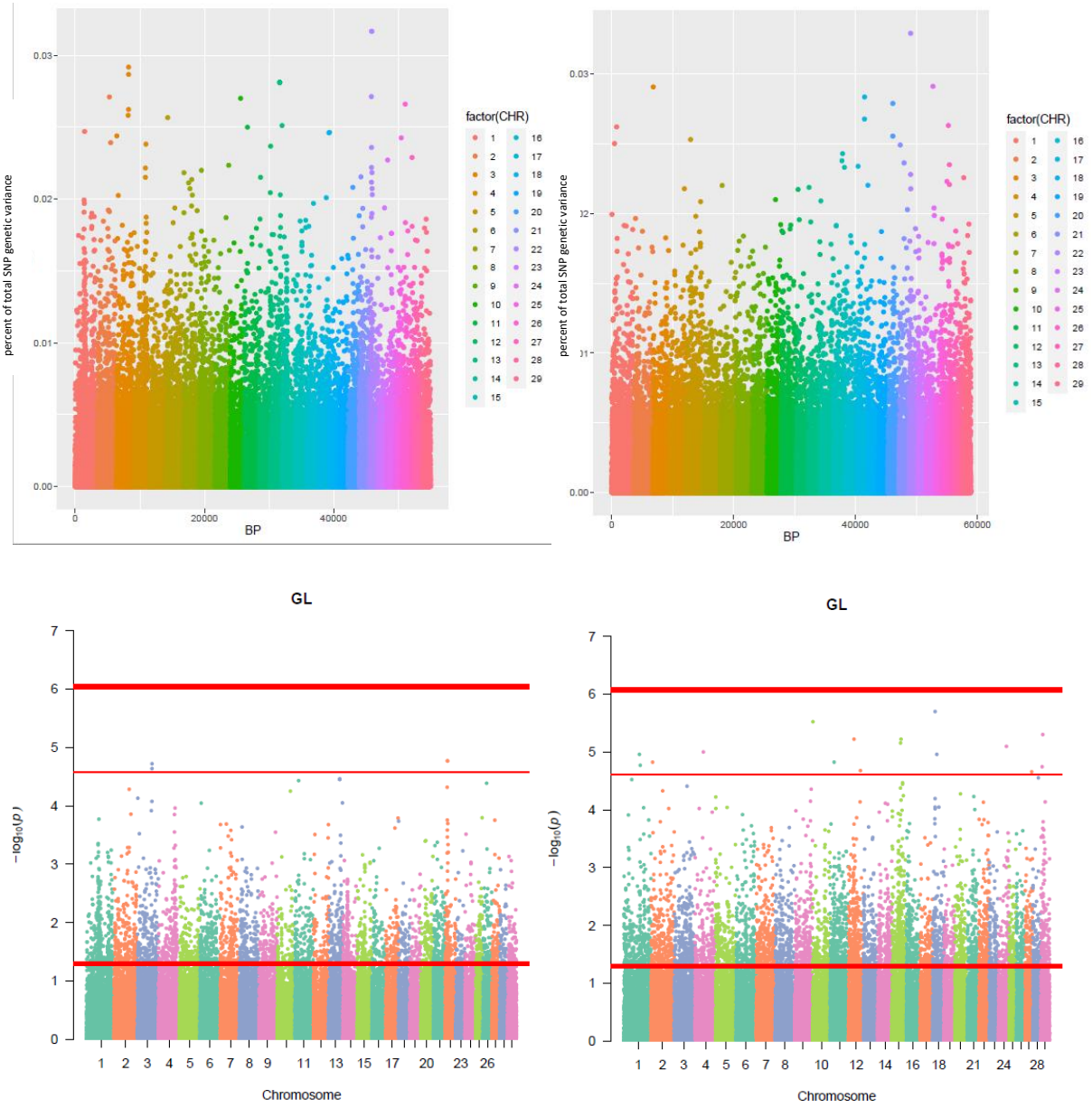


Figure 4.5.14: The percent of total SNP genetic variance (top row) and Manhattan plot (bottom row) for gestation length for Brahman (left) and Droughtmaster (right)

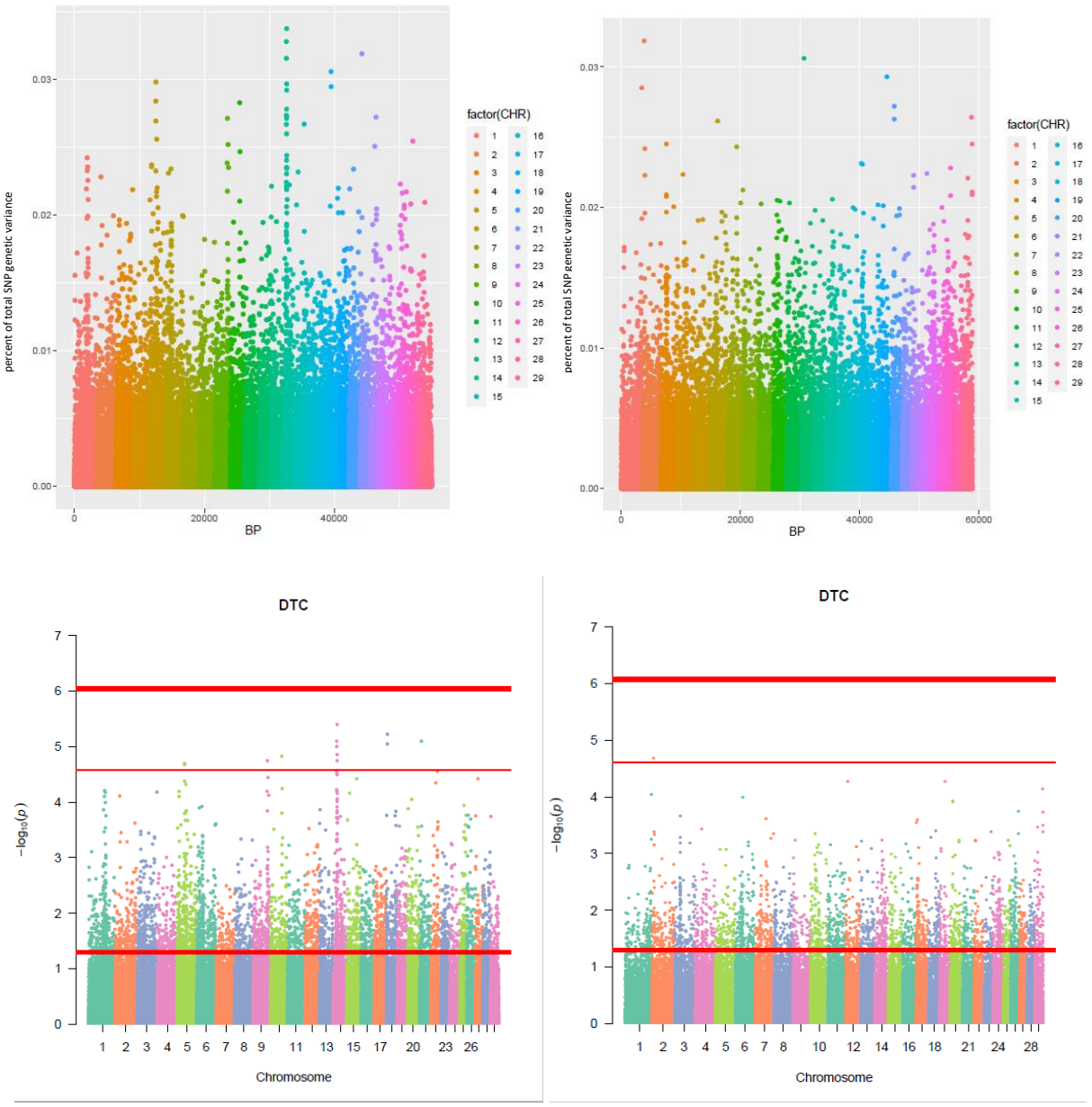


Figure 4.5.15: The percent of total SNP genetic variance (top row) and Manhattan plot (bottom row) for 1st parity days to calving for Brahman (left) and Droughtmaster (right)

4.6 Effect of myostatin mutations on the performance of tropical beef cattle

Introduction: Myostatin mutations have been identified in beef cattle (and other species), causing animals to be 'double-muscled' with increased muscle development. This study aimed to estimate the frequency of these mutations in tropical beef breeds and investigate their effect on a wide range of traits.

Dataset: Myostatin mutation genotypes for Repronomics animals (MLA projects B.NBP.0759 and P.PSH.1221) were obtained from Neogen, where animals were genotyped on Neogen's GGP TropBeef

chip. There were 6,119 observations. Observations were removed because the test failed or was still pending (n=167), were duplicated (n=6), were unable to be matched or were a project sire (n=113). This left 5,946 myostatin observations, but only 5,782 were matched to Repronomics animals, including animals that died at or shortly after birth. Of these records, there were 2,317 (40%) where the dam was also recorded for F94L and NT821 and 1,080 (19%) where the dam was also recorded for Q204X.

The final dataset included 2,467 Brian Pastures and 3,315 Spyglass animals born between 2015 and 2023. The numbers by year are shown in Table 4.6.1, with low numbers for 2015 and 2017-born animals. 3,040 (53%) were female and 2,736 (47%) were male.

Table 4.6.1: Number of Repronomics animals with myostatin genotypes by birth year

Year	2015	2016	2017	2018	2019	2020	2021	2022	2023
N	23	415	140	923	920	951	716	792	902

Myostatin segregation: Nine (C313Y, D182N, E226X, E291X, F94L, NT419, NT821, Q204X, S105C) myostatin variants were tested, but only five (C313Y, E226X, F94L, NT419, NT821) have been validated on the GGP TropBeef chip. Results showed only three variants were segregating in the Repronomics animals, although no Brahman animals were identified with a myostatin mutation. NT821 was the most common variant, with an allele frequency 0.05 found across Droughtmaster and Santa Gertrudis animals. It was the only variant with animals that were homozygous for the myostatin allele. Allele frequencies were similar across sexes.

Table 4.6.2: Myostatin allele frequency across Repronomics animals by sex (NR = no result)

		N alleles			Male		N alleles			Female
Variant	NR	0	1	2	Frequency (0-1)	NR	0	1	2	Frequency (0-1)
F94L	0	2,709	27	0	0.005	2	2,982	56	0	0.009
NT821	0	2,484	249	3	0.047	0	2,746	284	10	0.050
Q204X	478	2,236	22	0	0.005	801	2,221	18	0	0.004

Differences were observed within breeds, with no Brahman animal showing any of the myostatin variants. Droughtmaster was the only breed with the Q204X variant segregating, but it was only present in the progeny of one sire. The allele frequency of the NT821 variant was highest in Santa Gertrudis (0.12 compared to 0.08 for Droughtmaster). Given the segregation differences observed for breeds, it can be seen that 19.1% of Droughtmaster animals and 26.0% of Santa Gertrudis animals had at least one myostatin allele. The F94L heterozygotes in Droughtmaster and Santa Gertrudis were sired by 21 and 13 different sires, respectively. The NT821 heterozygotes (and double copy homozygotes) in Droughtmaster and Santa Gertrudis were sired by 50 and 32 different sires, respectively. The remainder of the study focused on Droughtmaster and Santa Gertrudis for the effects of the myostatin variants F94L and NT821.

Table 4.6.3: Myostatin allele frequency across Repronomics animals by breed (NR = no result)

		N alleles			Brahman
Variant	**NR**	**0**	**1**	**2**	**Frequency (0-1)**
F94L	0	2,554	0	0	0
NT821	0	2,554	0	0	0
Q204X	583	1,971	0	0	0
		N alleles			**Droughtmaster**
Variant	**NR**	**0**	**1**	**2**	**Frequency (0-1)**
F94L	2	2,138	48	0	0.011
NT821	0	1,852	331	5	0.078
Q204X	532	1,616	40	0	0.012
Combined*		1,806	375	7	
		N alleles			**Santa Gertrudis**
Variant	**NR**	**0**	**1**	**2**	**Frequency (0-1)**
F94L	0	872	32	0	0.018
NT821	0	697	199	8	0.119
Q204X	165	739	0	0	0
Combined*		669	223	12	

*Combined is the number of myostatin alleles across F94L and NT821

Table 4.6.4: Frequency of genotypes across all variants for Droughtmaster and Santa Gertrudis animals (NR = no result)

Droughtmaster					Santa Gertrudis			
F94L	**NT821**	**Q204X**	**N**	**%**	**F94L**	**NT821**	**N**	**%**
0	0	0	1,295	59.2	0	0	669	74.0
0	0	1	37	1.7				
0	0	NR	473	21.6				
0	1	0	281	12.8	0	1	195	21.6
0	1	1	3	0.1				
0	1	NR	44	2.0				
0	2	0	4	0.2	0	2	8	0.9
0	2	NR	1	0.0				
1	0	0	34	1.6	1	0	28	3.1
1	0	NR	12	0.5				
1	1	0	2	0.1	1	1	4	0.4
NR	0	NR	1	0.0				
NR	1	NR	1	0.0				

Table 4.6.5: Frequency of genotypes for calf-cow combinations across all variants across Droughtmaster animals (NR = no result)

F94L-calf	F94L-cow	N	%	NT821-calf	NT821-cow	N	%
0	0	891	40.7	0	0	708	32.4
0	1	8	0.4	0	1	36	1.6
0	NR	1,239	56.6	0	NR	1,108	50.6
1	0	12	0.5	1	0	131	6.0
1	1	8	0.4	1	1	41	1.9
1	NR	28	1.3	1	NR	159	7.3
NR	NR	2	0.1	2	1	3	0.1
				2	NR	2	0.1

Table 4.6.6: Frequency of genotypes for calf-cow combinations across all variants across Santa Gertrudis animals (NR = no result)

F94L-calf	F94L-cow	N	%	NT821-calf	NT821-cow	N	%
0	0	406	44.9	0	0	301	33.3
0	1	15	1.7	0	1	29	3.2
0	NR	451	49.9	0	NR	367	40.6
1	1	14	1.5	1	0	60	6.6
1	NR	18	2.0	1	1	39	4.3
				1	2	2	0.2
				1	NR	98	10.8
				2	1	4	0.4
				2	NR	4	0.4

Hardy-Weinberg equilibrium: With the allele frequencies observed for Droughtmaster and Santa Gertrudis, the expected genotype frequencies under Hardy-Weinberg are presented in Table 4.6.7. While F94L for both breeds was observed to be in Hardy-Weinberg equilibrium (critical value=3.84, p=0.05 and df=1), for NT821, Droughtmaster frequencies were not in Hardy-Weinberg equilibrium. Although not significant, the chi-square value for Santa Gertrudis was closer to the critical value than 0, and perhaps with more records, NT821 for Santa Gertrudis may also be shown not to be in Hardy-Weinberg equilibrium. There were fewer 2-copy animals in both breeds than the expected number. The reason for this discrepancy is unknown, but several reasons could be embryo loss, myostatin being linked to poorer reproduction or a non-random population. In Repronomics, the policy is no calf, no stay, and if myostatin is linked to embryo loss or poor reproduction, this may have impacted the observed genotype frequencies. The Hardy-Weinberg equilibrium test assumes a random mating population. While project sires are not selected for genetic merit, they are chosen to represent the wider breed populations and to include influential sires, and this may have resulted in a non-random subset and influenced the genotype frequencies observed in the population. Furthermore, it is possible that 2-copy sires are not retained for breeding and thus are unavailable for inclusion in the Repronomics project.

Table 4.6.7: Hardy-Weinberg equilibrium test with the frequency and number of expected and observed genotypes and chi-square value

	Droughtmaster				Santa Gertrudis			
	Expected		Observed		Expected		Observed	
F94L	**Freq.**	**N.**	**Freq.**	**N.**	**Freq.**	**N.**	**Freq.**	**N.**
0	0.9781	2,138.17	0.9780	2,138	0.9343	871.75	0.9646	872
1	0.0218	47.57	0.0220	48	0.0354	31.96	0.0354	32
2	0.0001	0.26	0.0000	0	0.0003	0.29	0.0000	0
	X2=0.264				X2=0.290			
NT821								
0	0.8501	1,855.73	0.8464	1,852	0.7762	695.44	0.7710	697
1	0.1443	315.02	0.1513	331	0.2114	189.38	0.2201	199
2	0.0061	13.28	0.0023	5	0.0142	12.69	0.0089	8
	X2=5.981				X2=2.226			

Myostatin allele effects on phenotype traits: The number of animals with two copies of the myostatin alleles was very low, as shown in Table 4.6.3. Therefore, no analysis included 2 copy animals. The impact of having one copy of the myostatin variant was investigated for Droughtmaster and Santa Gertrudis animals. Many traits were considered, including carcase, body weight and composition, adaptation, maternal, and female reproduction traits. Fixed effects models were developed as part of the Repronomics project EBVs or from the standard BREEDPLAN analysis. Sire was fitted as a random effect. The myostatin genotype was fitted as a fixed class effect (i.e. 0 or 1). For traits recorded on both sexes, the sex x myostatin interaction was tested, and it was not significant for all traits and mutations. Least squares means were only reported for traits with 10 or more heterozygote animals recorded. For traits with a maternal component (birth and weaning weight), the impact of the cow myostatin genotype was also tested with the cow genotype nested within the cow genotype status (Y/N), and included as an interaction with the calf myostatin genotype.

Birth and weaning weight (kg) – Results showed the myostatin mutation NT821 significantly ($p<0.05$) affected birth weight for both breeds and weaning weight for Santa Gertrudis. The maternal component of birth and weaning weight was not significant for both breeds. Calves that were heterozygote for NT821 were heavier at birth compared to calves that had no copies of the NT821 mutation. The effect of one copy was 1.06kg and 2.58kg in Droughtmaster and Santa Gertrudis, respectively, equating to a 3.05% and 7.16% increase in the birth weight of calves. Heterozygote Santa Gertrudis calves were also 6.66kg heavier (3.01% increase) at weaning.

Table 4.6.8: Significant NT821 myostatin effects (EFF) and the corresponding percentage change (%) observed of one copy of the myostatin variant

	Droughtmaster				Santa Gertrudis			
	N(0)	**N(1)**	**EFF**	**%**	**N(0)**	**N(1)**	**EFF**	**%**
Birth weight (kg)	1860	296	1.06	3.05	673	190	2.58	7.16
Weaning weight (kg)					637	172	6.66	3.01

F94L significantly ($p<0.05$) affected Santa Gertrudis's birth and weaning weight, with a significant interaction between the calf and cow genotypes. Table 4.6.9 presents the least squares means for the different calf-cow genotype combinations for birth and weaning weight. It should be noted that the

numbers of some combinations were low. It can be seen that a F94L heterozygote calf had no impact on birth weight when the cow genotype was unknown. In comparison, a 5.04kg increase was observed between calves with and without one copy of the F94L allele when the cow was an F94L heterozygote. A similar pattern was observed for weaning weight. Heterozygote calves with ungenotyped dams were 4.46kg lighter at weaning compared to homozygotes, but when the cow was a heterozygote, her heterozygote calves were 21.3kg heavier than her homozygote calves.

Table 4.6.9: Number of records and least squares means (standard errors in brackets) for calf-cow F94L genotype combinations for Santa Gertrudis

	Birth weight			Weaning weight		
Calf genotype	**Cow genotype**			**Cow genotype**		
Number of records	**NR**	**0**	**1**	**NR**	**0**	**1**
0	434	390	15	401	370	15
1	17	0	14	16	0	13
LSM (SE)						
0	36.42	37.39	35.00	225.58	221.96	209.57
	(0.49)	(0.56)	(1.36)	(1.95)	(2.31)	(5.84)
1	36.46		40.05	221.12		230.87
	(1.49)		(1.40)	(6.35)		(6.23)

Heifer, 400-day, mating 1, mating 2 and carcase traits – Table 4.6.10 records the effect of myostatin mutations for traits where a significant myostatin effect was estimated. There was a drop in the total number of records available for mating 1 and mating 2 traits. This was expected due to the time lag in record collection, and cows that did not wean a calf from mating 1 were not retained for mating 2.

The F94L variant was not observed to significantly affect many traits. The exceptions were Droughtmaster, which had a significant decrease in P8 fat as a heifer and an increase in EMA at mating 2, and Santa Gertrudis, which had a significant decrease in P8 fat as a heifer.

The NT821 variant was observed to impact numerous traits in both breeds. The presence of one copy of NT821 was shown to decrease P8 fat levels and increase body condition scores in both breeds. Compared to 0 copy animals, P8 fat decreased by 15.9% and 31.8% for Droughtmaster and Santa Gertrudis, but the increase in body condition score was relatively smaller (2.0 to 2.6%).

Across all recording ages (i.e. heifer, 400-day scans, into mating 1 and 2 and carcase traits) and fat (subcutaneous and intramuscular) traits, one copy of NT821 resulted in leaner animals in both breeds. For Droughtmaster, the decrease in fat ranged from an 11.5% decrease for carcase P8 fat to a 58.0% decrease for ultrasound P8 fat at approximately 400 days. For Santa Gertrudis, fat decreased by 21.0% for carcase rib fat to 66.1% for ultrasound P8 fat at approximately 400 days. Santa Gertrudis heterozygotes were shown to have a 2.6% decrease in body condition score at mating 1.

For both breeds, heterozygote NT821 animals had larger eye muscle areas and live weight across all time periods. In Droughtmaster, the increase in eye muscle area ranged from 7.2% at mating 1 to 11.2% at 400 days, and in Santa Gertrudis, the increase ranged from 7.3% at mating 1 to 12.7% at slaughter. Heterozygote Droughtmaster animals were between 1.7% (at mating 1) and 4.1% (at slaughter) heavier than homozygotes, and heterozygote Santa Gertrudis animals were between 2.0% (400 days) and 3.2% heavier (at slaughter) than homozygotes. In addition to being more muscular,

heterozygote Droughtmasters were shown to have a 10.1% reduction in shear force (i.e. more tender) than homozygote (0) animals.

NT821 was also shown to increase the heifer puberty age. Droughtmaster and Santa Gertrudis heterozygotes were 49 (8.5% increase) and 31 (5.5% increase) days older at puberty than homozygote (0) animals. For Droughtmaster, the second days to calving also increased by 20 days, a 5.8% increase compared to homozygotes.

Calving difficulty—Given the low incidence, there was limited data on calving difficulty. However, of the 27 Droughtmaster animals recorded as calf deaths from calving difficulties, 10 (37%) had at least one copy of the NT821 variant. Of the 18 Santa Gertrudis animals recorded as calf deaths from calving difficulties, 9 (50%) had at least one copy of the NT821 variant.

Traits with no significant myostatin effect – There were a large number of traits where no significant effect ($P<0.05$) of myostatin mutation was observed: gestation length, coat score, flight time, sheath score, hip height, mothering score, teat score, udder score and lactation anoestrus interval.

Conclusion: F94L and NT821 myostatin variants were shown to segregate in the Droughtmaster and Santa Gertrudis populations. NT821 had the biggest impact on production traits, with heterozygote animals being heavier and more muscular, improved tenderness and leaner, but had delayed puberty age, increased days to calving, and an indication of higher incidence of calving-related deaths. An AAABG paper has been submitted for 2025, and a series of full scientific journal articles are planned. These results will be communicated to breed societies, and extension messages will be developed in conjunction with the breed societies. The key messages for extension will include that myostatin is present in the breeds, that the impact of having myostatin is dependent on which mutation the animal has, while carcase attributes may be favourable, there are unfavourable effects on reproduction traits and strategies to manage the number of animals with myostatin mutations in the breed.

Table 4.6.10: Significant F94L and NT821 Myostatin effects (EFF) and the corresponding percentage change (%) observed for heterozygote animals

	F94L								NT821							
	Droughtmaster				Santa Gertrudis				Droughtmaster				Santa Gertrudis			
	N(0)	N(1)	EFF	%	N(0)	N(1)	EFF	%	N(0)	N(1)	EFF	%	N(0)	N(1)	EFF	%
Heifer traits																
Ultrasound P8 scan (mm)	977	26	-0.46	-18.70	404	21	-0.52	-24.53	844	159	-0.40	-15.94	332	87	-0.71	-31.84
Body condition score (1-5)									880	163	0.08	2.61	346	88	0.06	1.99
BREEDPLAN 400 day traits																
400-day live weight (kg)													503	148	6.05	2.03
Ultrasound eye muscle area (cm^2)									1143	175	4.95	11.16	442	112	4.23	9.04
Ultrasound rib fat (mm)									1049	156	-0.65	-52.00	444	112	-1.02	-58.96
Ultrasound P8 fat (mm)									1049	156	-1.48	-58.04	444	112	-1.99	-66.11
Mating 1 traits																
Age at puberty via ovarian scan (day)									700	105	48.59	8.48	261	64	31.11	5.45
Ultrasound eye muscle area (cm^2)									767	127	4.04	7.15	290	82	4.15	7.28
Ultrasound rib fat (mm)									730	126	-0.40	-14.13	241	74	-0.75	-30.36
Ultrasound P8 fat (mm)									768	127	-1.32	-23.70	292	82	-1.63	-35.21
Live weight (kg)									772	128	6.80	1.71				
Body condition score (1-5)													292	82	-0.08	-2.55
Mating 2 traits																
Ultrasound eye muscle area (cm^2)	493	10	5.21	10.69					458	45	4.40	9.09	186	39	3.61	7.66
Ultrasound rib fat (mm)													186	39	-0.75	-43.86
Ultrasound P8 fat (mm)													186	39	-1.38	-58.97
Live weight (kg)									473	49	14.40	3.08				
Days to calving of the 2nd calf (days)									249	21	20.34	5.80				
Carcase traits																
carcase weight (kg)									420	51	9.60	4.10	141	31	8.10	3.16
Carcase eye muscle area (cm^2)									115	20	7.33	9.52	51	12	8.99	12.66
Carcase rib fat (mm)													141	31	-1.36	-20.96
Carcase P8 fat (mm)									420	51	-1.17	-11.53	141	31	-2.08	-19.62
Carcase intramuscular fat (%)									420	51	-0.56	-20.36	141	31	-0.82	-28.57
Shear force (kg)									403	46	-0.42	-10.12				

4.7 Relationship between non-BREEDPLAN carcase traits and reproduction

Carcase and reproduction traits are both economically important in the beef industry. Genetic correlations exist between carcase traits and reproduction traits in the BREEDPLAN evaluations of all breeds, and this work aimed to assess the genetic relationships between carcase traits recorded in the Steer BIN project, which are not currently traits in BREEDPLAN, and female Reproduction traits from the Repronomics project.

Female reproduction traits were recorded as part of the Repronomics project (MLA projects B.NBP.0759 and P.PSH.1221), while carcase traits were recorded for Repronomics steers as part of the Northern BIN project (MLA projects P.PSH.0743, P.PSH.0774, P.PSH.1386, P.PSH.1408, P.PSH.2131 and P.PSH.2132). The data was edited to include only purebred animals, and outliers with more than three standard deviations from the mean were removed. Non-BREEDPLAN carcase traits were recorded for 3,311 steers born in the Brian Pastures 2015-2022 and Spyglass 2013-2022 cohorts. Carcase records were available for 1,491 Brahman, 1,334 Droughtmaster and 486 Santa Gertrudis steers. The average number of animals per cohort was 174.3, ranging between 106 and 253. Traits extracted from BREEDPLAN were recorded on 4,583 heifers and 4,367 steers born in the Brian Pastures 2011-2023 and Spyglass 2011-2023 cohorts. BREEDPLAN records were available for 4,150 Brahman, 3,441 Droughtmaster and 1,359 Santa Gertrudis. The average number of animals per cohort was 186.5, ranging between 76 and 301. Summary statistics for the traits considered are shown in Table 4.7.1.

ASReml univariate models were used to estimate variance components and heritabilities, and bi-variate models estimated genetic and phenotypic correlations. All analyses used an animal model, with maternal and maternal permanent environment tested for significance for birth weight, gestation length and weaning weight. A three-generation pedigree was constructed for the dataset. For BREEDPLAN traits, the phenotype was pre-adjusted for fixed effects, and the statistical model included the BREEDPLAN contemporary group and breed as class fixed effects. For non-BREEDPLAN traits, the statistical model was the project cohort (all animals in a cohort had the same kill date) and sire breed as class fixed effects. Covariate adjustment (linear and quadratic) was considered for kill age, carcase weight, or no adjustment. Results showed that the estimated variance components were similar for each covariate adjustment model, so only results from models without adjusting for age or weight were reported.

Table 4.7.2 reports the variance component estimates for all traits. Estimates for BREEDPLAN traits were similar to previously reported parameters. Non-BREEDPLAN traits were shown to have variation, and heritability estimates ranged from 0.13 (MQ_LD_b) to 0.44 (MSA_Hump).

Table 4.7.3 reports the genetic and phenotypic correlations between the traits. Genetic correlations between the BREEDPLAN traits were similar to previously reported estimates. Moderate positive genetic correlations were estimated for gestation length with birth weight, age at puberty and 1st and 2nd parity days to calving, indicating that animals with shorter gestation lengths also were lighter at birth, reached puberty earlier and had shorter days to calving. Genetic correlations were close to 0 between gestation length and lactation anoestrus interval, weaning weight, carcase weight and shear force. Birth weight was estimated to have strong positive genetic correlations with weaning weight, carcase weight and days to calving at both parities. Moderate positive genetic correlations were estimated between birth weight and the ovarian ultrasound scan traits (age at puberty and lactation anoestrus interval), indicating that lower birth weight calves had better fertility. The correlation between birth weight and shear force was small and not significantly different from 0. Weaning weight

had moderate to strong positive genetic correlations with carcase weight and 2nd parity days to calving. No significant correlations were estimated between weaning weight and ovarian ultrasound scan traits, 1st parity days to calving and shear force. Estimated genetic correlations between gestation length, birth and weaning weight are similar to those reported by Moore et al. (2025).

Table 4.7.1: Summary statistics for female reproduction and steer carcase traits

Female reproduction traits						
Trait	**Trait**	**N**	**Mean**	**Std**	**Min**	**Max**
Age of puberty	AP	3,436	626.88	114.62	318.17	1007.10
Lactation anoestrus interval	LAI	2,343	73.27	65.24	-87.05	311.78
Days to calving 1	DTC1	3,097	328.65	39.05	274.13	437.06
Days to calving 2	DTC2	1,897	353.08	43.68	280.72	432.84
Birth weight	BW	8,424	34.57	5.29	18.35	53.13
Gestation length	GL	2,762	289.73	5.97	267.99	305.41
Weaning weight	WWT	8,271	210.01	27.67	119.48	320.97
Steer carcase traits						
Trait^	**Trait**	**N**	**Mean**	**Std**	**Min**	**Max**
Carcase weight	CWT	2,809	315.19	40.22	207.04	463.50
Shear force	SF	2,698	4.49	1.16	2.30	9.02
Longissimus dorsi cooking loss %	MQ_LD_LOSS	3,058	25.71	2.58	16.42	34.12
Longissimus dorsi a* colour	MQ_LD_a	3,283	22.89	2.52	11.73	31.62
Longissimus dorsi b* colour	MQ_LD_b	3,291	11.25	2.46	4.14	18.56
Longissimus dorsi L* colour	MQ_LD_l	3,284	39.72	2.90	30.19	49.24
MSA hump height (mm)	MSA_Hump	3,300	134.32	39.39	60	305
MSA USDA Ossification	MSA_Uos	3,272	142.46	16.06	100	200
MSA Index	MSA_Index	3,062	54.88	2.91	45.17	64.84
days	Kill age	3,311	882.74	67.34	619	1036

Phenotypes for BREEDPLAN female reproduction traits, carcase weight and shear force were pre-adjusted phenotypes from BREEDPLAN. Phenotypes for non-BREEDPLAN steer carcase traits are not pre-adjusted for carcase weight. Trait definitions for non-BREEDPLAN carcase traits are: MQ_LD_LOSS = Cooking loss measured as percentage difference in weight between a cooked and pre-cooked sample, MQ_LD_a = a* Colour space lightness measurement (red-green) on the 'bloomed' surface of the muscle using a Minolta Chroma Meter, MQ_LD_b = b* Colour space lightness measurement (blue-yellow) on the 'bloomed' surface of the muscle using a Minolta Chroma Meter, MQ_LD_l = l* Colour space lightness measurement (black-white) on the 'bloomed' surface of the muscle using a Minolta Chroma Meter, MSA_Hump = Hump height assessed by MSA certified graders: measured as the greatest height of the hump from the spinal column, as an assessment of *Bos Indicus* content, MSA_Uos = Ossification score assesses age, as the degree of conversion of cartilage to bone at the sacral, lumbar and thoracic vertebrae: 50-point subjective score measured from 100 (young ~9 months) to 590 (old ~96 months or older). Assessed by MSA-certified graders, MSA_Index = A single number, ranging from 30 to 80, that predicts the eating quality of a beef carcase based on MSA recorded traits aimed at describing tenderness, juiciness, flavour and overall liking of beef.

Carcase weight and shear force generally had low correlation estimates that were not significantly different from 0 with the ovarian ultrasound scan traits, both days to calving traits and with each other. Strong genetic correlations were estimated, indicating that cows that reached puberty earlier also had shorter lactation anoestrus interval and days to calving at both parities. Lactation anoestrus interval was also estimated to have positive genetic correlations with both days to calving measures, in particular, the genetic correlation between lactation anoestrus interval and 2nd parity days to calving was not significantly different from 1, indicating that these traits are genetically the same. Days to calving at the 1st and 2nd parities were also strongly correlated, and although not significantly different from 1 in this study, Johnston and Moore (2019) reported that days to calving at the different parities are different traits.

Genetic correlations between the non-BREEDPLAN carcase traits were generally not significantly different from zero. However, the two meat colour measures, MQ_LD_a and MQ_LD_b, were strongly correlated. The MSA_Index was positively correlated with all three meat colour traits and negatively correlated with ossification. Although generally not significant, genetic correlation estimates indicated small to moderate negative correlations between cooking loss and the three meat colour traits MQ_LD_a and MQ_LD_l, ossification and MSA index. A small positive genetic correlation was estimated between cooking loss and hump height. Except for the correlations mentioned above, the three meat colour traits generally had small correlations with each other, hump height and ossification. Although MSA_Hump was included in the construction of the MSA_Index, the genetic correlation between these traits was small and not significantly different to 0. This is most likely because breed was fitted in the model, which would remove the difference in hump height across the breeds. Hump height and ossification were also estimated to have a small genetic correlation.

Many of the genetic correlations between non-BREEDPLAN carcase traits and BREEDPLAN carcase and reproduction traits tended not to be significantly different from 0. However, ossification was estimated to have moderate negative genetic correlations with age at puberty, 1st parity days to calving, birth weight and weaning weight. This indicates that animals with carcases identified as being physiologically older were genetically those with earlier puberty, shorter days to calving, and lighter birth and weaning weights. Negative, but not significant, correlations were estimated between ossification and lactation anoestrus interval, 2nd parity days to calving, gestation length and carcase weight. There was no relationship between ossification and shear force, and small non-significant genetic correlations were estimated between ossification and other eating quality traits. Shear force was estimated to have moderate to strong negative genetic correlations with all three meat colour traits and a positive correlation with cooking loss. Although not significant, shear force was positively correlated with hump height but not MSA_index. Meat colour (MQ_LD_l) was estimated to have moderate positive genetic correlations with age at puberty and 1st parity days to calving. This indicates that animals with higher colour scores had later puberty and longer days to calving. Positive correlations not significantly different from 0 were also estimated between MQ_LD_l and lactation anoestrus interval, 2nd parity days to calving, birth weight, weaning weight and carcase weight. There was no genetic relationship between gestation length and MQ_LD_l. In contrast, the colour traits MQ_LD_a and MQ_LD_b were estimated to have negative genetic correlations with the ovarian scan traits, both days to calving traits, gestation length, birth weight, weaning weight and carcase weight. However, except for the correlation between MQ_LD_a and the traits 1st parity days to calving and weaning weight, and MQ_LD_b and birth weight, the correlations were not significantly different from 0. Cooking loss was positively correlated with ovarian scan traits, indicating that traits with greater cooking loss were older at puberty and had longer lactation anoestrus interval. Although not significant, cooking loss was positively correlated with 2nd parity days to calving, birth weight and gestation length, and negatively correlated with 1st parity days to calving, weaning weight and carcase weight. Hump height and MSA_Index were estimated to have small correlations not significantly different from 0 with ovarian scans, days to calving at both parities, birth weight and gestation length. Positive correlations were estimated between hump height and MSA_Index both weaning and carcase weight.

The estimated variance components indicate that the non-BREEDPLAN carcase traits considered in this study were heritable and could be included in genetic evaluations. There were no strong unfavourable correlated responses with the BREEDPLAN reproduction, growth and carcase traits. However, as shear force was moderately to strongly correlated with cooking loss and the three meat

colour traits, including these traits, may be of limited value. Ossification may have potential for genetic evaluation describing the physiological age of the carcase. Ossification was estimated to be moderately correlated with age at puberty and growth traits, and further research could investigate if there is merit in developing an ossification breeding value to describe the physiological development of animals. The other non-BREEDPLAN eating quality traits considered in this study had moderate to strong genetic correlations with shear force, which is already a BREEDPLAN trait, and thus, including these new traits as separate EBVs may be of limited value.

Table 4.7.2: Additive (V_a), maternal (V_m), maternal permanent environment (V_{pe}), residual (V_e) and phenotypic (V_p) variance estimates and direct (h^2) and maternal (h_m^2) heritability estimates and standard errors (SE) from a pooled breed dataset

Trait	V_a	SE	V_m	SE	V_{pe}	SE	V_e	SE	V_p	SE	h^2	SE	h_m^2	SE
MSA_Uos	65.72	9.00					94.84	7.15	160.56	4.59	0.41	0.05		
MQ_LD_LOSS	1.27	0.22					3.45	0.20	4.73	0.13	0.27	0.04		
MQ_LD_a	0.62	0.13					2.90	0.13	3.51	0.09	0.18	0.04		
MQ_LD_b	0.20	0.05					1.39	0.06	1.59	0.04	0.13	0.03		
MQ_LD_l	1.05	0.21					4.03	0.20	5.08	0.13	0.21	0.04		
MSA_Hump	193.11	24.01					242.15	18.72	435.26	12.45	0.44	0.05		
MSA_Index	0.78	0.12					1.51	0.10	2.28	0.07	0.34	0.05		
AP	6135.3	524.41					5058.1	353.14	11193	320.72	0.55	0.04		
LAI	1546.4	214.8					2632.4	173.64	4178.8	134.21	0.37	0.05		
DTC1	75.03	33.34					1355.7	45.77	1430.7	36.82	0.05	0.02		
DTC2	250.26	69.87					1217.2	70.73	1467.5	49.76	0.17	0.05		
BW	11.85	0.85	2.58	0.46	0.61	0.32	8.02	0.49	23.05	0.49	0.51	0.03	0.11	0.02
GL	17.57	2.26	2.42	0.86			8.27	1.26	28.26	0.98	0.62	0.07	0.09	0.03
WWT	192.01	16.12	73.28	10.62	43.27	7.42	134.48	9.08	443.05	9.71	0.43	0.03	0.17	0.02
CWT	341.77	42.97					286.99	31.96	628.77	20.22	0.54	0.06		
SF	0.34	0.06					0.79	0.05	1.13	0.03	0.30	0.05		

Table 4.7.3: Genetic (above diagonal) and phenotypic (below diagonal) correlations (standard errors) between carcase and reproduction traits from a pooled breed dataset

	MQ_LD_LOSS	MQ_LD_a	MQ_LD_b	MQ_LD_l	MSA_Hump	MSA_Uos	MSA_Index	AP	LAI	DTC1	DTC2	BW	GL	WWT	CWT	SF
MQ_LD_LOSS		-0.23 (0.13)	**-0.31 (0.15)**	-0.21 (0.13)	**0.12 (0.10)**	-0.11 (0.11)	-0.19 (0.11)	**0.25 (0.11)**	**0.25 (0.11)**	-0.24 (0.21)	0.15 (0.15)	0.11 (0.08)	0.21 (0.11)	-0.16 (0.09)	-0.10 (0.11)	0.36 (0.12)
MQ_LD_a	0.02 (0.02)		0.89 (0.03)	-0.05 (0.15)	-0.13 (0.12)	0.03 (0.12)	**0.26 (0.12)**	-0.13 (0.10)	-0.23 (0.13)	**-0.48 (0.23)**	-0.43 (0.18)	-0.33 (0.09)	-0.20 (0.12)	-0.29 (0.10)	-0.19 (0.12)	-0.55 (0.11)
MQ_LD_b	-0.02 (0.02)	0.91 (0.003)		0.25 (0.15)	-0.02 (0.13)	-0.01 (0.14)	0.41 (0.13)	-0.07 (0.12)	-0.19 (0.14)	-0.42 (0.26)	-0.34 (0.20)	**-0.27 (0.11)**	-0.21 (0.14)	-0.19 (0.11)	-0.12 (0.13)	-0.64 (0.12)
MQ_LD_l	0.01 (0.02)	0.29 (0.02)	0.45 (0.01)		0.02 (0.11)	-0.21 (0.11)	**0.29 (0.12)**	0.32 (0.10)	0.14 (0.12)	0.52 (0.20)	0.26 (0.17)	0.17 (0.09)	0.05 (0.12)	0.15 (0.10)	0.15 (0.11)	-0.36 (0.12)
MSA_Hump	-0.04 (0.02)	0.00 (0.02)	0.01 (0.02)	0.00 (0.02)		-0.08 (0.09)	-0.02 (0.10)	0.00 (0.07)	-0.08 (0.09)	-0.26 (0.18)	-0.10 (0.13)	0.00 (0.06)	0.05 (0.09)	**0.19 (0.07)**	0.26 (0.08)	0.28 (0.10)
MSA_Uos	-0.04 (0.02)	0.04 (0.02)	0.01 (0.02)	**-0.09 (0.02)**	0.03 (0.02)		-0.30 (0.09)	-0.24 (0.09)	-0.18 (0.09)	-0.50 (0.17)	-0.09 (0.13)	-0.30 (0.07)	-0.13 (0.09)	**-0.20 (0.08)**	-0.09 (0.09)	0.05 (0.11)
MSA_Index	-0.03 (0.02)	**0.08 (0.02)**	0.12 (0.02)	0.11 (0.02)	-0.17 (0.02)	-0.40 (0.02)		-0.16 (0.08)	-0.12 (0.10)	0.06 (0.19)	-0.23 (0.14)	0.00 (0.05)	-0.12 (0.10)	0.27 (0.08)	**0.25 (0.10)**	-0.04 (0.12)
AP	0.06 (0.03)	-0.04 (0.03)	-0.01 (0.02)	**0.08 (0.03)**	0.00 (0.04)	-0.07 (0.03)	-0.07 (0.04)		0.60 (0.06)	0.56 (0.16)	0.63 (0.10)	0.34 (0.05)	**0.17 (0.08)**	0.04 (0.06)	0.08 (0.08)	0.03 (0.09)
LAI	**0.08 (0.03)**	-0.06 (0.03)	-0.04 (0.03)	0.04 (0.03)	-0.03 (0.04)	-0.07 (0.04)	-0.04 (0.04)	0.30 (0.02)		0.35 (0.20)	0.99 (0.05)	0.22 (0.07)	-0.09 (0.10)	0.09 (0.08)	-0.07 (0.09)	0.18 (0.11)
DTC1	-0.03 (0.02)	**-0.05 (0.02)**	-0.03 (0.02)	**0.06 (0.02)**	-0.04 (0.03)	**-0.08 (0.03)**	0.01 (0.03)	0.14 (0.02)	**0.07 (0.03)**		0.75 (0.19)	0.56 (0.14)	**0.40 (0.19)**	-0.07 (0.16)	-0.06 (0.18)	-0.27 (0.20)
DTC2	0.03 (0.03)	**-0.07 (0.03)**	-0.05 (0.03)	0.05 (0.03)	-0.03 (0.04)	-0.02 (0.04)	-0.05 (0.03)	0.20 (0.03)	0.62 (0.02)	0.33 (0.03)		0.46 (0.10)	0.37 (0.15)	**0.26 (0.11)**	-0.02 (0.13)	0.28 (0.16)
BW	0.03 (0.02)	**-0.07 (0.02)**	**-0.05 (0.02)**	**0.08 (0.02)**	0.02 (0.02)	-0.10 (0.02)	0.02 (0.02)	0.17 (0.02)	0.10 (0.02)	0.04 (0.02)	**0.09 (0.03)**		0.36 (0.06)	0.71 (0.03)	0.45 (0.06)	0.10 (0.09)
GL	0.01 (0.03)	**-0.07 (0.03)**	**-0.07 (0.03)**	0.00 (0.03)	-0.01 (0.03)	-0.04 (0.03)	**-0.08 (0.03)**	0.04 (0.03)	-0.02 (0.04)	0.02 (0.03)	-0.02 (0.04)	0.32 (0.02)		-0.02 (0.07)	0.00 (0.08)	-0.02 (0.11)
WWT	-0.03 (0.02)	-0.02 (0.02)	-0.01 (0.02)	0.00 (0.02)	0.11 (0.02)	-0.01 (0.02)	**0.05 (0.02)**	**-0.08 (0.02)**	-0.01 (0.02)	-0.02 (0.02)	0.00 (0.03)	0.43 (0.01)	**0.05 (0.02)**		0.81 (0.03)	0.08 (0.09)
CWT	-0.04 (0.02)	-0.04 (0.02)	0.00 (0.02)	**0.08 (0.02)**	0.25 (0.02)	0.01 (0.02)	0.11 (0.02)	0.04 (0.04)	-0.03 (0.04)	-0.01 (0.03)	-0.01 (0.04)	0.35 (0.02)	0.02 (0.03)	0.54 (0.01)		0.13 (0.11)
SF	0.18 (0.02)	-0.29 (0.02)	-0.30 (0.02)	-0.31 (0.02)	0.00 (0.02)	0.02 (0.02)	-0.02 (0.02)	0.01 (0.04)	0.06 (0.04)	-0.03 (0.03)	0.06 (0.03)	0.01 (0.02)	**-0.07 (0.03)**	0.01 (0.02)	0.01 (0.02)	

Value is significantly different from 0, (estimate – upper 95% CI limit) <= 0.05; Value is significantly different from 0, (estimate – upper 95% CI limit) > 0.05

4.8 The relationship between Brahman content and carcase traits phenotypes

The MSA index predicts meat-eating quality based on several factors. One aspect is an adjustment for hump height as a proxy for tropical breed content, with larger humps impacting the MSA index up to a cap of 120mm hump height. The reasoning is that meat-eating quality is lower for animals with higher tropical breed content. Higher levels of calpastatin have been associated with higher tropical breed content and inhibit calpain activity, which impacts meat tenderisation. This work aimed to investigate the relationship between Brahman content and abattoir carcase traits, in particular with hump height and shear force.

Defining Brahman content

All Repronomics-born animals were genotyped. For this analysis, the estimated percentage of Brahman was considered as a proxy for the *Bos indicus* content. The estimated breed makeup was calculated using a subset of approximately 6,000 SNPs where the breed composition of genotyped Northern BIN steers (MLA projects P.PSH.0743, P.PSH.0774, P.PSH.2131 and P.PSH.2132) (males born from the Repronomics project) was estimated using genomic reference datasets. This work did not look at individual SNPS and their association with the traits (i.e. a GWAS study), and the Brahman content was determined using a relatively small subset of SNPS that are most likely not causative SNPS on the traits analysed. Genotypes had already undergone quality control, and any animal unrelated (defined by a relatedness to the reference QC metric) to the within-breed reference population was excluded before being considered in the current analysis.

Brahman content was available for 1,533 steers with carcase information from the Spyglass and Brian Pastures 2015-2018 cohorts and is recorded in Table 4.8.1. Figure 4.8.1 shows the percentage of Brahman for steers sired by Brahman (BB), Droughtmaster (DM), and Santa Gertrudis (SG) sires. The sum of each breed has to add up to 1, and if a foundation breed is not considered in the genomic reference dataset, the analysis will assign the proportion of that breed to another breed. The percentage of Brahman identified was very high for the Brahman steers; the average Brahman composition was 98.9%, ranging from 87.6% to 100%. Droughtmaster steers had composition mixes dominated by Brahman. On average, they were identified as 57.2% Brahman (between 34.7% and 79.1%). Santa Gertrudis steers, on average, were identified as being 38.9% Brahman (ranging between 27.8% and 50.9%).

Table 4.8.1: Summary of the breed composition for the Brahman, Droughtmaster and Santa Gertrudis Northern BIN steers.

	655 Brahman steers				650 Droughtmaster steers				228 Santa Gertrudis steers			
	Mean	**Std**	**Min**	**Max**	**Mean**	**Std**	**Min**	**Max**	**Mean**	**Std**	**Min**	**Max**
Brahman	0.989	0.019	0.876	1.000	0.572	0.068	0.347	0.791	0.389	0.044	0.278	0.509

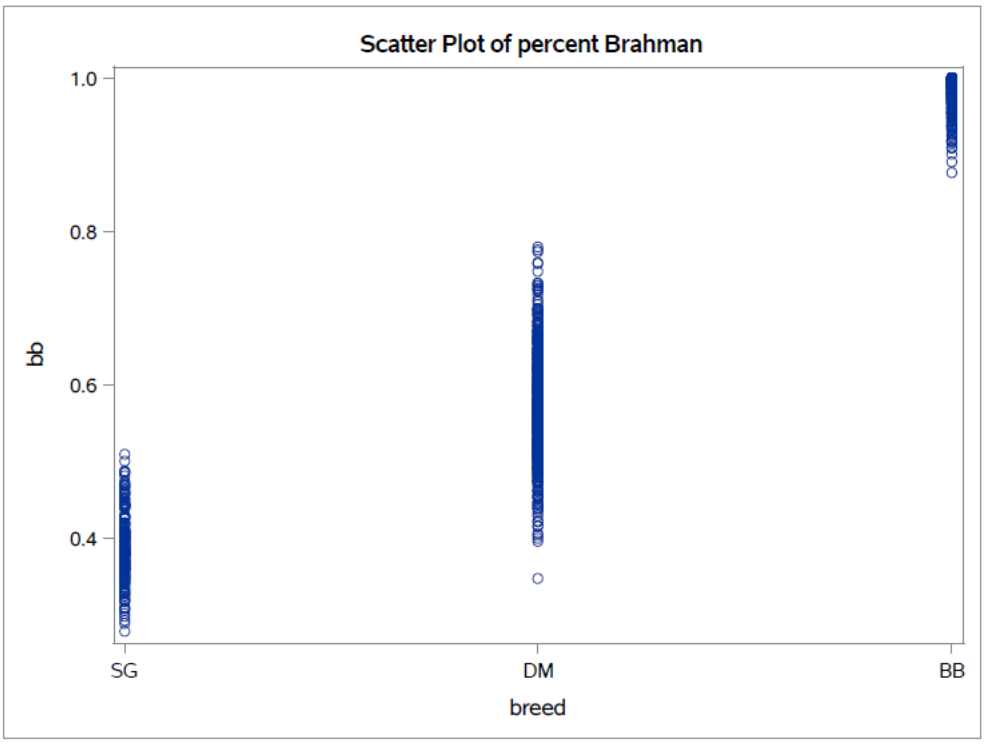


Figure 4.8.1: Percentage of Brahman in the breed composition for Santa Gertrudis (SG), Droughtmaster (DM) and Brahman (BB) Northern BIN steers

Carcase dataset

Carcase data was extracted from the 2013-2018 Spyglass and Brian Pastures 2015-2018 cohorts from the project database. The traits recorded were hot carcase weight (kg), hot P8 fat depth (mm), intramuscular fat percentage, Longissimus dorsi cooking loss%, Longissimus dorsi shear force (kg), Longissimus dorsi a* colour, Longissimus dorsi b* colour, Longissimus dorsi L* colour, Longissimus dorsi ultimate pH, MSA marble score, AUSMEAT marble score, MSA EMA, MSA rib fat at 12/13th rib (mm), MSA hump height (mm), MSA USDA Ossification, MSA Loin Temperature (degrees Centigrade), MSA Ultimate pH, MSA Index, MSA Fat Colour and MSA Meat Colour. Table 4.8.2 summarises the hump height, shear force and MSA index for the cohorts with breed composition results.

Table 4.8.2: Summary of hump height, shear force and MSA index phenotypes within cohort for Brahman, Droughtmaster and Santa Gertrudis steers

	Brahman					Droughtmaster					Santa Gertrudis				
	N	Av	std	Min	Max	N	Av	std	Min	Max	N	Av	std	Min	Max
MSA hump height (mm)															
SP15	98	190.3	34.6	105.0	260.0	107	126.3	13.0	90.0	160.0					
SP16	52	215.9	38.2	110.0	350.0	69	123.1	19.1	95.0	180.0					
SP16X	73	221.2	31.1	145.0	305.0	58	124.4	13.9	100.0	160.0					
SP17	110	146.7	24.8	95.0	240.0	100	106.9	12.9	85.0	145.0					
SP18	106	194.5	39.3	115.0	300.0	127	106.4	14.5	80.0	145.0					
BP15	55	171.2	24.4	130.0	220.0	37	109.9	15.1	85.0	140.0	63	101.5	12.1	70.0	135.0
BP16	50	176.3	21.3	120.0	225.0	53	104.7	12.6	80.0	130.0	65	91.0	11.7	60.0	120.0
BP17	47	152.7	21.0	105.0	195.0	41	105.7	12.6	90.0	135.0	53	89.1	9.8	70.0	115.0
BP18	60	168.7	34.4	115.0	315.0	56	112.1	13.1	85.0	145.0	48	95.2	10.7	65.0	115.0
Longissimus dorsi shear force (kg)															
SP15	98	5.4	1.0	3.2	7.9	107	4.7	1.1	3.0	9.9					
SP16	52	4.9	1.5	3.0	10.2	69	4.6	1.4	2.4	9.5					
SP16X	73	4.6	1.1	2.5	8.4	58	4.3	1.2	1.5	7.7					
SP17	110	5.6	1.3	3.5	9.5	100	4.9	1.4	3.1	9.2					
SP18	106	4.5	1.3	2.9	10.8	127	3.8	1.0	2.3	7.6					
BP15	55	4.7	0.9	3.0	7.3	37	4.2	0.9	2.7	5.9	63	4.2	0.8	2.6	7.0
BP16	50	5.2	0.9	4.0	7.8	53	4.7	1.0	2.5	7.7	65	4.6	0.9	2.7	7.3
BP17	47	5.7	1.3	3.8	8.9	41	5.4	1.5	2.6	9.0	53	4.6	1.1	3.3	7.8
BP18	60	5.0	1.2	3.0	9.0	56	3.9	0.9	2.7	7.4	48	4.3	1.1	3.0	8.1
MSA Index															
SP15	98	48.2	1.2	45.2	51.1	107	48.5	1.4	45.2	53.3					
SP16	52	53.7	1.4	50.7	57.1	69	54.3	1.6	51.6	58.7					
SP16X	73	53.0	1.2	49.9	55.5	58	54.1	1.6	50.7	58.6					
SP17	110	52.8	1.1	50.2	56.1	100	54.5	1.8	50.2	59.1					
SP18	106	53.3	1.2	50.2	56.1	127	55.7	1.8	51.5	60.4					
BP15	55	53.7	1.1	50.9	55.6	37	57.6	0.8	55.7	59.1	63	58.7	1.1	56.2	62.0
BP16	50	54.3	1.3	51.7	58.0	53	57.1	1.7	52.6	60.1	65	59.3	1.8	54.4	64.8
BP17	47	52.2	1.2	50.1	54.5	41	54.5	1.5	50.2	57.5	53	56.9	1.9	51.5	62.2
BP18	60	52.5	1.3	49.4	55.4	56	55.3	1.8	50.9	59.1	48	57.8	1.5	55.2	60.9

Dataset and analysis

The percentage of Brahman was considered a covariate, ranging from 27.8% to 100% for all animals. However, Figure 4.8.1 showed that each breed was not represented across the whole range of the covariate percentage of Brahman. Therefore, breed effects may influence these results. This analysis included a pooled breed dataset with no specific breed term in the model. Sire was not fitted in the model as this was confounded within breeds. A full model was fitted to test if the percentage of Brahman had a significant effect on each carcase trait, and non-significant terms ($P<0.05$) were sequentially removed. The full model considered was;

- cohort (BP15, BP16, BP17, BP18, SP15, SP16, SP16X, SP17, SP18)
- age at slaughter (days, covariate)
- percent Brahman (%, covariate)
- 1st-order interactions

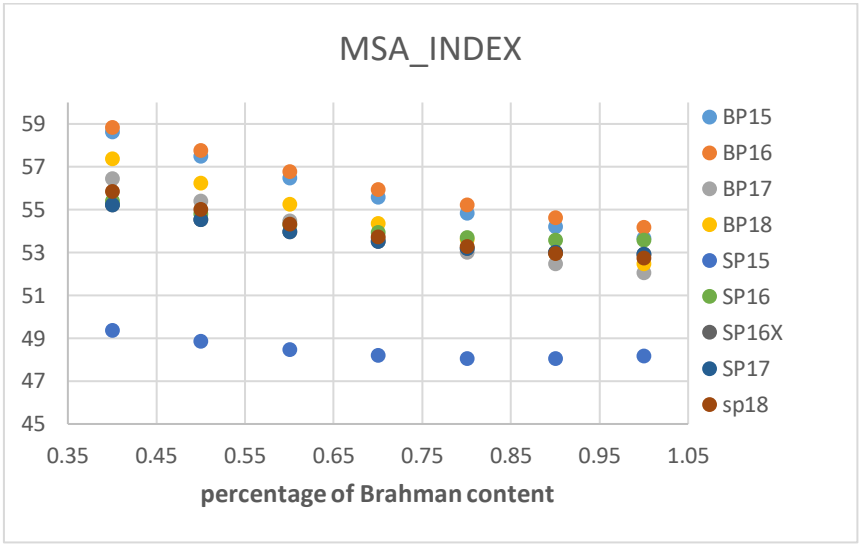
MSA hump height and MSA Index

The significant models for both traits included cohort, percentage of Brahman (linear and quadratic), and the interaction between the percentage of Brahman and cohort. Age at slaughter was also significant for MSA hump height.

Table 4.8.3: The average change in MSA index and hump height based on regression coefficient estimates when the percentage of Brahman content differs by 10% for Northern BIN steers

Impact of a 10% increase in the percentage of Brahman	MSA Index	MSA hump height
40% V 50%	-0.89	8.15
50% V 60%	-0.77	10.77
60% V 70%	-0.64	13.38
70% V 80%	-0.52	16.00
80% V 90%	-0.39	18.61
90% V 100%	-0.27	21.23

The regression coefficient for percentage Brahman from the significant models described above was used to quantify the impact of increasing Brahman content on carcase traits. Table 4.8.3 shows the average change in MSA index and hump height when the percentage of Brahman increases by 10%. For the MSA index, the biggest impact of a 10% increase in the percentage of Brahman was observed for lower Brahman content cattle (Droughtmaster and Santa Gertrudis animals), i.e. the difference between an animal with 40% and 50% percentage of Brahman was a reduction in the MSA Index of 0.89 MSA index units. For hump height, the impact was greatest for animals with larger Brahman content (Brahman). For example, the difference between an animal with 90% and 100% percentage of Brahman was an increase in hump height by 21.23 mm. Figure 4.8.2 illustrates the relationship between the percentage of Brahman and the solutions for MSA index and hump height. While the pattern is similar across cohorts, there are differences in the solutions obtained, with the greatest differences being at 100% Brahman content.



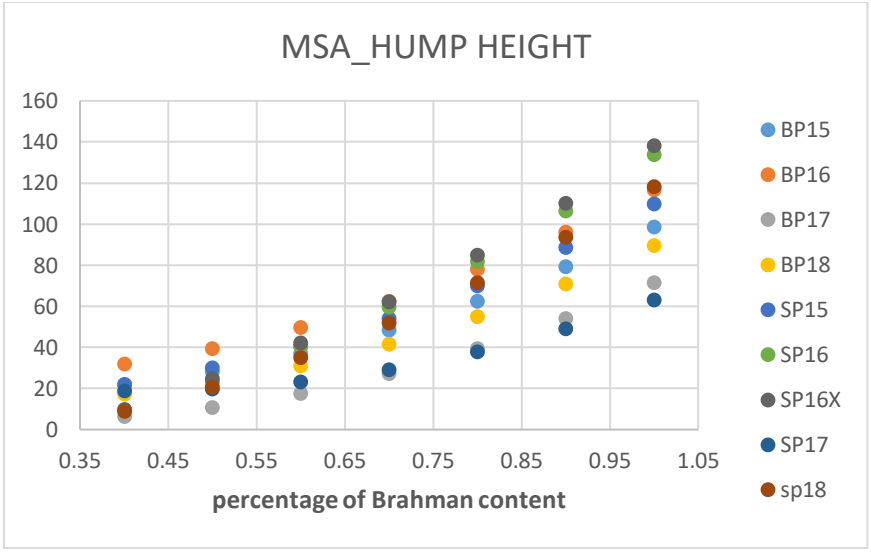


Figure 4.8.2: The relationship between the percentage of Brahman and MSA index and hump height for Northern BIN steers

Shear force

For shear force, only cohort, age at slaughter and percent Brahman were significant, with no interaction between Brahman content and cohort. A 10% increase in the percentage of Brahman resulted in a 0.14 increase in shear force.

Other carcase traits

The majority of the carcase traits were found to have a significant linear effect for the percentage of Brahman, with a significant interaction between the percentage of Brahman and the cohort. For most traits, the significant model was the cohort, age at slaughter, percentage of Brahman and percentage of Brahman X cohort. The exceptions were MQ_LD_a, MSA_pH_U, MSA_Afatcol and MSA_Amarbgn, where age was not significant. Table 4.8.4 shows the impact of a 10% increase in the percentage of Brahman for carcase traits. The effect of the percentage of Brahman varied across cohorts, and the interaction between the percentage of Brahman and cohort illustrates that the impact of breed genotypes varies depending on whether the season is favourable or not. For example, an animal with

low Brahman content may thrive in good seasons, but in more challenging seasons, performance may be affected, and a greater difference between low and high Brahman content animals may be observed. On average, a 10% increase in the percentage of Brahman resulted in a decrease of 2.93, 0.17, 0.86, 0.15, 0.06, 0.63, 0.16, 0.08, 0.01 and 4.50, respectively, for Hot carcase weight, Hot P8 fat depth, MSA EMA, MSA rib fat at 12/13th rib, Intramuscular Fat percentage, MSA USDA Ossification, Longissimus dorsi a* colour, Longissimus dorsi b* colour, MSA Loin Temperature and MSA Aust. Marbling score. Longissimus dorsi cooking loss and Longissimus dorsi L* colour increased by 0.20 and 0.04, respectively. Although there were cohort effects, MSA Ultimate pH and MSA Aust had no effect on average, and in the case of MSA Ultimate pH, showed a narrow range. The cohort X percentage of Brahman interaction for MSA Ultimate pH was significant, however, this was due to only one cohort level being significantly different from zero.

Table 4.8.4: Carcase trait linear solutions for a 10% increase in the percentage of Brahman

	Average across cohort	Minimum	Maximum
H_TotWt	-2.93	-8.49	-0.46
H_P8	-0.17	-0.43	0.28
MSA_EMA	-0.86	-2.04	0.47
MSA_Ribfat	-0.15	-0.47	0.10
MQ_LD_Fat_pct	-0.06	-0.12	0.01
MSA_Uos	-0.63	-3.06	0.46
MQ_LD_LOSS	0.20	0.04	0.53
MQ_LD_a	-0.16	-0.35	0.05
MQ_LD_b	-0.08	-0.18	0.03
MQ_LD_l	0.04	-0.11	0.17
MSA_lointemp	-0.01	-0.11	0.17
MSA_pH_U	0.00	-0.01	0.01
MSA_Afatcol	0.00	-0.13	0.07
MSA_Amarbgn	-4.50	-8.76	0.61

* H_TotWt = Hot Total Weight; H_P8 = Hot P8 fat depth; MSA_EMA = MSA EMA; MSA_Ribfat = MSA rib fat at 12/13th rib; MQ_LD_Fat_pct = Intramuscular Fat percentage; MSA_Uos = MSA USDA Ossification; MQ_LD_LOSS = Longissimus dorsi cooking loss%; MQ_LD_a = Longissimus dorsi a* colour; MQ_LD_b = Longissimus dorsi b* colour; MQ_LD_l = Longissimus dorsi L* colour; MSA_lointemp = MSA Loin Temperature; MSA_pH_U = MSA Ultimate pH; MSA_Afatcol = MSA Aust. Fat Colour; MSA_Amarbgn = MSA Aust. Marbling score;

Conclusion

This study compared Brahman content as defined by a subset of 6,000 SNPS with the abattoir carcase traits of Northern BIN animals. A relationship was observed between Brahman content and hump height, with higher Brahman content animals having higher hump heights. The relationship was not linear, and linear and quadratic regression solutions showed for animals with high Brahman content the increase in hump height was greater than for animals with low Brahman content animals. The relationship between Brahman content and shear force was linear, and showed that as Brahman content increased, the shear force also increased. A relationship was observed between Brahman content and MSA index, with higher Brahman content animals having lower MSA index values. Again, the relationship was not linear, and linear and quadratic regression solutions showed that animals with lower Brahman content had a greater decrease in MSA index as Brahman content increased. On average, it was observed that increasing Brahman content showed a decrease for Hot Total Weight, Hot P8 fat depth, MSA EMA, MSA rib fat at 12/13th rib, Intramuscular Fat percentage, MSA USDA Ossification, Longissimus dorsi a* colour, Longissimus dorsi b* colour, MSA Loin Temperature and

MSA Aust. Marbling score. An increase was observed with increasing Brahman content for Longissimus dorsi cooking loss% and Longissimus dorsi L* colour. These results showed that as Brahman content increased, the meat eating quality decreased, although this study could not assess if the adjustment for hump height in the MSA index was in alignment with these results.

4.9 Analysis of immune competence traits in Northern Australian tropically adapted beef breeds

Immune competence traits have been recorded in Northern BIN steers (MLA projects P.PSH.0743, P.PSH.0774, P.PSH.2131 and P.PSH.2132) at both locations for two cohorts, with a third cohort to be included in the dataset at a later analysis. This analysis considers the 2022 and 2023 cohorts with immune competence data recorded in tropical breeds.

In total, 784 steers were tested for the immune competence traits of cell-mediated and antibody-mediated immune responses. At weaning, immune competence traits, flight time and live weights were recorded. At the time of the analysis, carcase records were unavailable for these cohorts. Both traits were normally distributed, as shown in Figure 4.9.1, but there was an outlier animal (i.e. extremely positive) for cell-mediated immune response, and this animal was removed from the data analysis. Table 4.9.1 summarises the dataset available for analysis. Both immune competence traits show variation, with coefficients of variation of 30 and 19%, respectively, for cell and antibody-mediated response.

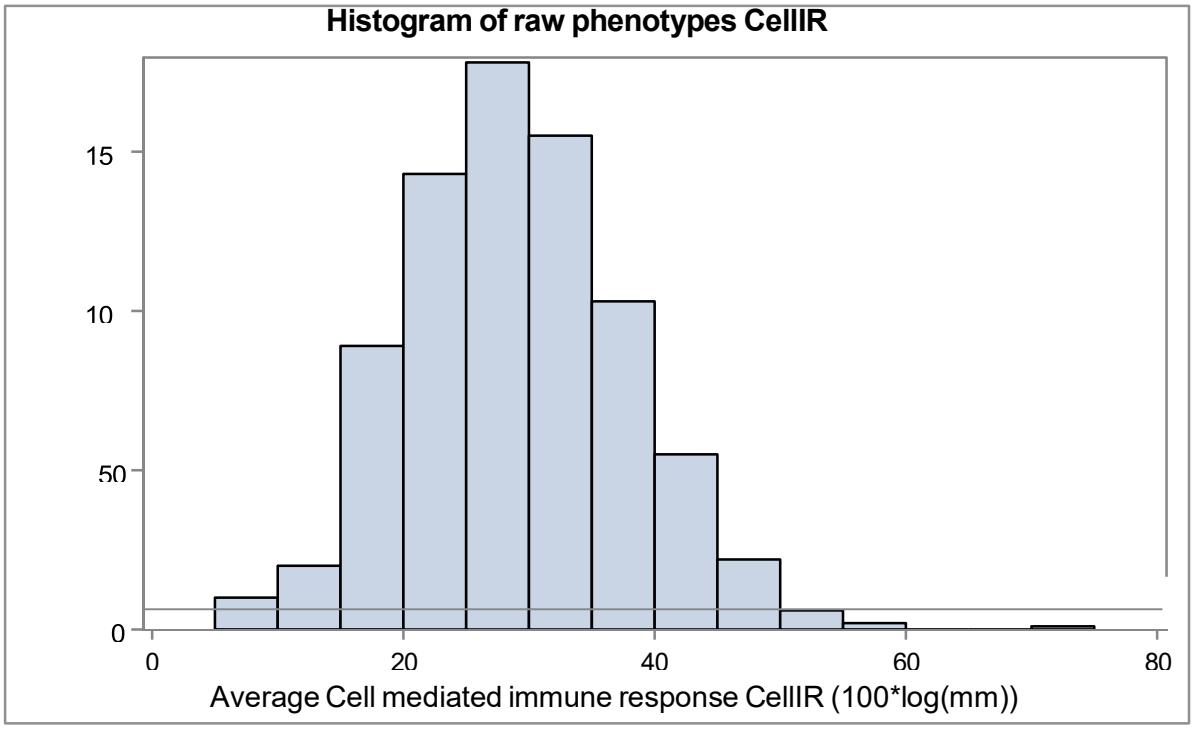
Description of immune competence traits

The cell-mediated immune response is a delayed-type hypersensitivity reaction recorded by measuring skin thickness under the tail when a small amount of commercially available 7-1 vaccine is injected into a test site, and saline is injected into a control site. The cell-mediated immune response was the log of the test site skin thickness divided by the control site skin thickness, measured two days after the injections. The cell-mediated immune response test was undertaken 14 days after the animal was vaccinated in the neck with the 7-1 vaccine.

The antibody-mediated immune response tested the blood antibody levels for tetanus and was recorded in optical density values. The blood sample was taken 14 or 16 days after the 7-1 vaccine was injected into the neck of the animal.

Table 4.9.1: Data summary of 2022 and 2023 cohorts for immune competence data recorded in three tropical beef breeds

	N	Mean	Std	Min	Max	CV%
Flight speed at day 12 (s)	783	0.75	0.25	0.34	2.60	33.3
Flight speed at day 14 (s)	773	0.66	0.21	0.34	2.06	31.8
Weight at day 0 (kg)	782	212.51	33.05	118.0	316	15.6
Weight at day 12 (kg)	783	221.09	33.83	121.5	336	15.3
Weight at day 14 (kg)	782	222.35	35.12	127.0	338	15.8
Skin thickness CST (log(mm))	783	-0.003	0.03	-0.11	0.09	
Cell-mediated immune response (100*log(mm))	783	28.93	8.61	5.65	55.22	29.8
Antibody-mediated immune response (100*OD units)	783	90.61	17.02	22.77	127.67	18.8



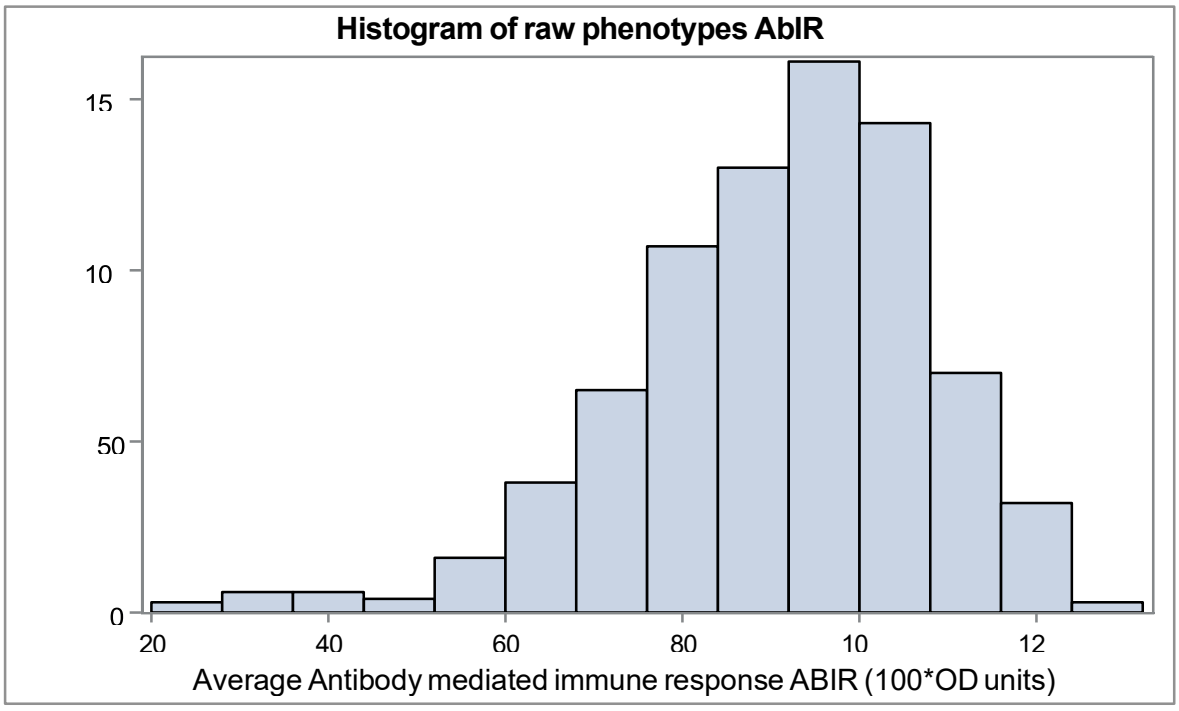


Figure 4.9.1: Histogram of raw immune competence traits recorded in tropically adapted beef breeds

Statistical Models and least squares means

Fixed effects were tested for significance using PROC MIXED in SAS with sire fitted as random. The initial models included effects for: age at weaning, weight at weaning, cohort (4 levels), sire breed (3 levels) and baseline skin thickness. Cow origin was not considered, as most cows were of the same origin, and those that were not were confounded with dam age (i.e. only older cows were from different origins). Data structure meant that dam age could not be fitted, with 5-year-old and older cows being mated by AI sires and 3- and 4-year-old dams naturally mated; therefore, the number of sires in common was limited.

The model considered age and weight effects separately and resulted in similar results. Weight-adjusted models are reported, but the most appropriate covariate of age or weight-adjustment should be determined when the larger dataset is available.

The final models were:

Cell-mediated immune response = sire breed + birth cohort + weaning weight + baseline skin thickness
Antibody-mediated immune response = sire breed + birth cohort

Least squares means for breed indicated that Santa Gertrudis animals had the highest immune responses for both traits, and Droughtmaster animals had the lowest. Brahman animals were not significantly different from Droughtmaster for cell-mediated immune response and were not significantly different from Santa Gertrudis for antibody-mediated immune response. Cohorts from Brian Pastures and Spyglass tended not to be significantly different within year groups, but there were significant year (season) effects observed, with animals born in the #22 cohort having higher responses than animals born in the #23 cohort.

Table 4.9.2: Least squares means for sire breed and cohort; subscripts indicate significant differences

Sire breed	Cell-mediated LSM	Antibody-mediated LSM
BBBB	28.35 ^{b} (0.59)	94.12 ^{a} (1.20)
DMDM	26.95^{b} (0.62)	86.48 ^{b} (1.28)
SGSG	35.51^{a} (0.94)	91.92 ^{ab} (1.93)
Cohort	**Cell-mediated LSM**	**Antibody-mediated LSM**
BP22	32.69 ^{a} (0.82)	93.92 ^{a} (1.60)
SP22	32.25 ^{a} (0.80)	91.52 ^{ac} (1.66)
BP23	28.72 ^{b} (0.75)	87.72 ^{b} (1.53)
SP23	28.79 ^{b} (0.72)	88.87 ^{bc} (1.44)

The covariates, baseline skin thickness and weight at weaning, were significant for cell-mediated immune response. The solutions for these covariates indicate a difference in cell-mediated immune response of approximately 0.7 standard deviations between animals at the extreme of the baseline skin thickness and approximately 0.8 standard deviations between animals with a 150kg weight difference.

Preliminary variance component estimates: Both traits were estimated to be heritable. Although the dataset was small when considering the cohort years as separate traits, the genetic correlations across years were strong (r_g=0.67 (0.57) for cell-mediated immune response and 0.50 (0.38) for antibody-mediated immune response), indicating that the traits were repeatable across years.

Table 4.9.3: preliminary variance component estimates

	Va	Ve	Vp	h^2	95% CI of h^2
Cell IR	11.17	51.87	63.03	0.18 (0.09)	0.00 to 0.36
Ab IR	62.20	214.71	276.91	0.22 (0.09)	0.04 to 0.40

Phenotypic and genetic correlations were estimated between the immune traits and flight time, with the statistical model for flight time fitting sire breed, birth cohort and weaning weight. The phenotypic correlation was low and not significantly different from 0 for both cell- and antibody-mediated immune responses. This was also the case for the genetic correlation between flight time and cell-mediated immune response (r_g=0.05 (0.30)), but a negative genetic correlation (r_g=-0.24 (0.27)) was estimated with the antibody-mediated immune response, indicating that animals that were high responders for the tetanus antibody were genetically the flightier animals albeit with a very large standard error. This is the opposite of what was reported in Angus.

Preliminary EBVs for immune competence: EBVs were produced for 3,263 animals from univariate models. Animals were either recorded themselves or were in the 3-generation pedigree of recorded animals. A Pearson correlation between the cell and antibody-mediated immune response EBVs for 80 sires with progeny recorded for immune competence was low (r=0.08), suggesting that the two immune traits describe different traits. As breed was fitted in the model, EBVs were adjusted for breed effects. However, each breed showed within-breed variation. The following plots show the EBVs for 80 sires by breed. It can be seen that for each breed, there is a highly negative sire. Investigation into these sires demonstrated that their progeny had low immune response phenotypes, and the ranking appears correct, including a large gap between the bottom two sires.

Conclusions: This study has shown that the cell- and antibody-mediated immune response traits are heritable in these tropically adapted breeds, with variation indicating that genetic selection would be possible for these traits. However, at this stage, more must be understood about the trait before it can be considered an additional trait for genetic evaluation, i.e., the antibody-mediated immune response tests for the tetanus antibody level after vaccination. Does this extrapolate to the other diseases in the vaccine and general diseases not vaccinated for? Ultimately, the value of these traits to beef production will be if it can be shown that selection for high responders in the immune traits translates to improved production and health outcomes and that recording immune traits is more viable than recording the actual traits themselves. Currently, carcase data is not yet available for these cohorts, and health traits are difficult to record, so the value of these traits cannot yet be considered. Late-in-life and survival traits are still being recorded and, once available, will be analysed to determine genetic links to immune competence phenotypes.

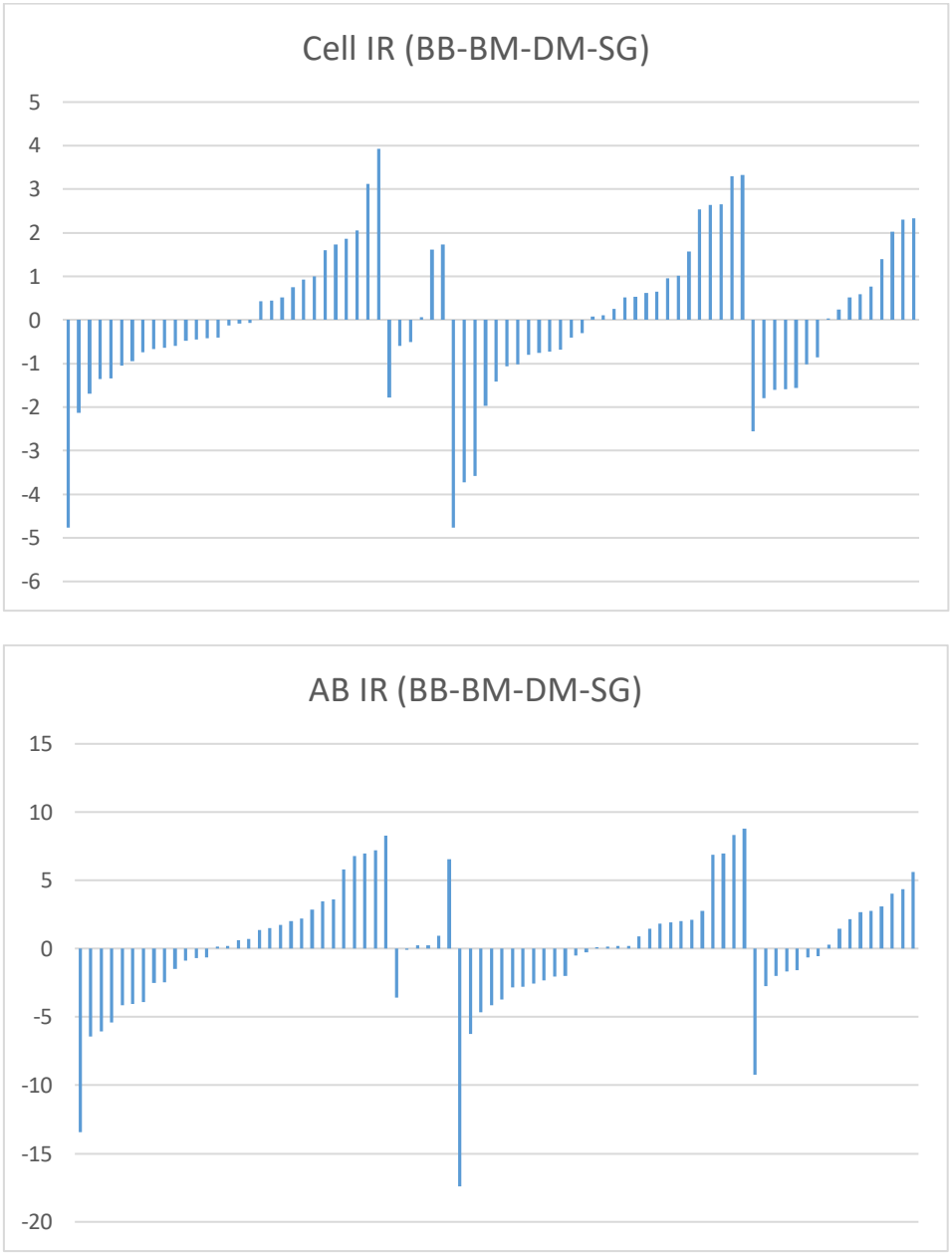


Figure 4.9.2: Cell and antibody-mediated immune response within breed EBVs for 80 sires

4.10 The potential of CSIRO eGrazor collars and Ceres ear tags to record pasture feed intake

Background

CSIRO research investigated whether sensor technologies could record individual feed intake of animals at pasture (Greenwood et al., 2017). The study was undertaken on Angus animals over pasture strips where the grazed pasture was monitored, and the sensor data from eGrazor collars were analysed. As a result, CSIRO developed a prediction equation converting the grazing time recorded

from eGrazor collars to a pasture DMI (kg DM/head/day). An example DMI prediction equation from this work was

Pasture intake (kg DM/head/d) = –4.13 + 2.325 x grazing (hours)

This research culminated in two products: the CSIRO eGrazor collar, which has been used for research but is not widely available, and the Ceres ear tag, which is available in the Australian marketplace.

Aim

The current work aimed to assess sensor technologies on Northern beef cattle and the ability to record grazing time as a proxy for DMI and determine whether there is a relationship with daily feed intake in the feedlot.

Summary of datasets

This study utilised Spyglass 2022-2023 and Brian Pasture 2023 cohorts. Below is an overview of the records collected for each cohort.

Spyglass 2022: 60 steers (27 Brahman and 29 Droughtmaster)

- CSIRO eGrazor collars were fitted at pasture between 22nd November 2022 and 18th December 2022 (on cattle recorded at Gatton)
- Feed intake in the feedlot at Gatton was recorded between 31st January 2023 and 30th May 2023

Spyglass 2023: 92 Brahman steers located at Warraka and 46 steers located at Darbalara (27 Brahman and 29 Droughtmaster); 60 steers (30 Brahman and 30 Droughtmaster) were located at Gatton for feed intake and CSIRO eGrazor collar data.

- CSIRO eGrazor collars were fitted at pasture between 20th November 2023 and 17th December 2023 (on cattle recorded at Gatton)
- Ceres ear tags were recording 7th March 2024 to 10th July (with an interim weight recorded on 15th April) at Warraka
- Feed intake in the feedlot at Gatton was recorded between 14th February 2024 and 23rd April 2024
- Note, animals with the Ceres ear tags were not the same animals recorded at Gatton for CSIRO eGrazor collars and feedlot feed intake

Brian Pastures 2023: 186 steers (64 Brahman, 49 Droughtmaster and 73 Santa Gertrudis)

- Ceres ear tags were recording 11th July 2024 to 7th November (with an interim weight recorded on 27th August)
- This cohort had no subset recorded for feed intake at Gatton or CSIRO eGrazor collars, which was only recorded at Gatton due to animal monitoring requirements.

CSIRO eGrazor collar data

Two Spyglass cohorts were recorded with CSIRO eGrazor collars. SP22 recorded 56 steers and SP23 60 steers. CSIRO provided data after editing out non-valid days (i.e., lost collars) and adjusting the algorithms to classify the behaviour of tropically adapted beef breeds. Each cohort had 27 days of

data, and weight was recorded at the start and end. SP22 steers gained, on average, 22.2kg over the period but ranged between 5 and 35kg. SP23 steers gained, on average, 30.7kg over the period but ranged between 17 and 41kg. The lower weight gain observed for SP22 has been attributed to a poorer season.

SP22 steers averaged (range) 8.8 (7.7-10.2) hours a day grazing, 7.2 (5.7-8.2) hours a day ruminating, 1.1 (0.8-1.4) hours a day walking and 5.6 (4.6-7.3) hours a day resting. SP23 steers averaged (range) 8.9 (7.1-10.6) hours a day grazing, 7.3 (5.9-8.3) hours a day ruminating, 0.8 (0.4-1.9) hours a day walking and 5.4 (4.1-8.3) hours a day resting.

Table 4.10.1: Summary of the CSIRO eGrazor collar data for Spyglass 22 and 23 cohort steers

	SP22 (n=56)				SP23 (n=60)			
All data	**average**	**std**	**min**	**max**	**average**	**std**	**min**	**max**
Weight gain kg (over 4 weeks)	22.2	7.0	5	35	30.7	6.0	17	41
Average grazing time hrs	8.8	0.5	7.7	10.2	8.9	0.8	7.1	10.6
Average rumination time hrs	7.2	0.5	5.7	8.2	7.3	0.6	5.9	8.3
Average walking time hrs	1.1	0.1	0.8	1.4	0.8	0.3	0.4	1.9
Average resting time hrs	5.6	0.5	4.6	7.3	5.4	0.7	4.1	8.3
Brahman subset								
Weight gain kg (over 4 weeks)	21.6	6.1	8	34	29.2	6.1	17	41
Average grazing time hrs	8.8	0.4	7.9	9.7	8.7	0.7	7.1	10.3
Average rumination time hrs	7.2	0.4	6.4	8.0	7.6	0.5	6.7	8.3
Average walking time hrs	1.2	0.1	0.9	1.4	0.8	0.3	0.5	1.9
Average resting time hrs	5.6	0.5	4.7	6.5	5.4	0.6	4.2	6.9
Droughtmaster subset								
Weight gain kg (over 4 weeks)	22.7	7.9	5	35	32.2	5.6	23	41
Average grazing time hrs	8.7	0.6	7.7	10.2	9.0	0.8	7.1	10.6
Average rumination time hrs	7.1	0.6	5.7	8.2	7.1	0.6	5.9	8.0
Average walking time hrs	1.1	0.1	0.8	1.3	0.8	0.4	0.4	1.8
Average resting time hrs	5.7	0.6	4.6	7.3	5.5	0.8	4.1	8.3

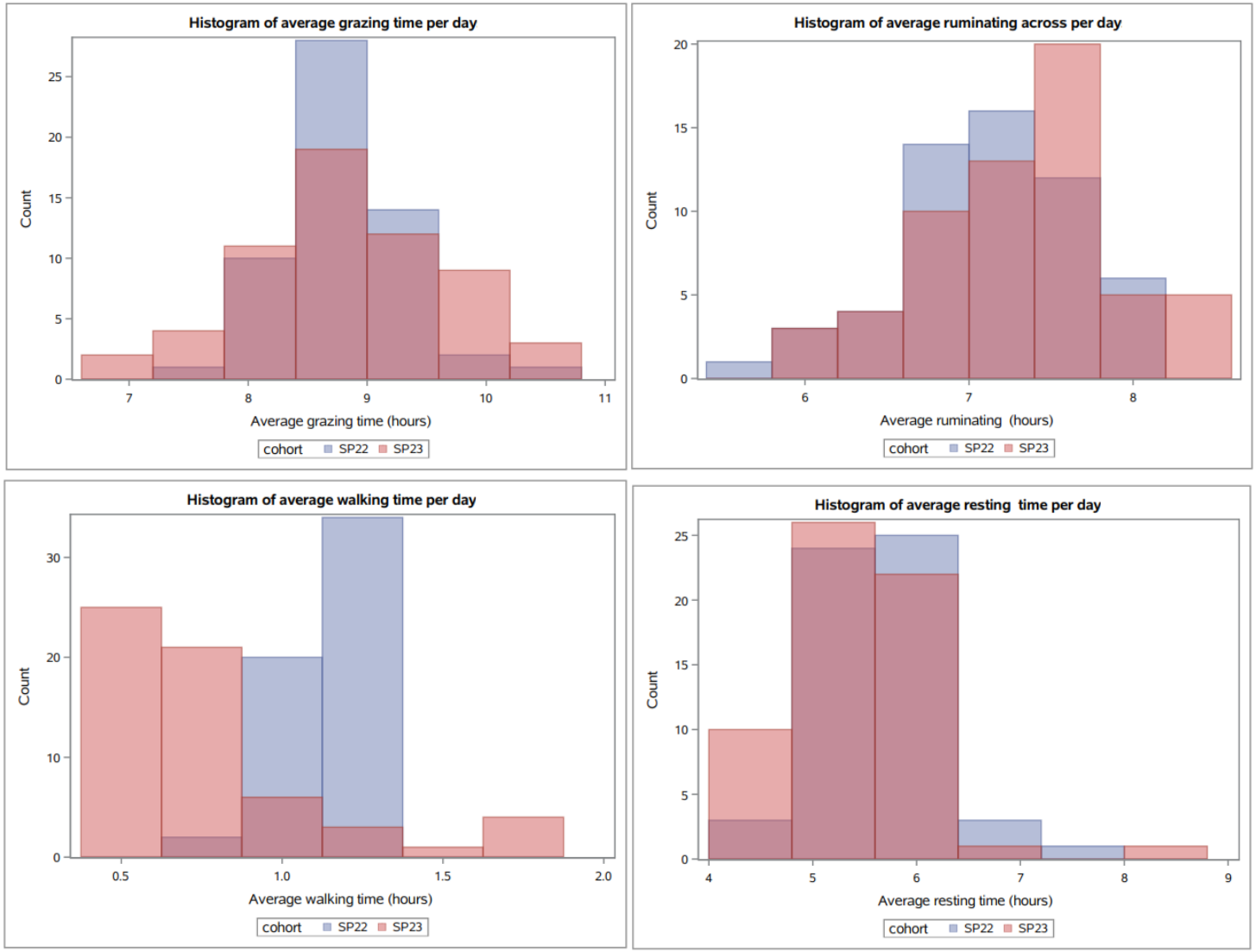


Figure 4.10.1: Histograms of animal behaviour recorded at pasture with the CSIRO eGrazor collars for Northern beef breeds

The distributions were similar across cohorts and breeds. The SP23 data show more variation, but grazing time was normally distributed. Figure 4.10.1 shows the distribution of each behaviour category. Grazing and rumination appear normally distributed, although there were large 'steps' in the rumination distribution for both cohorts. Walking and resting behaviours tended to have flatter profiles.

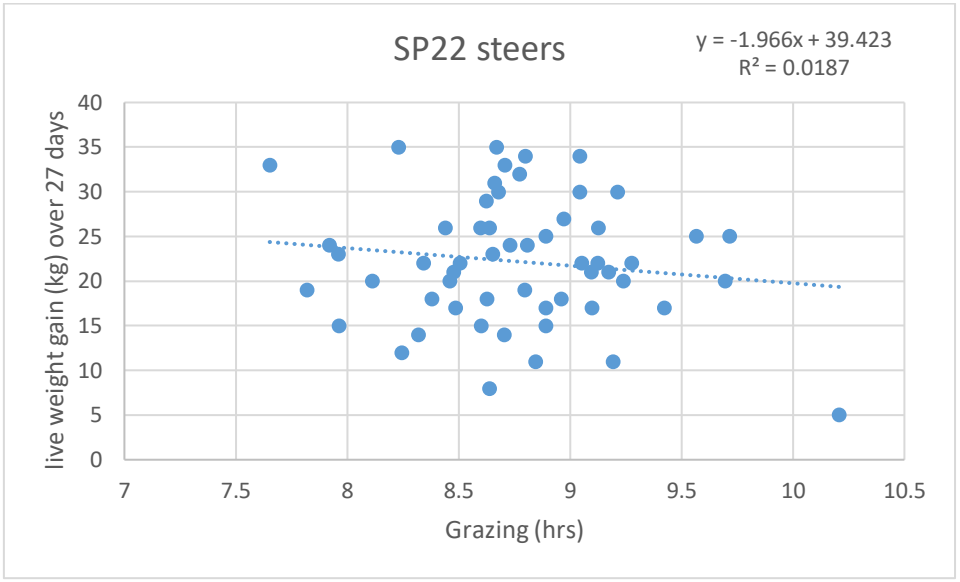
Pearson correlations between the pasture behaviours are shown below for both cohorts (Table 4.10.2). Both cohorts showed that as steers grazed longer, they spent less time ruminating, walking, and resting. The correlation with the weight gain over the month varied, with SP22 having a small negative relationship and SP23 having a moderate positive relationship. The positive relationship is more in line with the expectation that animals will grow more if they eat more. The direction and size of the correlations between traits also varied between the two cohorts.

Table 4.10.2: Pearson correlations between the pasture-recorded behaviour traits

	SP22				SP23			
	rumination	**walking**	**resting**	**wt gain**	**rumination**	**walking**	**resting**	**wt gain**
grazing	-0.42*	-0.44*	-0.25	-0.14	-0.22	-0.27*	-0.34*	0.36*
rumination		-0.13	-0.63*	0.24		0.16	-0.52*	-0.20
walking			0.24	-0.04			-0.33*	0.03
resting				-0.32*				-0.09

* indicates P<0.05 that the correlation is different from 0

Figure 4.10.2 shows the grazing time data versus the weight gain over the 1-month test. No relationship was observed for the SP22 steers, but a positive relationship can be seen in the SP23 data. There was a big difference in starting weights and weight gain between cohorts; on average, the SP22 steer weight gain was 8.5kg less than SP23. The grazing times were similar across cohorts, but there were likely factors other than grazing time that resulted in growth differences. Several factors, including grazing time, bite rate, mouth fill and pasture characteristics, determine feed intake. Previous research has indicated that grazing time accounts for 60% of the variation in intake (Greenwood et al. 2017, Charmley et al. 2023). Pasture quality is variable, but a feedlot diet is more standardised.



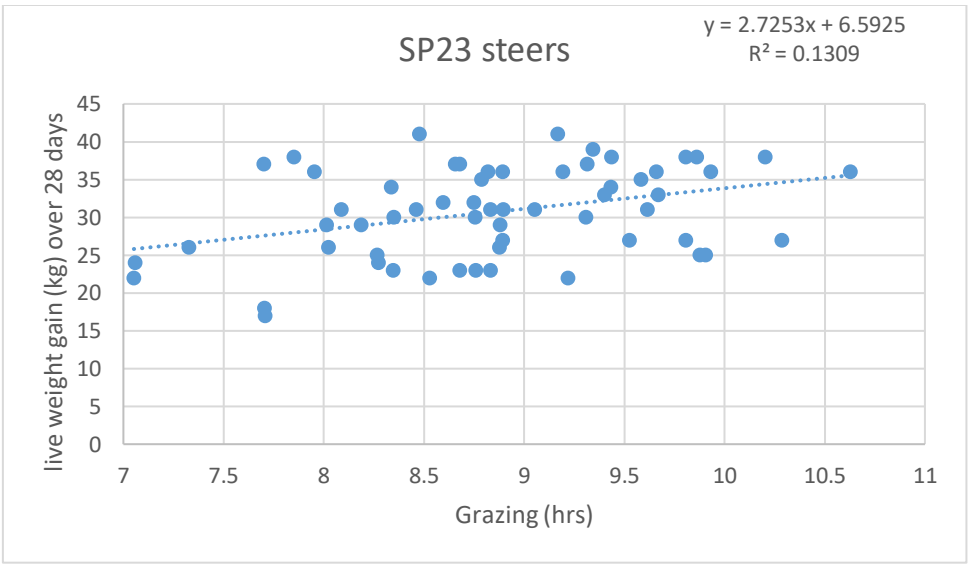


Figure 4.10.2: Relationship between grazing time and weight gain at pasture over the one-month period during which animals were recorded with the CSIRO eGrazor collars for Northern beef breeds

Relationship with feedlot DFI

Animals with CSIRO eGrazor collar data were also recorded for daily feed intake in the feedlot (Table 4.10.3). The 2022 Spyglass steers were at Gatton in the feedlot between 31st January 2023 and 30th May 2023, with a feed intake test undertaken between 14th March and 23rd May. This was approximately three months after the pasture eGrazor collar measurements were recorded. One steer was removed from the trial early, resulting in 59 steers with a DFI record. Animals consumed 10.7 kg/day on average but ranged from 8.4 to 13.2 kg/day. Although not a proper breed comparison, both breeds were similar, with Droughtmaster slightly (0.5 kg/day) consuming more than Brahman and gaining, on average, 4.5kg more during the test period.

The 2023 Spyglass steers were tested for feed intake at Gatton between 14 February and 23 April, approximately two months after the pasture eGrazor collar measurements were recorded. Two steers were removed from the trial early, resulting in 58 steers with a DFI record. Animals consumed 11.4 kg/day on average but ranged from 9.5 to 14.3 kg/day. Both breeds were similar, with Droughtmaster consuming more (1.0 kg/day) than Brahman and gaining, on average, 9.0 kg more during the test period.

Table 4.10.3: Summary of the feed intake data at the feedlot for Spyglass 22 and 23 cohort steers

	SP22 (n=59)				SP23 (n=58)			
	average	**std**	**min**	**max**	**average**	**std**	**min**	**max**
All data								
Start weight (kg)	393.1	31.7	314	467	303.6	28.0	242	362
End weight (kg)	500.5	42.8	405	603	405.9	33.8	327	466
Test weight gain (kg)	107.5	15.9	68	139	102.3	13.0	78	132
ADG (kg/day)	1.53	0.23	0.98	1.99	1.48	0.19	1.13	1.91
DFI (kg/day)	10.73	1.17	8.38	13.23	11.43	1.18	9.45	14.33
Brahman subset								
Start weight (kg)	389.4	32.4	314	448	294.2	27.3	242	339
End weight (kg)	494.7	45.2	405	565	392.1	32.4	327	452
Test weight gain (kg)	105.3	16.5	68	135	97.8	11.3	78	124
ADG (kg/day)	1.50	0.24	0.97	1.93	1.42	0.16	1.13	1.80
DFI (kg/day)	10.50	1.15	8.38	13.11	10.93	0.73	9.67	12.45
Droughtmaster subset								
Start weight (kg)	396.9	31.0	351	467	312.9	25.9	258	362
End weight (kg)	506.6	40.0	451	603	419.7	29.7	371	466
Test weight gain (kg)	109.8	15.3	85	139	106.8	13.2	84	132
ADG (kg/day)	1.57	0.22	1.21	1.99	1.55	0.19	1.22	1.91
DFI (kg/day)	10.98	1.15	9.14	13.23	11.92	1.35	9.45	14.33

55 SP22 and 58 SP23 steers had pasture collar and feed intake data. Pearson correlations (Table 4.10.4) between the traits varied across the cohorts. DFI was strongly related to weight gain and growth in SP22 (r=0.79) but only moderately correlated in SP23 (r=0.40). The weight gain from the pasture period did not show a relationship with the weight gain in the feed lot.

Table 4.10.4: Pearson correlations between the pasture activity and feedlot DFI intake

	SP22 feedlot		SP23 feedlot	
	DFI	**ADG**	**DFI**	**ADG**
	Pasture traits			
grazing	0.20	0.16	0.08	0.15
rumination	0.03	0.11	0.09	-0.10
walking	-0.34*	-0.32*	0.07	-0.15
resting	-0.02	-0.06	-0.10	-0.05
wt gain	0.01	0.08	-0.04	0.08
	Feedlot traits			
DFI		0.79*		0.40*

* indicates P<0.05 that the correlation is different from 0

The correlation between pasture grazing time and DFI measured in the feedlot was weak for both cohorts: r=0.20 and 0.08, respectively, for SP22 and SP23. The relationship between DFI and rumination or resting was minimal in both cohorts. In SP22, the strongest correlation to feedlot DFI was with walking, r=-0.34, but this relationship was not observed in SP23.

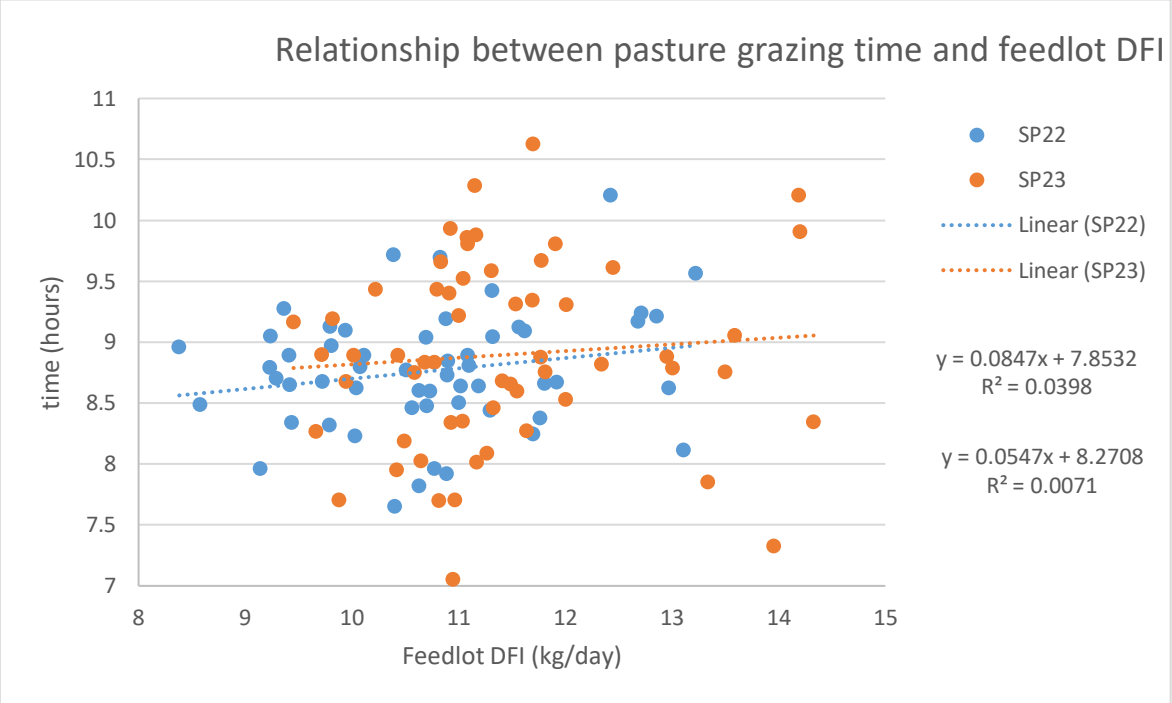


Figure 4.10.3: Relationship between CSIRO eGrazor grazing time at pasture and feedlot daily feed intake for Northern beef breeds

Discussion and Conclusion: Over two cohorts, 117 Brahman and Droughtmaster steers were recorded for both the CSIRO eGrazor collar and feedlot daily feed intake. The eGrazor collar data recorded daily behaviours that were within the expected ranges. Animals in this study were reported to graze approximately 9 hours a day, ranging from 7 to 11 hours a day. This is slightly higher than other studies, but with the eGrazor collars, the behaviour was recorded 24 hours a day. In the original research establishing the link between grazing time and DMI, the average grazing time on 10 Angus steers in individual plots was 6.7 hours, ranging from 5.3 to 7.7 hours (Greenwood et al. 2017). Kilgour et al. 2012 reported from a study involving five herds of beef cattle that cattle at pasture grazed 6.1 hours a day (range 5-7.3 hours) during the daylight observation period. In the same study, animals rested/ruminated for 7.6 hours and walked for 3.3 hours. Their study did not record behaviour during night-time. The grazing time was particularly interesting as it underpins the prediction equation for dry matter intake at pasture developed by CSIRO, and has been shown to account for 60% of the pasture feed intake of animals. Many factors, including pasture quality, paddock size and terrain, stocking rate, weather, and day length, will likely impact animal grazing behaviour. Despite different seasons and average daily gains, both cohorts recorded similar grazing times.

Although the numbers in this study were small, the pasture grazing time and feedlot DFI were poorly related, indicating that in the Brahman and Droughtmaster animals of this study, the pasture grazing time (as a proxy for pasture feed intake) had no relationship with feedlot DFI. This is perhaps not

unexpected, as the behaviour of animals at pasture and in the feedlot is likely to be different. There was also a two to three-month gap between recording animals at pasture and in the feedlot. The feeding behaviours of animals on pasture and in the feedlot may vary as they are in very different environments, which may impact their DFI. Because feed intake at pasture is difficult to record, the relationship between intake at pasture and the feedlot is unknown. While the two traits are likely to be different, it is reasonable to consider that there may be a relationship between intake at pasture and in the feedlot. Personal communication with CSIRO (Aaron Ingham, 2025) showed that the feedlot behaviour profile of animals in the feedlot differs from those at pasture, with feedlot animals reported to graze/feed for 5 hours, ruminate for 9 hours, rest for 8 hours, walk for 0.5 hours and other behaviours for 1.5 hours a day.

Ceres ear tag data

Two cohorts were recorded for behaviour using the commercially available Ceres ear tag (www.cerestag.com), which is based on the technology developed for the eGrazor collars. The SP23 and BP23 steer cohorts were fitted with the Ceres ear tags.

SP23 was recorded between 7 March 2024 and 10 July, with interim weights recorded on 15 April. BP23 was recorded between 11 July 2024 and 7 November, with interim weights recorded on 27 August.

In total, 136 and 144 SP23 and BP23 animals were tagged, respectively, and daily behaviours were recorded. The tag's algorithms are based on those developed for the CSIRO eGrazor collars. Tag data was downloaded approximately every 24 hours, and the time spent grazing, resting/rumination, walking, and drinking/other activities was recorded. There were 14,245 and 16,133 data points for SP23 and BP23 cohorts, respectively, and individuals had, on average, 105 and 112 data points (days) recorded for SP23 and BP23. The number of data points per animal ranged from 1 to 130, as some tags malfunctioned and/or were replaced. Data from 30 tags were removed where the number of data points was <70.

Tag data was downloaded approximately every 24 hours, and the time between data downloads was calculated as the time between a data point and the previous data point.

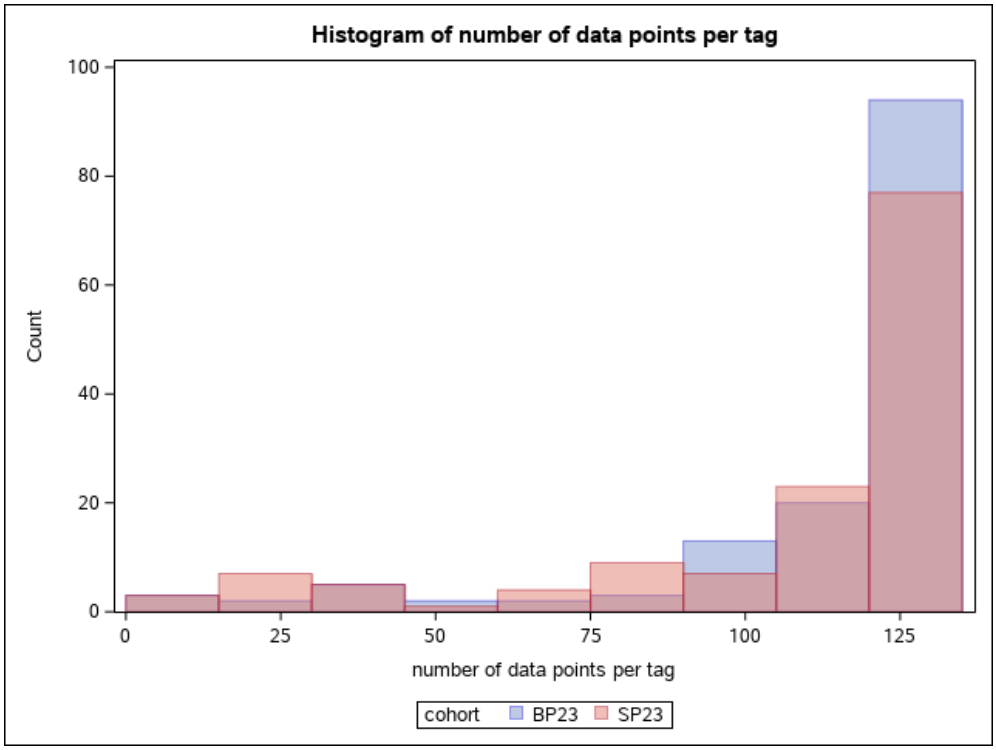


Figure 4.10.4: Histograms of the number of data points for animals recorded at pasture with the Ceres ear tags for Northern beef breeds

Tag data was downloaded approximately every 24 hours, and the time between data downloads was calculated as the time between a data point and the previous data point. Table 4.10.5 summarises the time between data downloads for records that captured between 1 and 50 hours of data.

Table 4.10.5: Average time between data uploads from the ear tag in a dataset filtered to include only records where the time ranged from 1 to 50 hours

Cohort	Total N datapoints	N datapoints with a previous datapoint between 1 and 50 hours	Avg	Std	Min	Max
All	28,357	27,841	24.6	4.3	1.3	50.0
SP23	13,780	13,527	24.7	4.5	1.3	50.0
BP23	14,577	14,314	24.5	4.0	2.0	49.9

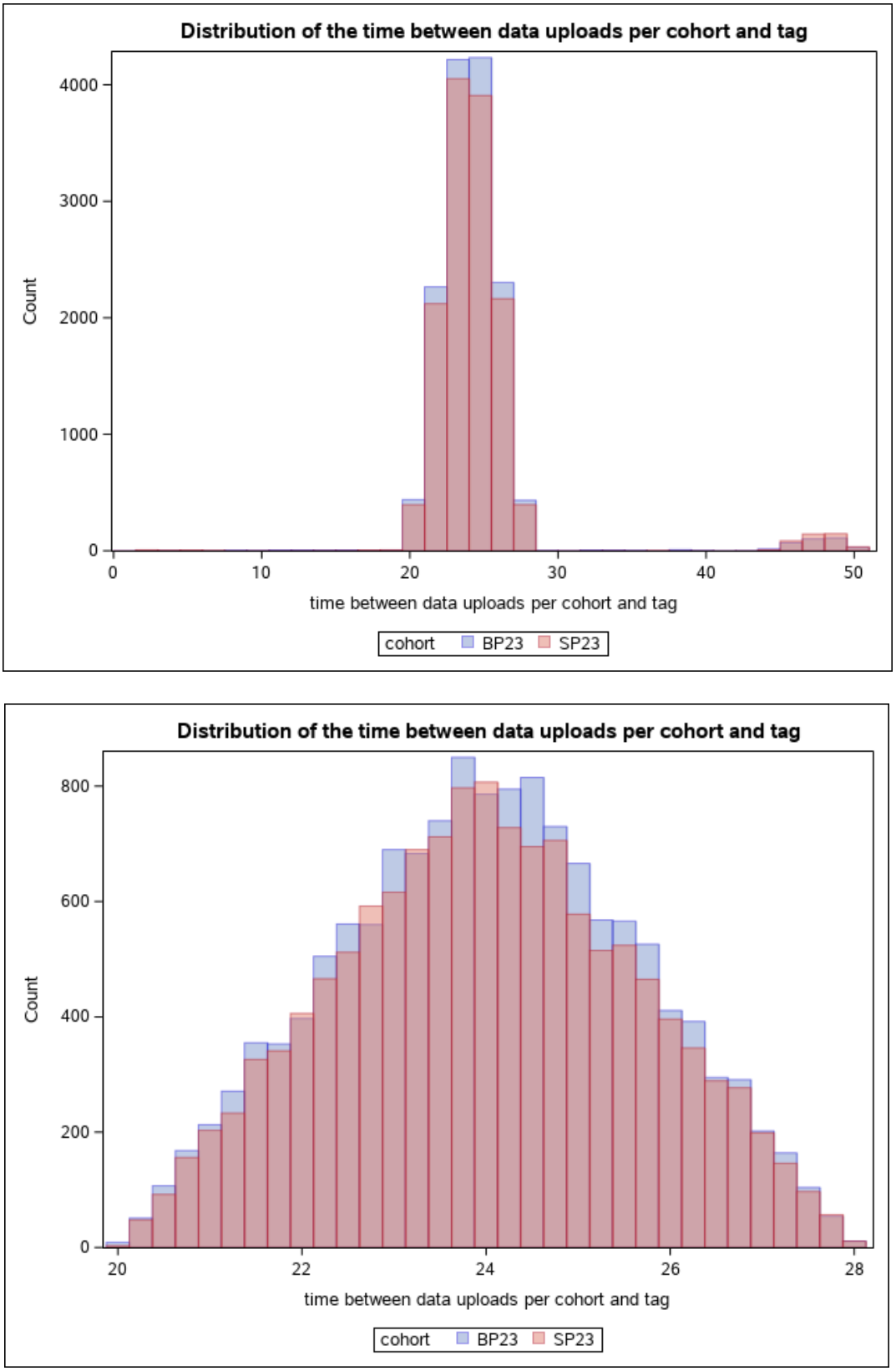


Figure 4.10.5: Histograms of the time between data uploads for all (top) animals and those within the 20-28 hour window (bottom) recorded at pasture with the Ceres ear tags for Northern beef breeds

Where the time between data uploads was restricted to between 20 and 28 hours, there were 26,918 (94.9%) data points with an average (standard deviation) of 24.0 (1.6) hours between data uploads.

Considering the records where the previous data point was recorded between 20 and 28 hours earlier, the total activity time recorded by the tag averaged 16.7 hrs per animal. However, Figure 4.10.6 shows that both cohorts had records of zero activity. For BP23, there were many records where animals spent precisely 24 hours resting/ruminating. Even after removing these erroneous records, the total time captured was less than the recording period, and there remained a large number of 24-hour captures, but only for BP23, which was unusual. On average, 6.8 hours of data were lost per record, ranging from an additional 3.9 hours to all 27.7 hrs being lost. Looking at the dataset, it appeared most data uploads occurred late afternoon at approximately 5 pm. It is unknown if the 5 pm to 12 pm data is lost or if the missing data occurred randomly across the recording period.

Table 4.10.6: The total activity time (hrs) recorded by Ceres ear tags for records where the previous tag read was 20 to 28 hours earlier.

	Before edit					After editing extremes				
	N	Avg	Std	Min	Max	N	Avg	Std	Min	Max
All	26,918	16.7	4.1	0	24.2	25,975	17.2	2.84	0.01	24.2
SP23	13,029	16.6	3.6	0	21.5	12,778	16.9	2.8	0.01	21.5
BP23	13,889	16.8	4.5	0	24.2	13,197	17.5	2.9	0.02	24.2

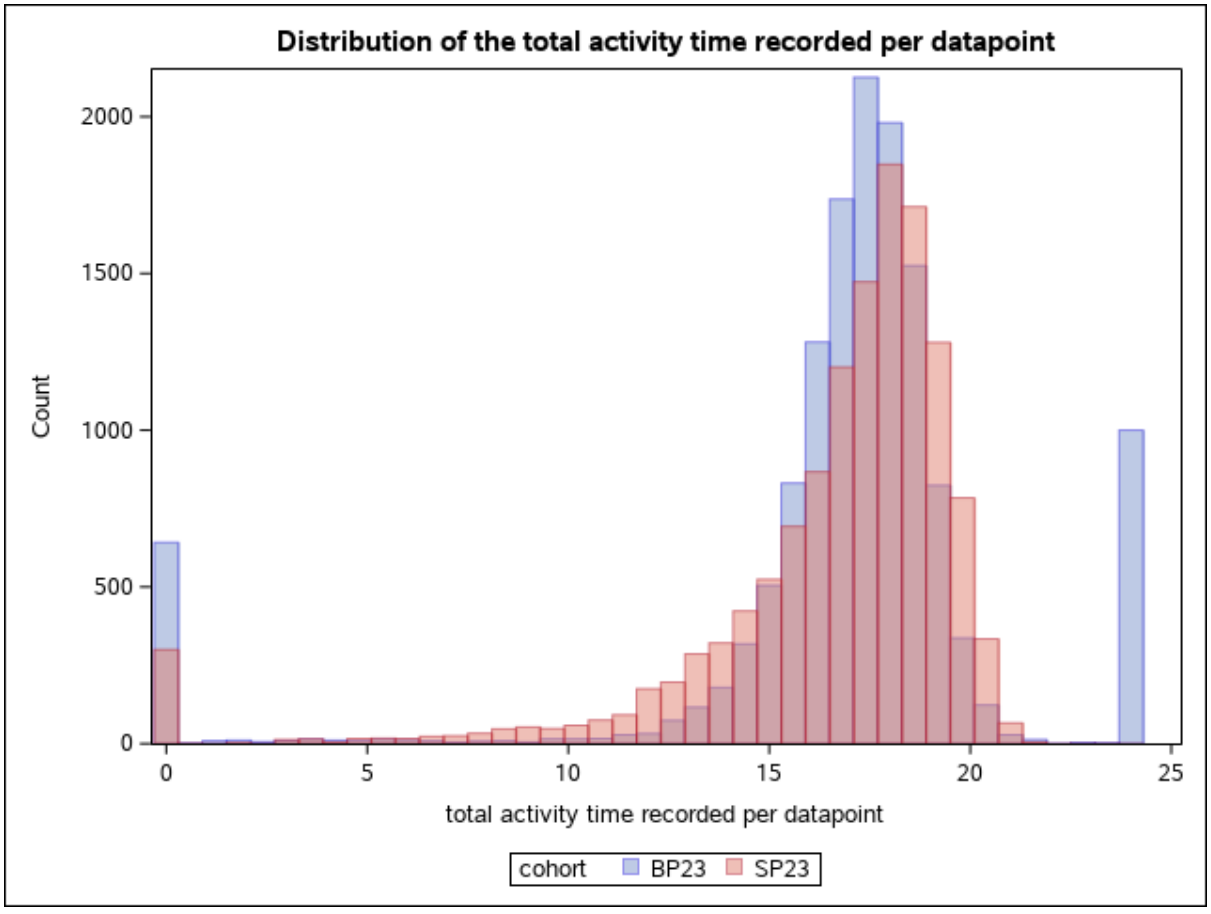


Figure 4.10.6: Histograms of the total activity time recorded for each data upload with the Ceres ear tags for Northern beef breeds

Table 4.10.7 and Figure 4.10.7 show the distribution of the activity times for the dataset with a recording period of 20-28 hrs.

Table 4.10.7: Summary of the individual behaviour activities (hrs) recorded by Ceres ear tags for records where the previous tag read was 20 to 28 hours earlier.

			grazing			Resting/rumination			
	N	Avg	Std	Min	Max	Avg	Std	Min	Max
All	25,975	6.2	3.2	0	15.7	7.7	2.2	0	23.9
SP23	12,778	7.6	3.2	0	15.7	7.5	1.9	0	14.9
BP23	13,197	4.9	2.5	0	13.5	7.9	2.4	0	23.9
			walking			Drinking/other			
	N	Avg	Std	Min	Max	Avg	Std	Min	Max
All	25,975	3.1	2.3	0	11.6	0.2	0.3	0	9.2
SP23	12,778	1.6	1.3	0	9.6	0.1	0.1	0	1.6
BP23	13,197	4.5	2.2	0	11.6	0.2	0.3	0	9.2

The SP and BP 23 cohorts showed very different distributions for grazing and walking behaviours. In both cohorts, there were large numbers of animals with unrealistically low grazing times. In the case of BP23, the average grazing time was 4.9 hours, which is lower than the 8.8-8.9 hours observed from the CSIRO eGrazor collars. Some BP23 animals also spent 20+ hours resting and ruminating. The maximum walking time in the CSIRO eGrazor collars was 1.9 hours, whereas most BP23 Ceres ear tag data walked longer than this, as did many SP23 animals.

Conclusion: Ceres ear tags were fitted to 280 steers from two cohorts, and 25,975 daily data points were recorded. Approximately 95% of the daily data points were uploaded 20 to 28 hours after the previous daily data point. Analysis of these daily data points showed that the average reporting period was 24.6 hours, but the total activity time recorded was much lower at 17.2 hours, with an average of 6.8 hours of activity a day missing. Although recorded on different animals, the average behaviour times did not reflect the distributions observed from the CSIRO eGrazor collar data. This was especially the case for BP23, where the average grazing time was lower, and the average walking time was higher than the distributions reported with CSIRO eGrazor collars. Although the average grazing and walking time was more in line for SP23, many records were still abnormally high or low. The resting/rumination time was similar for both cohorts but much lower than the time reported for these activities from the CSIRO eGrazor collar data. This dataset indicates that the Ceres ear tags do not accurately reflect the behaviours of animals and thus are not suitable as a predictor of the time animals spend grazing.

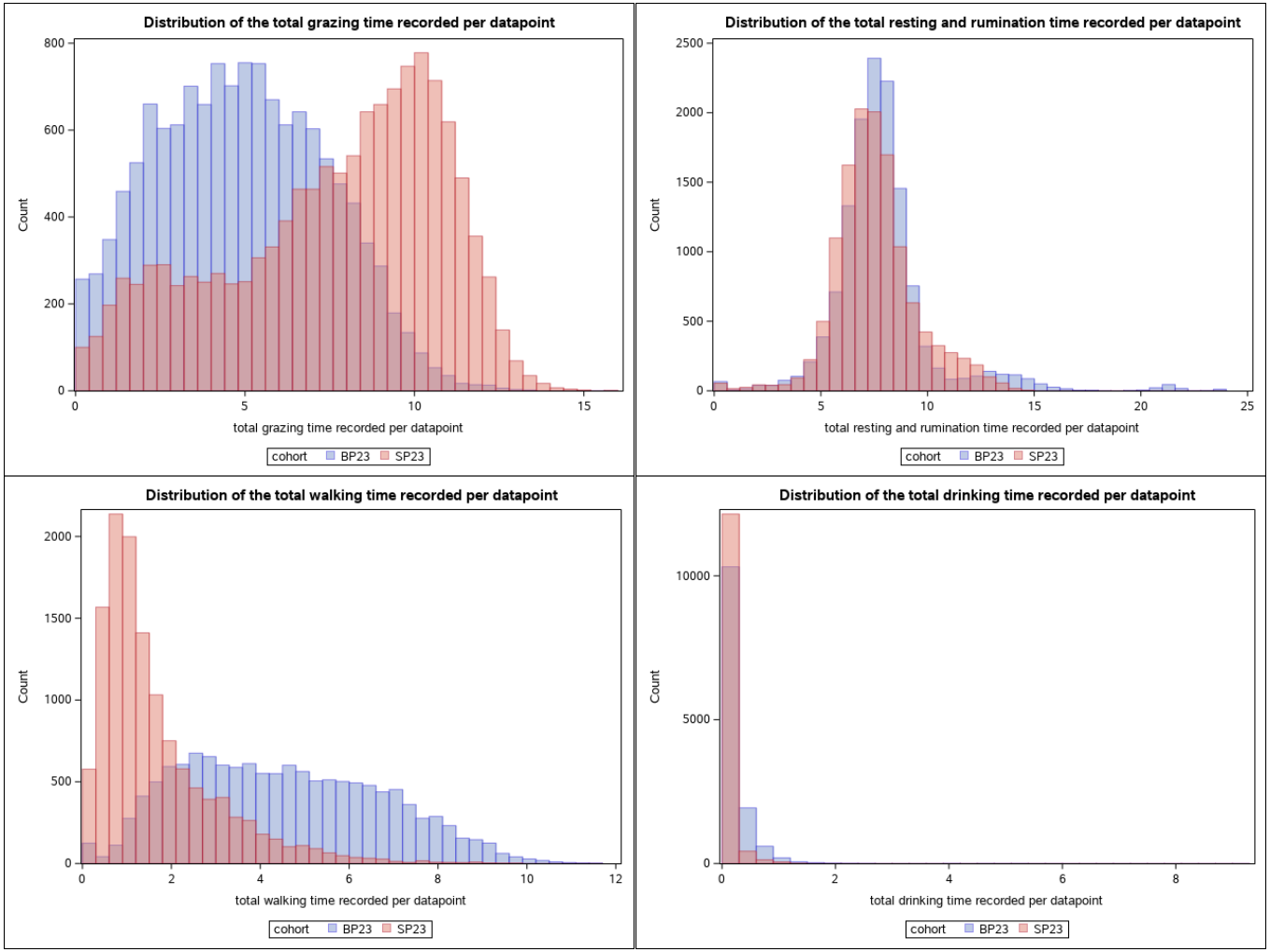


Figure 4.10.7: Histograms of animal behaviour recorded at pasture with the Ceres ear tags for Northern beef breeds

5. Methodology and Results for Objective 4

A reference population comprises animals with phenotypes and genotypes and is required for effective genomic selection. The design of the reference population determines the benefit observed from genomic selection. The ideal reference population is sufficiently large in size and has sufficient linkage to the population in which genomic selection is being implemented. This section reports on research into methods for describing the structure of existing beef reference populations, including linkage and coverage, prediction of accuracy, and phenotype quality.

5.1 Linkage and Coverage

A key design aspect of reference populations is the relatedness of animals used to build the reference. Scientific research has demonstrated that optimum design is when animals within the reference population are diversely related to each other but are then closely related to animals considered as selection candidates, where we want to use genomics to make selection decisions. Applying these design principles can be challenging for many practical reasons, including the fact that there are limited quantitative metrics and tools available to make informed decisions on sire selections for building reference populations. This work aimed to develop metrics that describe and assess the structure of reference populations to ensure suitability for genomic selection on a breed, herd or individual level.

5.1.1 A method to describe linkages between groups of animals

The average relatedness was computed to assess the linkage between defined groups of animals. Numerator relationship matrices were constructed with unpublished AGBU “nrmblock” software written by Mohammad Ferdosi based on algorithms by Aguilar et al. (2011) and Sargolzaei et al. (2005). The method was applied to Australian beef reference populations. For each animal born in 2010 or later, the average relatedness with all animals and trait-specific reference only animals was calculated based on the off-diagonal elements.

To then assess how trait-specific reference populations represented the whole population (i.e. breed), the average relatedness to reference animals (y-axis) was plotted against the average relatedness to all animals (x-axis). The regression slope for all animals and individual herds quantified this visual relatedness to the reference metric. If all animals in the population were phenotyped and genotyped, the figure (and slope) would be a 1:1 line with no deviations. Therefore, a regression slope close to 1 was considered optimum. However, when the slope was less than 1, this indicated a reference population that was generally under-representative of the whole population. A slope larger than 1 was often observed where the reference population was constructed from a small subset of herds, and some animals were over-represented and others under-represented.

This method has two applications: the first was used to describe the linkage between a general population and trait-specific reference populations, and the second was used to investigate the linkage between existing BIN or reference population projects. In the first instance, the method was applied to the Angus, Brahman, Charolais, Hereford, and Santa Gertrudis populations to assess how the breed’s reference populations represented animals born since 2010 in each breed.

5.1.2 Describing linkages to reference populations in Australian beef populations

To define the size of the reference population, reference populations were considered to include animals with both phenotype and genotype available, as well as genotyped but un-phenotyped sires with five or more progeny with phenotypes not already included in the reference. With single-step genomic evaluations, more animals contribute to the reference population, but these are difficult to define. Table 5.1.2.1 records the reference sizes for each breed for several traits, including the percentage of the 2010+ animals this represented. The number of herds with both phenotyped and genotyped animals is recorded in Table 5.1.2.2. The population-wide slope from the relatedness to the reference metric is recorded in Table 5.1.2.3, along with a series of figures showing the relatedness.

Reference size varied for each breed, but across all breeds, the reference size was very small for abattoir carcase traits, ranging from 0% (Charolais) to just 0.6% (Brahman). This small reference size and the results of the relatedness to the reference metric demonstrated that for all breeds, further investment into building the carcase reference population is required. The same conclusion can also be made for the female traits of days to calving and mature cow weight, with more investment required to build the size of these reference populations. Female fertility records are generally not recorded well, except for in the Repronomics and Southern Multi-Breed projects. Excluding Brahman and Santa Gertrudis (breeds included in the Repronomics project), the largest days to calving reference population represented just 0.3% of the Angus population. In contrast, the Brahman and Santa Gertrudis days to calving references were 1.3% and 2.0% of the total population, respectively. The same pattern can be observed for mature cow weight.

In contrast, for live weight, the reference population constituted between 3.6% (Charolais) and 13.1% (Angus) of the population since 2010.

The relatedness to reference metric plots demonstrated that the larger populations generally had a narrower data band on the plots. Brahman, Charolais and Hereford appeared to have similar plots for most traits. Santa Gertrudis's results suggested that the reference population was constructed on a few (well-recorded) herds.

The structure of a breed's reference population continually changes over time, and these metrics need to be recomputed, especially when new data is added. For example, adding recent cohorts of industry and project data, such as the Southern Multi-breed and Repronomics data, may result in significant increases in data, particularly for some breeds where the data will represent a large proportion of the total data for some traits, especially hard-to-measure traits.

Table 5.1.2.1: Description of the reference size (percentage) for animals born 2010+ for Australian Angus, Brahman, Charolais, Hereford and Santa Gertrudis populations.

	N animals born 2010+	Reference population							
		Gestation length	Birth weight	Live weights	Mature cow weight	Ultrasound scans	Carcase traits	Scrotal circumference	Days to calving
Angus	1,043,859	63,015 (6.0)	139,466 (13.4)	136,637 (13.1)	8,817 (0.8)	95,292 (9.1)	4,276 (0.4)	49,050 (4.7)	3,100 (0.3)
Brahman	165,714	1,670 (1.0)	3,724 (2.2)	12,896 (7.8)	2,023 (1.2)	5,610 (3.4)	932 (0.6)	3,729 (2.3)	2,161 (1.3)
Charolais	106,222	1,401 (1.3)	3,317 (3.1)	3,791 (3.6)	74 (0.07)	2,530 (2.4)	14 (0.01)	1,930 (1.8)	0 (0)
Hereford	410,167	9,478 (2.3)	28,878 (7.0)	31,379 (7.7)	2,038 (0.5)	22,691 (5.5)	972 (0.2)	14,247 (3.5)	949 (0.2)
Santa Gertrudis	80,085	279 (0.3)	1,026 (1.3)	4,619 (5.8)	1,027 (1.3)	3,572 (4.5)	111 (0.1)	1,011 (1.3)	1,628 (2.0)

Table 5.1.2.2: Description of the number of herds contributing phenotyped and genotyped reference data (the number of herds to reach 50% of data) for Australian Beef Angus, Brahman, Charolais, Hereford and Santa Gertrudis populations.

		Reference population							
	Genotypes	Gestation length	Birth weight	Live weights	Mature cow weight	Ultrasound scans	Carcase traits	Scrotal circumference	Days to calving
					Phenotype only				
Angus		999 (53)	1228 (80)	1022 (77)	387 (29)	709 (59)	33 (7)	662 (48)	71 (9)
Brahman		155 (4)	143 (3)	120 (9)	33 (4)	31 (4)	5 (2)	44 (4)	29 (4)
Charolais		262 (12)	369 (20)	224 (13)	65 (5)	149 (8)	7 (1)	128 (7)	200 (5)
Hereford		473 (38)	706 (69)	611 (62)	228 (18)	450 (47)	18 (2)	399 (44)	25 (3)
Santa Gertrudis		31 (2)	25 (2)	54 (5)	23 (3)	41 (3)	3 (1)	44 (4)	10 (3)
					Phenotype and genotype				
Angus	891 (34)	557 (23)	719 (30)	662 (30)	159 (8)	513 (25)	17 (5)	443 (21)	32 (5)
Brahman	339 (6)	37 (2)	38 (2)	73 (4)	15 (3)	22 (3)	5 (1)	27 (3)	16 (2)
Charolais	258 (7)	100 (5)	163 (6)	125 (4)	8 (2)	83 (3)	0	72 (3)	0
Hereford	523 (19)	265 (11)	375 (14)	390 (17)	72 (2)	330 (19)	12 (2)	302 (21)	13 (1)
Santa Gertrudis	41 (1)	8 (2)	7 (2)	24 (1)	9 (2)	17 (1)	2 (1)	18 (1)	5 (1)

Table 5.1.2.3: The regression slopes describing the reference populations for Australian Beef Angus, Brahman, Charolais, Hereford and Santa Gertrudis populations.

	Reference population							
	Gestation length	**Birth weight**	**Live weights**	**Mature cow weight**	**Ultrasound scans**	**Carcase traits**	**Scrotal circumference**	**Days to calving**
Angus	1.28	1.26	1.25	1.25	1.26	0.75	1.31	0.80
Brahman	0.89	0.80	0.79	0.46	0.94	0.91	0.77	0.64
Charolais	1.18	1.17	1.29	1.10	1.32	-	1.30	-
Hereford	1.05	1.26	1.15	1.43	1.13	0.57	1.18	1.57
Santa Gertrudis	1.49	1.29	1.24	1.44	1.26	1.37	1.26	1.34

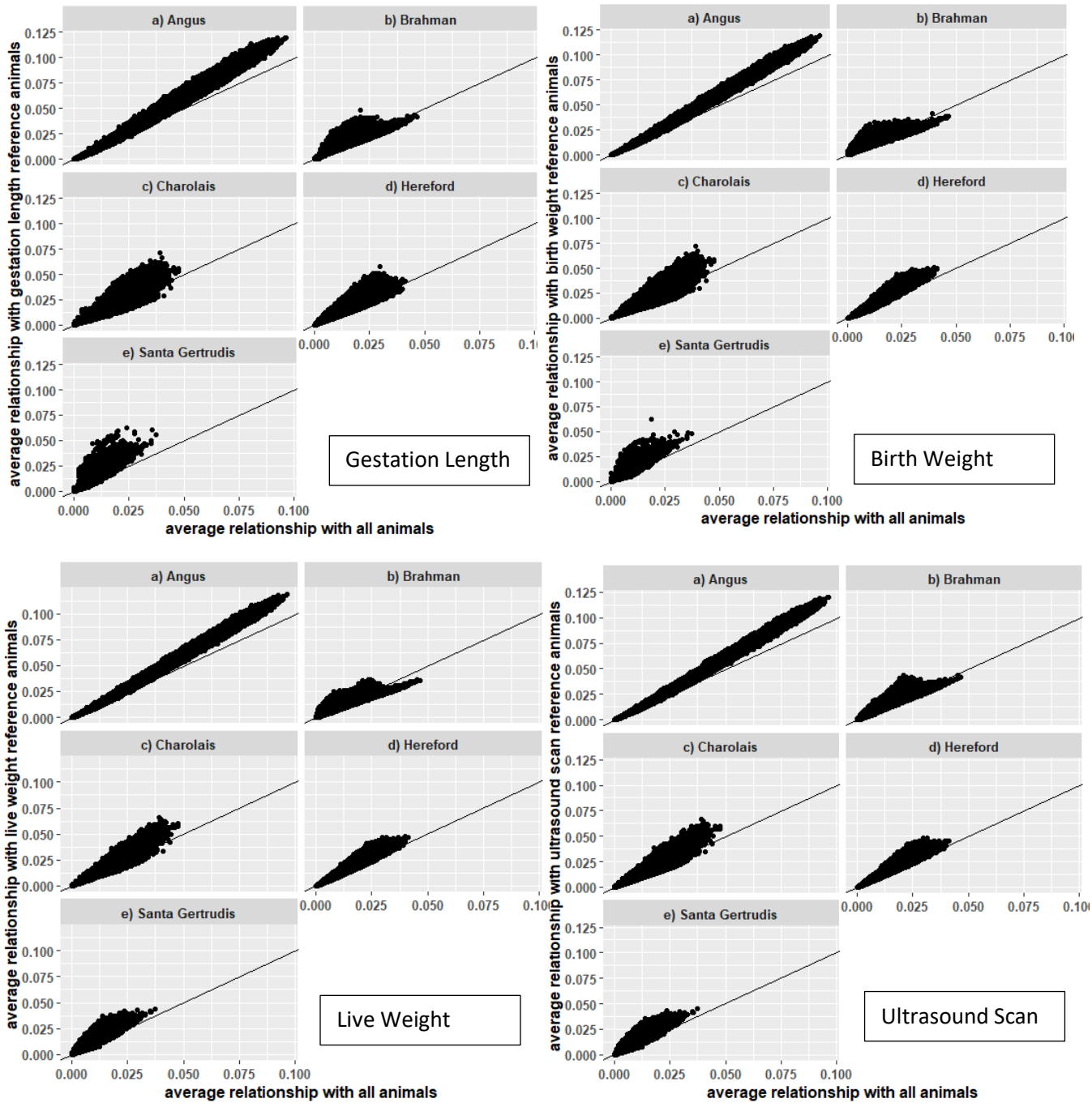


Figure 5.1.2.1: Relatedness to reference populations metrics for Australian Angus, Brahman, Charolais, Hereford and Santa Gertrudis populations for gestation length, birth weight, live weight and ultrasound scan traits.

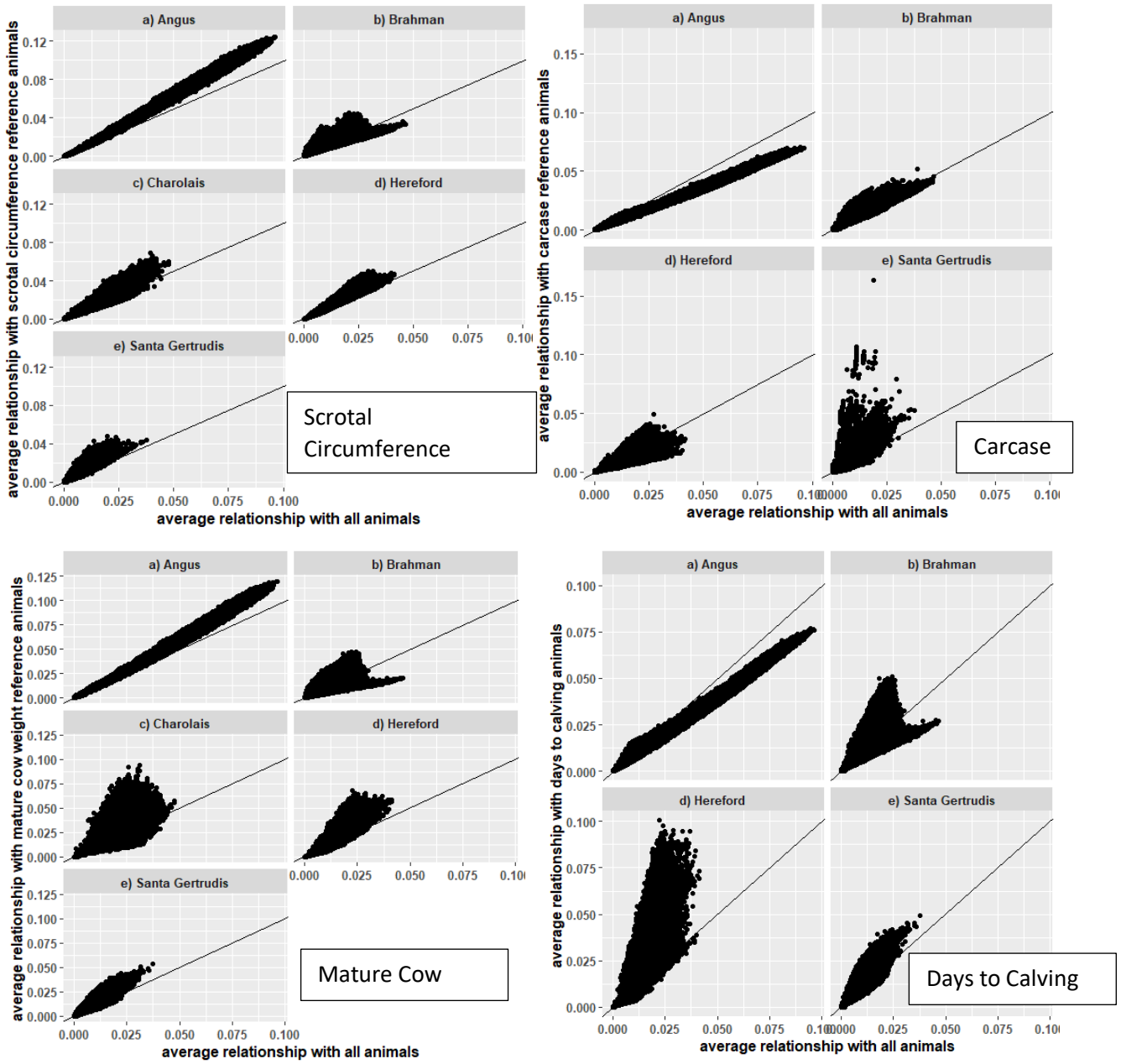


Figure 5.1.2.2: Relatedness to reference populations metrics for Australian Angus, Brahman, Charolais, Hereford and Santa Gertrudis populations for scrotal circumference, carcase, cow mature weight and days to calving traits.

5.1.3 Application of linkage metrics to the design of reference populations

Application for identifying potential sires for inclusion in the Southern Multi-Breed reference population

Support was provided to the Southern Multi-Breed project for future sire selection processes to ensure that the project sires used represented the broader populations and were not already represented in the project. Figure 5.1.3.1 illustrates how the linkage metrics were used to assess potential sires for inclusion in the Southern Multi-Breed project. Each dot represented one of 58 bulls available in a sales catalogue and thus potential project sires, the relationship coefficient to the closest relative already in the Southern Multi-Breed project, and the average relatedness to the broader population for the breed. The cluster of bulls (n=15) in the lower right quadrant (circled in the plot) offered the most advantage to the Southern Multi-Breed reference project as they represented animals with new genetics to include in the herd and had the higher average relationships to the breed population, increasing the impact of including that sire into the Southern Multi-Breed reference population.

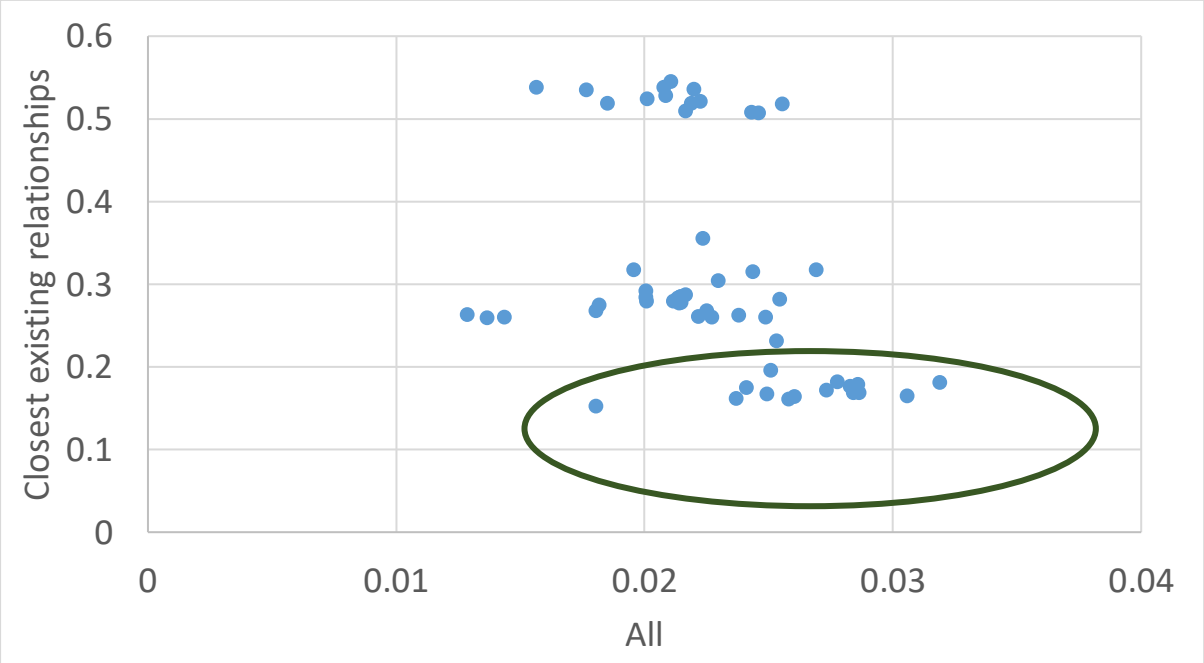


Figure 5.1.3.1: Example of applying the relatedness to reference metrics to identify sires for inclusion into reference populations.

Quantifying the linkage between genetics represented in the Southern Multi-Breed project and the broader beef populations

Southern Multi-Breed is a landmark reference data project involving six beef cattle breeds. Calves are born and managed in mixed-breed groups across five NSW Department of Primary Industries and Regional Development (DPIRD) sites. The overarching goal of Southern Multi-Breed is to collect high-quality reference data, particularly for hard-to-measure traits, to enhance genetic evaluations and facilitate the development of a multi-breed genetic evaluation. As such, the Southern Multi-Breed project's design is critical to ensure fair head-to-head across breed comparisons and ensure that the generated reference data genetically represents the breed populations. The relatedness to reference metrics described in section 5.1.1 of this report were used to describe and compare the relatedness of Southern Multi-Breed reference populations to a whole breed. A key element of the Southern Multi-Breed project design was the selection of foundation cows and sires to maximise relationships between the SMB herd and the wider breed. This work aimed to assess if the choice of foundation cows and sires has effectively ensured that Southern Multi-Breed data is genetically linked to the whole population within the respective breeds (Angus, Brahman, Charolais, Hereford, Shorthorn and Wagyu).

At the commencement of the Southern Multi-Breed project, foundation cows were purchased from industry seedstock herds. These were identified as herds that were BREEDPLAN recorded and influential in the breed (either using a wide range of sires or selling their genetics to other seedstock herds). Groups of cows were sourced from these herds. All cows were BREEDPLAN performance recorded with pedigree information and were selected to be representative of the national population (assessed via 400-day weight and reproduction EBVs), but especially if their sires were current influential sires (i.e. a large number of progeny). Angus foundation cows were also retained from the NSW DPIRD muscling and feed efficiency selection herds. Female progeny were retained in the project, with foundation cows exiting as the number of project-born females increased. Project sires were also BREEDPLAN performance recorded with pedigree information. Natural mate sires were purchased from industry herds, and nominations were sought by the industry for artificial insemination sires. Sires were selected to represent the breed, emphasising using current or emerging influential sires. This study considered the cows and sires that produced the first two cohorts of calves.

Linkage methods described previously were used to assess how the Southern Multi-Breed foundation cows and sires were related to the breed population for five of the six breeds represented in the project. This study did not consider one breed because pedigree information was unavailable for that breed. All known pedigree information was available for breeds A, B, C and E, but pedigree was only available for a subset of breed D. Of the 267 breed D foundation animals, 116 foundation cows and sires were present in the available pedigree subset, and these animals were considered in the current study. A numerator relationship matrix was constructed for each breed in the study based on the breed's recorded pedigree. The average relationship coefficient for each animal in the breed was calculated with 1) Southern Multi-Breed foundation cows and sires and 2) all animals within the breed. The visual metric (Figure 5.1.3.1) was produced for each breed, where the average relatedness to Southern Multi-Breed animals (y-axis) was plotted against the average relatedness to all animals (x-axis) in the breed. The regression slope and Pearson correlation coefficient were also calculated for each plot to quantify the relationships between Southern Multi-Breed and the whole breed population.

Table 5.1.3.1 summarises by breed the 1,149 foundation cows and 277 sires. Cows were from similar age structures and sourced from 5 to 13 herds per breed. The number of foundation cows per breed varied depending on the number of sites at which the breeds were present. Breed C had the largest number of cows (n=370) due to being present at four of the sites. Breeds B, D and E were located at two or three project sites, while Breed A was located at only one site. The number of sires per breed depended on the number of cows and sites the breeds were present at, and mating was either natural or artificial insemination.

Table 5.1.3.1: A summary of the Southern Multi-Breed project foundation cows and sires

Breed	A	B	C	D	E
Number of site locations	1	2	4	2	3
Number of foundation cows	166	182	370	219	212
Number of herds	7	5	13	10	9
Year of birth range	2008-18	2009-19	2009-18	2010-17	2010-18
Number of project sires	41	36	89	48	63

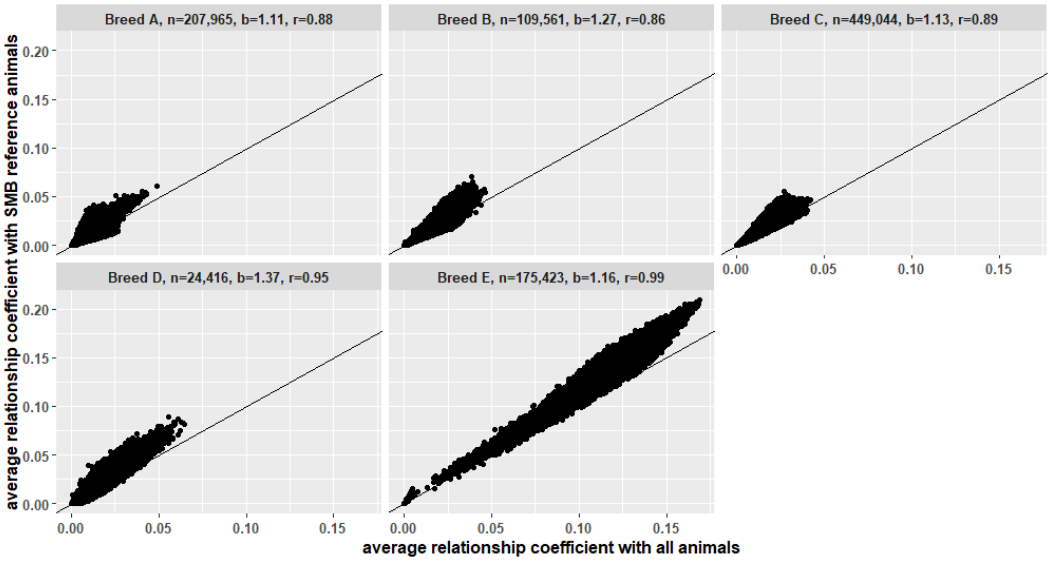


Figure 5.1.3.1: The average relatedness to all animals (x-axis) compared with animals in the Southern Multi-Breed reference population (y-axis), regression coefficient (b) and correlation (r) for all animals born after 2010 (n) in five of the breeds represented in Southern Multi-Breed

Figure 5.1.3.1 describes how animals in the breed were related to Southern Multi-Breed foundation cows and sires and the breed population. The average relatedness to all animals in the breed ranged between 0.0 and 0.05. The exception was breed E, where the average relatedness to all animals was much higher (0.0 to 0.2), reflecting breed E's reduced diversity due to being founded from a limited number of animals. These plots demonstrated that the genetics represented in Southern Multi-Breed are well linked to the breed population for all five breeds considered in this study. The shapes of the plots indicate that the animals with higher average relationship coefficients to all animals in the breed also demonstrated higher average relationship coefficients to Southern Multi-Breed animals. Data points in the plots generally followed the 1:1 line, although they tended to be slightly above the line. The 1:1 line is the expected relationship when the reference population is representative of the whole population. The slightly higher than 1 regression coefficients were found to align with the Southern

Multi-Breed strategy to target high-impact and diverse genetics when sourcing foundation cows and sires, and suggest that when selecting future project sires, more emphasis can be placed on increasing diversity, as high-impact animals are currently well represented.

This study confirmed that these foundation cows and sires used in Southern Multi-Breed are highly related to the breed population. Therefore, the reference data collected will benefit within-breed genomic selection programs.

5.1.4 Herds identified as being poorly linked to the Hereford reference population

The study examined Hereford herds with animals born since 2010, with the linkage metrics to the Hereford reference populations applied on a herd level to determine population linkage. Linkage on a herd level was considered to explore which herds had low linkage and better understand why they may be poorly linked. Herd-level regression slopes were obtained for 1,070 herds, and Table 5.1.4.1 summarises the herd-level regression slopes for live weight, ultrasound carcase scans, and abattoir carcase traits.

Table 5.1.4.1: Summary of herd-level regression slopes describing the linkage of herds to Hereford reference populations and the number of herds within brackets of regression slopes.

N herds=1070	Regression slope				N herds within slope categories					
	average	std	min	max	[<0.5]	[0.5-0.79]	[0.8-0.89]	[0.9-1.09]	[1.1-1.19]	[1.2+]
Phenotyped population										
Live weight	0.988	0.15	0.009	1.05	25	22	2	1021	0	0
Ultrasound scans	0.999	0.16	0.001	1.14	24	22	3	961	59	0
Abattoir carcase	0.611	0.15	0.001	1.44	175	803	42	43	4	1
Reference populations (phenotype and genotype)										
Live weight	1.028	0.18	0.001	1.66	23	22	42	722	187	72
Ultrasound scans	1.048	0.19	0.001	1.72	23	22	5	707	189	122
Abattoir carcase	0.565	0.15	0.0009	1.21	320	676	34	35	2	1

The average herd-level regression coefficient indicated that Hereford herds were generally linked to live weight and ultrasound-scanned reference populations, but were not well linked to the abattoir carcase reference populations. Results were similar for the phenotype only and reference (genotyped and phenotyped) populations, suggesting that linkage to abattoir carcase traits will not be improved by more genotyping but instead requires new carcase reference data (i.e. both phenotypes and genotypes) to be recorded in the Hereford population. The minimum regression slope demonstrated that some herds were poorly linked to the performance recorded and reference populations. The maximum herd regression slopes demonstrated that some herds are well linked to the reference population, and no further genetic links to these herds are required in the Hereford reference populations.

There were 49 and 87 herds for live weight with regression slopes <0.9 to the performance recorded and reference populations, respectively. Almost all the herds (n=1,020 and 1,030, respectively, for the abattoir carcase performance recorded and reference populations) had regression slopes <0.9 for abattoir carcase traits. We investigated the herds with low levels of linkage for live weight. We found that these herds could be characterised by being numerically small and containing more historical

animals, being overseas herds or being herds that did not have performance records and were disconnected from other herds that do have performance records.

5.1.5 Longevity of reference populations

Effective reference populations of sufficient size and linkage to breed populations are a significant investment that enables increased genetic improvement through genomic selection. However, reference populations require continued investment to ensure that recent generations remain sufficiently linked to the reference and obtain maximum benefit. The Angus Trans-Tasman Cattle Evaluation (TACE) and the Angus Sire Benchmarking Program were used to explore the longevity of the Angus reference population and quantify the importance of an evolving reference population that changes to reflect current and future Angus genetics each year.

Angus Australia commenced the Angus Sire Benchmarking Program in 2010. Since then, 12 cohorts (11 cohorts with data at the time of this study) of sires have produced progeny to help build a relevant genomic reference for Angus Cattle. The Trans-Tasman Angus population is managed by many breeders, predominantly spread across southern Australia and New Zealand, encapsulating a diversity of environments, production systems, and breeding objectives. The design of the Angus Sire Benchmarking Program is described in Appendix 9.1.1.

Linkage metrics described in section 5.1.1 of this report were calculated, and three relationship metrics were defined: 1) the sires' relationship to their closest relative, 2) the sires' average relationship with their 10 closest relatives, and 3) the sires' average relationship with the animals in the reference population cohort. Summary statistics across sire groups were weighted by the number of progeny sired by the individual within the Trans-Tasman pedigree. To test the influence of Angus Sire Benchmarking Program data on the accuracy of EBVs for sires represented in the TACE pedigree, a series of modified evaluations were conducted where the genetic evaluation was completed with subsets of the Angus Sire Benchmarking Program data excluded based on the TACE pedigree, genotypes and data available in August 2022. The analyses were 1) no Angus Sire Benchmarking Program data, 2) Cohort 1-3 data only, 3) Cohort 1-6 data only, 4) Cohort 1-9 data only, and 5) All Angus Sire Benchmarking Program data.

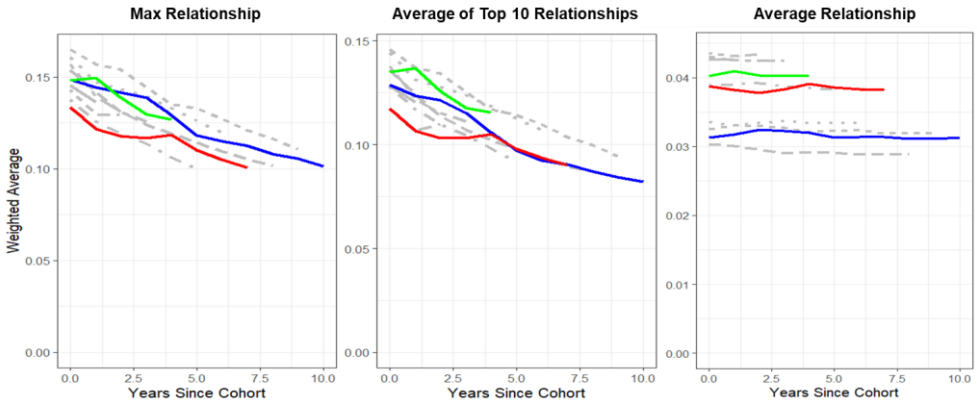


Figure 5.1.5.1. The average relatedness metrics, weighted by the sires' progeny count within a year, between Angus Sire Benchmarking Program cohort progeny and sires of calves born *n* years after the cohort mating: Cohort 1 (2011) = blue, Cohort 4 (2014) = red, Cohort 7 (2017) = green with other cohorts in grey

Figure 5.1.5.1 presents the average relationship coefficients between Angus Sire Benchmarking Program progeny and the sires of calves born *n* years after the cohort mating. The relationship of the progeny in Cohort 1 with the sires, which had progeny present in the TACE pedigree, declined over time. The average relationship remained reasonably consistent between the cohort progeny and the industry sires (blue line, Figure 5.1.5.1), and this was a by-product of the effective population size and that the top 10 sires genetically influential ancestors explained 42% of the genetic diversity in the population (Clark et al. 2019). However, whilst the average relationship remained relatively constant, the relationship metrics focusing on the strength of the relationship with the closest relatives were shown to decline noticeably (Figure 5.1.5.1). This rate of decline, while not uniform, was relatively consistent across all the cohorts. This suggested that the evolution of the Trans-Tasman Angus population was constant due to the effective population size and limitations on sourcing outside genetics. The merit of the Angus Sire Benchmarking Program ultimately depends on its ability to produce accurate estimated breeding values for hard-to-measure and economically important traits among future selection candidates.

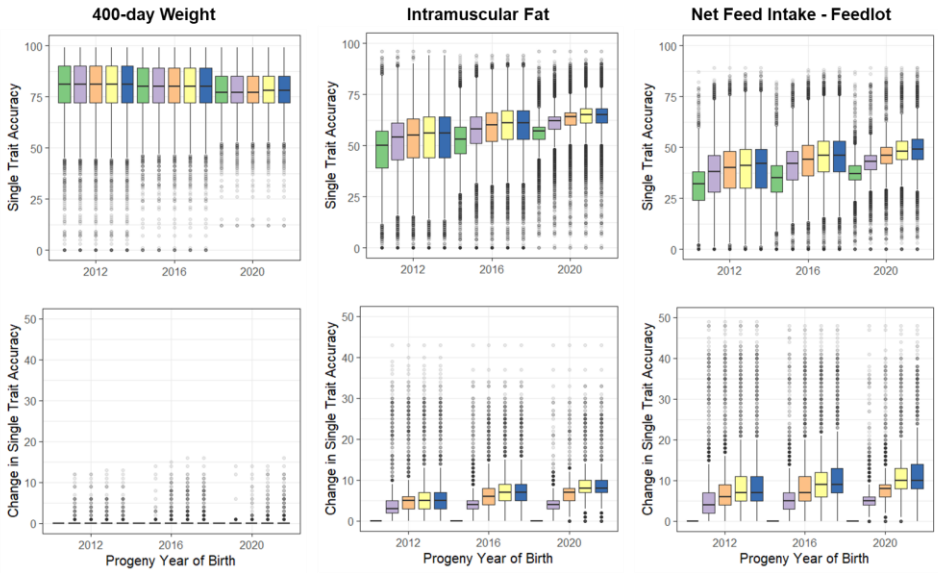


Figure 5.1.5.2. Impact of including Angus Sire Benchmarking Program phenotypes from Cohorts 1-3 (purple), Cohorts 1-6 (orange), Cohorts 1-9 (yellow) and All Cohorts (blue), compared to when no Angus Sire Benchmarking Program phenotypes (green) were available on the single trait accuracy of estimated breeding values of the sires of 2012, 2016 and 2020 progeny for 400-day weight, carcass Intramuscular Fat and Net Feed Intake – Feedlot

The importance of the Angus Sire Benchmarking Program reference population to the accuracy of selection candidate estimated breeding value (EBV) accuracy was largely governed by the baseline accuracy, which, in turn, was driven by the size of the reference population and the effective population size. It should be noted that within an ssGBLUP analysis, the reference expands beyond the Angus Sire Benchmarking Program and includes all animals from the broader industry with phenotypes and genotypes. Consequently, for highly recorded traits like 400-day weight, the contribution of the Angus Sire Benchmarking Program data was minimal. For the sires used across the Angus breed in 2012, 2016 and 2020, the mean change in accuracy was less than 1% (Figure 5.1.5.2). In contrast, for carcase intramuscular fat, the mean impact of the Angus Sire Benchmarking Program data for single-trait accuracy of the sires from the same three years was an accuracy increase of 5.7%, 7.5% and 8.2% (Figure 5.1.5.2), respectively. These estimates include the contribution to EBV accuracy

of correlated traits, a feature of the BREEDPLAN multi-trait analysis. After accounting for this, the Angus Sire Benchmarking Program data's impact on carcase intramuscular fat EBV accuracy was reduced for the three drops to +1.5%, +2.4% and +3.8%, respectively. The value of the Angus Sire Benchmarking Program data was most noticeable for net feed intake, where there is minimal recording outside of the reference, with the Angus Sire Benchmarking Program data leading to an average change in single trait accuracy (BREEDPLAN reported multi-trait analysis in brackets) of +8.7% (+2.0%), +10.3% (+3.2%) and +11.3% (+4.8%) for 2012, 2016 and 2020 sires (Figure 5.1.5.2), respectively.

The impact on EBV accuracy from the decline in relatedness between Angus Sire Benchmarking Program cohorts and sires appearing in the TACE pedigree in later years is most clearly observed for net feed intake (Figure 5.1.5.2). For industry sires used in 2012, the inclusion of Angus Sire Benchmarking Program data provided an extra 8.7% accuracy; however, if the ASBP had concluded after either the 3rd, 6th or 9th cohort, this gain would have only been +5.6%, +7.5% and +8.5%, respectively. As expected, most of the accuracy gain observed in the 2012 sires comes from the earlier cohorts, with cohorts 1-3 accounting for 67% of the overall accuracy improvement. In comparison, for 2020 sires, cohorts 1-3 only provided 46% (+5.2%) of the overall accuracy improvement observed when including the Angus Sire Benchmarking Program data, with 94% of the gains in accuracy achieved from the data from cohorts 1-9. This suggests that, for traits that Angus breeders cannot readily measure on the farm, the Angus Sire Benchmarking Program recording makes a valuable contribution and shows that investment in the reference needs to continue to reflect the diversity of genetics represented in the current selection candidates.

To maximise the contribution to EBV accuracy provided by reference population projects, this study demonstrates that relationships between reference animals should be low but need to be sufficiently genetically diverse so that their relationship to the broader population is high. As relatedness between Angus Sire Benchmarking Program cohorts and subsequently used industry sires declined, there was a corresponding fall in accuracy gains from the Angus Sire Benchmarking Program phenotypes. This shows that the Angus Sire Benchmarking Program remains highly valuable for lowly recorded traits in the broader Angus population. It also demonstrates that investment in reference populations must be ongoing to reflect the diversity of genetics represented within selection candidates.

5.2 Predicting accuracy from genomic evaluations

Predicting the expected EBV accuracy from genomic evaluations is important when designing reference populations and for producers considering the value proposition for genotyping, i.e. is the cost of genotyping worth the expected increase in accuracy? There are several theoretical predictions available. However, anecdotal reports have indicated that the observed accuracy tends to be lower than theoretical predictions, creating a challenge for reference design decisions and having implications for the adoption of genomics by breeders. A new empirical-based method was recently proposed, and this work aimed to implement and test this method to investigate if it generated more realistic predicted accuracies from genomics-only EBVs.

5.2.1 An empirical approach to predicting accuracy from genomic selection

Theoretical predictions

Several theoretical predictions of genomics-only accuracies have been published (Daetwyler et al. 2008, Goddard 2009, Goddard and Hayes 2009, Goddard et al. 2011). In this work, we considered two theoretical predictions that are commonly used:

1) Daetwyler et al. (2008) proposed a method that assumes that the markers capture all variance and show that accuracy is a function of the trait heritability, the effective number of chromosome segments (Me), and the reference population's size.

$$\text{Accuracy} = \sqrt{\frac{h2}{h2+\frac{Me}{N}}}$$

2) Goddard and Hayes (2009) produced a graphic based on Goddard's (2009) theoretical predictions, illustrating expected accuracies given different reference sizes and trait heritabilities. Goddard (2009) predicts the GEBV accuracy as the linkage disequilibrium between markers and QTL multiplied by the accuracy with which marker effects are estimated. The Goddard (2009) prediction equation was similar to Daetwyler et al. (2008) in that it considers the effective number of chromosome segments (Me), reference size and heritability. It also considers the number of markers and allows that not all the genetic variance is captured by the SNPs. It is equivalent to the Daetwyler et al. (2008) method when there are large numbers of markers, as you can then assume that the SNPS explain all the variance.

$$\text{Accuracy} = \sqrt{\frac{M}{Me+M} * \frac{N}{N+\frac{Me}{\frac{M}{Me+M}*h^2}}} \qquad \text{Me} = \frac{2NeLk}{\ln(4NeLk)}$$

The Goddard and Hayes (2009) plot (Figure 5.2.1.1) is widely used in the beef industry to discuss the expected accuracy. It assumes the effective population size = 100 and the effective number of chromosome segments = 639.

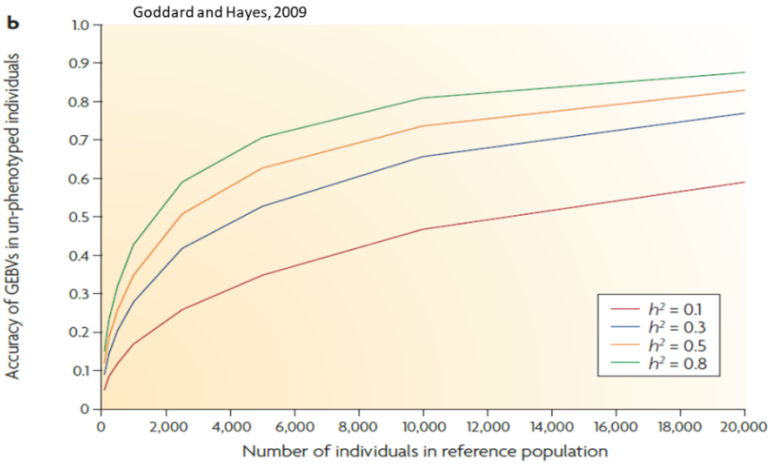


Figure 5.2.1.1: Accuracy of GEBVs in un-phenotyped individuals for different-sized references and trait heritabilities: reproduced from Goddard and Hayes (2009)

The prediction equation Goddard et al. (2011) reported is the same as that from Goddard (2009). However, the equation for computing the Me term is different, which results in a higher Me for a given effective population size and, thus, lower accuracy prediction, assuming all other model parameters are constant except the equation for computing Me.

$$\text{Accuracy} = \sqrt{\frac{M}{Me+M} * \frac{N}{N+\frac{Me}{\frac{M}{Me+M}*h^2}}} \qquad \text{Me} = \frac{2NeLk}{\ln(NeL)}$$

Empirical prediction approach

Dekkers et al. (2021) published an empirical approach for predicting genomic accuracies. In addition to the predicted accuracy, the method also empirically estimates Me, the proportion of variance explained by SNPs and the decay in accuracy as the number of generations between the target animals and reference animals increases. This method also has the flexibility to consider different sets of target animals (i.e. unphenotyped, phenotyped and more distantly related animals) and predict the accuracy increase with genomics for the various target subsets. In contrast, all the theoretical predictions consider only unphenotyped animals related to the reference population.

The method

The method applies a series of equations but requires two analyses before it can be applied. Therefore, the method can only be applied once a breed has a reference population, but it may be reasonable to use predictions based on a similar population.

To apply this method, reference and target animals need to be identified. Reference animals are animals with both a genotype and a phenotype. In contrast, target animals can be any group of animals to which we are interested in applying genomic selection.

Two analyses are undertaken using genetic parameters from the routine genetic evaluation. In these analyses, the whole breed pedigree for reference and target animals is used, but only phenotypes and genotypes of reference animals are used.

1. A BLUP evaluation with full pedigree, reference population phenotypes and no genotypes
2. A GBLUP evaluation with phenotypes and genotypes of reference animals

Any software can be utilised, but exact accuracy based on model parameters must be calculated for each animal and not an approximated accuracy. This study used WOMBAT software (Meyer, 2007) for the BLUP and GBLUP analysis. Due to the large size of the Angus reference population, a different approach was needed for the Angus GBLUP analysis. The new BREEDPLAN accuracy methodology recently developed by AGBU was used for the Angus (Li et al. 2023), and when applied to GBLUP, as in this study, provided exact accuracy.

Application of method

The following outlines the 12 steps of the Dekkers et al. (2021) method. Steps are parameters taken from the abovementioned analysis, defined population parameters or calculations based on the formula provided.

1. r_{Gr} – Average **accuracy of reference** animals from GBLUP run
2. r_{Ar} – Average **accuracy of reference** animals from pedigree BLUP run

3. r_{Dr} – Compute **the contribution of G above that of A** with the following formula, which uses the accuracy values of reference animals

$$r_{Dr} = \sqrt{\frac{r_{Gr}^2 - r_{Ar}^2}{1 + r_{Ar}^2(r_{Gr}^2 - 2)}}$$

4. q^2_D – Calculate the proportion of genetic variance captured. Set the initial value as 1.0
5. θ_{Dr} – Calculate **Fisher's information statistic** with the following formula, which uses the contribution of G above A, the proportion of genetic variance captured and the heritability (as used in the routine genetic evaluation)

$$\theta_{Dr} = \frac{r_{Dr}^2(1 - r_{Dr}^2 q_D^2 h^2)}{q_D^2 - r_{Dr}^2}$$

6. Me – calculate the **effective number of chromosome segments** with the following formula, which uses the number of reference animals, the proportion of genetic variance captured, heritability and Fisher's information statistic

$$Me = \frac{N q_D^2 h^2}{\theta_{Dr}}$$

7. q_D^2 – Calculate the **proportion of genetic variance captured** with the following formula, which uses the number of markers and Me

$$q_D^2 = \frac{M}{M + Me}$$

8. Replace q_D^2 in step 4 and repeat the steps 4-8 loop until the Me estimate is stable and doesn't change across iterations.
9. r_{At} – Average **accuracy of target** animals from pedigree BLUP run
10. p_{rt} – Calculate the **loss of accuracy** between the reference and target animals with the following formula, which uses the effective number of chromosome segments, ϒ=2, k=number of chromosomes (29), L is the size of the chromosomes in morgans (1.017 as reported in Snelling et al. 2007) and the number of generations between the closest maternal and paternal relatives in the reference)

$$p_{rt} = \frac{(1 - \gamma k L)^{(l_p + l_m)}}{Me}$$

11. r_{Dt} – Compute the **contribution of G above that of A** in the target population with the following formula, which uses the contribution of G above that of A in the reference population and the loss of accuracy between the reference and target populations

$$r_{Dt} = p_{rt} r_{Dr}$$

12. r_{Gt} – Calculate the **predicted average accuracy of target animals** from a GBLUP run with the following formula, which uses

$$r_{Gt} = \sqrt{\frac{r_{At}^2 + r_{Dt}^2 - 2 r_{At}^2 r_{Dt}^2}{1 - r_{At}^2 r_{Dt}^2}}$$

5.2.2 Validation of the empirical approach in Australian beef populations

Several traits from an Australian Brahman data set were used to validate the empirical approach, and a forward validation was undertaken with the reference data split by year of birth into reference and target subsets. The birth year that defined reference and target groups varied for each trait, such that approximately 70% of the data was from the reference and the remaining 30% from the target animals. The method was applied as described above, and the predicted accuracy of target animals was obtained. An additional GBLUP was then undertaken where phenotypes of the reference animals and genotypes of both reference and target animals were included. The achieved and predicted accuracy for target animals was compared, and the results are shown in Table 5.2.2.1. The achieved accuracy was lower than predicted by between 0.9% and 3.6%. In contrast, the achieved accuracy was lower than the theoretical accuracy by between 5.2% and 21.8%. The empirical predicted accuracy was closer to the achieved accuracy than the theoretical predictions – this was especially true for traits with larger reference population sizes. These results demonstrated that the empirical method does provide a predicted accuracy that is more representative of the achieved accuracy.

Table 5.2.2.1: Forward validation results comparing the predicted and achieved accuracy of target animals

	Number of animals		Accuracy of target animals		
Trait	**reference**	**target**	**Predicted[1]**	**Achieved[1]**	**Theoretical[1]**
Age of puberty	1,670	806	0.521	0.485	0.601
Lactation anoestrous interval	1,048	470	0.419	0.395	0.447
Shear force	982	511	0.294	0.276	0.363
Percent normal sperm	1,366	583	0.316	0.296	0.411
400-day live weight	8,730	4,832	0.628	0.610	0.825
200-day live weight	11,541	4,415	0.595	0.583	0.795
600-day live weight	7,805	3,673	0.661	0.632	0.839
Scrotal size	4,351	1,988	0.557	0.526	0.744
Ultrasound EMA (heifer/steer)	2,565	1,393	0.408	0.399	0.493

[1] Predicted accuracy is the empirical accuracy from Dekkers et al. (2021); Achieved accuracy is the accuracy obtained from a GBLUP analysis when genotypes were included; Theoretical prediction based on the Daetwyler et al. (2008) method, where Me was 1680.23 (Ne = 141.6)

5.2.3 Prediction of genomic accuracy in Australian beef populations using an empirical approach

The previous section validated the Dekkers et al. (2021) empirical method in a subset of Brahman traits, where reference animals were split into reference and target/validation subsets. This section applied the method to several breeds to determine the predicted accuracy based on current reference populations. Here, all reference animals remained in the reference, and the target population was defined as genotyped animals born in 2019 or later but were not part of the reference population (i.e., genotype only with no phenotype – note that the genotypes of these animals have not been considered in the method described in section 5.2.1). For example, Brahman's current 400-day live weight reference size was 13,562. In the validation analysis, the reference population was split so that 8,730 animals remained reference animals, and 4,832 were considered target animals to validate the method. In these application analyses, all 13,562 records remain reference animals.

The Dekkers empirical method was applied to each breed (Angus, Brahman, Hereford and Santa Gertrudis) for an extensive range of traits (as univariate models) in the national genetic evaluation. Reference animals were animals with both genotypes and phenotypes. Target animals were genotyped animals born in 2019 or later but were not part of the reference population (i.e., genotype only with no phenotype – note that the genotypes of these animals have not been considered in the method described in section 5.2.1). Tables 5.2.3.1-5.2.3.4 record the results from the empirical method for each of the four breeds in this study. All traits were single-trait analyses; therefore, the accuracy would be expected to be higher in a multi-trait context.

These analyses demonstrated that there are boundaries for when the empirical method will be effective.

- Small reference sizes (approximately 1,000 or fewer) showed that the effective number of chromosome segments (Me) estimates were not sensible, however, a stable estimate (from the loop in the method) was possible.
- Very large reference sizes may have difficulty obtaining a stable Me estimate (from the loop in the method). This upper range varied depending on the trait heritability – the higher the heritability, the lower the maximum number of records that obtained stable Me estimates.

Provided that the reference size was within these upper and lower bounds, the empirical method provided estimates for predicted EBV accuracy and Me. Although difficult to see clearly (due to traits having different heritabilities and population sizes), the results showed the expected trends: traits with higher heritability and larger reference population sizes had higher predicted accuracy. Me estimates varied across breeds, heritabilities and different reference sizes. The empirical Me estimates were larger than the theoretical Me in all cases.

Effective population size (Ne) was estimated for each breed using RelaX2 (Stranden, 2014) software using the whole breed pedigree file (i.e. not trait specific); Ne was estimated to be 141.50, 141.56, 184.05 and 266.77 for Angus, Brahman, Hereford and Santa Gertrudis, respectively. Applying the theoretical Me equation outlined earlier in this report resulted in theoretical Me estimates of 1679.67, 1680.23, 2074.97 and 2808.32 for Angus, Brahman, Hereford and Santa Gertrudis, respectively. Pedigree completeness may have impacted the theoretical Ne estimates, especially for breeds with incomplete pedigree recording.

Although this method appears better for predicting the accuracy of genotyped and un-phenotyped animals, it relies on a suitable dataset for the initial BLUP and GBLUP analysis. This is of limited value to breeds and traits yet to be recorded or for providing predictions for reference sizes other than the current reference size (i.e. if an additional 1,000 reference records were available). An alternative may be to use results from another similar breed or trait, or to subset data from a well-recorded trait to fill in the population size gaps.

Table 5.2.3.1: Predicted accuracy of genotyped and un-phenotyped Angus animals and effective number of chromosome segments (Me) of the Angus population from empirical methods

		Accuracy from data analysis			Empirical predictions	
Trait*	**Reference size**	**BLUP reference**	**BLUP target**	**GBLUP reference**	**GBLUP target**	**Estimated Me**
crby	1,019	0.759	0.222	0.788	0.478	2278.461
crib	3,621	0.685	0.279	0.752	0.564	3777.035
cema	3,959	0.621	0.277	0.700	0.529	3749.060
cimf	4,035	0.603	0.275	0.686	0.522	3746.738
cp8	4,077	0.614	0.278	0.696	0.531	3832.274
cwt	4,090	0.66	0.286	0.737	0.566	3831.788
mcwt	8,758	0.663	0.381	0.784	0.689	4182.573
hp8	41,647	0.709	0.489	0.890	0.854	5255.064
hrib	41,744	0.689	0.484	0.879	0.843	5290.016
hema	41,797	0.625	0.463	0.837	0.800	5051.547
ss	47,588	0.685	0.493	0.888	0.856	5290.363
bp8	51,694	0.633	0.479	0.858	0.826	5298.930
brib	51,917	0.602	0.467	0.834	0.802	5265.048
bema	52,145	0.613	0.471	0.843	0.811	5323.711
wt600	55,230	0.666	0.485	0.881	0.850	5588.285
gl	62,412	0.792	0.492	0.952	#	#
wt400	95,811	0.649	0.492	0.891	0.864	5404.475
wt200	121,660	0.562	0.438	0.876	0.846	3884.167
bwt	136,119	0.677	0.432	0.931	#	#

* bema, bp8 and brib= ultrasound scanned bull eye-muscle area, p8 fat and rib fat; bwt=birth weight; cema, cimf, cp8, crib, crby and cwt= abattoir carcase eye-muscle area, intra-muscular fat, p8 fat, rib fat, retail beef yield and weight; gl=gestation length; hema, hp8 and hrib= ultrasound scanned heifer and steer eye-muscle area, p8 fat and rib fat; mcwt=mature cow weight; ss=scrotal size; wt200, wt400 and wt600=live weight at 200, 400 and 600 days of age. # Stable estimates were unable to be obtained

Table 5.2.3.2: Predicted accuracy of genotyped and un-phenotyped Brahman animals and effective number of chromosome segments (Me) of the Brahman population from empirical methods

		Accuracy from data analysis			Empirical predictions	
Trait*	**Reference size**	**BLUP reference**	**BLUP target**	**GBLUP reference**	**GBLUP target**	**Estimated Me**
crby	217	0.279	0.016	0.288	0.079	11134.22
cema	929	0.584	0.110	0.608	0.274	4248.951
sf	1,493	0.512	0.123	0.549	0.290	4530.000
crib	1,515	0.565	0.132	0.601	0.320	4630.186
lai	1,518	0.685	0.133	0.711	0.368	4059.000
cimf	1,555	0.481	0.119	0.517	0.269	4528.163
cp8	1,557	0.546	0.130	0.584	0.315	4500.457
cwt	1,558	0.586	0.136	0.624	0.343	4427.263
gl	1,710	0.560	0.151	0.596	0.324	4099.407
pns	1,949	0.517	0.122	0.559	0.308	4795.000
brib	2,396	0.535	0.140	0.587	0.356	4631.803
bp8	2,405	0.575	0.148	0.626	0.384	4745.283
ap	2,476	0.779	0.181	0.806	0.506	4479.000
mcwt	2,757	0.728	0.218	0.769	0.519	4556.638
bema	2,874	0.517	0.142	0.573	0.355	4908.603
hrib	3,709	0.676	0.213	0.726	0.493	5129.167
hp8	3,913	0.749	0.227	0.793	0.566	5091.849
hema	3,957	0.548	0.185	0.604	0.391	5027.587
bwt	4,778	0.678	0.180	0.737	0.521	5350.555
ss	6,339	0.680	0.255	0.753	0.585	6281.957
ft	7,799	0.641	0.195	0.714	0.526	5824.432
wt600	11,478	0.712	0.292	0.803	0.684	7025.402
wt400	13,562	0.676	0.284	0.778	0.662	7166.831
wt200	15,965	0.586	0.252	0.708	0.596	6972.595

* ap= age at puberty; bema, bp8 and brib= ultrasound scanned bull eye-muscle area, p8 fat and rib fat; bwt=birth weight; cema, cimf, cp8, crib, crby and cwt= abattoir carcase eye-muscle area, intra-muscular fat, p8 fat, rib fat, retail beef yield and weight; ft=flight time; gl=gestation length; hema, hp8 and hrib= ultrasound scanned heifer and steer eye-muscle area, p8 fat and rib fat; lai=lactation anoestrus interval; mcwt=mature cow weight; pns=percent normal sperm; sf=shear force; ss=scrotal size; wt200, wt400 and wt600=live weight at 200, 400 and 600 days of age.

Table 5.2.3.3: Predicted accuracy of genotyped and un-phenotyped Hereford animals and effective number of chromosome segments (Me) of the Hereford population from empirical methods

		Accuracy from data analysis			Empirical predictions	
Trait*	**Reference size**	**BLUP reference**	**BLUP target**	**GBLUP reference**	**GBLUP target**	**Estimated Me**
crby	179	0.373	0.006	0.401	0.171	2952.928
cema	1,014	0.469	0.101	0.512	0.278	2559.972
crib	1,387	0.433	0.103	0.490	0.296	3643.774
cp8	1,473	0.515	0.119	0.574	0.356	3700.667
cimf	1,582	0.530	0.125	0.590	0.371	3727.166
cwt	1,584	0.587	0.132	0.646	0.415	3741.824
mcwt	2,289	0.565	0.207	0.632	0.441	4048.791
hrib	9,794	0.616	0.327	0.742	0.650	5210.119
hp8	9,802	0.653	0.340	0.773	0.682	5203.243
hema	9,852	0.563	0.308	0.693	0.600	5075.529
gl	11,593	0.675	0.350	0.799	0.719	5464.154
ss	18,299	0.650	0.419	0.810	0.763	6321.345
brib	19,530	0.536	0.379	0.714	0.668	6329.530
bp8	19,547	0.562	0.392	0.739	0.693	6381.786
bema	19,582	0.543	0.382	0.720	0.673	6389.342
wt600	21,732	0.592	0.396	0.774	0.730	6526.949
wt400	31,039	0.579	0.428	0.778	0.747	6325.288
bwt	35,163	0.662	0.352	0.849	0.813	6362.538
wt200	35,125	0.566	0.401	0.777	0.744	5968.626

* bema, bp8 and brib= ultrasound scanned bull eye-muscle area, p8 fat and rib fat; bwt=birth weight; cema, cimf, cp8, crib, crby and cwt= abattoir carcase eye-muscle area, intra-muscular fat, p8 fat, rib fat, retail beef yield and weight; gl=gestation length; hema, hp8 and hrib= ultrasound scanned heifer and steer eye-muscle area, p8 fat and rib fat; mcwt=mature cow weight; ss=scrotal size; wt200, wt400 and wt600=live weight at 200, 400 and 600 days of age.

Table 5.2.3.4: Predicted accuracy of genotyped and un-phenotyped Santa Gertrudis animals and effective number of chromosome segments (Me) of the Santa Gertrudis population from empirical methods

		Accuracy from data analysis			Empirical predictions	
Trait*	Reference size	BLUP reference	BLUP target	GBLUP reference	GBLUP target	Estimated Me
lai	40	0.578	0.037	0.605	0.269	216
ap	114	0.730	0.066	0.749	0.352	500
crby	133	0.240	0.006	0.264	0.117	3537
cema	138	0.278	0.027	0.307	0.144	1369
pns	304	0.313	0.066	0.334	0.144	3953
gl	311	0.498	0.110	0.513	0.187	2620
sf	392	0.395	0.053	0.423	0.186	3127
cp8	393	0.392	0.054	0.419	0.182	3180
crib	394	0.442	0.060	0.472	0.213	3047
cimf	397	0.448	0.060	0.479	0.219	3047
cwt	398	0.434	0.059	0.464	0.209	3097
bwt	1,056	0.653	0.262	0.688	0.390	3176
brib	1,341	0.465	0.155	0.508	0.297	3973
bema	1,355	0.508	0.168	0.553	0.329	3929
bp8	1,356	0.524	0.172	0.569	0.340	4005
mcwt	1,366	0.663	0.175	0.699	0.411	3324
ss	1,464	0.578	0.187	0.627	0.393	3699
hema	2,764	0.627	0.189	0.684	0.460	3973
hrib	2,769	0.603	0.183	0.661	0.439	3958
hp8	3,260	0.652	0.201	0.713	0.502	4045
wt400	4,086	0.587	0.206	0.659	0.472	4264
wt600	4,343	0.627	0.218	0.699	0.513	4516
ft	4,487	0.639	0.225	0.707	0.516	3883
wt200	5,053	0.565	0.353	0.646	0.477	4373

* ap= age at puberty; bema, bp8 and brib= ultrasound scanned bull eye-muscle area, p8 fat and rib fat; bwt=birth weight; cema, cimf, cp8, crib, crby and cwt= abattoir carcase eye-muscle area, intra-muscular fat, p8 fat, rib fat, retail beef yield and weight; ft=flight time; gl=gestation length; hema, hp8 and hrib= ultrasound scanned heifer and steer eye-muscle area, p8 fat and rib fat; lai=lactation anoestrus interval; mcwt=mature cow weight; pns=percent normal sperm; sf=shear force; ss=scrotal size; wt200, wt400 and wt600=live weight at 200, 400 and 600 days of age.

Comparison of predicted accuracy and theoretical accuracy

Figures 5.2.3.1-5.2.3.4 show the predicted accuracy from the empirical method and the predicted accuracy from two theoretical predictions, where Me was as described earlier in this report, based on the effective population size. Angus, Brahman and Hereford showed much higher theoretical predictions than empirical predictions; on average, theoretical predictions were 11%, 18% and 12.5% higher, respectively. Santa Gertrudis showed more variable results, with the difference being smaller on average. However, they had many traits where the reference contained less than 1,000 animals, and at smaller reference sizes, the empirical method was shown to perform poorer. For the Santa Gertrudis traits with larger references, the differences were greater between the empirical and theoretical predictions.

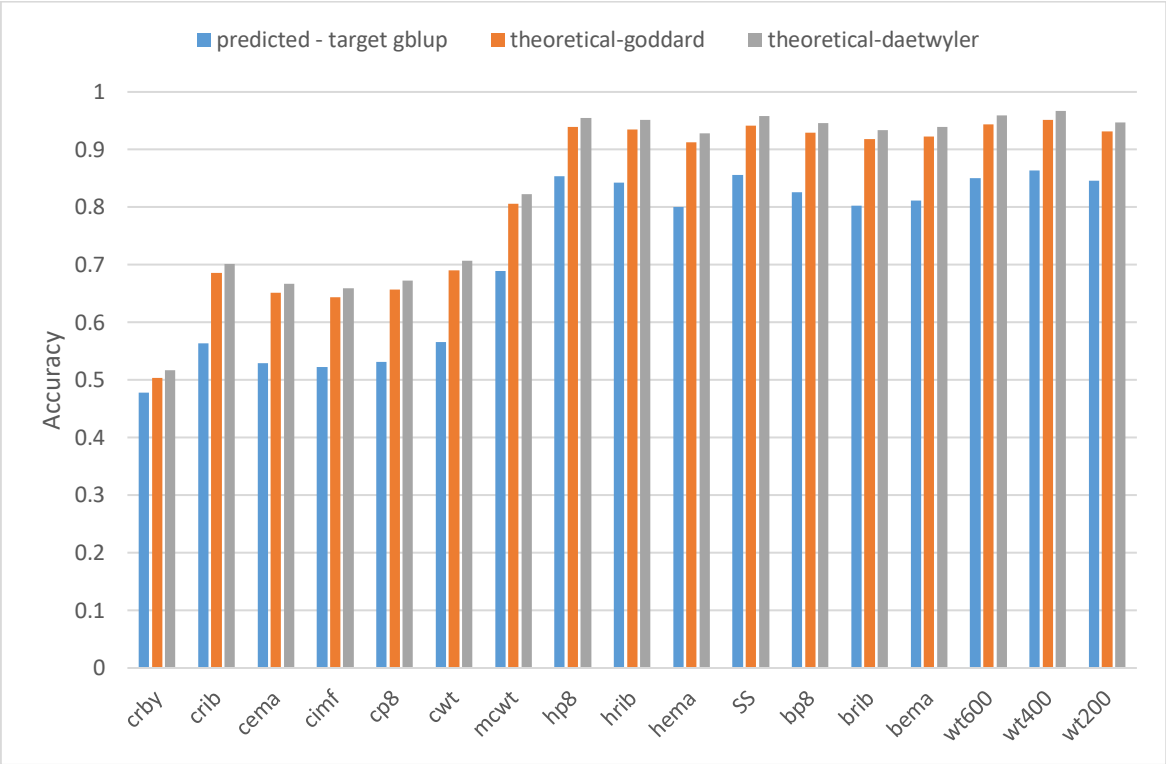


Figure 5.2.3.1: Comparison of empirical accuracy prediction with those from theoretical predictions for Angus

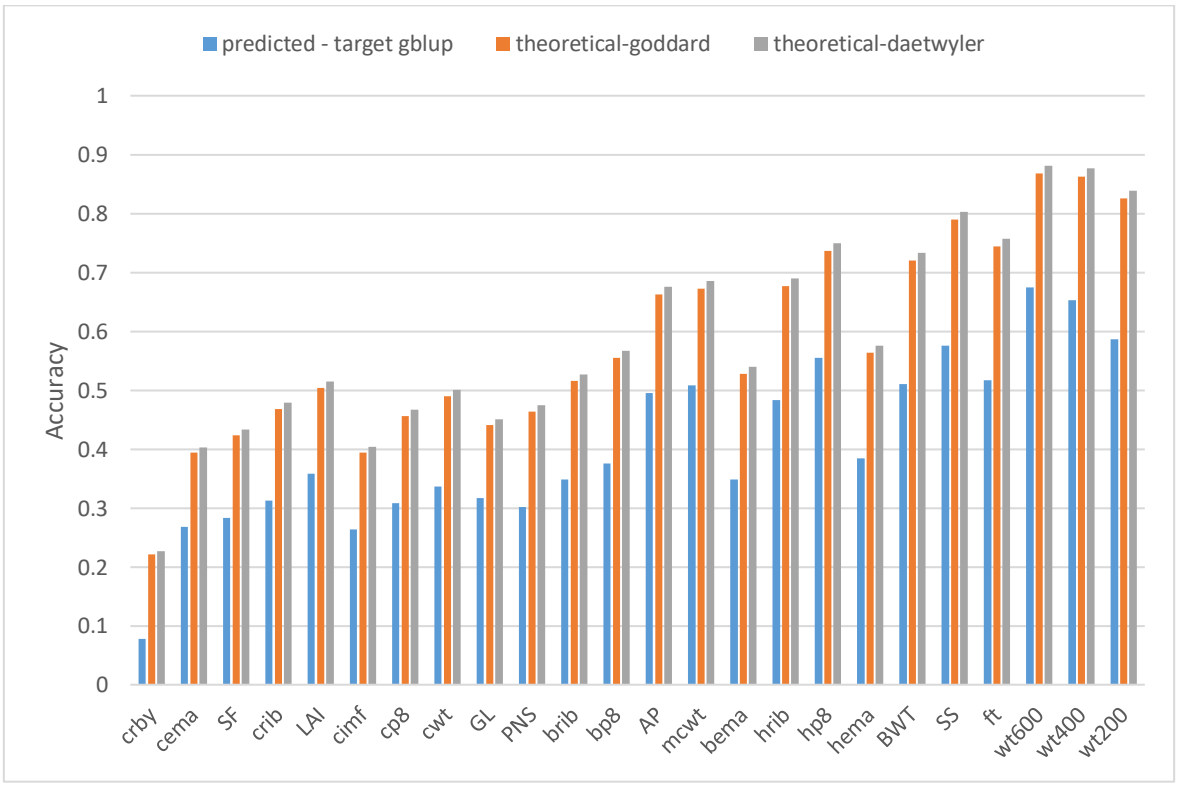


Figure 5.2.3.2: Comparison of empirical accuracy prediction with those from theoretical predictions for Brahman

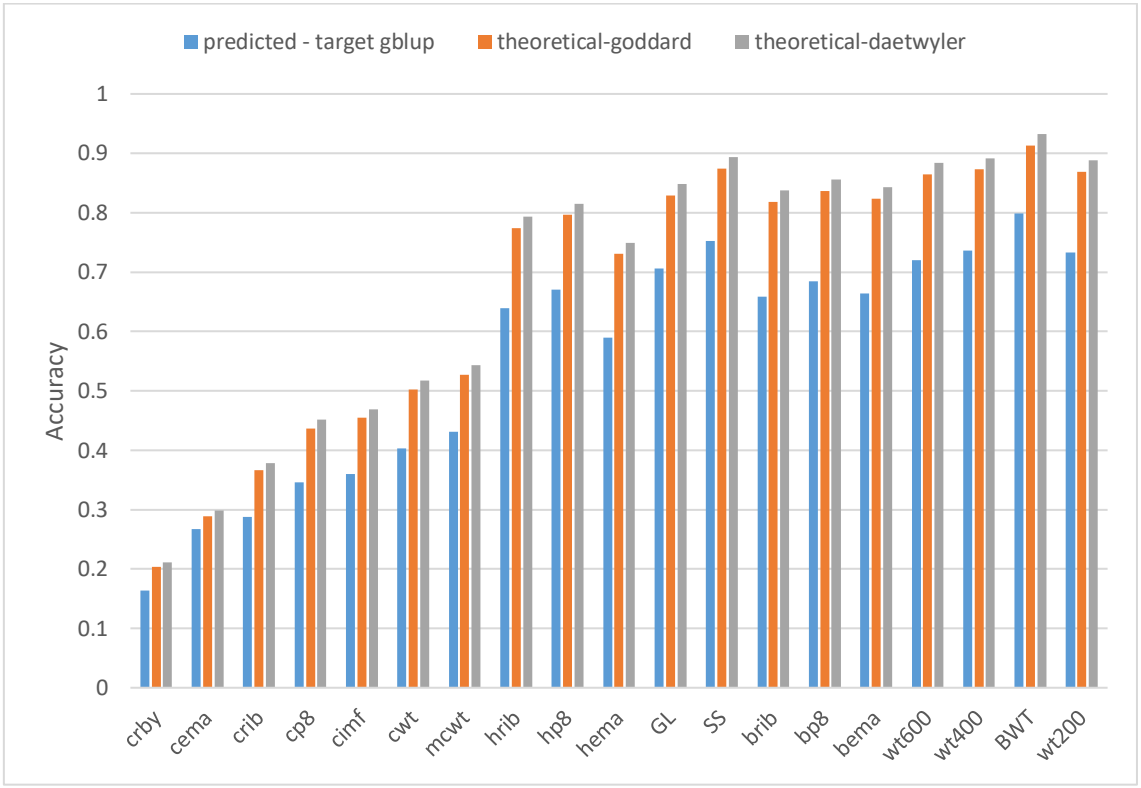


Figure 5.2.3.3: Comparison of empirical accuracy prediction with those from theoretical predictions for Hereford

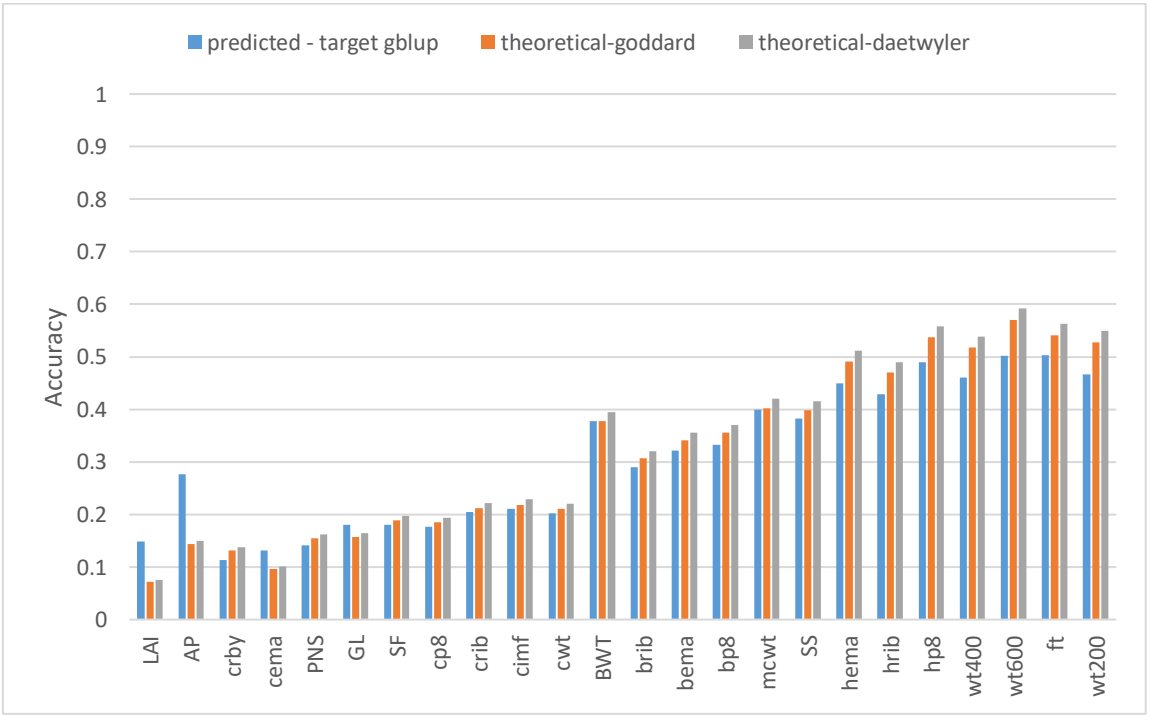


Figure 5.2.3.4: Comparison of empirical accuracy prediction with those from theoretical predictions for Santa Gertrudis

Theoretical predictions performed similarly to Dekkers et al. (2021) empirical predictions when the empirical Me term (estimated via the Dekkers et al. (2021) method) was used in the equations instead of the theoretical Me. Figures 5.2.3.5-5.2.3.8 demonstrate this for each of the breeds. For all breeds, the accuracy prediction by Daetwyler et al. (2008) using the empirical estimate of Me performed closest to the empirical method. On average, the Daetwyler et al. (2008) accuracy prediction (using the empirically estimated Me) was only 1% different compared to the empirical method, and the difference between Daetwyler et al. (2008) (using the empirically estimated Me) and Dekkers et al. (2021) methods ranged from -2% to 4%. There was more variation with the Goddard (2009) accuracy prediction using the empirical Me estimate than with the empirical method. On average, the Goddard (2009) prediction (using the empirically estimated Me) was 3% to 4% lower than the empirical method, and the difference between methods ranged from -7% to 1%. These results clearly show that the accuracy overestimation observed from theoretical methods was due to poor theoretical Me calculations, and when using empirically estimated Me, both empirical and theoretical methods performed similarly.

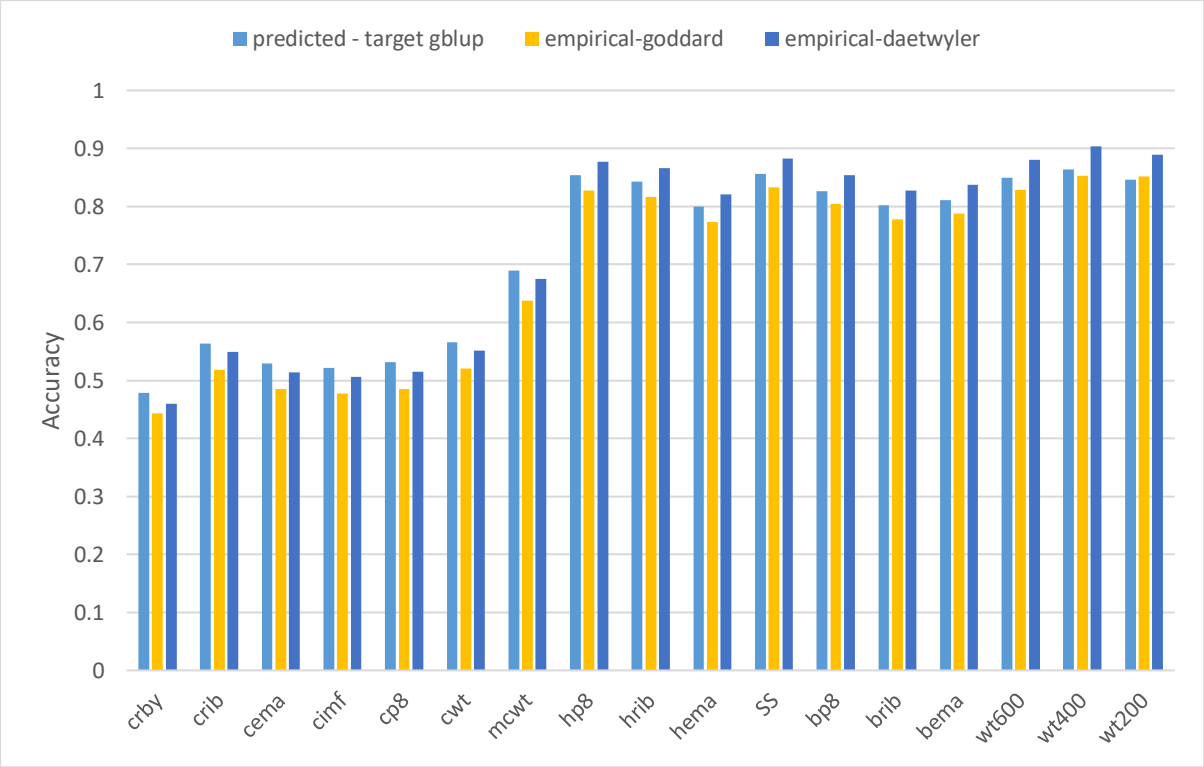


Figure 5.2.3.5: Comparison of empirical accuracy prediction with those from theoretical predictions using the empirical effective number of chromosome segments for Angus

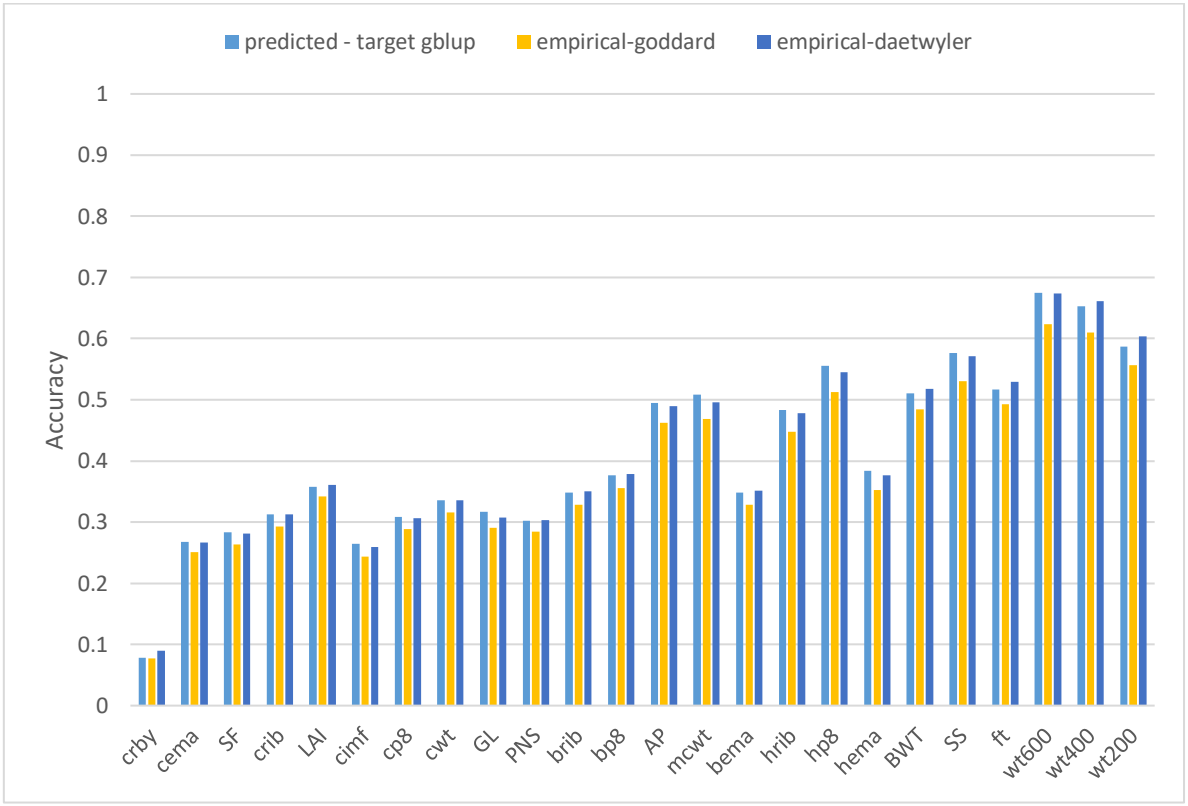


Figure 5.2.3.6: Comparison of empirical accuracy prediction with those from theoretical predictions using the empirical effective number of chromosome segments for Brahman

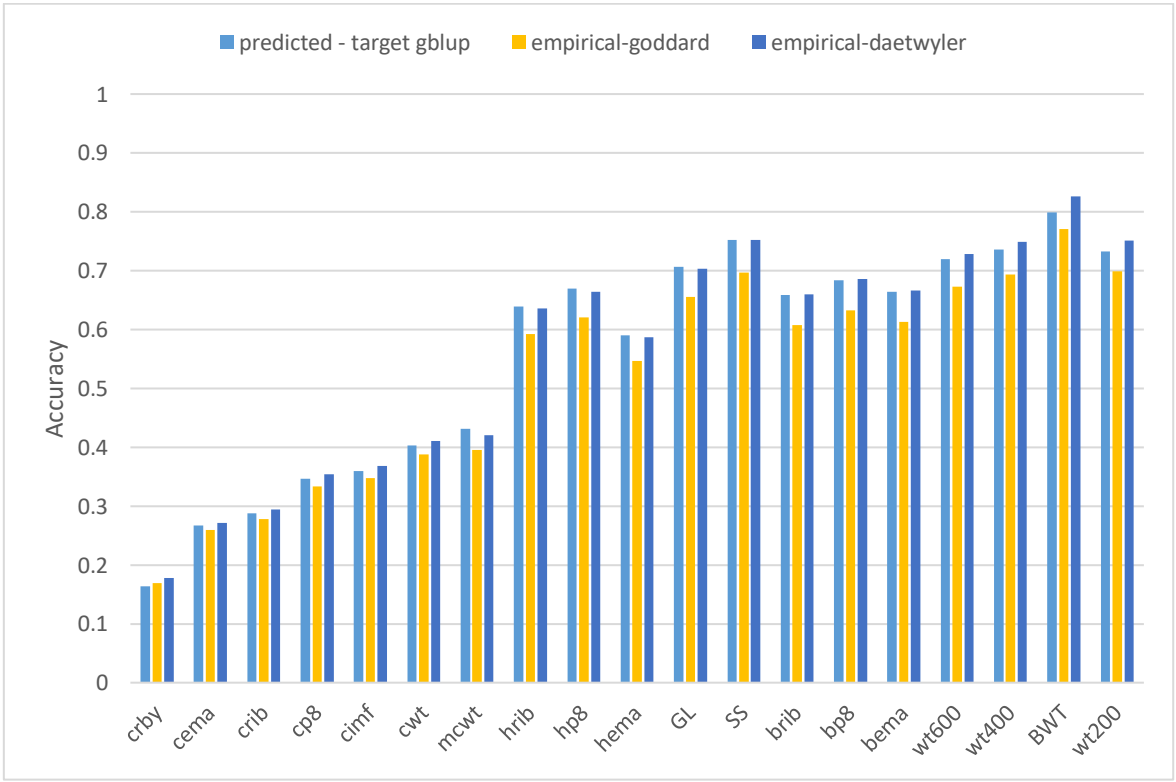


Figure 5.2.3.7: Comparison of empirical accuracy prediction with those from theoretical predictions using the empirical effective number of chromosome segments for Hereford

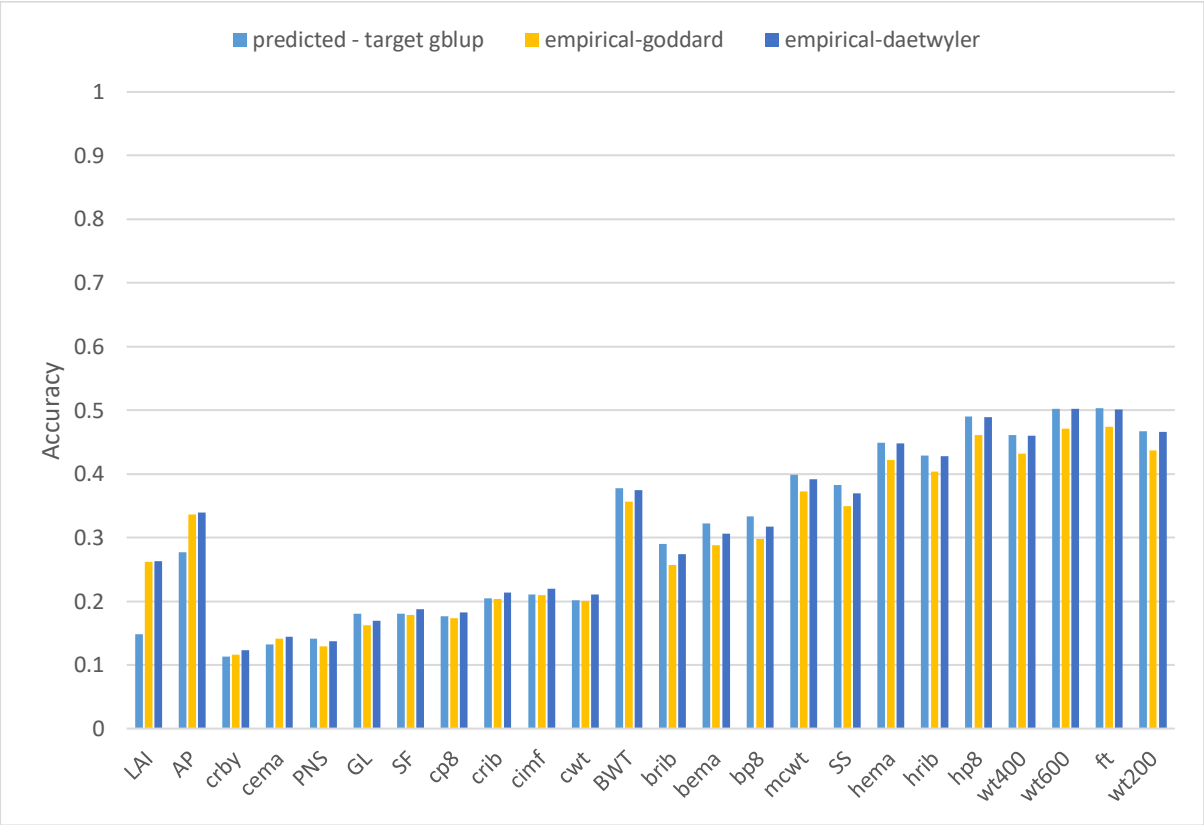


Figure 5.2.3.8: Comparison of empirical accuracy prediction with those from theoretical predictions using the empirical effective number of chromosome segments for Santa Gertrudis

Conclusions from applying an empirical approach for the prediction of accuracy in Australian beef datasets

These results have shown that the Dekkers et al. (2021) empirical method of accuracy prediction is a good predictor of accuracy. However, there are limitations to the widespread application due to the requirement of an existing dataset. Predictions of accuracy will be challenging for breeds that do not yet have a reference population, breeds that have a small reference (n<approximately 1,000) or have a very large reference population (especially if the trait heritability is high) and for predictions for reference sizes not yet already represented in the existing datasets.

A big advantage of the Dekkers et al. (2021) method is the ability to vary how the target animals are defined and how related the target is to the reference population. These attributes are not currently possible with the standard theoretical predictions. A key advantage of the Dekkers et al. (2021) method is the ability to empirically estimate the effective number of chromosome segments (Me), especially for large reference populations. This research has shown that theoretical accuracy predictions overestimate accuracy due to poor estimates of Me from theoretical equations. Using empirical Me in the theoretical calculations showed that the accuracy predictions between the theoretical and empirical methods were comparable.

5.2.4 Development of methods to quantify the effective number of chromosome segments (Me) in different-sized reference populations

The application of the empirical method of Dekkers et al. (2021) for predicting accuracy from genomic selection was shown in the previous section to be effective in Australian beef populations. However, there are limitations to the widespread application due to the requirement of an existing dataset. Therefore, predictions of accuracy will be challenging for breeds that do not yet have a reference population, have a small reference (n<approximately 1,000), have a very large reference population (especially if the trait heritability is high) and for predictions for reference sizes not yet already represented in the existing datasets. Furthermore, it was shown that estimating the empirical Me and using this Me in existing theoretical accuracy prediction equations resulted in similar predictions of genomic accuracies. This work aimed to develop methods and approaches to overcome these limitations and extend the application of empirical methods.

All prediction equations use the Me term for the effective number of chromosome segments. This term is based on effective population size (Ne) and chromosome size. The theoretical formula has several variations, but they tend to be similar. The following formula comes from Goddard et al. (2011), and the theoretical prediction of Me may not necessarily reflect the real Me. This is likely the reason for the discrepancy between theoretically predicted and achieved accuracy from applying genomic selection, especially for larger population reference sizes.

$$\text{Me} = \frac{2NeLk}{\ln(NeL)}$$

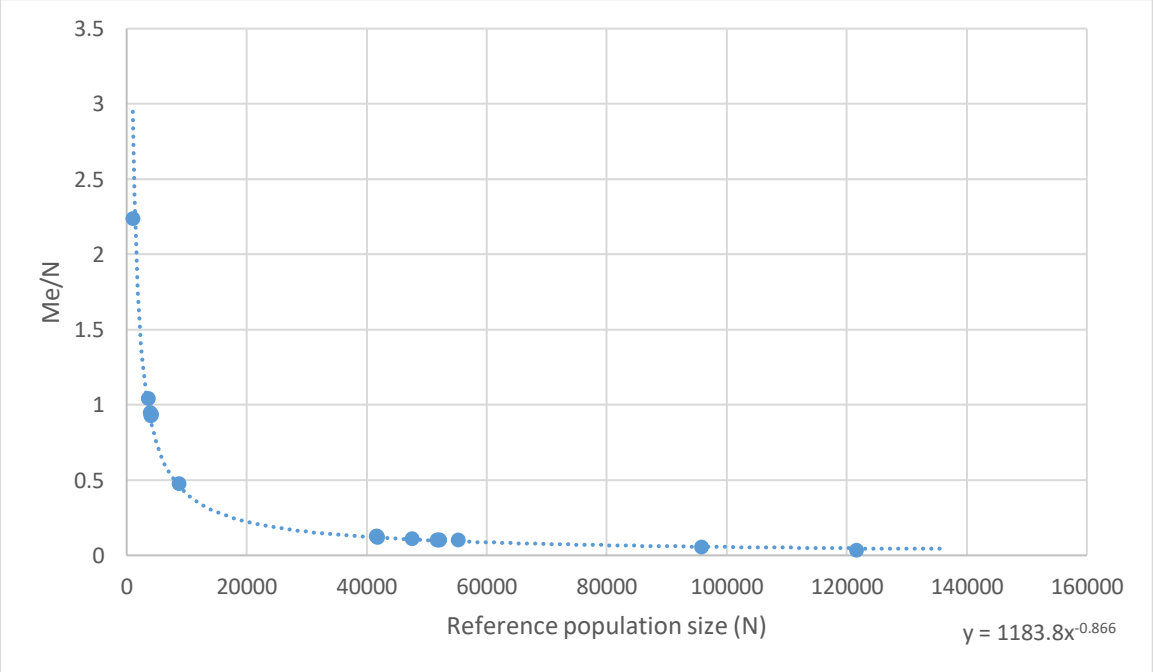


Figure 5.2.4.1: Cubic relationship between the empirically estimated effective number of chromosome segments (Me)/N for each trait in the reference population with the Reference population size (N) for the Angus population

Plotting the empirical Me/N for each trait showed a cubic pattern (Figure 5.2.4.1) that can be described via a power equation. Thus, Me/N can be predicted for a given reference population size.

However, the ability to describe this curve depends on the number of reference traits and size, resulting in gaps on the x-axis.

To fill in the gaps for different-sized references, the 400-day weight reference population was reduced in size based on year of birth, and the empirical Me was calculated using the Dekkers et al. (2021) method. These empirical Me estimates were added to the plot to better describe the cubic relationship between Me/N and N (Figure 5.2.4.2). This produced a better-defined cubic relationship. These plots show that the trait heritability does not impact Me/N, and this makes sense based on the theoretical equations for Me, which are based on the effective population size and genome size. The flatter the shape of the curve, the lower the intercept value.

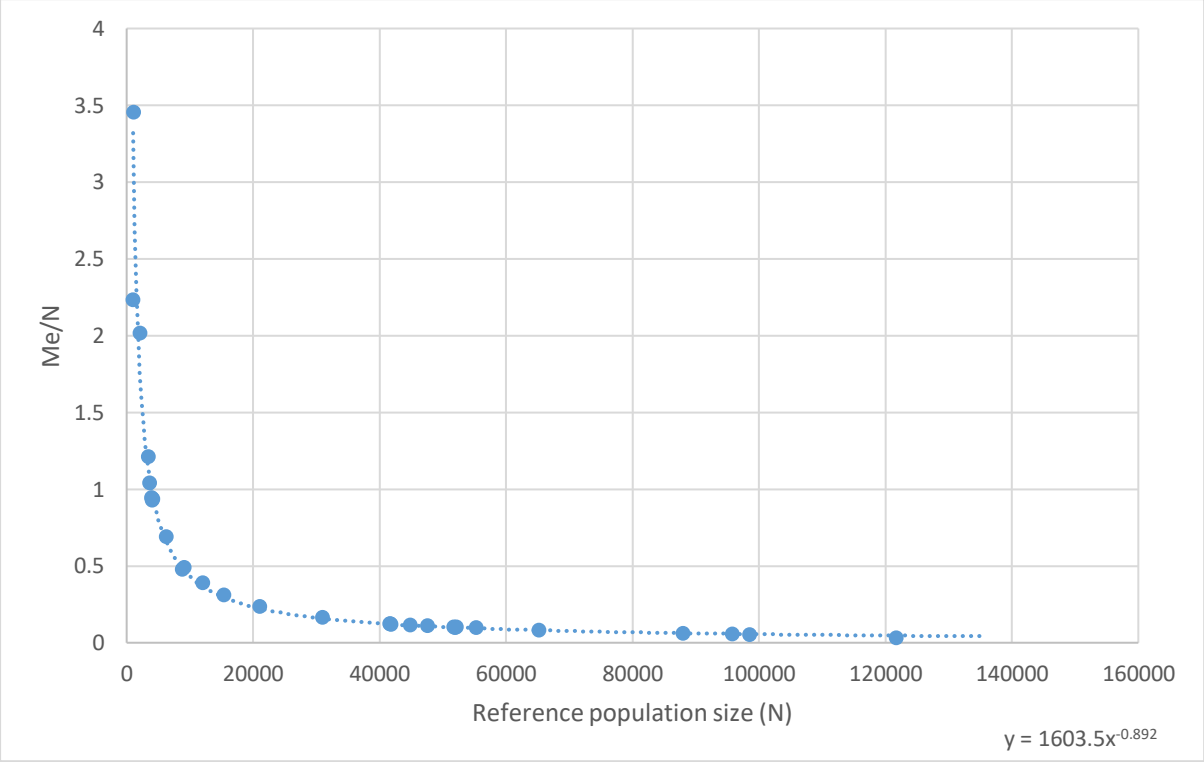


Figure 5.2.4.2: Cubic relationship between the empirically estimated effective number of chromosome segments (Me)/N for each trait in the reference population, including subsets of the 400-day weight reference population, with the Reference population size (N) for the Angus population

Applying the breed-specific prediction (based on the curve described in Figure 5.2.4.2) of Me/N to the Daetwyler et al. (2008) accuracy prediction equation provided similar accuracy results to those predicted from the empirical Dekkers et al. (2021) method. The exception was when the reference population was small (Figure 5.2.4.3). This showed that the breed-specific predictions of Me/N provided accuracy predictions that were the same as using the empirical estimated Me, allowing for accurate accuracy predictions for all reference sizes, not just those where data is currently available, and thus overcoming one of the limitations of applying the empirical Dekkers et al. (2021) method.

Ignoring retail beef yield where larger differences were observed due to the small reference size, the difference between the accuracy from the Dekkers et al. (2021) method using empirical Me and the breed-specific predicted Me/N term differed by a maximum of 4%. On average, across the traits, there was no difference between the two predictions. This demonstrates that provided the breed-specific

Me/N curve has been defined using Dekkers empirical methods, accurate accuracy predictions are possible for all reference sizes and traits for that breed. The breed-specific Me/N curve can be defined using the often-larger reference populations of easier-to-measure traits.

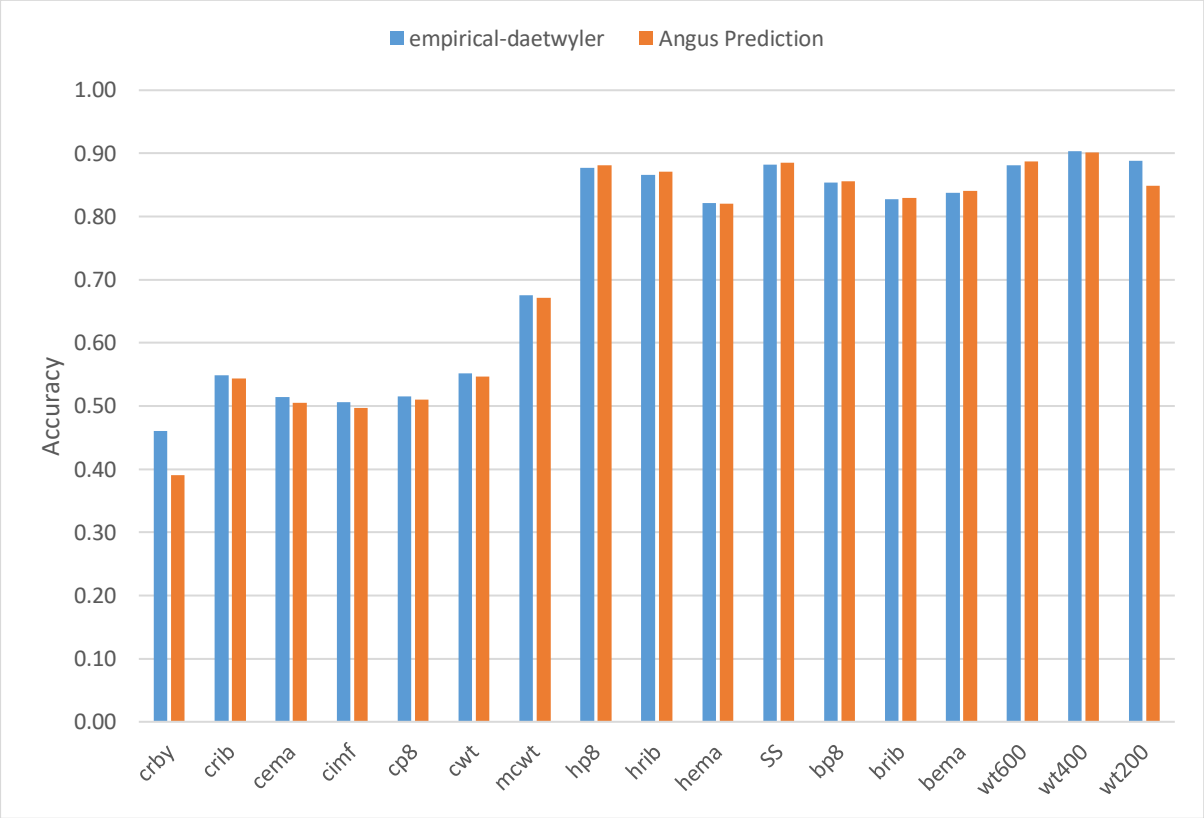


Figure 5.2.4.3: Comparison of empirical accuracy prediction with those from theoretical predictions using the predicted empirical effective number of chromosome segments divided by reference size (Me/N) for Angus

This process was repeated for each breed, and Figure 5.2.4.4 shows the cubic relationships between the four breeds in this study. The shape of the curve was similar for each of the four breeds, but there were differences, likely due to differences in the genomic diversity of the breed. Angus tended to have lower Me/N, and Brahman had higher Me/N for a given reference size. The power function, $Me/N=IX^{y}$, describes the curve where I is the intercept, X is the reference population size, and y is the exponential, defining the line shape. The equations describing the cubic relationship for each breed were as follows;

Angus	$Me/N=1603.5X^{-0.892}$
Brahman	$Me/N=846X^{-0.777}$
Hereford	$Me/N=1149.4X^{-0.831}$
Santa Gertrudis	$Me/N=1402.7X^{-0.868}$

Like Angus, the theoretical accuracy prediction using the predicted Me/N term yielded similar accuracy predictions where the reference population size was greater than 250. The difference between the accuracy from the Dekkers et al. (2021) method using empirical Me and the breed-specific predicted Me/N term differed by a maximum of 4%, 2%, 4%, and 2% for Angus, Brahman, Hereford, and Santa Gertrudis, respectively. On average, there was no difference between the two predictions for all breeds and across the traits.

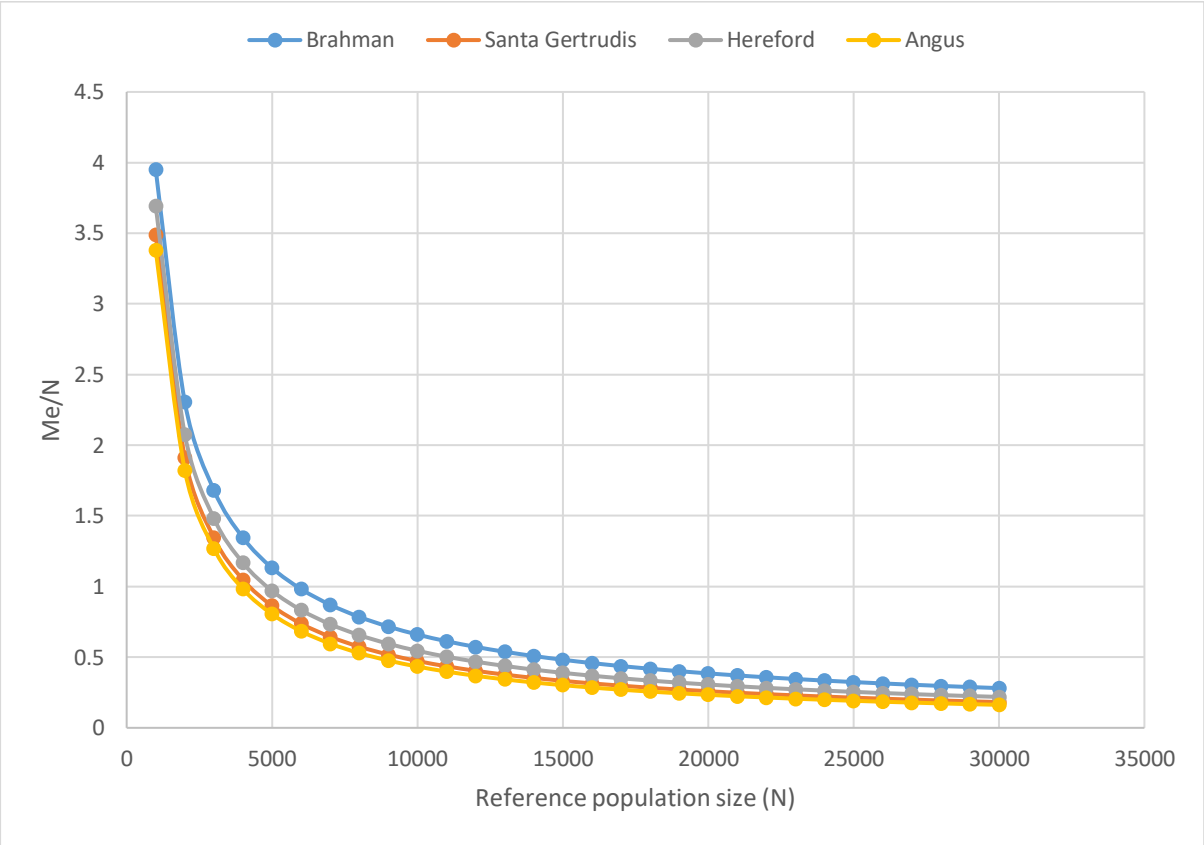


Figure 5.2.4.4: Cubic relationship between the empirically estimated effective number of chromosome segments (Me)/N for each trait in the reference population, including subsets of the 400-day weight reference population, with the Reference population size (N) for the Angus, Brahman, Santa Gertrudis and Hereford populations

The impact of applying another breed prediction equation for Me/N to the Daetwyler et al. (2008) theoretical accuracy prediction was examined. Table 5.2.4.1 summarises the accuracy prediction for traits other than retail beef yield or those with a reference size of less than 250. The biggest differences were observed when the Angus prediction equation was used to predict Brahman and vice versa. This makes sense as these were the most extreme differences observed in Figure 5.2.4.4.

Table 5.2.4.1: Summary of the differences observed from predicting accuracy using different breeds' power functions to predict Me/N compared to the breed-specific Me/N prediction

	Breed prediction equation for Me/N							
	Angus		Brahman		Hereford		Santa Gertrudis	
Breed	**Avg**	**Range**	**Average**	**Range**	**Avg**	**Range**	**Avg**	**Range**
Angus	0.00	-0.04 to 0.01	-0.08	-0.14 to -0.06	-0.04	-0.06 to -0.01	-0.02	-0.06 to -0.03
Brahman	0.05	0.02 to 0.08	0.00	-0.02 to 0.01	0.02	0.00 to 0.04	0.04	0.01 to 0.07
Hereford	0.03	-0.03 to 0.06	-0.04	-0.07 to -0.02	-0.01	-0.04 to 0.01	0.02	-0.04 to 0.04
Santa Gertrudis	0.01	-0.01 to 0.02	-0.02	-0.06 to 0.02	-0.01	-0.04 to 0.02	0.00	-0.02 to 0.02

Conclusions

The Me/N term can be predicted for a breed, and this predicted Me/N term can then be used to predict accuracy for a given reference population size. The predicted accuracy given different-sized reference populations can now be compared using empirical methods, which provide more realistic accuracy predictions. However, this still requires a suitable-sized reference population for at least one trait to derive the cubic Me/N with N relationship.

An alternative is to use the cubic Me/N relationship with N of another breed. This was tested, and although the accuracy prediction from another breed was not as accurate as using a breed-specific cubic Me/N with N relationship, it does provide better accuracy predictions than theoretical methods, especially for traits with larger references.

The ability to predict empirical Me/N now means that the improved empirical predictions have a wider range of applications that benefit the Australian beef industry. A full scientific journal is being prepared for submission to the Genetics Selection Evolution journal, with publication likely to be in 2026.

5.2.5 Development of accuracy prediction tools

Breed-specific predicted accuracy plots for different reference population sizes and trait heritability were generated based on the empirical methods described in this report (breed-specific Me/N based on Figure 5.2.4.4 and applying the Daetwyler et al. (2008) theoretical accuracy prediction equation) and are shown in Figures 5.2.5.1-4.

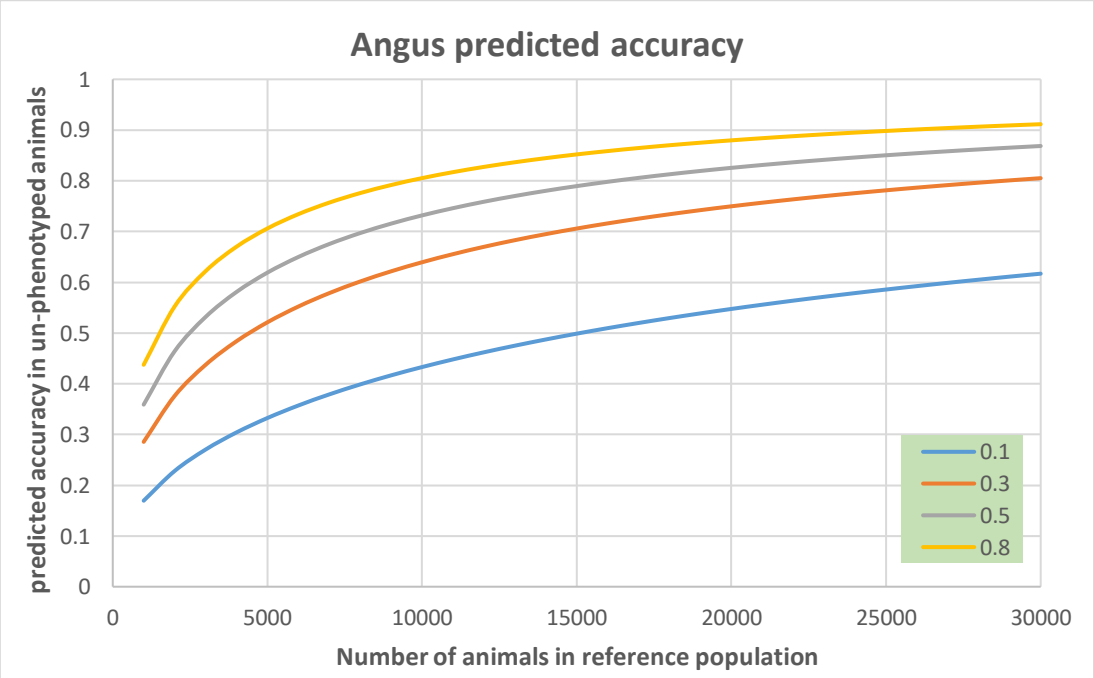


Figure 5.2.5.1: Angus predicted GEBV accuracy of un-phenotyped animals for different-sized reference populations and heritabilities

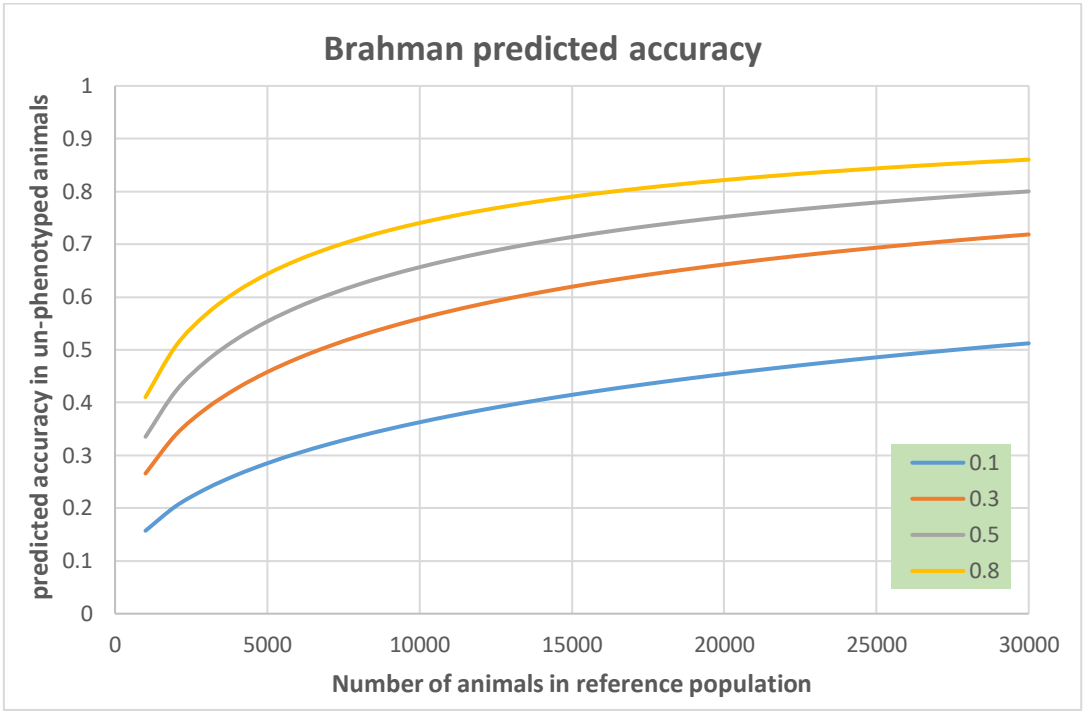


Figure 5.2.5.2: Brahman predicted GEBV accuracy of un-phenotyped animals for different-sized reference populations and heritabilities

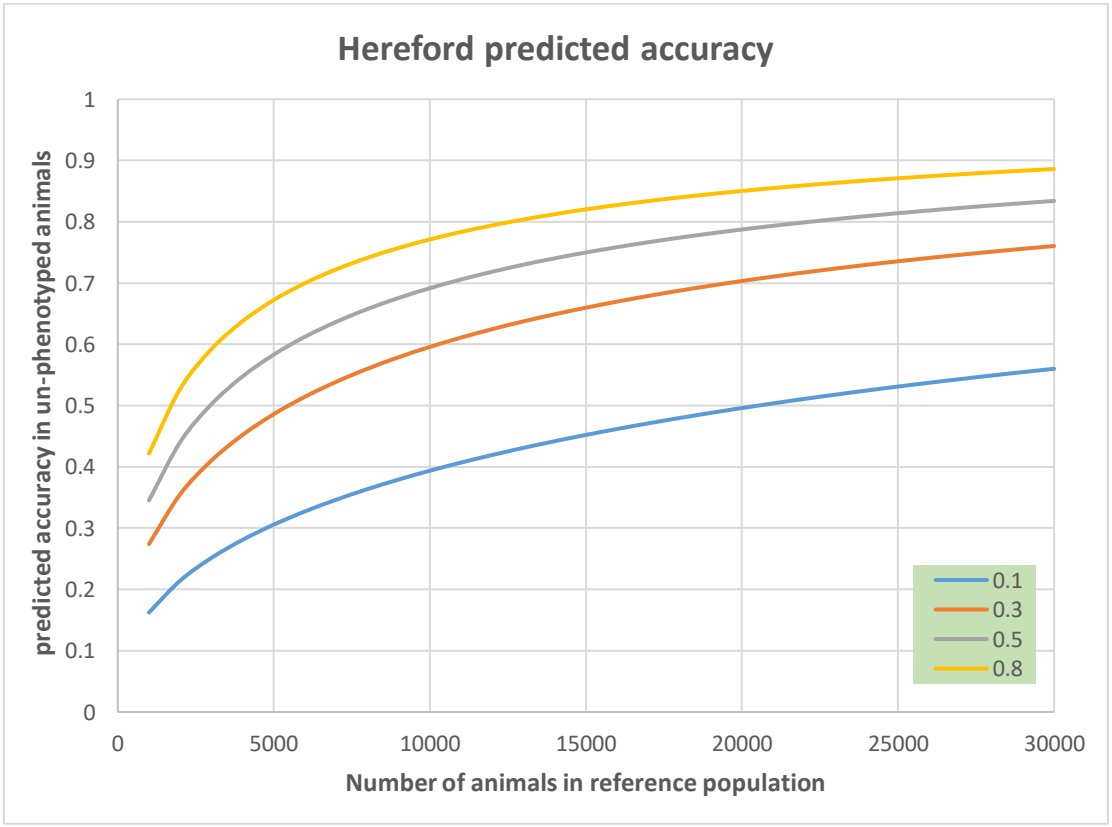


Figure 5.2.5.3: Hereford predicted GEBV accuracy of un-phenotyped animals for different-sized reference populations and heritabilities

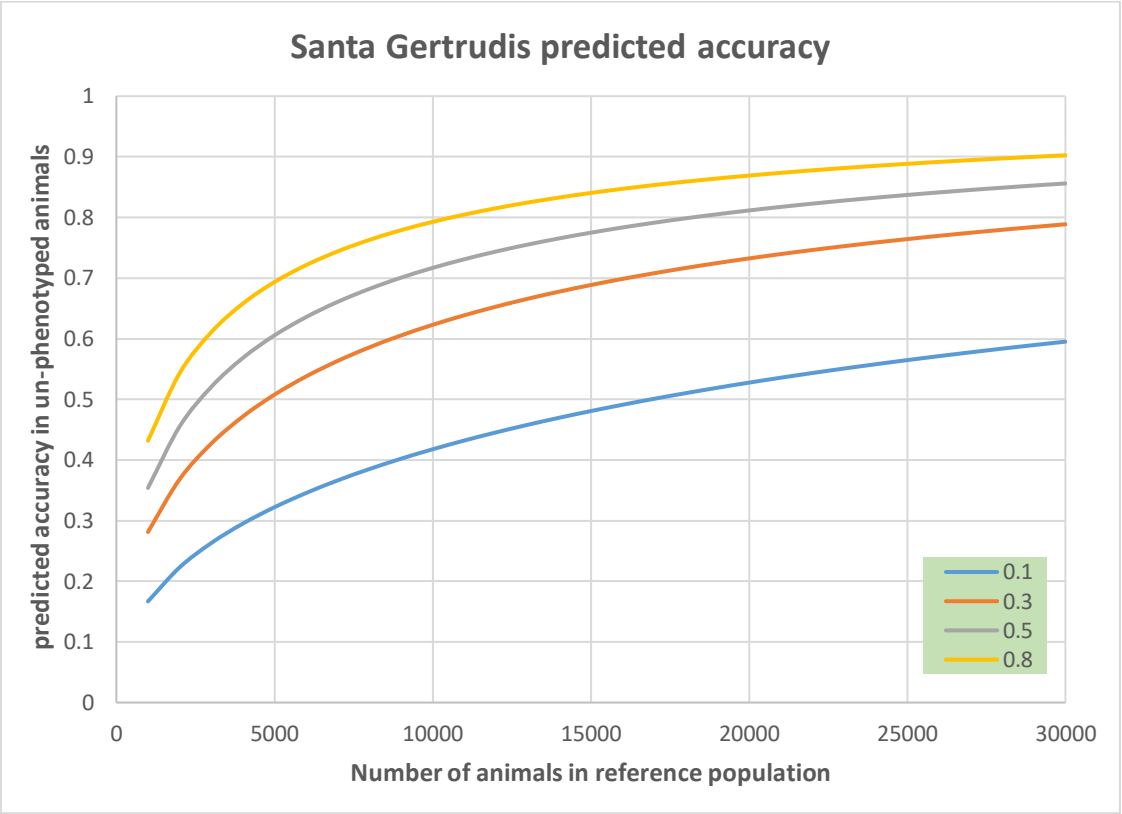
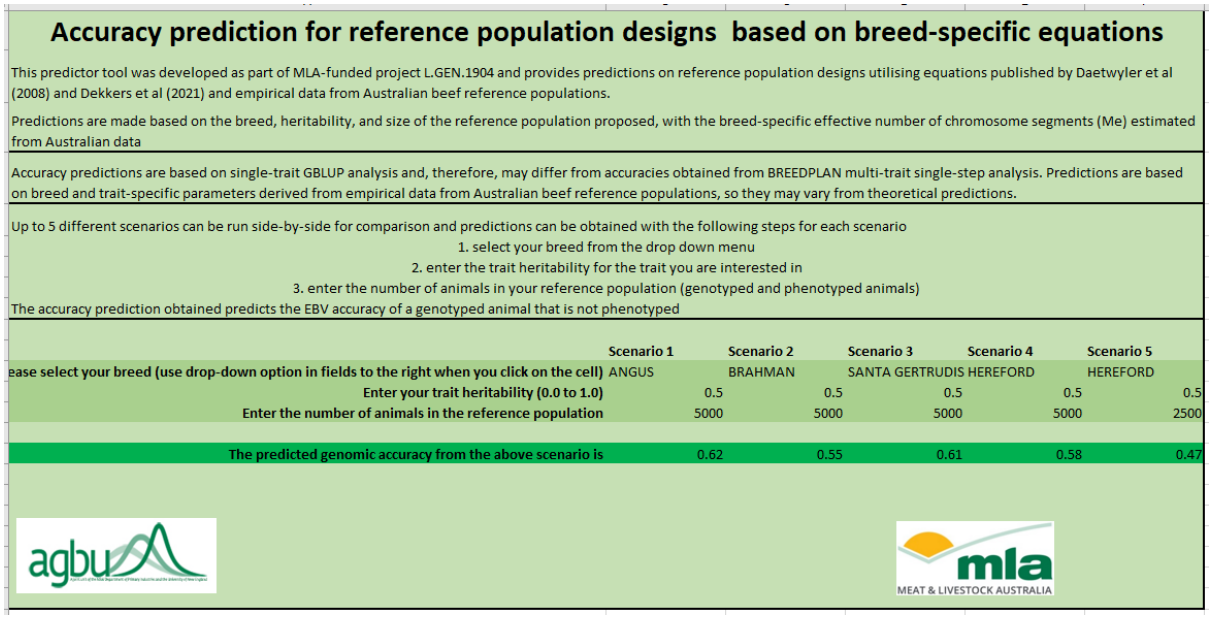


Figure 5.2.5.4: Santa Gertrudis predicted GEBV accuracy of un-phenotyped animals for different-sized reference populations and heritabilities

Two Excel-based tools were created that predict genomic accuracy at a population and individual animal level. These prediction tools are based on the breed's actual reference data using empirical methods rather than just theoretical calculations, making them novel in industry. These methods were previously shown to be more accurate. Access to these tools is available from MLA under a licence agreement, and although developed for all breeds in one tool, they will be distributed as breed-specific tools.

Population-level – This tool was designed for reference design questions. For up to 5 different scenarios, the predicted genomic accuracy can be tested side by side. The user must select the breed, trait heritability and reference population size to obtain a genomic accuracy prediction. The Daetwyler et al. (2008) theoretical accuracy equation was used, but the Me term was based on empirical estimates utilising Dekkers et al. (2021) empirical methods and the method developed in this project (section 5.2.4) to determine the empirical Me for any reference population size. A screenshot of this tool is shown below in Figure 5.2.5.5.



Accuracy prediction for reference population designs based on breed-specific equations

This predictor tool was developed as part of MLA-funded project L.GEN.1904 and provides predictions on reference population designs utilising equations published by Daetwyler et al (2008) and Dekkers et al (2021) and empirical data from Australian beef reference populations.

Predictions are made based on the breed, heritability, and size of the reference population proposed, with the breed-specific effective number of chromosome segments (Me) estimated from Australian data

Accuracy predictions are based on single-trait GBLUP analysis and, therefore, may differ from accuracies obtained from BREEDPLAN multi-trait single-step analysis. Predictions are based on breed and trait-specific parameters derived from empirical data from Australian beef reference populations, so they may vary from theoretical predictions.

Up to 5 different scenarios can be run side-by-side for comparison and predictions can be obtained with the following steps for each scenario

1. select your breed from the drop down menu
2. enter the trait heritability for the trait you are interested in
3. enter the number of animals in your reference population (genotyped and phenotyped animals)

The accuracy prediction obtained predicts the EBV accuracy of a genotyped animal that is not phenotyped

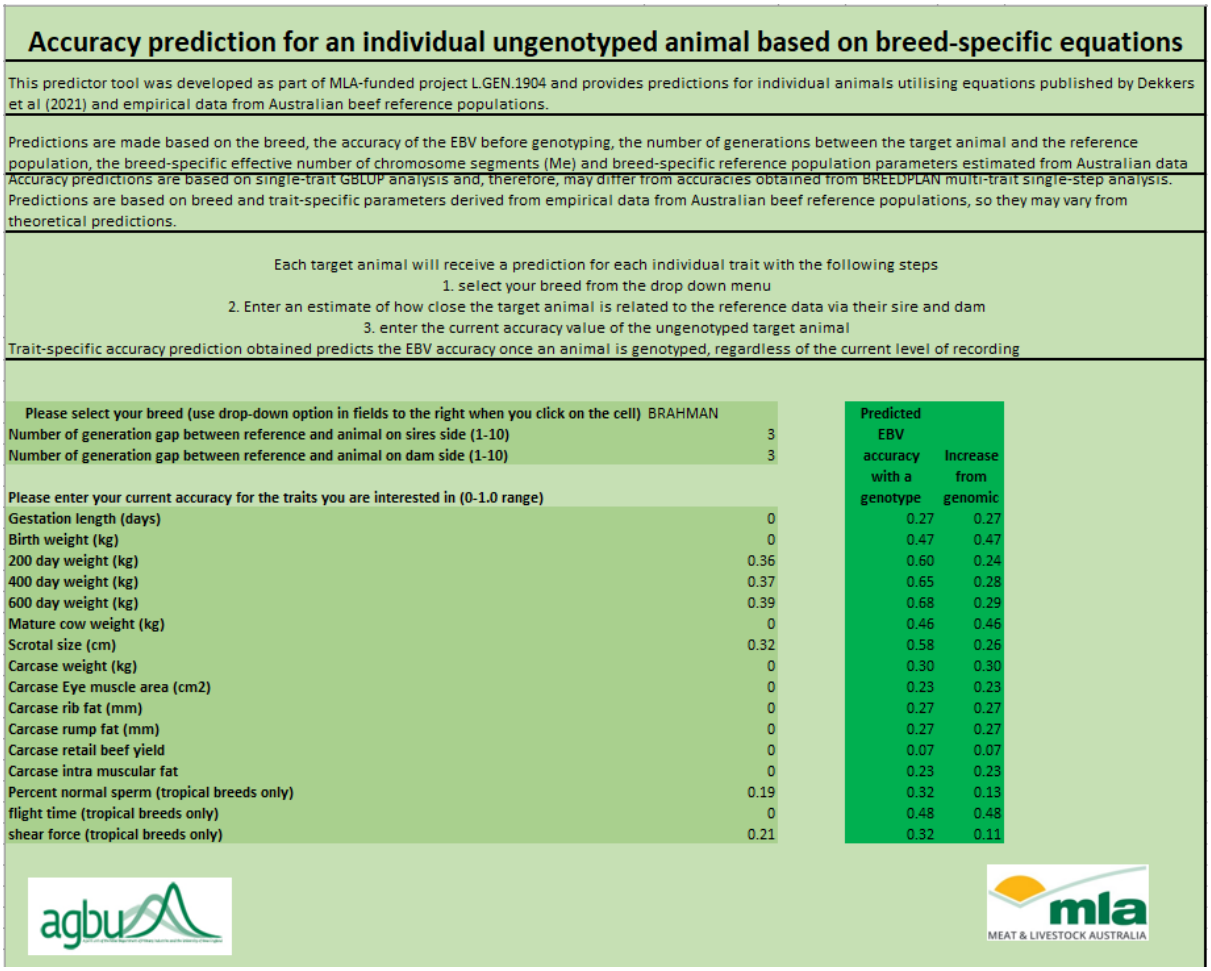
	Scenario 1	Scenario 2	Scenario 3	Scenario 4	Scenario 5
ease select your breed (use drop-down option in fields to the right when you click on the cell)	ANGUS	BRAHMAN	SANTA GERTRUDIS	HEREFORD	HEREFORD
Enter your trait heritability (0.0 to 1.0)	0.5	0.5	0.5	0.5	0.5
Enter the number of animals in the reference population	5000	5000	5000	5000	2500
The predicted genomic accuracy from the above scenario is	0.62	0.55	0.61	0.58	0.47

agbu

mla MEAT & LIVESTOCK AUSTRALIA

Figure 5.2.5.5: Population-based genomic accuracy prediction tool to assist in reference population design

Individual-level – this tool was designed to consider expected increases in genomic accuracy based on the animal's current accuracy level; those already with information (i.e. phenotypes) will experience a smaller increase than those with genomics only. The user must select the breed, the number of generations between the target animal and animals in the reference population, and the current accuracy of each trait the user is interested in. In return, the user receives the predicted EBV accuracy with genomics and compares it with the initial accuracy entered into the tool. The methodology for these calculations was based on Dekkers et al. (2021) empirical methods and reference population parameters derived from the accuracy work and reported in previous sections. A screenshot of this tool is shown in Figure 5.2.5.6.



Accuracy prediction for an individual ungenotyped animal based on breed-specific equations

This predictor tool was developed as part of MLA-funded project L.GEN.1904 and provides predictions for individual animals utilising equations published by Dekkers et al (2021) and empirical data from Australian beef reference populations.

Predictions are made based on the breed, the accuracy of the EBV before genotyping, the number of generations between the target animal and the reference population, the breed-specific effective number of chromosome segments (Me) and breed-specific reference population parameters estimated from Australian data

Accuracy predictions are based on single-trait GBLUP analysis and, therefore, may differ from accuracies obtained from BREEDPLAN multi-trait single-step analysis. Predictions are based on breed and trait-specific parameters derived from empirical data from Australian beef reference populations, so they may vary from theoretical predictions.

Each target animal will receive a prediction for each individual trait with the following steps
1. select your breed from the drop down menu
2. Enter an estimate of how close the target animal is related to the reference data via their sire and dam
3. enter the current accuracy value of the ungenotyped target animal

Trait-specific accuracy prediction obtained predicts the EBV accuracy once an animal is genotyped, regardless of the current level of recording

Please select your breed (use drop-down option in fields to the right when you click on the cell)	BRAHMAN		
Number of generation gap between reference and animal on sires side (1-10)	3		
Number of generation gap between reference and animal on dam side (1-10)	3		
Please enter your current accuracy for the traits you are interested in (0-1.0 range)		Predicted EBV accuracy with a genotype	Increase from genomic
Gestation length (days)	0	0.27	0.27
Birth weight (kg)	0	0.47	0.47
200 day weight (kg)	0.36	0.60	0.24
400 day weight (kg)	0.37	0.65	0.28
600 day weight (kg)	0.39	0.68	0.29
Mature cow weight (kg)	0	0.46	0.46
Scrotal size (cm)	0.32	0.58	0.26
Carcase weight (kg)	0	0.30	0.30
Carcase Eye muscle area (cm2)	0	0.23	0.23
Carcase rib fat (mm)	0	0.27	0.27
Carcase rump fat (mm)	0	0.27	0.27
Carcase retail beef yield	0	0.07	0.07
Carcase intra muscular fat	0	0.23	0.23
Percent normal sperm (tropical breeds only)	0.19	0.32	0.13
flight time (tropical breeds only)	0	0.48	0.48
shear force (tropical breeds only)	0.21	0.32	0.11

Figure 5.2.5.6: Animal-level genomic accuracy prediction tool to assist in predicting the increase in accuracy that would occur by genotyping animals based on their current EBV accuracy

5.3 Does poor data quality impact genomic predictions?

Genomic evaluations have increased the EBV accuracy in livestock herds, especially for hard or late-to-measure and low heritability traits. Genomic accuracy is a direct function of the reference data size, increasing with size until a plateau is reached. However, this assumes that all reference data is of suitable quality, which may not always be true. This work aimed to investigate whether poor reference data quality impacts genomic accuracy.

Birthweight data from a November 2023 BREEDPLAN extract of a single breed was used, although the results of this study are likely to apply to other breeds and traits. The birth weight trait was selected as the breed data audit report demonstrated that there were herds with lower data quality scores in the dataset. Figure 5.3.1 illustrates the data quality scores for all herds with recorded birth weights. Lower data quality scores reflect data outside the normal range for several metrics specific to each trait.

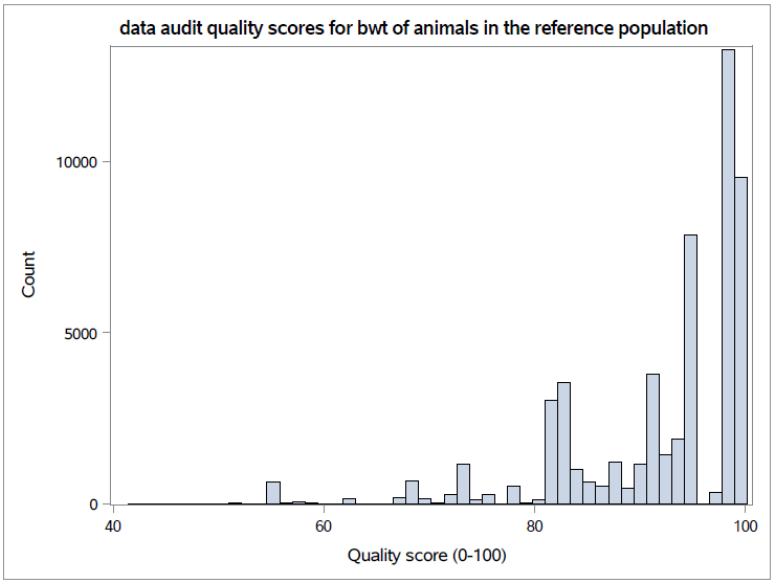


Figure 5.3.1: Data audit quality scores for the birth weight reference population

There were 42,204 genotyped animals born in 2018-2023 and recorded for birth weight, although there were very few 2023-born animals in the data. This data was used in this study. Approximately 8% and 30% of the dataset had data audit scores of less than 80 and less than 90, respectively. Genetic parameters were those from BREEDPLAN evaluations. Wombat software was used to undertake GBLUP genetic evaluations, and LR statistics were used to assess the impact of different data quality scenarios. All six years of data were included in the 'whole' scenario, and only the first three years were included in the 'partial' scenario. The 'partial' dataset represented approximately 30% of the data, with the recent data (born 2020+) removed from the whole dataset, representing approximately 70%. Five LR statistics (Legarra and Reverter, 2018) were calculated for the focal animals: bias, stability, population accuracy, dispersion and slope. Focal animals were defined as all animals born 2020-2023 that were part of the reference population (i.e. in the 'whole' evaluation), but the phenotypes were removed in the 'partial' scenario.

Three scenarios were considered based on the size of the reference population: the full (n=42,204) reference population, a reference size of 5,000, which was approximately 12.5% of animals and akin to a typical live weight reference size and a reference size of 1,000, which was approximately 2.5% of animals and akin to a typical carcase trait reference size.

Four GBLUP evaluations were undertaken for each reference size scenario, each having a 'whole' and 'partial' evaluation (based on birth year).

1. All data (ALL)
2. All phenotypes from herds with data quality scores <80 removed (80+)
3. A subset of phenotypes from herds with data quality scores of 90+ was removed. The number of randomly selected herds removed was such that record numbers were similar to the 80+ scenario to act as a control to mitigate against the reduced reference size (80+ control)
4. All phenotypes from herds with data quality score <90 removed (90+)

The number of phenotypes for all runs varied according to the scenario, but the 42,204 genotypes were always included. When the reference size = 42k, this was simply the whole dataset, but when the reference size was 5k or 1k, a random subset of herds was chosen to construct the required

reference size. However, the random subset of herds was modified to ensure that approximately 8% of the reference data had data quality scores <80. All data from a herd were either included or excluded in each scenario. This was done for five replications, and the average of the replicates was presented in the results. No restrictions were placed on the proportion of the reference data with data quality scores <90, and indeed, the amount of data with 80-90 data quality and 90+ data quality scores varied across the replicates. Figure 5.3.2 shows how the complete dataset (42k) was divided into the 1k and 5k scenarios used in this study.

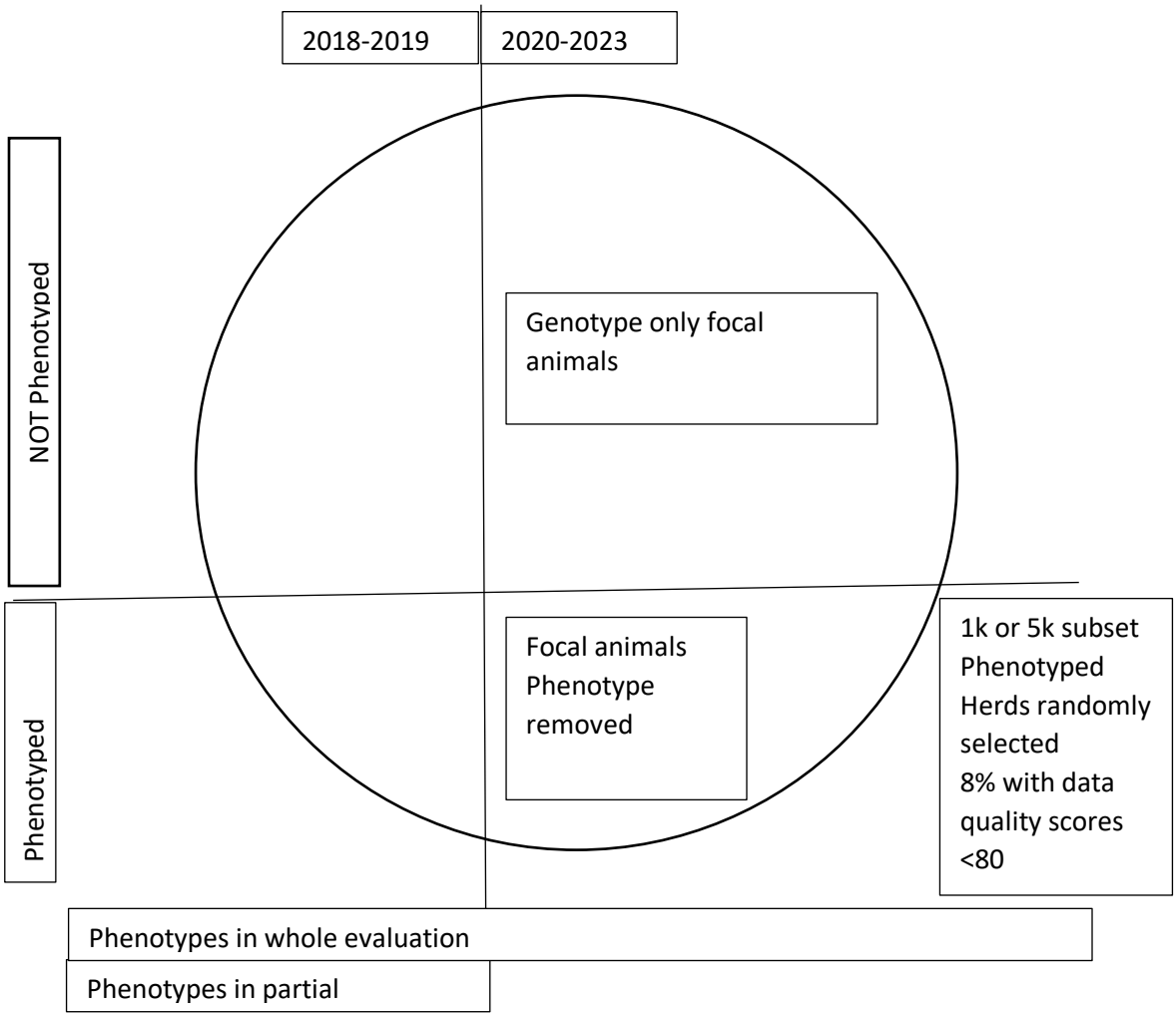


Figure 5.3.2: Diagram illustrating the subsets of animals analysed for the 1k and 5k reference size

Table 5.3.1 describes the 11 datasets considered in this study. The full reference population (n=42k) does not represent a scenario we observe in practice, with all animals being genotyped and phenotyped. Approximately 8% of the data was considered low-quality, 23% mid-quality, and 69% high-quality. When the reference size was reduced (n=5k or 1k), the proportion of low-quality data was kept similar to 8% in all replicates, but all other factors depended on which herds were randomly selected to be part of the population. Therefore, five replicates were run, and the average of the replicates was presented. There was variation across the replicates in the proportion of the data classified as mid-quality. This was mainly observed for the 1k reference size, where the proportion of mid-quality data (41%) was higher than the other reference sizes.

This analysis was based on real data, so the 'truth' is unknown. Therefore, the impact of removing subsets of data was compared with results obtained when all data, regardless of the data score, for the given scenario, were considered. For example, when the reference size was 5k, results were obtained using all 5k data and removing the subset of the 5k data with data quality scores less than 80. The impact of removing data with data quality scores less than 80 was assessed by comparing the results with all 5k data metrics. Three LR statistics, bias, dispersion, and slope (not reported), showed no trends across the analyses when low-quality data were removed. These statistics were similar for analyses with and without low-quality data for the different subsets of focal animals. Focal animals were born 2020-2023; there were 30,443, 3,679 and 664 focal animals for the 42k, 5k and 1k reference populations. To provide further insight, these focal animals were subsetted into those from herds with low, mid and high-quality data quality scores. Although not focal animals, LR statistics were also reported for genotype-only animals from herds that were not included in the reduced 1k and 5k reference population sizes.

Impact of removing low-quality data

Table 5.3.2 records the LR statistics for stability and population accuracy for the All evaluation (i.e. with no data removed) and when low-quality data (defined as data score < 80) was removed. Also recorded was the control, where similar numbers of high-quality animals were removed to control for the reduction in accuracy expected due to reduced reference size.

When considering the population as a whole (the All subset), removing low-quality data had no impact for all three reference sizes, with the change in stability and accuracy values ranging from 0% to 1%. The control comparison showed changes in accuracy ranging from 0% to 4%. Focal animals (born 2020-2023) with low-quality data (i.e. the data being removed in this scenario) did show an improvement when the low-quality data was removed from the reference sizes 1k and 5k. Removing the low-quality data improved the stability and accuracy for animals with low-quality data by 10% and 14%, whereas the control only saw changes between -1% and 4%, indicating that the changes observed were not solely due to changes in the amount of data. For the full (42k) reference size, removing low-quality data had no impact on stability and accuracy. Focal animals with mid- or high-quality data showed no effect from removing low-quality reference data for all population sizes, with the change in stability and accuracy values ranging from -1% to 0%. The control comparison showed changes in accuracy and stability ranging from -2% to 13%. When the reference size was very small (1k) for high-quality focal animals, an increase in stability and accuracy was observed in the control analysis. This can be attributed to the very low stability and accuracy value of replicate 5 for the All and 80+ scenarios. This extreme replicate (which had a much lower proportion of high-quality records) occurred in a scenario with already small numbers, and more replicates being undertaken would be beneficial. When considering animals that had genotype only at all times (i.e. herds not selected to be part of the 1k and 5k reference populations), there was no impact of removing low-quality data for all reference sizes, with the change in stability and accuracy values ranging from 0% to 1%. The control comparison showed changes in accuracy ranging from 0% to 2%.

Impact of removing low and mid-quality data

Table 5.3.3 records the stability and accuracy statistics for the All evaluation (i.e. with no data removed) and when low and mid-quality data (defined as data score < 90) were removed. For this scenario, there was no control analysis. Compared to the low-quality data scenario, the number of mid-quality records varied across the five replicates (Table 5.3.1), ranging from 3.9% to 71.4%.

When considering the population as a whole (the All subset), no improvement was observed for all three reference sizes when low and mid-quality data were removed. Instead, the decrease in reference size reduced stability and accuracy estimates. The decrease ranged from -10% to 0%. Focal animals (born 2020-2023) with low-quality data scores (i.e. the data being removed in this scenario) showed no improvement over that already observed from removing just low-quality reference data. Instead, removing the mid-quality data decreased the stability and accuracy values from -13% to 4%, likely due to reduced reference size. Focal animals with mid-quality data (i.e. the data being removed in this scenario) showed a small improvement in stability and accuracy, with increases ranging from 1% to 5% observed. This small improvement is likely due to removing the low and mid-quality data, as all other focal groups showed decreased stability and accuracy resulting from reduced reference size. Focal animals from herds with high-quality data scores showed no impact of removing low and mid-quality reference data for all population sizes, with the change in stability and accuracy values ranging from -4% to -1%. When considering animals that had genotype only at all times (i.e., herds not selected to be part of the 1k and 5k reference populations), removing low and mid-quality data for all reference sizes reduced stability and accuracy, with the change in stability and accuracy values ranging from -11% to -5 %.

Conclusions

Removing low-quality data positively impacted the stability and accuracy of the genetic evaluations for focal animals from herds with low-quality data scores, but not on animals from herds with mid or high-quality data scores. This demonstrates that while low-quality phenotypes have an impact, this impact is mainly restricted to only those herds with low-quality phenotyping and not the herds that collect quality phenotypes. The effect of removing low-quality data was greatest for smaller reference sizes, demonstrating that where a trait is hard to measure and consequently will have a small reference size (e.g., abattoir carcase traits), it is essential that these phenotypes are high-quality. However, the phenotyping quality was still important for the scenario similar to what is currently observed for live-weight reference populations.

The relationship between herds may also influence the impact, but this was not considered in this study. However, herds with low-quality data scores generally had lower regression coefficients describing relationships with animals in the birthweight reference population. There were 330 herds with data quality scores and herd-specific regression coefficients describing the relationship of the herd with the breed's birthweight reference population. A moderate positive Pearson correlation of 0.23 was observed between the data quality score and the regression coefficient. This indicates that herds with higher-quality phenotypes tended to be more closely related to animals in the breed reference population (those with a phenotype and genotype, like the dataset in this study). This was further supported by 26% of herds with high-quality data having regression coefficients of 1.1+ compared to only 9% and 11% observed for herds with low- and mid-quality data, respectively. Furthermore, 21% of herds with low-quality data had regression coefficients less than 1, compared to 14% and 10% observed for mid and high-quality data, respectively. Should herds with low-data quality be those that are also highly influential (regression coefficients 1.1+) in the reference population, then their data may unduly impact the results for herds with mid and high-quality data.

There was no benefit to the removal of mid-quality data from the analysis. While modest increases in accuracy and stability were observed for animals with mid-quality data, there were decreases in accuracy and stability for other animal groups; this was particularly the case for genotyped animals from herds that had no data in the reference population. The reduction can be attributed to the

decline in reference size, as removing low and mid-quality data resulted in approximately 30 to 50% of the reference data being removed. This demonstrates the balance that is required between quality and quantity. Both are important for overall accuracy and stability. The current study showed that removing low-quality data improved results for animals from herds with low-quality data, with no change to animals from herds with mid- and high-quality data. If the proportion of low-quality data was higher than the 8% observed in this data, the reduction in the quantity of data may have inversely impacted the animals with mid- and high-quality data, as we observed when the mid-quality data was removed.

Table 5.3.1: Description of the data subsets analysed, where the reference population size was 1k, 5k or 42k, and for the smaller subsets, five replicates were generated.

Reference size (replicate)	**42k**	**5k (avg)**	**1k (avg)**	**5k (1)**	**5k (2)**	**5k (3)**	**5k (4)**	**5k (5)**	**1k (1)**	**1k (2)**	**1k (3)**	**1k (4)**	**1k (5)**
Scenario – All data													
N phenotypes in whole	42,204	5,101	1,005	5,346	5,060	5,050	5,056	4,993	1,058	1,029	984	973	979
N phenotypes in partial	11,761	1,452	341	1,779	1,154	1,415	1,698	1,214	427	346	338	255	339
N (%) data quality score <80	3,288 (7.8)	424 (8.3)	97 (9.7)	484 (9.1)	417 (8.2)	432 (8.6)	395 (7.8)	391 (7.8)	83 (7.8)	95 (9.2)	111 (11.3)	89 (9.1)	105 (10.7)
N (%) data quality score 80-90	9,749 (23.1)	868 (17.0)	413 (41.1)	967 (18.1)	416 (8.2)	1,479 (29.3)	199 (3.9)	1,280 (25.6)	222 (21.0)	603 (58.6)	480 (48.8)	63 (6.5)	699 (71.4)
N (%) data quality score 90+	29,167 (69.1)	3,809 (74.7)	495 (49.3)	3,895 (72.9)	4,227 (83.5)	3,139 (62.2)	4,462 (88.3)	3,322 (66.5)	753 (71.2)	331 (32.2)	393 (39.9)	821 (84.4)	175 (17.9)
Scenario – removal of low-quality (<80) data													
N phenotypes in whole	38,916	4677	908	4,862	4,643	4,618	4,661	4,602	975	934	873	884	874
N phenotypes in partial	10,734	1945	302	1,677	4,057	1,280	1,630	1,079	403	306	273	221	308
Scenario – removal of high-quality (90+) data to form control													
N phenotypes in whole	38,870	4662	889	4,824	4,642	4,591	4,633	4,620	978	915	839	855	856
N phenotypes in partial	11,019	1333	318	1,566	1,070	1,313	1,553	1,165	393	334	321	224	318
Scenario – removal of low and mid-quality (<90) data													
N phenotypes in whole	29,167	3809	495	3,895	4,227	3,139	4,462	3,322	753	331	393	821	175
N phenotypes in partial	8,287	1045	154	1,376	912	804	1,577	558	334	95	81	219	39

Table 5.3.2: Stability and Accuracy results[#] for different focal animal groups when the reference population size was 1k, 5k or 42k and low-quality data was removed from the analysis.

	All focal animals			Subsets of focal animals based on their herd data quality score									Genotype only animals from herds not included in the reference population		
	All			low-quality (<80)			mid-quality (80-90)			high-quality (90+)					
	42k	5k	1k	42k	5k	1k	42k	5k	1k	42k	5k	1k	42k	5k	1k
N	30,443	3,649	664	2,261	314	58	7,302	571	265	20,880	2,764	341	0	26,794	29,779
Stability															
full dataset	0.79	0.56	0.46	0.76	0.48	0.47	0.77	0.60	0.47	0.79	0.54	0.39		0.68	0.65
low-quality data (<80) removed	0.79	0.56	0.46	0.81	0.62	0.58	0.78	0.60	0.47	0.79	0.54	0.38		0.69	0.65
Impact of removing low-quality data	**0.00**	**0.00**	**0.00**	**0.05**	**0.14**	**0.12**	**0.01**	**0.00**	**0.00**	**0.00**	**0.00**	**-0.01**		**0.01**	**0.00**
control animals removed*	0.79	0.56	0.50	0.81	0.48	0.51	0.77	0.58	0.48	0.79	0.55	0.51		0.68	0.67
Impact of removing control animals	**0.00**	**0.00**	**0.04**	**0.05**	**0.00**	**0.04**	**0.00**	**-0.02**	**0.01**	**0.00**	**0.01**	**0.13**		**0.00**	**0.02**
Accuracy															
full dataset	0.77	0.55	0.46	0.76	0.52	0.52	0.77	0.59	0.47	0.77	0.54	0.40		0.65	0.64
low-quality data (<80) removed	0.77	0.56	0.46	0.77	0.63	0.62	0.77	0.58	0.47	0.77	0.54	0.39		0.65	0.64
Impact of removing low-quality data	**0.00**	**0.01**	**0.00**	**0.01**	**0.11**	**0.10**	**0.00**	**-0.01**	**0.00**	**0.00**	**0.00**	**-0.01**		**0.00**	**0.00**
control animals removed*	0.78	0.55	0.50	0.81	0.51	0.55	0.77	0.58	0.48	0.78	0.54	0.51		0.65	0.66
Impact of removing control animals	**0.01**	**0.00**	**0.04**	**0.05**	**-0.01**	**0.04**	**0.00**	**-0.01**	**0.01**	**0.01**	**0.00**	**0.11**		**0.00**	**0.02**

* Absolute numbers vary as animals in focal groups differ. # results for reference sizes 1k and 5k were the average of five replicates

Table 5.3.3: Stability and Accuracy results[#] for different focal animal groups when the reference population size was 1k, 5k or 42k, and low and mid-quality data were removed from the analysis.

	All focal animals			Subsets of focal animals based on their herd data quality score									Genotype only animals from herds not included in the reference population		
	All			low-quality (<80)			mid-quality (80-90)			high-quality (90+)					
	42k	**5k**	**1k**	**42k**	**5k**	**1k**	**42k**	**5k**	**1k**	**42k**	**5k**	**1k**	**42k**	**5k**	**1k**
N	30,443	3,649	664	2,261	314	58	7,302	571	265	20,880	2,764	341	0	26,794	29,779
Stability															
full dataset	0.79	0.56	0.46	0.76	0.48	0.47	0.77	0.60	0.47	0.79	0.54	0.39		0.68	0.65
low-quality data (<80) removed	0.79	0.56	0.46	0.81	0.62	0.58	0.78	0.60	0.47	0.79	0.54	0.38		0.69	0.65
Low and mid-quality data (<90) removed	0.79	0.53	0.36	0.80	0.56	0.48	0.82	0.64	0.49	0.78	0.51	0.34		0.64	0.54
Additional Impact of removing mid-quality data	**0.00**	**-0.03**	**-0.10**	**0.04**	**-0.06**	**-0.10**	**0.05**	**0.04**	**0.02**	**-0.01**	**-0.03**	**-0.04**		**-0.05**	**-0.09**
Accuracy															
full dataset	0.77	0.55	0.46	0.76	0.52	0.52	0.77	0.59	0.47	0.77	0.54	0.40		0.65	0.64
low-quality data (<80) removed	0.77	0.56	0.46	0.77	0.63	0.62	0.77	0.58	0.47	0.77	0.54	0.39		0.65	0.64
Low and mid-quality data (<90) removed	0.76	0.52	0.38	0.75	0.58	0.49	0.78	0.59	0.49	0.75	0.51	0.35		0.60	0.53
Additional Impact of removing mid-quality data	**-0.01**	**-0.04**	**-0.08**	**-0.01**	**-0.05**	**-0.13**	**0.01**	**0.01**	**0.02**	**-0.02**	**-0.03**	**-0.04**		**-0.05**	**-0.11**

results for reference sizes 1k and 5k were the average of five replicates

6. Conclusion

This project has successfully advanced research on reference population design and provided support and value-added to existing reference populations. The activities within this project have been varied, ranging from assisting reference population projects with their design to undertaking research that will enable more effective reference populations in the future. Many studies were undertaken, helping to evaluate new traits and phenotyping technologies, investigating the impact of SNPs of large effect on key production and reproduction traits and better understanding the traits recorded in reference populations. Current breed reference populations were assessed using the methodology developed in the project to determine whether Australian beef references were sufficiently related to their wider breed populations. The project also developed new methods and tools for predicting EBV accuracy from genomics-only animals. These tools can be used to more effectively evaluate the impact of reference design decisions and the expected increase in accuracy for genotyped animals. The effect of reference phenotype quality on genomic predictions was assessed. The key findings from this project are listed below.

6.1 Key findings

- Descriptions of Australian beef genomic reference populations were compiled to capture the reference population design and summarise the data generated. This information will allow future investment in reference populations to be targeted for maximum benefit and better leverage existing reference populations for genetic improvement.
- An SQL database was created to capture an inventory of the animals and data collected as part of reference population projects. The database captures information on the project design and the information collected on reference animals.
- Genomic prediction accuracy is directly related to how the genotyped selection candidate is related to the genomic reference. A relatedness to reference metric was developed to describe how two groups of animals were related. This method had many applications, including assessing how animals and/or herds were related to reference populations and identifying sires to include in reference populations.
- The relatedness to reference metric was used to assess how animals in the wider breed populations were related to trait-specific reference populations. The results showed that for hard-to-measure traits (i.e. abattoir carcase traits, female reproduction traits and mature cow weight), most of the breed reference populations still required additional investment to ensure the full benefits of genomic selection for the whole breed.
- The relatedness to reference metric was used to describe and compare the relatedness of the Southern Multi-Breed reference population to a whole breed. The study confirmed that the foundation cows and sires used in the Southern Multi-Breed Project were highly related to the breed population. Therefore, the reference data collected will benefit within-breed genomic selection programs.
- The longevity of the Angus reference population was explored using the relatedness to reference metric. As relatedness between Angus Sire Benchmarking Program cohorts and subsequently used industry sires declined, there was a corresponding fall in accuracy gains from the Angus Sire Benchmarking Program phenotypes.

- A new empirical-based method for predicting genomic predictions was applied and was shown to better predict accuracy than current theoretical approaches. The predicted accuracy of genomic predictions was calculated based on current Angus, Brahman, Hereford, and Santa Gertrudis reference populations. Analysis showed that the benefit of the empirical method was an improved estimate of the effective number of chromosome segments, which is an important factor in genomic accuracy.
- Applying the empirical-based method for predicting the accuracy of genomic predictions was limited to existing reference populations. Therefore, the method was extended to allow its application to a wider range of scenarios.
- Using the extended empirical-based method for accuracy prediction, two tools were developed to predict genomic accuracy when designing future reference populations and determining the potential benefit of genotyping individual animals. The accuracy prediction tools are available by license from MLA.
- The impact of poor phenotype quality of reference animals on genomic selection was limited to those herds recording phenotypes considered poor quality and did not impact herds that recorded phenotypes classified as medium or high quality or genomic-only breeding values.
- In addition to genetic improvement, the management decisions of producers also impact phenotypic performance and profitability. The following management strategies were identified to improve phenotypic performance and profitability for carcase and fertility traits.
    - Managing the age spread of a cohort – If the age spread is large, the spread of carcase weight within a cohort will be greater, and profitability will be impacted due to animals being slaughtered before meeting market specs or being kept longer, incurring additional costs. An age spread in the cohort that was too large was also shown to impact the number of pubertal heifers at the start of mating and the time it took for a cow to start cycling after weaning a calf.
    - Season of birth – Analysis showed that calves born late in the calving season were more likely to have delayed puberty, resulting in fewer heifers being pubertal at the start of mating. Furthermore, heifers that calve late in the season were also shown to take longer to cycle again after the calf was weaned.
    - Body weight and growth – Managing the live weight of heifers affected whether the heifers were pubertal at the start of mating. In tropical beef breeds, it was shown that for 85% of heifers to be pubertal at the start of mating, the average weight should be 221 kg as yearlings and 353 kg at the start of mating. Body weight and composition at the start of the 2nd mating period affected the lactation anoestrus interval.
    - Puberty status at mating – Heifers that were pubertal at the start of mating were more likely to have cycled again when the calf was weaned.
    - Tailoring management decisions in response to annual seasonal effects – Annual seasonal effects were shown to impact carcase weight, age at puberty and lactation anoestrus interval. Tailoring management decisions in response to annual seasonal changes may help mitigate the effect of the season.
    - Culling older cows – calves of older cows were shown to be lighter at slaughter.

- The myostatin mutations (double-muscling) NT821 and F94L were shown to segregate in Droughtmaster and Santa Gertrudis. NT821 had the biggest impact on production traits, with heterozygote animals being heavier and more muscular, improved tenderness and leaner, but had delayed puberty age, increased days to calving, and an indication of higher incidence of calving-related deaths.
- Immune competence traits (cell- and antibody-mediated immune response) were found to be heritable, with variation indicating that selection is possible for these traits in northern beef breeds. However, more needs to be understood about the impacts of these traits on economically important traits before they can be effectively used in breeding programs.
- New sensor technology was trialled. Sensor data from eGrazor collars classified behaviours of tropically adapted beef breeds at pasture that aligned with literature reports, but showed no relationship with feedlot feed intake. Sensor data from Ceres ear tags was inconsistent, and no beneficial outcomes could be made at this stage.
- The relationship between carcase traits currently not included in BREEDPLAN evaluations and BREEDPLAN traits for female reproduction, weaning weight, carcase weight and shear force was estimated. Estimated variance components indicate that the non-BREEDPLAN carcase traits were heritable and could be included in genetic evaluations. There were no strong unfavourable correlated responses with the BREEDPLAN reproduction, growth and carcase traits. Shear force was moderately to strongly correlated with cooking loss and the three meat colour traits. Ossification was estimated to be moderately correlated with age at puberty and growth traits, and further research could investigate if there is merit in developing an ossification breeding value to describe the physiological development of animals.
- Analyses showed that animals with higher Brahman content had higher hump heights, lower MSA index, decreased hot carcase weight, hot P8 fat depth, MSA EMA, MSA rib fat at 12/13th rib, intramuscular fat percentage, MSA USDA Ossification, Longissimus dorsi a* colour, Longissimus dorsi b* colour, MSA Loin Temperature and MSA Marbling score and increased shear force, Longissimus dorsi cooking loss and Longissimus dorsi L* colour. These results showed that as Brahman content increased, the meat eating quality decreased, although this study could not assess if the adjustment for hump height in the MSA index were in alignment with these results.
- Principal component analysis of Brahman, Droughtmaster and Santa Gertrudis breeds showed that the Brahman and Droughtmaster genetics represented in the Repronomics project represented the genotyped Brahman and Droughtmaster industry animals. Santa Gertrudis animals in the Repronomics project did not represent the full range of genotyped Santa Gertrudis industry animals.
- Genome-wide association studies found several significant SNPs for heifer age at puberty and birth weight of Brahman and Droughtmaster animals. The significant SNPs for heifer age at puberty were in regions close to significant regions reported previously in the literature for tropical beef and dairy breeds.
- Multi-breed project EBVs for novel traits recorded at different times (as a heifer, into mating one, and into mating two) were developed for tropically adapted breeds.

- A preliminary analysis of Wagyu feed efficiency records estimated moderate heritability. Variation was observed for preliminary EBVs of 29 sires with progeny recorded for net feed intake.

6.2 Benefits to industry

The main benefit to the industry arising from this research was the development of evidence-based guidance on where future investment in genomic reference populations is required. Descriptions of the current effectiveness of beef reference populations and the development of improved accuracy tools and linkage metrics will allow more effective reference populations to be designed. The new tools developed can be utilised to construct future reference populations. This will help inform investment decisions and ultimately improve the genetic gain and profitability of the beef industry.

The project has provided the first research into myostatin mutations in Droughtmaster and Santa Gertrudis. Exploiting these results for tropical beef populations will help to inform the northern beef industry on managing these myostatin mutations in their populations. Work undertaken for this project has provided new information about genetic relationships between traits, the development of new EBVs, and an understanding of how managing fixed effects can improve carcase and female reproduction traits, and several SNPs were identified as significantly associated with female reproduction traits.

Investigations into applying new sensor-derived phenotypes for pasture feed intake are important to enable future genetic improvement in feed intake and feed efficiency traits. However, results from this project show that more work is required on the technologies before they can be widely used for genetic improvement programs.

7. Future research and recommendations

Investment in beef reference populations should continue. This is especially the case for hard-to-measure traits, smaller breeds, and maintaining reference populations' relatedness to current beef industry animals. Given the limited resources available for investment, investing in reference populations that achieve multiple aims and building reference populations would be advantageous. It would be beneficial to ensure that reference populations measure a wide range of traits to estimate genetic relationships and for new technology and traits to be evaluated and included successfully in BREEDPLAN multi-trait evaluations. With a major focus being the development of beef multi-breed genetic evaluations, reference populations that include multiple breeds with head-to-head comparisons are essential and may be the primary source of their reference data for smaller breeds.

The relatedness to reference metrics and prediction of accuracy tools developed in this project is available via license from MLA. Future reference populations can use them to assist with project design and identify influential new genetics for inclusion.

Recording hard-to-measure phenotypes is a major cost for reference populations. Therefore, future research should focus on new phenotyping technologies that yield high-value phenotypes more cost-

effectively. Genotyping costs are also not insignificant, and research that resulted in cheaper genotyping would be advantageous.

Extension and adoption activities should continue to promote the value and importance of reference populations, both for industry education and to motivate industry investment in reference populations.

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9. Appendix

9.1 Description of Australian Beef Reference Populations

9.1.1 Angus Information Nucleus and Sire benchmarking program

Organisation: Angus Australia

Breeds: Purebred Angus

Project Duration and size: Approximately 800 to 1,100 calves from 30 to 40 sires annually from 2010 and continuing

Project Status: Active and ongoing

Project contact: Christian Duff (Angus Australia General Manager Genetic Improvement)

Project overview: The Angus Sire Benchmarking Program (ASBP) has operated since 2010 with three objectives: 1) progeny test modern Angus bulls, 2) generate records on hard-to-measure traits, including abattoir carcase traits, and 3) generate data for genetic evaluation and contribute to a genomic reference dataset. ASBP cohorts 1 - 11 were co-funded with MLA, and cohorts 12 and onwards were self-funded by Angus Australia. Several overlay projects with ASBP cohorts and additional traits may have been co-funded via these overlays, i.e. net feed intake and methane records were collected on ASBP cohorts 12 – 15 and co-funded as part of the UNE-led methane project. Cows are mated via Artificial Insemination (AI) to progeny test approximately 30 to 40 sires annually. The resulting calves are recorded for traits from birth to slaughter for steers and from birth to first calf for heifers.

Project herds: Project herds generally were commercial purebred Angus herds from the industry, although registered herds were part of the project in some cases. Initially, herds are part of the ASBP project for three cohorts, with the option to remain in the project longer. Within a cohort, there tended to be 4-6 project herds at a time, and over ASBP cohorts, 1 - 9 in total, 16 herds located in NSW and VIC were involved. ASBP herds required approximately 300 purebred Angus cows of any age to be available to be mated via AI mating. Herds agreed to manage and record progeny according to ASBP protocols provided by Angus Australia. No pedigree or fixed effect information was required for the cows, but cows were identified whilst part of the ASBP project (i.e., maternal half-sibs were identified). Angus Australia financed the AI program, but herds were financially compensated with activity-based payments (i.e. at weaning) to contribute towards the labour costs of recording the phenotypes. Herds also retained the female progeny sired by project sires.

Project sires: A sire nomination process was open to all Angus members in Australia and New Zealand, with Angus Australia selecting project sires from the nominations. Sires tended to be predominantly young bulls (2-3 years), but some older influential bulls were also included and were assessed for genetic diversity to ensure they were free of genetic conditions. Sire genetic merit was also considered, with sires exhibiting a range of EBVs. However, sires with low genetic merit were unlikely

to be selected as the progeny produced was required to meet the specs of the feedlot. Sires were used across herds and, in some cases, across years to provide linkage. All matings were via AI, with the project herds providing backup bulls. However, only calves sired by project sires were recorded in the project. Owners of selected sires pay a fee ($2,500+GST for Australian bulls and $4,000+GST for international bulls) and supply 100 semen straws for the AI program. Over 13 cohorts, 436 different sires were used, with 56 of these bulls being from New Zealand, the USA or the UK.

Project cows: Project cows tended to be purebred commercial Angus cows, but some were crossbred, with unknown parentage and birth dates. A small number of herds were registered pedigree cows. The herds retained female progeny, and they could become project cows in subsequent years.

Management of project animals: Project animals were all from AI matings, with each sire having, on average, approximately 25 progeny. Animals born in the same herd were managed together. Birth and early growth performance traits were measured on all calves at the co-operator herds. Males were castrated, steers were grown to feedlot entry, where they undertook a feed intake test before being finished in a commercial feedlot. Carcases were assessed for a range of meat quality traits. Heifers were grown out in the co-operator herds and joined by a natural service sire in multi-sire groups with sires provided by co-operator herds to obtain first-parity days to calving. The BIN did not record individual service sire, but the multi-sire mating group information was recorded.

Traits recorded: A range of traits and fixed effects (i.e. date of birth) from birth through to slaughter or first-parity calving were recorded by the BIN program utilising project protocols provided by Angus Australia. All animals were recorded for birth (weight and calving ease), early growth, ultrasound scanning, temperament (docility), coat score and structural assessment traits. Steers were recorded for feed intake and carcase traits, including meat quality traits. Heifers were also recorded for first-parity days to calving. For hard-to-measure traits, the BIN animals represent the majority and, in some cases, the entire reference population. Additional novel traits were recorded as part of additional overlay projects for subsets of the BIN animals. These novel traits included immune competence, methane emissions, heat tolerance, retail beef yield and carcase fatty acid profile.

Overview of records collected: The table on the next page summarises the number of records (rounded to the nearest hundred) collected throughout the BIN projects for a range of traits. For some traits, only steers, heifers or only some cohorts were recorded.

The number of records (rounded to the nearest hundred) collected for BIN animals for a range of different traits from birth to slaughter

	Included in Angus TACE[4]	Cohorts[1] 1-13
Birth weight (kg)	Y	11,500
Calving difficulty (score)	Y	8,800
200-day weight (kg)	Y	11,600
400-day weight (kg)	Y	8,200
600-day weight (kg)	Y	7,100
Docility (score)	Y	11,400
Flight time (s)	N	4,500
Coat score (score)	N	7,000
Structural Soundness[2] (score)	Y	8,900
Live ultrasound traits[3]	Y	9,700
Live condition score (score)	N	6,000
Live muscle score (score)	N	8,000
Hip Height (cm)	N	1,700
Sheath score (score)	N	2,200
Carcase weight (kg)	Y	5,100
Carcase EMA	Y	5,000
Carcase P8 fat	Y	5,000
Carcase rib fat	Y	4,700
Carcase Intra-muscular fat	Y	4,700
Ausmeat marble score	Y	5,000
MSA marble score	Y	5,100
MSA index	N	5,000
Shear force	N	1,200
Carcase ossification	N	5,100
Carcase cooking loss	N	1,200
Carcase PH	N	4,200
Carcase lab PH	N	1,500
Carcase meat and fat colour	N	5,100
Carcase lab meat colour	N	1,500
Carcase meat temperature - chiller	N	5,000
Carcase hump score (score)	N	3,300
Net feed intake (kg/day)	Y	5,100
First parity days to calving (days)	Y	3,800
Immune competence traits	Y	4,700
Retail beef yield (%)	Y	900
Carcase fatty acid profiles	N	1,100
Capacity score	N	5,900

1 The time lag between birth and later-in-life records means incomplete datasets may exist.

2 Structural soundness measures include feet angle front and rear, claw set front and rear and rear legs from behind and side

3 Live ultrasound measures include P8 fat, rib fat, eye muscle area and intra-muscular fat

4 Most traits are evaluated using the BREEDPLAN system, but the American Angus Association analyses Structural Soundness traits, and CSIRO analyses immune competence traits

Genotyping: Project sires were genotyped, and sires were verified. All project calves were sire-verified and genotyped. The density of the genotype varied over time, with the chip density increasing with time. Initially, the chip density was 5k, and the current SNP chip density used by the BIN program is 70k.

Additional Notes: BIN cohorts have been involved in the ALMTech project, testing several technologies: Hyperspectral, Microwave, MIJ and VIA scans. Further information can be found on the Angus Australia website, where progeny performance reports are published for each cohort. More information on the project design can be obtained from the Proceedings of the Association for the Advancement of Animal Breeding and Genetics 2019 conference.

Parnell, P.F., Duff, C.J., Byrne, A.I, and Butcher, N.M. (2019) The Angus sire benchmarking program – A major contributor to future genetic improvement in the Australian beef industry. Proc. Assoc. Advmt. Anim. Breed. Genet. 24: 492.

Information storage: All data has been stored in the Angus Australia database located with Angus Australia. Extracts are provided to ABRI for undertaking BREEDPLAN evaluations for the Trans Tasman Angus Cattle Evaluation (TACE). All raw data from the BIN animals are stored in their database by Angus Australia. Tissue samples (hair or TSU) for genotyping were taken on the farm and sent to Angus Australia, which then sent the samples to the genotyping lab. The genotyping lab stores any remaining samples and provides genotype files, which are loaded into the Angus database.

Information collated by Kirsty Moore (AGBU) and Christian Duff (Angus Australia)
10th February 2024

9.1.2 Hereford Information Nucleus and Young Sire Progeny test

Organisation: Herefords Australia Ltd

Breeds: Purebred Hereford

Project Duration and Size: Approximately 450 calves from 15 sires annually from 2011 and ongoing

Project Status: Active and ongoing

Project contact: Hamish Chandler (Hereford Breed Development Manager)

Project overview: The Hereford BIN project has operated over three phases, focusing on terminal carcase traits. The first two phases received MLA Donor Company funding, and the current phase three was self-funded by Herefords Australia Limited. Cows are mated via Artificial Insemination to progeny test approximately 15 sires annually, and the resulting calves are recorded for traits from birth to slaughter.

Project herds: Since the start of the progeny test, 15 herds have been involved. Pedigree and commercial Hereford herds were eligible, provided they had 50+ cows available for AI mating, standard production and management practices (i.e. compatible joining dates), and they agreed to performance record progeny according to the project protocols. Eight herds participated each year in phase one, with four herds located in the southern (VIC and SA) and northern (NSW and QLD) regions. In the later phases, two herds located in the southern region participated predominantly.

Project sires: A sire nomination process was open to all Hereford members. Herefords Australia, often in consultation with AGBU, selected project sires from the nominations to represent the diversity of the wider Hereford population and linkage to other Hereford projects. Owners of selected sires paid a nomination fee and to the project herds a royalty per live calf at 400 days. Project sires were used across herds and years to provide linkage. Over ten years, 114 different sires produced 10 or more BIN progeny. International sires are eligible for nomination, and several New Zealand sires are represented. However, the nomination process meant that sires were predominantly Australian-bred.

Project cows: Project cows tended to be purebred commercial Hereford cows with unknown parentage and birth dates. A few herds in phase one used pedigree cows to produce project animals. Female progeny from the project were not retained for breeding in the project. The cow structure of the BIN means that female reproduction traits cannot be recorded, and the BIN focus has been on terminal carcase traits. Over ten years, 3,097 cows produced project calves, with 649 cows producing two or more calves for the BIN project.

Management of project animals: Project animals were predominantly the result of AI matings, and in some herds, there were additional naturally mated animals. Animals born in the same herd were managed together until weaning. In phase one at weaning, steers were purchased and grouped within the region (i.e. the steers from the four southern herds were combined) for backgrounding and slaughter. In the later phases, animals born in the same herd were managed together from birth to slaughter. Only steers were taken through to slaughter, except for a few heifer cohorts in later phases.

Traits recorded: A range of traits and fixed effects (i.e. date of birth) from birth through to slaughter were recorded by the herd utilising project protocols. Herefords Australia oversaw this process to maintain data quality. The key focus traits were abattoir carcase and chiller, meat quality, feed efficiency and structural soundness traits. BIN animals represent the largest proportion of Hereford data available for these traits. Female fertility traits were not recorded, and females were not retained for breeding.

Overview of records collected: The table on the next page summarises the number of records (rounded to the nearest hundred) collected throughout the BIN projects for a range of traits. For some traits, only steers or some cohorts were recorded.

The number of records (rounded to the nearest hundred) collected for BIN animals for a range of different traits from birth to slaughter

	Hereford BREEDPLAN trait	Phase 1 (2011-2014)	Phase 2 (2015-2017)	Phase 3[1] (2018-2020)	Total (2011-2020)
Gestation length (days)	Y	1500	700	700	2800
Birth weight (kg)	Y	1600	1100	1300	4000
Calving difficulty (score)	Y	1600	900	1300	3900
200-day weight (kg)	Y	1400	800	700	2900
400-day weight (kg)	Y	1200	600	600	2400
600-day weight (kg)	Y	800	600	500	1900
Docility (score)	Y	1200	500	300	2000
Live condition score (score)	N	100	200	300	700
Live muscle score (score)	N	900	400	300	1600
Structural Soundness[2] (score)	N	1000	400	300	1700
Live ultrasound traits[3]	Y	1200	600	400	2300
Carcase weight (kg)	Y	800	500	200	1500
Carcase P8 fat	Y	700	500	300	1500
Carcase rib fat	Y	400	500	300	1200
Carcase EMA	Y	700	500	300	1600
Carcase Intra-muscular fat	Y	700	500	300	1600
Ausmeat marble score	Y	700	500	300	1600
MSA marble score	Y	700[4]	500	300	1600
MSA index	N	700	500	300	1600
Shear force	N	700	500	200	1400
Carcase ossification	N	200	500	300	1000
Carcase cooking loss	N	700	500	200	1400
Carcase PH	N	700	500	300	1500
Carcase lab PH	N	700	500	300	1500
Carcase meat and fat colour	N	500	500	200	1200
Carcase meat colour (a, b and l)	N	700	500	200	1400
Carcase muscle score (score)	N	300	200	100	600
Net feed intake (kg/day)	Y	400	200	100	700

1 The time lag between birth and later-in-life records means incomplete datasets may exist.
2 Structural soundness measures include feet angle front and rear, claw set front and rear and rear legs from behind and side
3 Live ultrasound measures include P8 fat, rib fat, eye muscle area and intra-muscular fat
4 In phase one, 400 were scored under the old MSA marble score, and 300 with the current MSA marble score

Genotyping: Project sires were genotyped, and where possible, their sires were verified. Project calves, especially calves produced via AI mating, were sire-verified with later cohorts and genotyped. Very few early cohort animals were genotyped as, at that time, the genotyping costs were prohibitive. Instead, sires were genotyped predominantly with a 150k chip (50k and 30k chips were also used for sires). Since 2015, all BIN progeny were genotyped, initially with 30K chips, then 50k chips and recently 100k chip density.

Additional Notes: BIN cohorts have been involved in the ALMTech project (2018-2020), testing several technologies, including hyperspectral, Microwave, MIJ, and VIA scans. The COVID-19 pandemic affected the BIN project, particularly for 2019-born animals, where meat samples for one herd could

not be taken for meat quality measures. In another two herds, there were plant issues, and carcase EMA records were unreliable.

Information storage: All data was stored in the Hereford database with ABRI. This included traits incorporated into existing BREEDPLAN evaluations and those yet to be included, i.e. meat quality traits. Herefords Australia Ltd also has the original MSA feedback data from the abattoirs. Raw phenotypes collected by BIN herds were sent to Herefords Australia Ltd, which then submitted the records to ABRI for inclusion in BREEDPLAN. Likewise, tissue samples (hair or TSU) for genotyping were taken on the farm and sent to Herefords Australia Ltd, which then sends the samples to the genotyping lab, who then store any remaining samples and provides back genotype files, which are loaded into the Herefords database.

Information collated by Kirsty Moore (AGBU) and Michael Beattie (formerly Herefords Australia Ltd)

1st July 2021

9.1.3 Repronomics reference population

Organisation: 'Repronomics' - Jointly run by the Animal Genetics and Breeding Unit (AGBU) and Queensland Department of Primary Industries (DPI)

Breeds: Purebred Brahman, Droughtmaster and Santa Gertrudis

Project Duration and Size: Approximately 400, 350 and 130 Brahman, Droughtmaster and Santa Gertrudis calves from 25, 23 and 10 Brahman, Droughtmaster, and Santa Gertrudis sires have been produced annually since 2014.

Project Status: Active with funding until 2023

Project contact: David Johnston (Repronomics project leader)

Project overview: The Repronomics project has operated over two phases, focusing on female reproduction traits. Both phases received MLA Donor Company funding. Two DPI Research herds in QLD run cows from the three breeds (Santa Gertrudis are only at one site). Project calves are naturally mated for their first two matings (to allow ovarian scan traits to be collected), after which cows are mated using artificial insemination. Calves are extensively recorded for traits from birth and following the females through their reproductive lives. The Northern BIN source Repronomics steers for recording from weaning to slaughter.

Project herds: Two DPI research herds in Queensland were the key Repronomics herds. 'Spyglass' is located 120km NW of Charters Towers and runs two of the three project breeds: Brahman and Droughtmaster. 'Brian Pastures' is located in Gayndah, and all three project breeds are run on the property. DPI staff manage both herds. Within a herd, all animals were managed together regardless of breed.

Project sires: Project sires were selected to be representative of the wider population. In particular, current or emerging influential sires and sires with limited female reproduction information were sourced for the project. Natural mate and AI sires were identified by the Repronomics project team, and bulls or semen were purchased by the project. Project sires were used across herds and years to provide linkage. In addition, some sires were used as natural mate and AI sires to provide links between 1st and 2nd parity cows naturally mated and 3rd and later parity cows mated via AI. Since 2014, 165 different sires (78 Brahman, 64 Droughtmaster and 23 Santa Gertrudis) produced 10 or more BIN progeny. Repronomics Brahman animals are linked to the Southern Multi-breed Brahmans via the use of common sires. Sires are predominantly Australian-bred, but a small number of USA Brahman sires have been included in AI.

Project cows: Base project cows were the existing herds on-site at the commencement of the project. Additional cows were purchased, including some tropical composite cows, which were mated to Droughtmaster and Santa Gertrudis sires to make up the numbers. Base cows were pedigree and performance recorded and included a portion of the beef CRC cows. Female progeny from the project were retained in the project, with some of the calves since 2017 being from project females.

Management of project animals: Animals born in the same herd and year were managed together as a cohort unit. Cohorts generally remain on the property where they were born, but in bad seasons, some complete cohorts are agisted elsewhere. After weaning, only females were retained, with steers sold to the Northern BIN. The project's focus was female reproduction, and the first two matings were natural mates to allow ovarian scanning traits to be recorded, with subsequent matings via AI. Cows that failed to wean a calf were removed from the herd.

Traits recorded: A large number of traits and fixed effects (e.g., date of birth) from birth through reproduction were recorded by trained DPI staff utilising project protocols. Accredited scanners measured ultrasound body composition and ovarian scan traits. The key focus traits were reproduction traits, particularly ovarian scanned age at puberty and lactation anoestrus interval. However, many novel traits, often repeated at different ages, were also recorded.

Overview of records collected: The table on the next page summarises the number of records (rounded to the nearest hundred) collected throughout the Repronomics projects for each trait.

The number of records (rounded to the nearest hundred) collected for BIN animals for a range of different traits from birth to reproduction traits

	BREEDPLAN trait	Phase 1 (2011[2]-2017)			Phase 2[1] (2018-2020)			Total (2011[2]-2020)		
Breed		**BB**	**DM**	**SG**	**BB**	**DM**	**SG**	**BB**	**DM**	**SG**
Birth to weaning (Females and males)										
Gestation length (days)	Y	500	400	100	500	300	100	1000	700	200
Birth weight (kg)	Y	1400	1200	500	1200	1000	400	2600	2200	900
Calving difficulty (score)		1400	1200	400	1300	1100	400	2700	2300	800
200-day weight (kg)	Y	1500	1300	500	1200	1000	400	2700	2300	900
Flight time (seconds)	Y	1500	1300	500	1200	1000	400	2700	2300	900
Coat score (score)		1100	1100	400	1200	1000	400	2300	2100	800
Mothering score (score)		700	600	200	1000	900	400	1700	1500	600
Horn status (score and genotype)		2000	1700	700	1200	1000	400	3200	2700	1100
Coat colour (score)		2100	1900	600	1300	1100	400	3400	3000	1000
Calf vigour (score)		1400	1200	400	1300	1100	400	2700	2300	800
Coronet circumference (cm)		1100	1000	400	400	400	100	1500	1400	500
Pompes (genotype)		400	500	200	1300	1100	400	1700	1600	600
Post-weaning (Females only)										
400-day weight (kg)	Y	800	700	300	400	300	100	1200	1000	400
600-day weight (kg)	Y	900	700	300	200	200	50	1100	900	350
Live ultrasound traits[3]	Y	600	500	200	100	100	50	700	600	250
Mature cow weight (kg)	Y	700	600	200	0	0	0	700	600	200
Days to Calving (days)	Y	900	700	300	0	0	0	900	700	300
Ovarian scan Age at puberty (days)	Y[4]	800	600	300	200	200	50	1000	800	350
Ovarian scan Lactation anoestrus interval (days)	Y[4]	600	500	200	0	0	0	600	500	200
Body condition score – heifer (score)		700	600	300	400	300	100	1100	900	400
Body condition score – into mating 1 (score)		800	700	300	200	200	50	1000	900	350
Body condition score – calving 1 (score)		700	600	200	0	0	0	700	600	200
Body condition score – into mating 2 (score)		700	600	200	0	0	0	700	600	200
Hip height – heifer (cm)		700	600	300	300	300	100	1000	900	400

Hip height – into mating 1 (cm)	800	700	300	200	200	50	1000	900	350
Hip height – into mating 2 (cm)	700	600	200	0	0	0	700	600	200
Naval score (score)	600	500	200	200	200	50	800	700	250
Teat and udder scores (score)	700	600	300	0	0	0	700	600	300
Live ultrasound P8 fat – heifer	700	600	300	300	300	100	1000	900	400
Live ultrasound traits[3] – into mating 1	800	600	300	200	150	50	1000	750	350
Live ultrasound traits[3] – into mating 2	600	600	200	0	0	0	600	600	200
Live weight (kg) – heifer (kg)	700	600	300	400	300	100	1100	900	400
Live weight (kg) – into mating 1 (kg)	800	700	300	50	50	50	850	750	350
Live weight (kg) – into mating 2 (kg)	700	600	200	0	0	0	700	600	200
Buffalo fly (score)	100	100	100	0	0	0	100	100	100

1 The time lag between birth and later-in-life records means there may be incomplete datasets. 2 Base cows born in 2011-2013 were also phenotyped for some traits. 3 Live ultrasound measures include P8 fat, rib fat and eye muscle area. But NOT intra-muscular fat 4 The traits are included in BREEDPLAN with correlations to days to calving, but the individual traits are not published

Genotyping: All Repronomics animals (males and females) are DNA verified and genotyped with the 35k GGP TropBeef chip (some earlier animals with a 25k chip), and all project sires are genotyped with an 80k Bos indicus DNP chip. Many seedstock industry animals were genotyped in the project, particularly sires with high accuracy days to calving EBVs.

Additional Notes: Normally, there is only one cohort per location and year; however, for Spyglass 2016 calves, there are two cohorts, SP16 and SP16X, where SP16X was born in a location separate from SP16 because of needing to agist project animals during a bad season.

A paper presented in the Proceedings of the Association for the Advancement of Animal Breeding and Genetics 2017 conference provides more information on the project design.

Johnston, D.J., Grant, T.P., Schatz, T.J., Burns, B.M., Fordyce, G. and Lyons, R.R. (2017) The Repronomics Project – enabling genetic improvement in reproduction in northern Australia. Proc. Assoc. Advmt. Anim. Breed. Genet. 22: 385-388.

Information storage: The project has a detailed SQL database storing all raw data. Records collected on-site are sent to AGBU, which loads the data into the Repronomics database. Data eligible for inclusion into BREEDPLAN is then extracted from the Repronomics database, formatted, and then loaded into ABRI's northern multi-breed research database, which can be accessed for inclusion in national genetic evaluations. DNA samples are sent to the genotyping lab, who store any remaining samples and provides genotype files back to the project, where the genotypes are stored in the Repronomics database and are also loaded into the Northern Multi-Breed Genomics Database, where they are available for inclusion into the breed genomic evaluations.

Information collated by Kirsty Moore (AGBU) and David Johnston (AGBU/Repronomics project leader)

27th January 2022

9.1.4 Northern BIN reference population

Organisation: The northern BIN is a joint project between the Australian Brahman Breeders Association (ABBA), Droughtmasters Stud Breeders Society (DSBS) and a consortium of Santa Gertrudis Breeders.

Breeds: Purebred Brahman, Droughtmaster and Santa Gertrudis

Project Duration and Size: Approximately 195, 175 and 66 Brahman, Droughtmaster and Santa Gertrudis calves from 22, 21 and 10 Brahman, Droughtmaster, and Santa Gertrudis sires have been produced annually since 2014.

Project Status: Active and ongoing

Project contact: John Croaker (Manager – ABBA BIN Projects)

Project overview: The Northern BIN uses steers produced from the Repronomics research project from the 2014 Spyglass and 2015 Brian Pastures cohorts onwards. For more information regarding the details from birth until weaning, refer to this series's Repronomics genomic reference population overview sheet. Post-weaning Repronomics steers were purchased for inclusion into the Northern BIN, where the focus was on recording carcase traits. The cohort structure was maintained for slaughter, where abattoir traits were recorded. The projects are funded by project herd with Spyglass (P.PSH.0743) and Brian Pastures (P.PSH.0774) considered separate projects, but included together for analysis and this document.

Project herds: From birth until weaning, steers were managed on the two DPI research herds utilised by Repronomics. Brahman and Droughtmaster were present at the Spyglass herd, while at Brian Pastures, Brahman, Droughtmaster and Santa Gertrudis breeds were represented. All animals were managed together within each herd regardless of breed, which continued post-weaning. Post-weaning steers were backgrounded as complete cohorts at several locations. The property Warraka, located about 40km southwest of Taroom, is where most steers have been finished on grass and Leucaena. However, cohorts have been finished in feedlots where grass is unavailable in seasons.

Project sires: All sire decisions were made during the Repronomics project. Project sires were selected to be representative of the wider populations. In particular, current or emerging influential sires and sires with limited female reproduction information were sourced for the project. Natural mate and AI sires were identified by the Repronomics project team, and bulls or semen were purchased by Repronomics. Project sires were used across herds and years to provide linkage. In addition, some sires were utilised as natural mate and AI sires to provide links between 1st and 2nd parity cows naturally mated and 3rd and later parity cows mated via AI. Eighty-one different sires (35 Brahman, 36 Droughtmaster and 10 Santa Gertrudis) produced 10 or more northern BIN steers. Repronomics/ Northern BIN Brahman steers are linked to the Southern Multi-breed Brahmans using common sires. Sires are predominantly Australian-bred, but a small number of USA Brahman sires have been included in AI.

Project cows: Project cows were part of the Repronomics project, with Northern BIN only utilising the steer progeny. The Repronomics base project cows were the existing herds on-site at the commencement of the Repronomics project. Additional cows, including some tropical composite cows mated to Droughtmaster and Santa Gertrudis sires, were purchased to make up the numbers. Base cows were pedigree and performance recorded, and included a portion of the beef CRC cows. Female Repronomics progeny were retained, with some of the Repronomics and northern BIN calves since 2017 being from Repronomics-born females.

Management of project animals: Animals born in the same herd and year were managed together as a cohort unit. Cohorts generally remain on their birth property, but some complete cohorts are agisted elsewhere in bad seasons. After weaning, steers were sold to the Northern BIN, where they were backgrounded and finished before being slaughtered. The locations where animals were backgrounded and finished varied, but the cohort structure was maintained. Finishing was predominantly via grass and Leucaena, but some cohorts have been finished in the feedlot where grass was unable. Steers were slaughtered in abattoirs as a cohort, and abattoir carcase traits were collected.

Traits recorded: As part of the Repronomics project, a large number of traits and fixed effects (e.g., date of birth) from birth through weaning were recorded by trained DPI staff utilising project

protocols. Post-weaning to slaughter, further traits and fixed effects were recorded by the northern BIN. Accredited scanners measured ultrasound body composition traits, and abattoir carcase traits were recorded by trained MSA and abattoir staff.

Overview of records collected: The table on the next page summarises the number of records (rounded to the nearest hundred) collected throughout the Northern BIN projects for each trait.

Genotyping: All steers were genotyped with the 35k GGP TropBeef (some earlier animals with a 25k chip) as part of the Repronomics project and were DNA verified.

Additional Notes: Normally, there is only one cohort per location and year; however, for Spyglass 2016 calves, there are two cohorts, SP16 and SP16X, where SP16X was born in a location separate from SP16 because of needing to agist project animals during a bad season.

Information storage: Additional information from the Northern BIN is stored in the Repronomics database, keeping all data from birth to slaughter in one place. Records collected on-site are sent to AGBU, which loads the data into the Repronomics database. Data eligible for inclusion into BREEDPLAN is then extracted from the Repronomics database, formatted, and then loaded into ABRI's northern multi-breed research database, which can be accessed for inclusion in national genetic evaluations. Post-slaughter abattoir kill sheets are sent to the northern BIN, and this data is forwarded to AGBU, where it is also loaded into the Repronomics database.

Information collated by Kirsty Moore (AGBU) and John Croaker (Manager – ABBA BIN Projects)
27th January 2022

ABBA AUSTRALIAN BRAHMAN BREEDERS' ASSOCIATION LIMITED
DROUGHTMASTER Australia's natural wonder
CONSORTIUM OF SANTA GERTRUDIS BREEDERS
agbu

The number of records (rounded to the nearest hundred) collected for BIN animals for a range of different traits from birth to slaughter

	BREEDPLAN trait	Phase 1 (2011[2]-2017)			Phase 2[1] (2018-2020)			Total (2011[2]-2020)		
Breed		**BB**	**DM**	**SG**	**BB**	**DM**	**SG**	**BB**	**DM**	**SG**
Birth to weaning (Females and males)										
Gestation length (days)	Y	500	400	100	500	300	100	1000	700	200
Birth weight (kg)	Y	1400	1200	500	1200	1000	400	2600	2200	900
Calving difficulty (score)		1400	1200	400	1300	1100	400	2700	2300	800
200-day weight (kg)	Y	1500	1300	500	1200	1000	400	2700	2300	900
Flight time (seconds)	Y	1500	1300	500	1200	1000	400	2700	2300	900
Coat score (score)		1100	1100	400	1200	1000	400	2300	2100	800
Mothering score (score)		700	600	200	1000	900	400	1700	1500	600
Horn status (score and genotype)		2000	1700	700	1200	1000	400	3200	2700	1100
Coat colour (score)		2100	1900	600	1300	1100	400	3400	3000	1000
Calf vigour (score)		1400	1200	400	1300	1100	400	2700	2300	800
Coronet circumference (cm)		1100	1000	400	400	400	100	1500	1400	500
Pompes (genotype)		400	500	200	1300	1100	400	1700	1600	600
Post-weaning (Males only)										
400-day weight (kg)	Y	400	400	200	200	200	100	600	600	300
600-day weight (kg)	Y	500	500	200	400	400	100	900	900	300
Live ultrasound traits[3]	Y	400	400	200	200	200	100	600	600	300
Structural Soundness[4] (score)		300	300	100	200	200	50	500	500	150
Carcase weight (kg)	Y	500	500	200	200	200	50	700	700	250
Carcase composition traits[3]	Y	500	500	200	200	200	50	700	700	250
Shear force (kg)	Y	500	500	200	200	200	50	700	700	250
Marble score (Ausmeat and MSA) (score)		600	600	200	200	200	50	800	800	250
MSA index		600	500	200	200	200	50	800	700	250

Carcase ossification	500	400	100	0	0	0	500	400	100
Carcase cooking loss	600	600	200	200	200	50	800	800	250
Carcase PH	600	600	200	200	200	50	800	800	250
Carcase meat and fat colour	600	600	200	200	200	50	800	800	250
Carcase meat colour (a, b and l)	600	600	200	200	200	50	800	800	250
Butt Score (Score)	300	300	100	200	200	50	500	500	150
Ultimate pH	600	600	200	200	200	50	800	800	250
MSA hump height (mm)	500	400	100	0	0	0	500	400	100
MSA loin temperature (degrees centigrade)	600	600	200	200	200	50	800	800	250
Buffalo fly (score)	100	100	0	0	0	0	100	100	0

1 The time lag between birth and later-in-life records means incomplete datasets may exist.

2 Base cows born in 2011-2013 were also phenotyped for some traits

3 Live ultrasound measures include P8 fat, rib fat and eye muscle area. But NOT intramuscular fat

4 Structural soundness measures include feet angle front and rear, claw set front and rear and rear legs from behind and side

9.1.5 Southern Multi-Breed reference population

Organisation: The Multi-Breed Genomic Beef Cattle Resource project, also known as the Southern Multi-Breed (SMB) project, is a collaborative R&D project between the NSW Department of Primary Industries and Regional Development (DPIRD), the University of New England (UNE), and MLA. The SMB project team, along with the steering and technical committees, facilitates the overall running of the project.

Breeds: Purebred Angus, Brahman, Charolais, Hereford, Shorthorn, Wagyu, Brahman x Angus and Brahman x Hereford.

Project Duration and Size: The first two project cohorts (2020 & 2021) generated 2,715 calves and will continue to produce approximately 1,300 calves annually.

Project Status: Active and ongoing with funding until 2025

Project contact: Faye Haynes (Project leader)

Project overview: SMB has been co-funded by NSW DPIRD, UNE, Meat & Livestock Australia and the Commonwealth Government through the MLA Donor Company over the five years, 2020 to 2025. The project aims to benefit within-breed genetic evaluations and inform the development of a multi-breed genetic evaluation. Five NSW DPIRD research stations run cows from six beef breeds, producing purebred and Brahman x Hereford and Brahman x Angus calves. A wide range of traits are recorded, including existing BREEDPLAN traits, cow composition, horn/polled, reproduction, feedlot and abattoir carcase traits. Mating is generally via Artificial Insemination/backup, but project female calves will be naturally mated for their first two matings to allow ovarian scan traits to be collected.

Project herds: Five NSW DPIRD research stations located in NSW were the SMB herds. Angus was a link breed present at all sites. In addition to Angus, Trangie Agricultural Research Centre (Trangie) also ran Hereford and Wagyu cows, Tocal Agricultural Centre (Tocal) ran Charolais and Shorthorn cows, Glen Innes Agricultural Research and Advisory Station (Glen Innes) ran Hereford and Wagyu cows, Elizabeth MacArthur Agricultural Institute (EMAI, Menangle) ran Charolais, Hereford, Shorthorn and Wagyu cows, and Grafton ran Hereford and Brahman cows. At Grafton Primary Industries Institute (Grafton), Brahman and Angus/Hereford first-cross calves are also produced. NSW DPI staff manage all herds.

Project sires: All project sires were BREEDPLAN performance recorded with full pedigree information. Project sires were selected to be representative of the wider breed populations. In particular, current or emerging influential sires or sires that provide genetic links with other BIN projects (past and present) were sourced for the project. AI sire nominations were sourced from the industry, with final natural mate (backup) and AI sires selected by the SMB project team and technical committee. Bulls were purchased, and semen was donated for use in the project. Project sires were used within breeds and across herds and years to provide linkage. 154 and 202 sires generated cohorts one (R) and two (S) calves, respectively.

Project cows: Base project cows were purchased from key industry seedstock herds. All purchased cows were BREEDPLAN performance recorded with full pedigree information. Cows were sourced to be representative of the national population (assessed via 400-day weight and reproduction EBVs), especially if their sires were currently highly influential. Angus cows were also retained from the NSW

DPIRD muscling and feed efficiency selection herds. Female progeny from the project will be retained for breeding, and full reproduction data will be collected.

Management of project animals: NSW DPI staff manage the animals, with animals born in the same herd and year managed together as a cohort unit. However, several sub-groups were required for management purposes with large herd sizes. These groups were formed by balancing the fixed effects (i.e., cow age), breed, and sires across the groups to ensure data analysis will not be unduly affected. Females are retained in the project, and steers are backgrounded at two locations (EMAI and Duck Creek Agricultural Field Station at Ballina) before entering the UNE Research Feedlot (Tullimba) for feed intake testing and finishing, before abattoir carcase records are collected.

Traits recorded: A large number of traits and fixed effects (e.g., date of birth) from birth through reproduction or slaughter were recorded by trained NSW DPI staff utilising project protocols. Accredited scanners measured ultrasound body composition and ovarian scan traits. The following traits are being recorded.

- Current BREEDPLAN traits
  - Live weight (birth, weaning, yearling, final and mature)
  - Reproduction (gestation length, calving ease and days to calving)
  - Carcase (live ultrasound scan, carcase weight, intramuscular fat*, fat, EMA and shear force tenderness*) * samples taken for future phenotyping
  - Net feed intake, temperament and structure
- Calf bellow and calf vigour
- Reproduction traits
  - Puberty – age, weight, height, p8 fat and body condition score
  - 1st lactation anoestrous
  - Pregnancy success
- Cow composition traits (joining and weaning)
  - Live ultrasound scans (EMA, P8 fat, rib fat, IMF)
  - Body condition score
- Horn, poll or scurs
- Abattoir carcase traits and eating quality traits
- Worm egg counts
- Methane at the feedlot

Genotyping: Base females were DNA sampled and will be genotyped with at least a 50k SNP chip. Likewise, all sires will be genotyped, and 51 AI sires across all breeds have had full genomic sequences at 10X coverage. All calves were DNA sampled by weaning and genotyped with a high-density SNP chip. Genotypes were used for parentage verification and inclusion into reference populations.

Additional Notes: More information on the project design can be obtained from papers published in the Proceedings of the Association for the Advancement of Animal Breeding and Genetics 2021 conference.

Donoghue, K.A., Walmsley, B.J., Siddell, J.P, Granleese, T., Penrose, L, and Arthur, P.F. (2021) Southern multi-breed resource population: Generation of cohorts one and two. Proc. Assoc. Advmt. Anim. Breed. Genet. 24: 98.

Connors, N.K., Walmsley, B.J., and Donoghue, K.A. (2021) Addressing scur phenotypic challenges with the Southern Multi-breed Project. Proc. Assoc. Advmt. Anim. Breed. Genet. 24: 70.

Walkom, S.F., Donoghue, K.A., Arthur, P.F., Clark, S.A., and Walmsley, B.J. (2021) Using matesel to aid sire allocation in genomic reference populations – southern multi-breed an example. Proc. Assoc. Advmt. Anim. Breed. Genet. 24: 419.

Walmsley, B.J., Donoghue, K.A., Johnston, D.J., Clark, S.A., Siddell, J.P, Granleese, T. and Arthur, P.F. (2021). Initiating the Southern multi-breed resource population. Proc. Assoc. Advmt. Anim. Breed. Genet. 24: 423.

Information storage: Project records are stored using the Stockbook software, with each DPIRD site having its own stockbook. Systems are being developed where project data will be extracted and stored in a multi-breed database with ABRI, which will ultimately allow project data to be included in the BREEDPLAN genetic evaluations. DNA samples are sent to the genotyping lab, which stores any remaining samples and returns genotype files. All SNP data will be quality checked, stored on a project database and loaded into ABRI's southern multi-breed research database.

Information collated by Kirsty Moore (AGBU), Kath Donoghue (DPIRD) and Brad Walmsley (DPIRD/AGBU)

14th January 2022

9.1.6 Beef CRC projects

Organisation: The Beef Cooperative Research Centre (CRCs) operated over three projects with many research organisations as partners.

Breeds: CRC1: Purebred Angus, Belmont Red, Brahman, Hereford, Murray Grey, Santa Gertrudis and Shorthorn. Brahman first-cross with the following breeds: Angus, Belmont Red, Hereford, Murray Grey, Santa Gertrudis and Shorthorn sires. CRC2 and CRC3: purebred Brahman and Tropical Composite.

Project Duration and Size: The CRC's ran for approximately 20 years - CRC1 operated from 1993-1999, CRC2 from 1999-2005 and CRC3 from 2005-2012. In total, CRC1 produced nearly 8,000 purebred calves, representing 388 sires. The breakdown per breed, as reported by Upton et al. (2001), was;

- Angus – 117 sires, 1,849 progeny (233 heifers and 1,616 steers)
- Belmont Red – 64 sires, 1,588 progeny (575 heifers and 1,013 steers)
- Brahman – 44 sires, 893 progeny (438 heifers and 455 steers)
- Hereford – 57 sires, 1,138 progeny (134 heifers and 1,004 steers)
- Murray Grey – 23 sires, 458 progeny (73 heifers and 385 steers)
- Santa Gertrudis – 48 sires, 1,342 progeny (594 heifers and 748 steers)
- Shorthorn – 35 sires, 513 progeny (0 heifers and 513 steers)

CRC1 produced first-cross calves over three years (1996-1998) from 1,000 Brahman cows. In total, 1,894 calves (male and female) were produced from 96 sires. The breakdown per sire breed, as reported by Upton et al. (2001), was;

- Angus – 10 sires and 157 calves
- Belmont Red – 14 sires and 393 calves
- Brahman – 14 sires and 330 calves
- Charbray – 4 sires and 89 calves
- Charolais – 16 sires and 231 calves
- Hereford – 8 sires and 138 calves
- Limousin – 14 sires and 294 calves
- Santa Gertrudis – 8 sires and 142 calves
- Shorthorn – 8 sires and 120 calves.

CRC2 focused on two tropical-adapted breeds, with calves produced for Brahman and Tropical composite breeds over 2000-2003. At the commencement of first mating, there were 1,020 Brahman and 1,117 Tropical Composite females, and 1,007 Brahman and 1,209 Tropical Composite steers post-weaning. These progeny represented 53 Brahman and 50 Tropical Composite sires. CRC3 continued the design of CRC2 and produced Brahman and Tropical composite calves from 2004-2011, with an additional 3,694 Brahman and 5,035 Tropical Composite calves produced from 136 sires.

Project Status: Historic

Project contact: Clara Bradford (MLA) or Heather Burrow (outgoing CRC CEO)

Project overview: CRC1 aimed to research the genetics of carcase and beef quality considering two different finishing diets. CRC2 shifted focus to female reproduction and the relationship to the carcase traits. This was extended in CRC3 to consider lifetime female reproduction and male reproduction traits. CRC1 purebred calves were bred at 34 different commercial herds, with the CRC purchasing calves at weaning. Crossbred CRC1 animals were generated at two research properties with base Brahman cows donated by industry herds. CRC2 cattle were bred from 8 co-operator properties with calves purchased at weaning by the CRC and transferred to one of 4 Queensland research stations. Five Queensland research stations were used to generate calves born in CRC3. Once at the CRC research stations, calves were managed together as a cohort.

Project herds: CRC1 and CRC2 purebred animals were generated from 34 and 8 co-operator herds, respectively. Calves were bred by artificial insemination (AI) or natural mating, and herds were required to use the CRC project sires. In CRC1, the herd requirements were that they needed to be able to produce 15 progeny per sire for at least three sires annually, and within a given breed, there needed to be at least three herds participating. Although there were herds with BREEDPLAN-recorded cows, most sires were mated to non-pedigreed commercial cows. Post-weaning, CRC1 calves were transferred to a southern and northern Australia CRC-controlled property. Temperate breeds were generally located in southern Australia, and the Tropical breeds were in northern Australia. Crossbred CRC1 animals were generated at 2 Brahman herds ('Duckponds' near Comet and Brigalow Research Station near Theordore). CRC2 and CRC3 controlled properties were Swans Lagoon (Ayr), Belmont (Rockhampton), Toorak (Julia Creek), Brian Pastures (Gayndah) and Brigalow Research Station (Theordore), which represented a wide range of Queensland environments.

Project sires: In CRC1, individual collaborating breeders and breed societies selected the sires, not the beef CRC. However, sires were performance recorded with BREEDPLAN, genetic links across herds,

and years were generated using common link sires in all herds. The project sires for the crossbred CRC1 animals were a subset of the sires used for CRC1 purebred matings. CRC2 and CRC3 were involved in the sire selection process for the respective stages, although collaborating breeders could nominate sires. CRC2 and CRC3 sires were selected to represent divergence for EBVs for retail beef yield and intramuscular fat percentage. In addition, heterozygosity for gene markers identified in CRC1, EBVs for scrotal size or days to calving, and the impact of the sire within the breed were also considered. Genetic links were again created by link sires across herds and years, with CRC1 animals and industry data. In CRC1 and CRC2, mating was via natural mating and AI. In CRC3, only natural mating in multi-sire groups was undertaken to allow ovarian scans and male fertility traits to be assessed.

Project cows: CRC1 purebred base cows came from 34 collaborating breeders and tended to be non-pedigree commercial cows. 1,000 Brahman cows donated from numerous Brahman breeders were used to generate the crossbred calves in CRC1. No females were retained from CRC1. In CRC2, the base cows were industry animals at eight co-operator herds. Female progeny were retained and were naturally mated as part of CRC3, forming the project cows for CRC3 located at five research herds. Several of these cows were later used as project cows for the Repronomics project.

Management of project animals: For CRC1 and CRC2, cows were mated by natural mating or artificial insemination (AI) in the cooperator herd. Herds recorded accurate calving dates at calving, and the sire was recorded. DNA was used to determine the sire where the sire was not known (i.e., multi-sire mating groups). All males were castrated at branding or immediately after purchase by the CRC. In CRC1, breeders could select heifer calves and retain up to 50%, but all male calves were transferred to the CRC. After purchase, calves were moved to properties managed by CRC and were managed together within cohort groups. For CRC3, cattle were managed and mated onsite at CRC-controlled properties, all matings were via natural mating, and all males were kept entire.

Traits recorded: Many traits were recorded over the 3 CRCs depending on the CRC focus. As a direct result of CRC1, three new traits were added to BREEDPLAN – carcase weight, intramuscular fat percentage and retail beef yield percentage. For CRC1 and 2, birth information to weaning was recorded by the co-operator herds. After weaning and for all CRC3 traits, trained technicians and farm staff on the CRC-controlled properties were recorded using project protocols. Accredited scanners measured ultrasound body composition and ovarian scan traits. Animals were slaughtered at processing plants, and in CRC1, meat samples were taken to analyse meat quality in the laboratory.

Overview of records collected: The table on the next page summarises the number of records (rounded to the nearest hundred) collected throughout the CRC projects for each trait. In addition to actual traits and records recorded in the database (and reported in the table), several additional phenotypes were derived from stored data. For CRC2 and CRC3, these include gestation length (based on AI dates and early pregnancy fetal age ultrasound), mortality/survival/embryo loss records, age at puberty and return to cyclicity of lactating females based on regular ovarian scan results, conception rates, lifetime annual weaning rate and days to calving.

Genotyping: DNA was extracted for all sires (either by blood or semen) and used for marker evaluation studies in CRC1. With the advancement of DNA technologies, the sires were later genotyped for the 50k SNP panel, and these genotypes have been made available for inclusion into

BREEDPLAN single-step genomic analyses. Genotypes are stored with AGBU as part of the beef genomic pipeline database structure, and the CRC phenotype database has been annotated.

Additional Notes:

More information on the project design can be obtained from the following CRC design papers;

Bindon, B. M. (2001). Genesis of the Cooperative Research Centre for the Cattle and Beef Industry: integration of resources for beef quality research (1993–2000). *Australian Journal of Experimental Agriculture*, *41*(41), 843–853. https://doi.org/10.1071/EA00067

Burns B. M., Corbet N. J., Corbet D. H., Crisp J. M., Venus B. K., Johnston D. J., Li Y., McGowan M. R., Holroyd R. G. (2013) Male traits and herd reproductive capability in tropical beef cattle. 1. Experimental design and animal measures. Animal Production Science 53, 87-100.

Burrow, H. M., & Bindon, B. M. (2005). Genetics research in the Cooperative Research Centre for Cattle and Beef Quality. *Australian Journal of Experimental Agriculture*, *45*(7–8), 941–957. https://doi.org/10.1071/EA05069

Burrow HM, Johnston DJ, Barwick SA, Holroyd RG, Barendse W, Thompson JM, Griffith GR, Sullivan M (2003) Relationships between carcass and beef quality and components of herd profitability in northern Australia. Proceedings of the Association for the Advancement of Animal Breeding and Genetics 15, 359–362.

Johnston DJ, Barwick SA, Fordyce G, Holroyd RG, Williams PJ, Corbet NJ (2014) Genetics of early and lifetime annual reproductive performance in cows of two tropical beef genotypes in northern Australia. *Animal Production Science* **54**, in press. doi:10.1071/AN13043

Upton, W.; Burrow, H.M.; Dundon, A.; Robinson, D.L. and Farrell, E.B. (2001). "CRC breeding program design, measurements and database: methods that underpin CRC research results." *Aust. Journal of Experimental Agriculture* 41: 943-952

Information storage: Data from the CRC projects are stored in a relational database designed for the CRC programs. The database has a web front-end interface that can be accessed at http://beefcrc.une.edu.au to allow data access by all participating research organisations. However, this front-end interface is currently temporarily unavailable. In addition, data for BREEDPLAN evaluations have been added to the breed databases at ABRI for inclusion in genetic evaluation. Genotypes are stored in an internal AGBU database, and links have been made between the phenotype and genotype databases.

Information collated by Kirsty Moore (AGBU)

14th June 2023

The number of records* (rounded to the nearest hundred) collected for CRC animals for various traits from birth to reproduction and slaughter traits. * some traits were recorded multiple times

Project (years of birth)	CRC1 (1993-1999)		CRC2 (2000-2003)		CRC3 (2004-2012)		Total
	Purebred	Crossbred	Brahman	Tropical Composite	Brahman	Tropical Composite	
Birth and calving traits							
Birth weight (kg)	1,300	1,300	700	700	3,200	5,000	12,200
Calving difficulty (score)	0	0	0	0	3,200	4,500	7,700
Growth and body composition traits							
Weaning weight (kg)	6,600	1,900	2,000	2,300	3,200	4,600	20,600
Live weights (kg)	145,700	32,500	77,900	89,400	19,100	26,700	391,300
Body condition score (score)	39,100	4,000	63,700	74,900	9,400	13,900	205,000
Muscle score (score)	17,500	2,800	0	0	0	0	20,300
Hip height (cm)	14,100	5,100	23,300	24,000	1,600	2,200	70,300
Live ultrasound traits[1]	70,700	17,800	117,100	135,100	4,400	6,500	351,600
Live ultrasound intramuscular fat	0	0	9,800	11,300	0	0	21,100
Maturity score (score)	1,700	0	0	0	0	0	1,700
Abattoir carcase measurements							
Hot left and right side weight (kg)	15,100	3,700	2,000	2,400	0	0	23,200
Hot P8 fat depth (mm)	7,500	1,900	1,000	1,200	0	0	11,600
Carcase composition traits[2]	25,200	6,800	4,400	5,100	0	0	41,500
Fat and meat colour traits[3]	60,600	15,900	5,200	6,200	0	0	87,900
Marbling score[3]	10,700	2,400	700	1,000	0	0	14,800
Deep butt temperature (degrees)	7,500	1,900	0	0	0	0	9,400
Chiller muscle score (score)	7,500	1,900	0	0	0	0	9,400
Bone traits[4] (g)	38,500	6,000	0	0	0	0	44,500
Total Bone out[5] traits	41,800	6,500	8,900	10,000	0	0	67,200
Primal cut[6] traits	290,700	42,900	5,600	6,100	0	0	345,300
MSA carcase[7] traits	42,400	15,100	6,900	8,500	0	0	72,900
MQ Carcase cooking loss[8]	14,900	3,700	1,900	2,200	0	0	22,700
MQ Shear force measures[8] (kg)	25,400	5,100	1,900	2,200	0	0	34,600

MQ Ultimate pH[8]	14,900	3,700	1,000	1,100	0	0	20,700
MQ Carcase intramuscular fat	7,500	1,900	800	1,200	0	0	11,400
MQ muscle measures[9]	29,300	7,600	1,900	2,200	0	0	41,00
Fatty acid profiles[10]	38,200	0	0	0	0	0	38,200
Carcase value and market grade (left and right)	0	0	3,200	3,900	0	0	7,100
Number of permanent incisors	0	0	500	700	0	0	1,200
Butt score	0	0	1,000	1,200	0	0	2,200
Temperament							
Crush score (score)	8,700	5,100	0	0	0	0	13,800
Flight speed (sec)	13,800	5,100	8,100	8,200	10,300	14,600	60,100
Visual flight score (score)	7,500	3,100	0	0	0	0	10,600
Blood counts and hormonal traits							
Blood counts[11]	103,600	20,000	0	0	0	0	123,600
Blood IGF-1 (ng/ml)	1,300	0	4,700	5,300	2,600	3,700	17,600
Luteinising hormone concentration[12] (ng/ml)	0	0	0	0	1,800	2,800	4,600
Inhibin concentration (ng/ml)	0	0	0	0	1,200	1,800	3,000
Adaption traits							
Ambient Temperature (C)	0	0	1,700	1,700	3,900	5,800	13,100
Relative humidity (%)	0	0	700	900	0	0	1,600
Rectal temperature (C)	0	0	2,000	1,700	1,100	1,800	6,600
Buffalo Fly Lesion score (score)	0	0	2,700	2,600	0	0	5,300
Cattle tick (count or score)	0	0	600	500	0	0	1,100
Coat Colour (score)	0	0	4,300	4,600	4,300	5,400	18,600
Coat score (score)	0	0	6,400	6,600	3,500	6,100	22,600
Eggs per gram (EPG) (count)	0	0	3,900	4,300	0	0	8,200
Sheath/naval (score) / preputia eversion (mm)	2,700	1,200	3,300	4,000	6,300	7,600	25,100
Female reproduction traits							
Teat and Udder (score)	0	0	44,300	63,600	0	0	107,900
Ovarian scans (CL presence, follicle and tract size)	0	0	98,200	99,800	0	0	198,000
Male reproduction traits							

Scrotal size (cm)	0	0	9,900	14,800	8,300	12,300	45,300
Semen mass activity (score)	0	0	0	0	3,200	5,700	8,900
Progressive sperm motility (%)	0	0	0	0	3,200	5,700	8,900
Percent morphologically normal sperm	0	0	0	0	2,100	4,700	6,800
Testicular tone (score)	0	0	0	0	3,900	5,800	9,700
Ejaculate volume, colour and density	0	0	0	0	9,600	17,100	26,700
Sperm abnormalities[13] (counts)	0	0	0	0	59,600	137,000	196,600
ACV classification[14] (counts)	0	0	0	0	15,700	36,100	51,800
Additional traits							
Horn Status (score)	0	0	0	0	4,300	6,500	10,800
Daily feed intake (kg/day)	1,600	500	700	800	0	0	3,600
Tooth wear (score)	0	0	500	400	0	0	900
Structural traits[15]	0	0	2,900	3,000	9,800	16,200	31,900
Skin Inflammation score (score)	0	0	0	100	0	0	100

1 Live ultrasound measures include P8 fat, rib fat and eye muscle area. But NOT intramuscular fat

2 Carcase measures include P8 fat, rib fat and eye muscle area and were either actual (MSA) or technological (VIA) measures

3 Lab-based (a, b & l), chiller assessed and VIA assessed colour and chiller assessed and VIA assessed marbling score

4 Bone traits include the weight of the femur, forequarter, humerus, lumbar vertebra, neck, patella, pelvis, radius/ulna, scapula, tibia and the total weight of forequarter and hindquarter bones.

5 Total bone out traits were the weight of adjusted 85% chemical lean, weight-adjusted fat, adjusted retail beef yield, adjusted saleable beef yield, the weight of bones, cold side weight, recovered weight, weight of retail primal cuts, total intermuscular far, total subcutaneous fat, wholesale weight of primal cuts, the cold weight of the forequarter and hindquarter.

6 Primal cuts include blade, chuck, chuck tender, cube roll, eye round, thin flank, flap, hind shank, inside skirt, intercostals, knuckle, outside, rump, striploin, sub-sample of striploin, navel end brisket, outside-flat, point end brisket, rib set, shank, shin, tenderloin, tritips and topside. Traits included the untrimmed weight, retail weight, intramuscular fat, subcutaneous fat and total fat weight

7 MSA carcase traits were AUS_MEAT fat and meat colour, AUS-MEAT marbling score, consumer panel flavour score, juiciness score, tenderness score and overall liking score, loin temperature, eating quality score, ultimate pH, hump height and USDA lean score, marbling and ossification.

8 longissimus and semitendinosus muscles

9 longissimus and semitendinosus muscles measured for Instrom compression, initial yield, sarcomere length and shorthose adhesion

10 Fatty acid profiles include C140, C141, C150, C160, C161C, C170, C171, C180, C181C, C181C11, C181T, C182, C183, C190, CLA, MONO, MONO2, POLY, POLY2, RAT1, RAT2, SAT1 and SAT2

11 Blood counts include total basophil, eosinophil, lymphocyte, monocyte and neutrophil counts and percentage, presence of T cell markers, haematocrit percentage, haemoglobin concentration, counts of platelets, erythrocyte and white blood cells and distribution of red cell widths as a percentage

12 basal and stimulated measures

13 Abnormality traits included counts of the head (total, detached, pyriform, tapered, microcephalic, macrocephalic, teratoids, knobbed acrosomes, nuclear vacuoles, diadem defects, rolled heads, flattened acrosomes, nuclear crests, double head and loose acrosomes), midpiece (total, abaxial, broken necks, bent, distal reflexes, dag defects and segmental aplasia), tail (total, reflex, coiled, stumped and multiple) and droplet (total, proximal and distal)

14 ACV classification includes counts per 100 of normal sperm, proximal droplets, midpiece abnormalities, abnormal tails and loose heads, pyriform heads, knobbed acrosomes, vacuoles and teratoids and swollen acrosomes

15 Structural traits include feet score, leg structure and foot structure

9.1.7 Kaiuroo Brahman Project

Organisation: Kaiuroo Brahman seedstock herd and AGBU. Funding was by MLA project P.PSH.0921.

Breeds: Purebred Brahman.

Project Duration and Size: The project operated as one seedstock herd over three concurrent weaning groups: 2016, 2017, and 2018. A total of 1,530 animals (765 bulls and 765 heifers) were genotyped, representing 72 sires.

Project Status: Historic

Project contact: Matt Wolcott (AGBU)

Project overview: The Kaiuroo project contributed genotypes and hard-to-measure male and female reproduction traits to the Brahman BREEDPLAN genetic evaluation. Records were collected from three progeny cohorts. Kaiuroo is a well-linked seedstock herd. Adding to the male and female reproduction reference populations increased the EBV accuracy for Kaiuroo and other herds undertaking genomic selection.

Project herds: Kaiuroo is a Brahman seedstock herd in central QLD, running 900 breeders and 3,000 commercial cattle. Within the seedstock herd, animals are recorded with BREEDPLAN, and the herd is well linked to other seedstock herds and genetics used in key research projects.

Project sires: All sires were BREEDPLAN-recorded Brahman bulls, with 72 different sires represented over the three project cohorts. Sire selection was undertaken by the management of the Kaiuroo herd and AGBU. Sires were homebred or purchased from other Brahman seedstock herds, and matings were natural and AI. Sires were selected based on genetic merit and to ensure genetic links with reference projects, particularly the Repronomics project.

Project cows: Project cows were the Kaiuroo breeder herd. Cows were purebred Brahman, and female progeny were retained in the breeding herd. Although Kaiuroo is operated over several properties, seedstock cows were run as one herd, but may be in different management groups.

Management of project animals: The Kaiuroo cows were all managed together as one herd. Cows were mated by natural mating and AI, with calves recorded via BREEDPLAN protocols. Females were retained in the herd, and males were kept entire and sold as bulls to other seedstock and commercial producers, including the Repronomics and Southern Multi-breed projects. All calves born in the same management group were managed together according to BREEDPLAN contemporary group guidelines, with sexes separated at weaning. Bull breeding soundness evaluations (BBSE) and sperm morphology testing were undertaken on project male calves at 12, 18 and 24 months. The 24-month measurement was submitted to the BREEDPLAN genetic evaluation. Heifers were naturally mated as 2-year-olds, and ovarian ultrasound scans were performed at 2-month intervals before mating. Heifers were pregnancy tested, and ovarian ultrasound and pregnancy test data were used to determine the age of puberty. Lactating first calf females were naturally mated and had monthly ovarian ultrasound scans from the start of the mating period to identify when the cow cycled post-calving (lactation anoestrous interval). All project calves were genotyped.

Traits recorded: Male and female reproduction traits were recorded, in addition to routine BREEDPLAN traits recorded by the Kaiuroo herd. Female reproduction traits were age at puberty and lactation anoestrous interval. Trained operators did ovarian scanning. Male reproduction traits were obtained from bull breeding soundness evaluations (BBSE) and sperm morphology testing. Sperm samples were analysed using the same methodology as the Beef CRC. Traits included percent normal sperm, proximal and distal droplets, abnormal mid pieces, abnormal tails and heads, pyriform heads, knobbed acrosomes, vacuoles and tertoids and swollen acrosomes.

Overview of records collected: The table below summarises the number of records (rounded to the nearest hundred) collected throughout the Kaiuroo project for each trait.

The number of records* (rounded to the nearest hundred) collected for Kaiuroo animals for male and female reproduction. * some traits were recorded multiple times

	Total
Male reproduction traits	
Bull breeding soundness evaluations (BBSE) and sperm morphology testing	500
Female reproduction traits	
Age at puberty (days)	600
Lactation anoestrus interval (days)	200

Genotyping: All males and females evaluated for reproduction traits were genotyped and sire verified. Hair samples were collected at weaning and submitted to the Australian Brahman Breeders Association. Genotyping was done with Neogen using the 50K TropBeef chip. All genotypes have now been included in the Brahman BREEDPLAN analysis.

Additional Notes:

More information on the project can be obtained from the final MLA project report.

Wolcott, ML (2019). Intensive phenotyping in industry to expand the Brahman reference population. Meat and Livestock Australia Donor Company project P.PSH.0921 final report

Information storage: Project records were collected on-site, sent to AGBU and stored in the AGBU project SQL database. DNA samples are sent to the genotyping lab, which stores any remaining samples and returns genotype files to the project. Data (phenotypes and genotypes) eligible for BREEDPLAN were loaded into ABRI's Brahman database for inclusion into national genetic evaluations.

Information collated by Kirsty Moore (AGBU)

28th September 2023

9.1.8 Optimizing temperate cow herd efficiency - a Trans-Tasman collaboration

Organisation: A collaboration between Australian and New Zealand organisations: Beef + Lamb New Zealand Genetics, AbacusBio, AGBU, University of Adelaide and Massey University. Funding was provided by MLA project P.PSH.0869, which brought together industry levy and government funds in the two countries.

Breeds: Purebred and commercial Angus and Hereford.

Project Duration and Size: The 3-year project ended in 2020. It collected fertility and related data on over 5,000 Australian seedstock and New Zealand commercial cattle and utilised existing datasets produced from other projects (e.g., beef CRC).

Project Status: Historic

Project contact: Matt Wolcott (AGBU)

Project overview: The Trans-Tasman project aimed to improve temperate cows' lifetime productivity and profitability. Several project objectives aimed to improve descriptions of cow composition, identify indicators of heifer and cow fertility, assess if there were genotype-by-country interactions, and assess the genomic predictions for cow traits. Data for these objectives was drawn from several existing sources in Australia (i.e. Beef CRC, Angus and Hereford Beef Information Nucleus herds and Hereford Black Baldy project) and New Zealand (i.e. Beef Progeny Test and the Tier 2 Maternal Cow Project) and the industry genetic evaluation datasets. Female fertility records were collected for approximately 4,000 Australian seedstock heifers and 1,400 New Zealand commercial heifers. Data collected on the seedstock heifers were included in BREEDPLAN for routine BREEDPLAN traits. Phenotypes collected on commercial animals were deemed not suitable to be included in BREEDPLAN.

Project herds: Over two years, ovarian ultrasound scanning, growth, and composition traits were recorded in 9 Angus and 3 Hereford Australian seedstock herds. The herds were identified with a history of high-quality pedigree and performance recording in BREEDPLAN. Data was collected from 5 New Zealand Beef Progeny Test commercial herds with Angus or Hereford cows. The Beef Progeny Test has operated since 2014.

Project sires: In the Australian seedstock herds, sires were BREEDPLAN-recorded Angus or Hereford bulls that the individual herds have chosen as part of their standard business operations. There were 97 Angus and 36 Hereford sires with eight or more progeny recorded in the datasets. The NZ BPT used five sire breeds (Angus, Hereford, Stabiliser, Simmental, and Charolais) with linkage generated over multiple years. New Zealand beef and lamb, which operate the progeny test, identified the project sires.

Project cows: Project cows in the Australian seedstock herds were purebred Angus and Hereford and were fully BREEDPLAN recorded. The cows were part of the standard herd being run as part of the herd's business operations. Cows in the New Zealand Beef Progeny Test were commercial Angus and Hereford and were managed according to New Zealand commercial conditions as part of a coordinated progeny test.

Management of project animals: Australian cows were managed according to their herd's standard operating procedures and following BREEDPLAN protocols. In New Zealand, cows were managed according to standard New Zealand commercial conditions as part of a structured progeny test. The commercial conditions of the New Zealand animals meant that the cows did not have recorded dates of birth. Mating in Australia was almost exclusively via AI, while natural mating occurred in the New Zealand Beef Progeny Test. Heifers were followed through to becoming cows in both countries, and records were collected. Australian herds were ultrasound scanned on average three times, while the New Zealand cows were ultrasound scanned once at the commencement of mating.

Traits recorded: Female reproduction traits were recorded in Australian seedstock herds and New Zealand commercial herds. In Australia, ovarian scans, live weight, hip height, body condition score, and P8 fat depth were recorded at approximately three different time points. In New Zealand, ovarian scans and pregnancy tests providing foetal aging data were recorded at the commencement of mating.

Overview of records collected: The table below summarises the number of animals (rounded to the nearest hundred) measured throughout the Trans-Tasman project for each trait.

The number of animals recorded* (rounded to the nearest hundred) for female reproduction and body composition. * some traits were recorded multiple times

	Australian Seedstock herds		New Zealand BPT	Total
	Angus	Hereford	Angus and Hereford	
post-weaning				
Live weight	3,100	900		4,000
Hip height	1,800	900		2,700
Condition score	3,100	900		4,000
P8 fat depth	3,000	800		3,800
into mating				
Live weight	3,100	900		4,000
Hip height	3,200	900		4,100
Condition score	3,200	900		4,100
P8 fat depth	3,200	900		4,100
Reproduction				
Ovarian scans	3,100	900	1,400	5,400
Conception rate			1,400	1,400
Foetal age			1,100	1,100

Genotyping: A genotyping strategy was developed to ensure all recorded animals were genotyped at 50k density. Most seedstock herds in Australia had already genotyped animals, but two herds required genotyping. All animals were routinely genotyped as part of the New Zealand Beef Progeny Test. Genotyping was undertaken with GeneSeek Australasia (University of Queensland), and all genotypes have now been provided in the appropriate breeds' BREEDPLAN genotype database.

Additional Notes:

More information on the project can be obtained from the final MLA project report.

Edwards, J., Linscott, E., Archer, J., Wolcott, M., Banks, R., Pitchford, W. and Garrick, D. (2020) Optimising Temperate Cow Herd Efficiency – A Trans-Tasman Collaboration. Meat and Livestock Australia Donor Company project P.PSH.0869 final report.

Information storage: Australian seedstock herds submitted performance data to BREEDPLAN as standard. The additional records collected as part of this project were collected on-site and stored on AGBU servers (/home/agbu/mwolcot3/ANZAC). DNA samples are sent to the genotyping lab, which stores any remaining samples and returns genotype files to the herds. Data (phenotypes and genotypes) eligible for BREEDPLAN were loaded into ABRI's breed databases for inclusion into national genetic evaluations. New Zealand Beef Progeny Test data was collected and stored according to the project's procedures. This data was not deemed unsuitable for inclusion in ABRI's breed databases for national genetic evaluations.

Information collated by Kirsty Moore (AGBU)

24th April 2024

9.2 GWAS Significant SNPS

Table 9.2.1: Across Genome Significant SNPs for Brahman Age at Puberty

name	chrom	location	fp	estimate	serror	-log10(P)	gvarpc
bovinehd1400004739	14	15125634	0.469	-16.340	3.238	6.345	0.039
bovinehd1400004799	14	15354624	0.633	17.130	3.332	6.564	0.040
bovinehd1400005412	14	17253714	0.331	20.615	3.365	9.047	0.055
bovinehd1400005462	14	17468729	0.266	17.830	3.614	6.092	0.036
bovinehd1400005554	14	17863393	0.303	18.485	3.605	6.531	0.042
bovinehd1400005573	14	17919760	0.727	-19.607	3.751	6.764	0.044
bovinehd1400005621	14	18060329	0.213	19.373	3.897	6.177	0.037
bovinehd1400005634	14	18104102	0.478	-16.426	3.167	6.668	0.039
bovinehd1400005729	14	18467112	0.564	-21.862	3.156	11.365	0.068
bovinehd1400005931	14	19080139	0.493	16.583	3.233	6.536	0.040
bovinehd1400005932	14	19084445	0.429	-20.426	3.297	9.236	0.059
hapmap25518-bta-129035	14	19378401	0.485	-16.662	3.248	6.537	0.040
bovinehd1400006221	14	19972663	0.592	-18.204	3.220	7.803	0.047
ars-bfgl-bac-1180	14	20574088	0.557	-26.724	3.263	15.654	0.102
bovinehd1400006451	14	20681192	0.269	24.416	3.666	10.561	0.068
bovinehd1400006490	14	20854662	0.586	-27.438	3.365	15.353	0.106
bovinehd1400006508	14	20917167	0.292	19.784	3.541	7.636	0.047
ars-bfgl-bac-12159	14	20931583	0.556	-27.324	3.381	15.176	0.107
bovinehd1400006558	14	21096233	0.564	-27.872	3.388	15.654	0.111
bovinehd1400006612	14	21258769	0.304	19.587	3.514	7.606	0.047
bovinehd1400006616	14	21275909	0.397	25.718	3.447	13.069	0.092
bovinehd1400006748	14	21610015	0.316	17.888	3.461	6.626	0.040
bovinehd1400006965	14	22353534	0.743	-19.674	3.699	6.980	0.043
bovinehd1400006966	14	22356681	0.552	-24.809	3.370	12.741	0.089
bovinehd1400007019	14	22554883	0.648	-18.753	3.444	7.288	0.047
bovinehd1400007058	14	22678296	0.701	-21.296	3.664	8.212	0.055
bovinehd1400007077	14	22741124	0.642	-23.991	3.443	11.494	0.077
bovinehd1400007106	14	22818334	0.701	-27.076	3.666	12.822	0.089
bovinehd1400007139	14	22921127	0.761	-28.919	3.818	13.441	0.088
bovinehd1400007159	14	22994360	0.25	27.890	3.658	13.612	0.085
bovinehd1400007190	14	23077502	0.788	-26.730	3.802	11.686	0.069
bovinehd1400007242	14	23264774	0.284	27.948	3.683	13.492	0.092
bovinehd1400007274	14	23402733	0.212	21.099	4.016	6.825	0.043
bovinehd1400007326	14	23614007	0.729	-22.907	3.631	9.551	0.060
bovinehd1400007371	14	23822296	0.719	-21.567	3.533	8.987	0.055
ars-bfgl-ngs-36089	14	24019648	0.712	-19.067	3.589	6.965	0.043
bovinehd1400007470	14	24158384	0.303	26.784	3.450	14.085	0.088
bta-97369-no-rs	14	24203438	0.606	-16.218	3.257	6.194	0.037
bovinehd1400007556	14	24533833	0.351	22.735	3.457	10.319	0.068
bovinehd1400007582	14	24632670	0.747	-21.302	3.824	7.594	0.050
ars-bfgl-ngs-35159	14	24825146	0.522	26.501	3.240	15.654	0.102

hapmap50665-bta-34310	14	24859655	0.49	-25.101	3.208	14.292	0.092
bovinehd1400007646	14	24868649	0.433	18.856	3.248	8.192	0.051
bovinehd1400007679	14	24967988	0.476	-25.944	3.246	14.875	0.098
bovinehd1400007711	14	25098969	0.394	23.010	3.379	11.009	0.074
bovinehd1400007716	14	25134563	0.394	23.739	3.357	11.814	0.078
bovinehd1400007750	14	25262684	0.644	-18.100	3.325	7.283	0.044
bovinehd4100011364	14	25316107	0.475	-25.702	3.257	14.540	0.096
bovinehd1400007784	14	25421224	0.337	20.099	3.347	8.717	0.052
hapmap27934-btc-065223	14	25472332	0.527	25.375	3.252	14.222	0.093
bovinehd4100011372	14	25525813	0.444	-26.188	3.283	14.808	0.098
bovinehd1400007805	14	25527841	0.33	20.016	3.386	8.469	0.052
hapmap23456-btc-072918	14	25744989	0.464	26.419	3.326	14.699	0.101
bovinehd4100011393	14	25890276	0.452	-23.666	3.199	12.856	0.081
bfgl-ngs-116462	14	25894192	0.491	-24.983	3.195	14.273	0.091
bovinehd1400007883	14	25920254	0.529	24.439	3.213	13.550	0.087
bovinehd1400007932	14	26044182	0.302	17.524	3.524	6.180	0.038
bovinehd1400007938	14	26062341	0.588	-19.027	3.227	8.430	0.051
bovinehd1400007958	14	26128047	0.539	21.799	3.171	11.204	0.069
bovinehd4100011410	14	26133849	0.461	-21.703	3.195	10.956	0.068
ua-ifasa-7947	14	26192223	0.431	-24.430	3.232	13.393	0.085
bovinehd1400008008	14	26271742	0.543	-20.372	3.190	9.769	0.060
bovinehd1400008100	14	26459339	0.484	24.413	3.230	13.389	0.087
bovinehd1400008115	14	26510755	0.456	17.908	3.271	7.357	0.046
bovinehd1400008129	14	26556408	0.373	19.719	3.320	8.545	0.053
btb-00560182	14	26560163	0.556	23.718	3.193	12.954	0.081
bovinehd1400008137	14	26591877	0.478	22.424	3.163	11.872	0.073
bovinehd1400008145	14	26614779	0.559	23.151	3.198	12.348	0.077
btb-00561430	14	26759764	0.442	-23.478	3.209	12.593	0.079
bovinehd1400008234	14	26870423	0.688	-18.207	3.491	6.735	0.041
hapmap44230-bta-34389	14	26963208	0.426	-23.729	3.231	12.687	0.080
bovinehd1400008298	14	27012616	0.418	-22.459	3.220	11.514	0.071
bovinehd1400008333	14	27111745	0.549	23.471	3.198	12.666	0.079
bovinehd1400008378	14	27243190	0.458	-18.162	3.163	8.028	0.048
bovinehd1400008417	14	27381507	0.746	-23.252	3.734	9.323	0.060
ua-ifasa-8638	14	27424502	0.578	-22.776	3.275	11.448	0.074
bovinehd1400008429	14	27427946	0.567	-23.405	3.268	12.099	0.078
bovinehd1400008522	14	27679937	0.553	18.625	3.147	8.490	0.050
bta-34455-no-rs	14	28253443	0.591	18.271	3.173	8.069	0.047
bovinehd1400008696	14	28337095	0.681	-18.382	3.346	7.405	0.043
bovinehd1400008734	14	28497812	0.392	17.559	3.180	7.472	0.043
btb-00562922	14	28758622	0.421	-17.481	3.149	7.546	0.043
bfgl-ngs-117404	14	28808111	0.48	-17.142	3.131	7.358	0.043
btb-02062304	14	29455092	0.604	17.315	3.173	7.315	0.042
bovinehd1400009004	14	29498072	0.411	-17.241	3.170	7.272	0.042
ars-bfgl-ngs-93878	14	29525841	0.385	-18.470	3.208	8.069	0.047
bovinehd1400009028	14	29589249	0.482	-17.111	3.149	7.257	0.043

bfgl-ngs-112787	14	29862243	0.384	-15.778	3.188	6.129	0.034
hapmap42549-bta-42953	14	29894372	0.618	15.771	3.184	6.137	0.034
bovinehd1400009135	14	30002923	0.489	-16.550	3.204	6.620	0.040
hapmap48764-bta-44326	14	30157993	0.558	18.194	3.137	8.176	0.047
bovinehd1400009183	14	30184825	0.498	16.723	3.080	7.249	0.041
hapmap49092-bta-24990	14	30307307	0.44	-15.457	3.119	6.142	0.034
bovinehd1400009250	14	30392641	0.59	17.198	3.094	7.563	0.042
bovinehd1400009381	14	30652577	0.552	-16.878	3.216	6.813	0.041
hapmap39646-bta-34536	14	30688417	0.518	-15.765	3.190	6.111	0.036
bovinehd1400009510	14	31163601	0.583	15.974	3.209	6.192	0.036
bovinehd1400009652	14	31600580	0.405	-17.767	3.180	7.636	0.044
btb-01336217	14	31656560	0.348	-16.945	3.270	6.660	0.038
bovinehd1400009833	14	32141429	0.363	-16.723	3.332	6.284	0.038
bovinehd1400009854	14	32181234	0.65	16.218	3.282	6.112	0.035

Table 9.2.2: Across Genome Significant SNPs for Brahman Birth weight

name	chrom	location	fp	estimate	serror	-log10(P)	gvarpc
hapmap50491-bta-85929	6	16963160	0.102	-0.661	0.121	7.342	0.019
bovinehd0600006841	6	23496143	0.863	-0.532	0.107	6.152	0.016
bovinehd0600007149	6	24561751	0.307	-0.439	0.079	7.587	0.020
bovinehd0600007385	6	25410028	0.278	-0.421	0.081	6.669	0.017
bovinehd0600007776	6	26693489	0.438	-0.453	0.073	9.190	0.024
bovinehd0600008071	6	27555467	0.749	-0.405	0.080	6.345	0.015
bovinehd0600008174	6	27887575	0.534	-0.529	0.073	12.286	0.033
hapmap43142-bta-107561	6	28131847	0.18	0.502	0.096	6.793	0.018
bovinehd0600008283	6	28275511	0.438	0.502	0.073	11.309	0.030
bovinehd0600008465	6	28927865	0.556	0.388	0.075	6.712	0.018
bovinehd0600008510	6	29057762	0.528	-0.480	0.071	10.737	0.027
bovinehd0600008592	6	29293834	0.494	-0.552	0.072	13.585	0.036
bfgl-ngs-117147	6	29357249	0.549	-0.474	0.074	9.715	0.026
bovinehd0600008721	6	29682908	0.754	0.703	0.085	15.654	0.044
bovinehd0600008735	6	29736189	0.552	0.355	0.071	6.211	0.015
bovinehd0600008749	6	29800328	0.586	-0.398	0.075	7.025	0.018
bovinehd0600008841	6	30120131	0.542	-0.535	0.074	12.348	0.034
bovinehd0600008946	6	30527064	0.498	0.379	0.074	6.548	0.017
bovinehd0600008962	6	30575474	0.46	0.533	0.071	13.074	0.034
bovinehd0600008998	6	30698453	0.476	0.544	0.074	12.638	0.035
bta-119035-no-rs	6	30872560	0.459	0.371	0.074	6.315	0.016
bovinehd0600009054	6	30879591	0.514	-0.577	0.074	14.375	0.040
bovinehd0600009055	6	30880926	0.459	0.588	0.072	15.353	0.041
bovinehd0600009084	6	30966466	0.224	0.568	0.086	10.368	0.027
ars-bfgl-ngs-84321	6	31016133	0.245	0.540	0.082	10.245	0.026
bovinehd0600009102	6	31028257	0.36	0.410	0.075	7.391	0.018
bovinehd0600009147	6	31233466	0.51	-0.408	0.073	7.576	0.020
bovinehd0600009149	6	31234969	0.159	0.504	0.096	6.788	0.016
bovinehd0600009165	6	31282171	0.301	0.401	0.080	6.304	0.016
bovinehd0600009203	6	31444117	0.665	0.516	0.077	10.644	0.028
bovinehd0600009222	6	31478274	0.508	-0.479	0.073	10.384	0.027
bovinehd0600009280	6	31714029	0.561	-0.499	0.072	11.243	0.029
bovinehd0600009303	6	31827597	0.592	-0.507	0.074	11.146	0.030
bovinehd0600009347	6	32038500	0.6	-0.466	0.076	9.141	0.025
bovinehd0600009564	6	32801223	0.421	-0.623	0.075	15.654	0.045
bovinehd0600009569	6	32830418	0.376	0.536	0.074	12.294	0.032
bovinehd0600009634	6	33132472	0.368	-0.435	0.078	7.560	0.021
bovinehd0600009651	6	33197375	0.724	-0.470	0.083	7.844	0.021
bovinehd0600009719	6	33498367	0.51	0.514	0.073	11.673	0.031
bovinehd0600009735	6	33565172	0.382	0.510	0.076	10.800	0.029
bovinehd0600009738	6	33567821	0.613	-0.532	0.075	11.745	0.032
ars-bfgl-ngs-43857	6	33774948	0.507	0.407	0.073	7.543	0.020
bovinehd0600009846	6	33956983	0.431	-0.579	0.077	13.403	0.039

bovinehd0600010031	6	34610791	0.466	-0.603	0.075	15.176	0.043
bovinehd0600010067	6	34738726	0.857	-0.521	0.103	6.344	0.016
bovinehd0600010155	6	35042532	0.544	-0.450	0.074	8.842	0.024
bovinehd4100004451	6	35288734	0.591	-0.537	0.072	12.971	0.033
bovinehd0600010277	6	35463808	0.218	0.650	0.087	12.997	0.034
bovinehd0600010286	6	35488586	0.426	0.585	0.074	14.477	0.040
bovinehd0600010292	6	35499152	0.695	-0.526	0.080	10.409	0.028
bovinehd0600010293	6	35500546	0.338	0.593	0.077	13.921	0.037
hapmap43675-bta-75814	6	36412092	0.648	-0.511	0.076	10.639	0.028
bovinehd0600010471	6	36422368	0.618	-0.626	0.077	15.176	0.044
bovinehd0600010480	6	36442952	0.375	0.553	0.077	12.076	0.034
bovinehd0600010581	6	36725781	0.354	0.381	0.075	6.394	0.016
bovinehd0600010637	6	36999602	0.537	-0.609	0.074	15.654	0.044
bovinehd0600010786	6	37672865	0.534	-0.618	0.075	15.654	0.045
hapmap53940-rs29026121	6	37778924	0.419	0.542	0.075	12.192	0.034
bovinehd0600010804	6	37812521	0.396	0.517	0.073	11.858	0.030
bovinehd0600010824	6	37919045	0.431	0.515	0.075	11.215	0.031
bovinehd4100004638	6	38114717	0.344	0.589	0.080	12.748	0.037
hapmap26618-btc-070864	6	38157637	0.606	-0.442	0.073	8.937	0.022
bovinehd0600010895	6	38273065	0.362	0.408	0.077	6.884	0.018
hapmap32513-btc-066089	6	38312868	0.304	0.450	0.079	7.973	0.020
bovinehd0600010917	6	38382877	0.683	-0.429	0.078	7.502	0.019
bovinehd4100004684	6	38400569	0.11	0.834	0.115	12.472	0.032
bovinehd0600010924	6	38426291	0.129	0.587	0.108	7.290	0.018
bovinehd0600010951	6	38548198	0.491	0.478	0.075	9.749	0.027
hapmap26233-bta-75846	6	38736912	0.466	-0.524	0.075	11.444	0.033
bovinehd0600034453	6	38747310	0.529	-0.448	0.075	8.621	0.024
bovinehd0600011056	6	39115634	0.419	0.426	0.072	8.390	0.021
bovinehd0600011098	6	39295180	0.636	-0.415	0.074	7.713	0.019
ars-bfgl-ngs-34023	6	39371669	0.542	-0.439	0.074	8.541	0.023
bovinehd0600011172	6	39703250	0.472	0.499	0.072	11.390	0.030
hapmap26843-btc-036644	6	39921679	0.442	-0.509	0.073	11.544	0.030
bovinehd0600011241	6	40066669	0.478	-0.385	0.074	6.780	0.018
bovinehd0600011312	6	40353309	0.46	0.419	0.074	7.747	0.021
bovinehd0600011331	6	40413649	0.483	-0.396	0.074	7.091	0.019
bovinehd0600011336	6	40428390	0.4	-0.450	0.075	8.738	0.023
bovinehd0600011409	6	40618176	0.426	0.390	0.073	6.972	0.018
bovinehd0600011411	6	40622585	0.58	-0.406	0.073	7.561	0.019
bovinehd0600011476	6	40798002	0.377	-0.599	0.076	14.331	0.040
bovinehd0600011496	6	40820102	0.646	0.579	0.078	12.981	0.037
bovinehd0600011497	6	40820818	0.642	0.579	0.077	13.139	0.037
bovinehd0600011524	6	40894524	0.689	0.605	0.081	13.250	0.037
bovinehd0600011527	6	40906713	0.51	-0.357	0.072	6.069	0.015
bovinehd0600011545	6	40968848	0.633	0.419	0.076	7.365	0.019
bovinehd4100004791	6	41457643	0.396	0.412	0.076	7.221	0.019
bovinehd0600011667	6	41522023	0.485	-0.369	0.072	6.574	0.016

bovinehd0600011821	6	42059973	0.523	0.379	0.073	6.712	0.017
bovinehd0600011822	6	42060686	0.477	-0.387	0.073	6.969	0.018
bovinehd0600012020	6	42554396	0.248	-0.645	0.086	13.073	0.037
bovinehd0600012024	6	42580767	0.675	0.509	0.078	10.244	0.027
bovinehd4100004801	6	42835314	0.465	-0.363	0.073	6.208	0.016
bovinehd0600012173	6	43097401	0.6	0.464	0.077	8.813	0.025
bovinehd0600012305	6	43607791	0.693	0.446	0.079	7.858	0.020
bovinehd0600012335	6	43791568	0.197	-0.699	0.095	12.844	0.037
bovinehd0600012443	6	44275065	0.377	-0.456	0.078	8.271	0.023
bovinehd0600012457	6	44315678	0.382	-0.486	0.077	9.566	0.027
bovinehd0600012487	6	44403384	0.5	-0.410	0.072	7.949	0.020
bovinehd0600012492	6	44410455	0.549	-0.416	0.073	7.877	0.020
bovinehd0600012509	6	44444883	0.558	0.468	0.074	9.647	0.026
bovinehd0600013869	6	48836508	0.207	-0.485	0.092	6.894	0.018
bovinehd4100011066	14	9618157	0.412	0.460	0.076	8.752	0.024
bovinehd1400003503	14	10929298	0.325	0.389	0.078	6.161	0.016
hapmap31038-btc-069141	14	11176477	0.295	0.406	0.081	6.218	0.016
hapmap23784-btc-010226	14	12249541	0.617	-0.448	0.077	8.173	0.023
bovinehd1400004132	14	13197456	0.225	0.531	0.086	9.211	0.023
bovinehd1400004254	14	13417829	0.228	0.518	0.086	8.770	0.023
hapmap31182-bta-159357	14	13894960	0.706	0.540	0.084	9.953	0.029
ars-bfgl-ngs-55359	14	14168274	0.527	-0.381	0.074	6.511	0.017
bovinehd1400004530	14	14494754	0.216	0.456	0.089	6.575	0.017
bovinehd1400004660	14	14874505	0.429	0.483	0.073	10.509	0.027
bovinehd1400004702	14	15023750	0.587	-0.368	0.074	6.201	0.016
bovinehd1400004741	14	15129474	0.246	0.445	0.085	6.736	0.018
bovinehd1400004789	14	15316922	0.743	-0.547	0.082	10.569	0.027
bovinehd1400004805	14	15367052	0.509	-0.599	0.074	15.353	0.043
bovinehd1400004808	14	15369492	0.607	-0.564	0.079	12.135	0.036
bovinehd1400004865	14	15533199	0.258	0.415	0.081	6.529	0.016
bovinehd1400005070	14	16181118	0.55	-0.445	0.073	9.013	0.023
bovinehd1400005128	14	16307150	0.292	0.519	0.079	10.376	0.027
bovinehd1400005154	14	16394712	0.744	-0.541	0.084	9.904	0.027
bovinehd1400005214	14	16602217	0.223	0.492	0.088	7.661	0.020
bovinehd1400005271	14	16784290	0.539	-0.453	0.076	8.605	0.024
bovinehd1400005462	14	17468729	0.278	0.529	0.081	10.185	0.027
bovinehd1400005504	14	17669699	0.368	0.512	0.077	10.487	0.029
bfgl-ngs-116233	14	17706620	0.644	-0.424	0.077	7.463	0.020
bovinehd1400005528	14	17767587	0.273	0.444	0.081	7.301	0.019
bovinehd1400005554	14	17863393	0.334	0.626	0.080	14.353	0.042
bovinehd1400005573	14	17919760	0.71	-0.533	0.080	10.454	0.028
ars-bfgl-ngs-32563	14	18039217	0.389	0.452	0.075	8.704	0.023
bovinehd1400005621	14	18060329	0.227	0.491	0.087	7.764	0.020
bovinehd1400005634	14	18104102	0.473	-0.528	0.075	11.795	0.033
hapmap54994-rs29026820	14	18237825	0.074	-0.728	0.136	7.064	0.017

bovinehd1400005692	14	18287648	0.514	-0.367	0.074	6.153	0.016
bovinehd1400005773	14	18613954	0.323	0.604	0.080	13.433	0.038
bovinehd1400005861	14	18885521	0.056	-0.971	0.157	9.162	0.024
bovinehd1400005882	14	18948852	0.513	0.576	0.075	13.667	0.039
bovinehd1400005927	14	19069077	0.393	0.555	0.075	12.853	0.035
bovinehd1400005946	14	19155844	0.55	-0.561	0.074	13.411	0.037
bovinehd1400005970	14	19234405	0.464	0.572	0.074	13.868	0.039
bovinehd1400006006	14	19341599	0.814	-0.631	0.096	10.327	0.029
ars-bfgl-ngs-6136	14	19424294	0.9	-0.699	0.123	7.820	0.021
ars-bfgl-ngs-28234	14	19710934	0.566	-0.549	0.073	13.211	0.035
bovinehd1400006243	14	20034943	0.162	0.495	0.095	6.722	0.016
bovinehd1400006245	14	20041368	0.754	-0.422	0.083	6.399	0.016
bovinehd1400006357	14	20422957	0.333	0.595	0.078	13.719	0.037
bovinehd1400006455	14	20704261	0.72	-0.662	0.083	14.955	0.042
bovinehd1400006483	14	20837271	0.773	-0.630	0.087	12.456	0.033
ars-bfgl-ngs-106196	14	21764414	0.259	0.577	0.082	11.730	0.030
bovinehd1400006818	14	21833493	0.696	-0.630	0.080	14.574	0.040
bovinehd1400006945	14	22293187	0.179	0.498	0.095	6.844	0.017
bovinehd1400007477	14	24182505	0.733	-0.424	0.078	7.199	0.017
bovinehd1400007539	14	24452175	0.69	-0.501	0.077	10.082	0.026
bovinehd1400007846	14	25771401	0.275	0.587	0.080	12.690	0.033
bovinehd1400007885	14	25924883	0.721	-0.548	0.080	11.081	0.029
bovinehd1400007949	14	26091788	0.575	-0.566	0.074	13.671	0.037
bovinehd1400007990	14	26197356	0.867	-0.508	0.103	6.087	0.014
ua-ifasa-8554	14	26691608	0.304	0.488	0.076	9.904	0.024
bovinehd1400008234	14	26870423	0.696	-0.540	0.079	11.000	0.029
bovinehd1400008282	14	26969707	0.357	0.451	0.076	8.593	0.022
bovinehd1400008397	14	27317920	0.314	0.512	0.078	10.375	0.027
bovinehd1400008543	14	27771064	0.739	-0.666	0.081	15.654	0.041
bovinehd1400008660	14	28221952	0.42	0.555	0.074	13.081	0.036
bovinehd1400008667	14	28236317	0.695	-0.443	0.080	7.574	0.020
bovinehd1400008669	14	28238883	0.305	0.443	0.080	7.574	0.020
hapmap49130-bta-34437	14	28616735	0.631	-0.550	0.074	12.979	0.034
bovinehd1400008768	14	28641097	0.422	0.455	0.073	9.366	0.024
bovinehd1400008803	14	28782311	0.417	0.571	0.073	14.122	0.038
bovinehd1400008903	14	29137370	0.594	-0.484	0.073	10.466	0.027
bovinehd1400008910	14	29154723	0.463	-0.455	0.073	9.434	0.024
bovinehd1400008922	14	29197010	0.42	0.556	0.073	13.396	0.036
bovinehd1400009018	14	29559142	0.842	-0.495	0.100	6.123	0.016
bovinehd1400009028	14	29589249	0.44	-0.596	0.072	15.654	0.042
bovinehd1400009065	14	29732770	0.335	0.497	0.071	11.599	0.026
bovinehd1400009073	14	29755776	0.39	0.550	0.073	13.162	0.034
bovinehd1400009141	14	30019152	0.612	-0.577	0.074	14.162	0.038
bovinehd1400009182	14	30175048	0.338	0.380	0.076	6.311	0.015
bovinehd1400009183	14	30184825	0.541	0.515	0.072	12.156	0.031
bovinehd1400009218	14	30323253	0.394	0.614	0.074	15.654	0.043

bovinehd1400009269	14	30451214	0.496	0.404	0.072	7.810	0.020
bovinehd1400009279	14	30471227	0.747	-0.435	0.083	6.745	0.017
bovinehd1400009291	14	30486374	0.391	0.472	0.074	9.815	0.025
bovinehd1400009361	14	30590960	0.41	-0.572	0.072	14.574	0.038
bovinehd1400009485	14	31052862	0.618	-0.572	0.073	14.176	0.037
bovinehd1400009520	14	31201984	0.671	-0.439	0.077	7.891	0.020
bovinehd1400009525	14	31218288	0.425	0.524	0.074	11.778	0.032
bovinehd1400009609	14	31460476	0.596	-0.563	0.074	13.492	0.036
bovinehd1400009665	14	31626008	0.592	-0.437	0.075	8.305	0.022
bovinehd1400009667	14	31627917	0.418	0.478	0.075	9.744	0.027
bovinehd1400009687	14	31687605	0.453	0.442	0.072	9.170	0.023
bovinehd1400009705	14	31728265	0.737	-0.460	0.086	7.049	0.020
bovinehd1400009715	14	31762108	0.299	0.394	0.079	6.220	0.016
btb-01336033	14	31854932	0.44	-0.582	0.073	14.699	0.040
bovinehd1400009738	14	31862327	0.299	0.450	0.080	7.744	0.020
bovinehd1400009743	14	31876000	0.381	0.404	0.075	7.112	0.018
hapmap40239-bta-20881	14	31936098	0.428	-0.502	0.073	11.183	0.029
bovinehd1400009769	14	31960319	0.486	-0.575	0.074	14.239	0.039
bovinehd1400009776	14	31987771	0.274	0.419	0.082	6.480	0.017
bovinehd1400009799	14	32053249	0.407	0.481	0.074	10.094	0.027
bovinehd1400009867	14	32214895	0.499	-0.430	0.073	8.482	0.022
bovinehd1400009875	14	32233101	0.336	0.471	0.077	9.124	0.024
bovinehd1400009933	14	32385827	0.512	-0.444	0.072	9.132	0.023
bovinehd1400009938	14	32393654	0.528	0.534	0.073	12.638	0.034
bovinehd1400009939	14	32394139	0.472	-0.529	0.073	12.408	0.033
ua-ifasa-7535	14	32398088	0.365	-0.601	0.074	15.176	0.040
bovinehd1400009958	14	32462811	0.39	0.407	0.075	7.230	0.019
bovinehd1400009976	14	32518018	0.673	-0.393	0.077	6.422	0.016
bfgl-ngs-112227	14	32712341	0.517	0.536	0.073	12.841	0.034
bovinehd1400010063	14	32763681	0.531	0.445	0.073	8.979	0.024
bovinehd1400010083	14	32824245	0.395	0.561	0.074	13.393	0.036
bovinehd1400010091	14	32867843	0.354	-0.566	0.077	12.772	0.035
bovinehd1400010148	14	33075924	0.937	0.775	0.146	6.986	0.017
bovinehd1400010191	14	33263829	0.467	0.373	0.073	6.527	0.016
bovinehd1400010202	14	33305558	0.433	-0.378	0.073	6.685	0.017
bovinehd1400010203	14	33311484	0.433	-0.379	0.073	6.713	0.017
bovinehd1400010241	14	33435774	0.44	0.576	0.072	15.052	0.039
bfgl-ngs-109998	14	33496009	0.379	0.549	0.074	12.924	0.034
bovinehd1400010298	14	33643309	0.79	-0.519	0.088	8.459	0.021
ars-bfgl-ngs-102418	14	33650257	0.272	-0.621	0.082	13.483	0.036
bovinehd1400010311	14	33674371	0.481	0.529	0.072	12.547	0.033
bovinehd1400010309	14	33705668	0.566	0.477	0.071	10.623	0.027
bovinehd1400010343	14	33809691	0.401	-0.460	0.073	9.633	0.024
bovinehd1400010348	14	33830236	0.565	0.445	0.071	9.475	0.023
bovinehd1400010349	14	33834184	0.424	-0.410	0.074	7.564	0.020
bovinehd1400010363	14	33872141	0.264	-0.611	0.081	13.368	0.035

bovinehd1400010375	14	33900317	0.38	-0.491	0.073	10.646	0.027
bovinehd1400010386	14	33931590	0.438	-0.477	0.072	10.345	0.027
bovinehd1400010394	14	33964901	0.407	-0.478	0.073	10.275	0.026
bovinehd1400010422	14	34085308	0.798	-0.525	0.091	8.117	0.021
bovinehd1400010424	14	34095030	0.202	0.523	0.091	8.052	0.021
bovinehd1400010432	14	34130102	0.442	-0.592	0.073	15.176	0.041
bovinehd1400010496	14	34370911	0.618	0.470	0.074	9.723	0.025
bovinehd1400010560	14	34666072	0.641	0.602	0.075	15.052	0.040
bovinehd1400010561	14	34670135	0.262	-0.666	0.082	15.353	0.041
bovinehd1400010572	14	34715820	0.547	0.398	0.073	7.340	0.019
ars-bfgl-ngs-19330	14	34828602	0.39	0.423	0.075	7.844	0.020
bovinehd1400010652	14	35016024	0.47	-0.563	0.072	14.135	0.038
bovinehd1400010667	14	35100954	0.47	-0.549	0.073	13.329	0.036
bovinehd1400010719	14	35346833	0.515	-0.513	0.073	11.714	0.031
bovinehd1400010828	14	35695152	0.477	0.451	0.074	8.966	0.024
bovinehd1400010924	14	36042750	0.661	-0.498	0.075	10.497	0.026
bovinehd1400010943	14	36100767	0.391	0.408	0.075	7.260	0.019
bovinehd1400010944	14	36101374	0.616	-0.413	0.076	7.345	0.019
bovinehd1400010956	14	36126743	0.403	-0.366	0.073	6.237	0.015
bovinehd1400010966	14	36158299	0.539	0.475	0.073	10.207	0.027
bovinehd1400010973	14	36177079	0.533	0.468	0.072	10.007	0.026
bta-107899-no-rs	14	36267667	0.407	0.359	0.072	6.177	0.015
bta-107905-no-rs	14	36322336	0.546	-0.345	0.068	6.489	0.014
bovinehd1400011071	14	36463224	0.499	-0.377	0.072	6.876	0.017
bovinehd1400011100	14	36554488	0.577	0.389	0.073	7.031	0.018
bovinehd1400011178	14	36752804	0.545	0.367	0.073	6.374	0.016
bovinehd1400011149	14	36831989	0.475	-0.402	0.071	7.738	0.019
bovinehd1400011205	14	36944262	0.287	-0.532	0.080	10.446	0.028
ars-bfgl-ngs-37766	14	37548790	0.299	-0.451	0.079	7.993	0.020
bovinehd1400011411	14	37588889	0.528	0.500	0.072	11.425	0.030
hapmap41239-bta-34703	14	37632845	0.249	-0.617	0.085	12.421	0.034
bovinehd1400011436	14	37719828	0.378	-0.468	0.074	9.480	0.025
ua-ifasa-5908	14	37884073	0.261	-0.602	0.084	12.145	0.033
ua-ifasa-6750	14	38020858	0.264	-0.625	0.083	13.235	0.036
btb-01837238	14	38188466	0.673	0.557	0.078	12.020	0.033
bovinehd1400011565	14	38209006	0.484	-0.451	0.072	9.523	0.024
bovinehd1400011661	14	38622008	0.234	-0.625	0.087	12.184	0.033
ua-ifasa-7391	14	38677519	0.787	0.651	0.090	12.352	0.034
bovinehd1400011686	14	38713677	0.47	0.369	0.073	6.381	0.016
bovinehd1400011720	14	38813162	0.682	0.440	0.080	7.422	0.020
bovinehd1400024106	14	38822904	0.569	0.578	0.074	14.097	0.039
btb-01387726	14	38833176	0.462	-0.463	0.074	9.395	0.025
btb-01387806	14	38865578	0.516	-0.383	0.073	6.764	0.017
bovinehd1400011779	14	39072632	0.228	0.516	0.084	9.082	0.022
ua-ifasa-6899	14	39147564	0.211	-0.573	0.091	9.516	0.026
bovinehd1400011802	14	39182760	0.387	-0.445	0.074	8.715	0.022

btb-00566183	14	39381019	0.757	0.538	0.086	9.414	0.025
bovinehd1400011944	14	39803916	0.665	0.516	0.077	10.727	0.028
btb-00566358	14	40565849	0.227	-0.522	0.087	8.766	0.023
bovinehd1400012247	14	40987099	0.471	-0.421	0.073	8.165	0.021
bovinehd1400012331	14	41386739	0.22	-0.454	0.087	6.804	0.017
bovinehd1400012419	14	41727409	0.436	-0.424	0.072	8.528	0.021
bovinehd1400012536	14	42125147	0.541	-0.415	0.072	8.166	0.020
bovinehd1400012980	14	43800963	0.497	0.364	0.072	6.419	0.016
bovinehd1400013136	14	44304675	0.586	0.416	0.074	7.673	0.020
bovinehd1400013233	14	44631766	0.766	0.447	0.085	6.814	0.017
bovinehd1400013483	14	45510975	0.608	0.433	0.074	8.356	0.021
bovinehd1400015117	14	51573048	0.396	0.408	0.076	7.106	0.019
bovinehd2100000230	21	454528	0.112	0.830	0.118	11.661	0.033
bovinehd2100000207	21	581734	0.766	-0.430	0.087	6.168	0.016
bovinehd2100000129	21	869237	0.13	0.773	0.110	11.675	0.032
bovinehd2100000118	21	982601	0.133	0.824	0.110	13.134	0.037
ars-bfgl-ngs-63493	21	995360	0.869	-0.754	0.109	11.241	0.031
bovinehd2100000106	21	1089296	0.87	-0.751	0.110	11.042	0.030
bovinehd2100000090	21	1196735	0.878	-0.928	0.116	15.052	0.044
bovinehd2100000078	21	1270512	0.871	-0.776	0.111	11.598	0.032
bovinehd2100000061	21	1399283	0.119	0.876	0.117	13.176	0.038
bovinehd2100000031	21	1632924	0.18	0.572	0.089	9.872	0.023
bovinehd2100000022	21	1749155	0.121	0.885	0.115	13.778	0.040
bovinehd2100000015	21	1850825	0.879	-0.874	0.115	13.501	0.039
ars-bfgl-ngs-90904	21	1924657	0.883	-0.875	0.117	13.080	0.038
bovinehd2100000001	21	1958412	0.872	-0.809	0.111	12.509	0.035
bovinehd2100000555	21	1970429	0.133	0.834	0.111	13.261	0.038
21-2138942-c-t-rs434742030	21	2097487	0.787	-0.615	0.089	11.200	0.030
bovinehd2100000271	21	2144071	0.866	-0.833	0.110	13.346	0.038
bovinehd2100000283	21	2214322	0.811	-0.560	0.092	8.856	0.023
bovinehd2100000398	21	2784617	0.843	-0.537	0.100	7.137	0.018
ars-bfgl-ngs-92774	21	2890136	0.863	-0.680	0.106	9.821	0.026
ars-bfgl-ngs-37987	21	2937636	0.904	-0.954	0.126	13.403	0.038
bovinehd2100000457	21	3027732	0.136	0.558	0.104	7.025	0.017
bovinehd2100000944	21	5154955	0.208	0.475	0.089	6.971	0.018
bta-52775-no-rs	21	5778152	0.89	-0.710	0.118	8.708	0.024
bovinehd2100001216	21	5945095	0.663	-0.426	0.077	7.523	0.019
bovinehd2100001409	21	6658991	0.132	0.660	0.109	8.878	0.024
ars-bfgl-ngs-62108	21	7099307	0.089	0.735	0.128	7.984	0.021
bovinehd2100001581	21	7125435	0.099	0.752	0.120	9.383	0.024
bovinehd2100001706	21	7726138	0.534	-0.392	0.073	7.168	0.018
bovinehd2100001710	21	7732401	0.912	-0.790	0.132	8.615	0.024
ars-bfgl-ngs-86900	21	7844296	0.911	-0.856	0.132	10.000	0.028
bovinehd2100001788	21	7999641	0.123	0.574	0.111	6.608	0.017
bovinehd2100001969	21	8498932	0.128	0.662	0.106	9.358	0.023

bovinehd2100002479	21	10068286	0.671	-0.399	0.077	6.601	0.017
bovinehd0500013289	5	46060164	0.052	0.946	0.174	7.273	0.021
hapmap24085-bta-143102	5	46159494	0.925	-0.717	0.143	6.254	0.017
ars-bfgl-ngs-98210	5	46249078	0.063	0.840	0.160	6.843	0.020
hapmap50523-bta-98407	5	46516496	0.936	-0.806	0.148	7.298	0.019
bovinehd0500013462	5	46541885	0.938	-0.952	0.150	9.605	0.025
bovinehd1000024900	7	110390355	0.524	-0.362	0.072	6.376	0.016
bovinehd0800009065	8	29808970	0.509	0.373	0.072	6.706	0.017
ars-bfgl-ngs-21158	13	40405868	0.131	-0.587	0.114	6.611	0.019
bovinehd1300020070	13	69530792	0.528	0.386	0.072	7.131	0.018
ars-bfgl-ngs-15187	16	52149496	0.15	0.500	0.099	6.301	0.015
bovinehd2500012246	25	41063898	0.534	-0.354	0.071	6.206	0.015

9.3 Project publications and presentations

Publications

Moore, K.L., Grant, T.P. and Johnston, D.J. (2021). Genetic analysis of body condition and growth traits in beef females within and across ages and physiological states. In Proc. Assoc. Advmt. Anim. Breed. Genet. 23:247

Moore, K.L., Gurman, P.M. and Johnston, D.J. (2023). Application of an empirical approach for predicting accuracy for genomic evaluations. Proc. Assoc. Advmt. Anim. Breed. Genet. 24:146

Moore, K.L., Ferdosi, M.H., Girard, C.G., Walkom, S.F. and Johnston, D.J. (2022). A new metric to assess reference populations for genomic selection in Australian beef breeds. In Proceedings of 12th World Congress on Genetics Applied to Livestock Production: 3-8 July; Rotterdam.

Moore K.L., Johnston D.J., Ingham A., Hine B., Grant T. and Croaker J. (2023). Preliminary analysis of immune competence traits in Australian tropically adapted beef breeds. In Proceedings of Northern beef research update conference.

Moore K.L, Johnston D.J., and Grant T. (2025) Myostatin alleles are segregating in Australian Droughtmaster and Santa Gertrudis populations but not in Brahman. Proc. Assoc. Advmt. Anim. Breed. Genet. 25: (submitted)

Moore K.L, Johnston D.J., Grant T. and Croaker J. (2025) Preliminary analysis of immune competence traits in northern Australian tropically adapted beef breeds. Proc. Assoc. Advmt. Anim. Breed. Genet. 25: (submitted)

Moore, K.L., Walkom, S.F., Siddell, J.P. and Walmsley, B. (2023). Quantifying the linkage between genetics represented in the southern multi-breed project and the wider beef populations. Proc. Assoc. Advmt. Anim. Breed. Genet. 24:330

Walkom, S.F., Duff, C.J., Girard, C. and Moore, K. (2023). Longevity of reference populations in a Trans-Tasman genetic evaluation: review of the Angus sire benchmarking program. Proc. Assoc. Advmt. Anim. Breed. Genet. 24:322

Presentations

"Investigating Net feed Intake in Australian Wagyu", presented at WagyuEDGE conference, 27-29th April 2021

"The role of reference populations", presented at the Repronomics information day, 1st April 2022

"New traits being measured", presented at Cattle Australia Industry Updates 26th February 2025