



final report

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Intensive phenotyping in industry to expand the Brahman reference population

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Abstract

This project aimed to contribute genotypes and hard-to-measure phenotypes for male and female reproduction to the Brahman BREEDPLAN analysis from a seedstock herd which is well linked to the current Brahman population and to key research herds. The project recorded age at puberty (AP) and lactation anoestrous interval (LAI) in females and percent normal sperm (PNS) in males from three concurrent weaning groups. BREEDPLAN results showed an increase in days to calving estimated breeding value (EBV) accuracy for the Kaiuroo females in which AP and LAI were recorded, and in PNS EBVs for the bulls recorded for the trait, as well as for their sire and other related animals, both within the Kaiuroo herd and in the wider Brahman population. Data contributed to the Brahman evaluation from this project presents opportunities for breeders to make more informed selection decisions to improve reproduction, and to increase rates of genetic progress for those traits and, therefore, whole herd profitability. The project has provided a model for collection and use of data from industry for genomic reference, including estimates of potential costs.

Executive summary

Research conducted by the Beef CRC showed that female reproduction was a key driver of profitability for northern beef producing enterprises (Johnston *et al.* 2009 and 2014a). Those studies also developed methods to more accurately describe female reproductive performance (ultrasound scanning for ovarian function to measure age at puberty (AP) and lactation anoestrus interval (LAI)) and demonstrated that these were significantly more heritable ($h^2 = 0.26$ to 0.57) than days to calving ($h^2 = 0.05$ to 0.22), which is the trait in the BREEDPLAN evaluation for tropical beef breeds that describes genetic merit for female reproduction. As part of the same project, new descriptors of male reproductive performance were evaluated and percent normal sperm (PNS) was reported to be heritable for Brahmans and Tropical Composite bulls when recorded within optimal age ranges ($h^2 = 0.25$ and 0.41), and to be moderately and favourably genetically correlated to female reproduction traits measured by ovarian scanning ($r_g = -0.24$ to -0.65). Subsequent research, undertaken as part of the MLA funded B.NBP.0759 (Repronomics™) project, has sought to create the critical mass of AP and LAI records required for the BREEDPLAN single-step evaluations in tropical beef breeds to underpin more effective genomic selection for these economically important traits. Absent from this research was the capacity to manage large numbers of bulls, and collect the percent normal sperm records required for the male component of reproductive performance to be as well described as the female in these evaluations. This project sought to expand the availability of both male and female reproduction data in the reference population for the Brahman breed by collecting percent normal sperm, age at puberty and lactation anoestrus interval data, in genotyped males and females, in a well-described Brahman seedstock herd with good genetic links to industry and to relevant research projects.

A key aim of this project was to include genomic information in the Brahman evaluation for the intensively recorded males and females involved in this project. In total there were 252, 262 and 251 bulls and 246, 252 and 267 females with genotypes included in the evaluation in 2016, 2017 and 2018 respectively. After data cleaning and editing, and the inevitable challenges of collecting research data under commercial conditions, 643 age at puberty, 244 lactation anoestrus interval and 543 percent normal sperm records were also submitted for analysis to the Brahman evaluation. Prior to submission of the data, genetic parameters were estimated for each trait using records from all three years of recording. Heritabilities for AP, LAI and PNS were 0.56, 0.39 and 0.17 respectively, which was extremely consistent with results reported from the Beef CRC ($h^2 = 0.57$, 0.51 and 0.15 to 0.25 respectively), providing some confidence in the consistency of the data submitted for this project to that from previous research.

Undertaking custom analyses to evaluate the exact impact on Brahman BREEDPLAN EBVs and their accuracy of the recording undertaken for this study was not within the scope of the agreements in place for this project. It has been possible, however, to obtain an estimate of breeding value responses to the data recorded for this project by comparing publically available EBVs generated prior to, and following the submission of these records for BREEDPLAN analysis. For 72 sires of Kaiuroo progeny evaluated as part of this project, EBV accuracies for days to calving, AP, LAI and PNS increased from 59.9 to 66.1, 40.4 to 70.9, 38.1 to 57.5 and 26.1 to 50.9 percent respectively. This group of sires included 26 bulls with a combined 2033 progeny in 89 herds outside of Kaiuroo. The accuracy gains generated via the genotypes submitted as part of this project will be included in the pre-submission values, meaning that the responses in EBV accuracy to the recording and genotyping undertaken for this project will be underestimated in the changes described above. This aside, these improvements to the accuracy of BREEDPLAN EBVs describing reproductive performance present clear opportunities for Brahman breeders to make better informed selection decisions to improve reproduction in their herds.

Intensive recording of reproduction phenotypes in a seedstock herd is an expensive proposition. The recording carried out for this project could be replicated in 500 heifers and lactating first calf females and 500 young bulls at a cost of approximately \$100,000 per year. This research has demonstrated that these costs are offset by significant improvements in reproduction EBV accuracy, with the exact impact at the breed level dependant on the degree of relationship of intensively phenotyped animals to the rest of the population. This highlights the importance of undertaking such work in carefully selected herds to maximise the benefit at the breed and industry levels.

Table of contents

Intensive phenotyping in industry to expand the Brahman reference population.....	1
1 Background	6
2 Project objectives	7
3 Methodology	8
3.1 Bull breeding soundness evaluation and sperm morphology traits	8
3.2 Heifer ovarian scanning to determine age at puberty	8
3.3 Scanning in lactating first calf females to determine lactation anoestrous interval ...	9
3.4 Genotyping	9
3.5 Statistical analysis.....	9
4 Results.....	10
4.1 BBSE records for 2016, 2017 and 2018 weaned bulls	10
4.2 Ultrasound scanning data for age at puberty in 2016, 2017 and 2018 weaned heifers	11
4.3 Ultrasound scanning data for lactation anoestrous interval in 2014, 2015 and 2016 weaned heifers	12
4.4 Genetic parameters for male and female reproduction traits recorded at Kaiuroo .	13
4.5 Impact of Kaiuroo phenotyping on BREEDPLAN reproduction EBVs	14
4.6 Extension of Kaiuroo MDC results to industry	20
5 Discussion.....	20
5.1 Resourcing, costs and returns associated with intensive phenotyping to describe male and female reproductive performance.....	20
5.2 Meeting project objectives.....	22
5.2.1 Objective 1.....	22
5.2.2 Objective 2.....	22
6 Conclusions/recommendations.....	22
7 Key messages	23
8 Bibliography	24
9 Appendix	25
9.1 Appendix 1: Beef central article by Wayne Upton – 10 th July 2018.....	25
9.2 Appendix 2: Beef central article by Alex McDonald 17 th April 2018.....	26
9.3 Appendix 3: MLA Feedback Magazine article – July 2018	27
9.4 Appendix 4: YouTube video produced by Kaiuroo management including material recorded during Beef 2018 tour - 7 th May 2018.....	29

1 Background

The following is copied directly from the original project proposal.

Genetic evaluation for beef cattle in northern Australia is entering the genomic prediction and selection stage, firstly through the incorporation of DNA information via the blending approach, and more recently, with the implementation of single-step genomic evaluation (MLA projects B.BFG.0050 and L. GEN.1704). For genomic selection to work reliably, reference population data is essential – i.e. animals representative of the population under selection which have both genotypes and phenotypes for traits of economic importance. The accuracy of breeding value predicted using single-step rises with the size of the reference population (Goddard and Hayes, 2009), and ensuring that the reference population maintains genetic linkage to the current breeding population is critical. As relatedness between the reference population and selection candidates declines, so does the accuracy of the breeding values generated. There are no hard and fast rules for how many new records are needed each year to maintain good accuracy, but a rule of thumb is to aim for approximately 5,000 animals with phenotypes and genotypes to achieve accuracy of EBVs similar to that of young animals with their own records. To maintain this level of accuracy, completely refreshing the reference population over approximately 2 generations (approximately 7 years) should be sufficient – meaning adding approximately 700 new animals to the reference each year. Where the population is more diverse, this target should be higher.

The key design aspects of reference populations are therefore that:

- The animals genotyped and phenotyped (or with close relatives that are phenotyped) are closely related to the current active breeding population, and
- The animals are recorded for traits that are as directly related to enterprise profitability as possible. In particular, specifically designed reference populations will usually need to include traits that are high value (large impact on either income or cost) and which are not routinely or widely recorded in the general recording population (Banks et al, 2006; Banks, 2011, Van der Werf *et al.*, 2010).

Beef CRC research and MLA project B.NBP.0761 (Johnston *et al.* 2014a, 2014b and 2019) identified new, but hard to measure traits which describe reproductive performance in tropical beef breeds (age at puberty, lactation anoestrous interval and percent normal sperm) with greater accuracy than has been possible using days to calving and scrotal circumference, the traits traditionally employed to describe reproduction in the BREEDPLAN evaluation. Reproductive rate is a key driver of profitability for northern beef breeding enterprises, and recording these new traits in a seedstock herd, well linked to the current industry and research populations, has been the key focus of the research undertaken for project.

In this project, the Kaiuroo Brahman seedstock herd worked with AGBU to optimise phenotypic recording and genotyping for reproduction (including male percent normal sperm, and female age at puberty and lactation anoestrus interval), and has invested in genotyping and recording eligible bulls and heifers from each of 3 drops, to contribute data to the Brahman Single-step BREEDPLAN evaluation. These records have been collected in one of the best described Brahman seed-stock herds, and matings were structured to insure good genetic linkage with the Brahman BIN project, as well as the MLA B.NBP.0759 (Repronomics™) project.

2 Project objectives

The following is copied directly from the original project proposal.

The project aims to collect genotypes and high quality phenotypes, for traits contributing to male and female reproductive performance in Brahman cattle, on approximately 500 animals (bulls and heifers equally) in each of 3 successive calf crops, in a Brahman stud that is well genetically linked to the overall Brahman breed in Australia, and to research herds. These records will contribute in realtime to the reference population for Brahman single step BREEDPLAN, and help ensure that genomic breeding values for reproduction traits in Brahman cattle are at useful levels of accuracy, and hence that genomic testing in Brahman cattle is as reliable as practically possible.

3 Methodology

3.1 Bull breeding soundness evaluation and sperm morphology traits

Bull breeding soundness evaluations (BBSE) and sperm morphology testing were undertaken in the 2017, 2018 and 2019 weaned bulls. These were timed to achieve the best description of variation in bull fertility, with an initial test conducted in March of each year and a second evaluation prior to the use of selected bulls in the stud breeding program, in September. An interim test for some bulls was also conducted in May to better describe variation in male puberty. The BREEDPLAN evaluation only analyses a single record for BBSE, with additional records contributing to ongoing research around male reproduction traits and their potential contribution to our understanding of the genetics of female reproduction, both key drivers of profitability for northern beef breeders.

Methods employed to collect and analyse sperm samples were consistent with those reported for Beef CRC bulls by Corbet *et al.* (2013). The bulls collected and analysed for this project comprised 199, 187, and 179 animals weaned in 2016, 2017 and 2018 respectively; with bull fertility traits evaluated described in Table 3.1.1.

Table 3.1. 1. Description of sperm abnormality traits measured in Kaiuroo bulls.

Trait	Code	Description
Percent normal sperm	PNS	Proportion of sperm cells evaluated displaying none of the abnormalities described below.
Proximal and distal droplets	PD	Spherical adhesions to the proximal or distal segment of the sperm cell tail, most commonly observed in peripubertal bulls
Abnormal mid pieces	MP	Includes several abnormalities of the sperm cell mid-piece.
Abnormal tails and heads	TH	Includes several abnormalities of the sperm cell tails and heads, including loose or detached heads and bent tails.
Pyriform heads	PY	Sperm cells which develop with an atypical (pear shaped) head which affects the cell nucleus and fertilising capacity.
Knobbed acrosomes	KA	Abnormal development of the acrosome which produces a flattened or indented apex to the sperm cell.
Vacuoles and teratoids	VT	Includes voids and irregular surfaces of the sperm cell indicative of severe disturbance in spermatogenesis.
Swollen acrosomes	SA	Atypical enlargement of the acrosome.

3.2 Heifer ovarian scanning to determine age at puberty

Ultrasound scanning to assess ovarian function in heifers was undertaken for 220, 199 and 224 heifers, weaned in 2016, 2017 and 2018 respectively. Scanning for each cohort commenced in February of those years and continued, at approximately 2 monthly intervals, until the start of the heifer's first mating, in October, as 2 year olds. For 2016 and 2017 weaned females, pregnancy testing results were applied to fine-tune estimates of age at puberty based on pre-mating ovarian scanning results. These results were not available for 2018 weaned heifers before the conclusion of the project, and a penalty of contemporary group maximum AP +42 days (2 cycles) was applied for females which failed to record a CL up to mating (N = 67). Consistent with the Beef CRC protocols described by Johnston *et al.* (2009), age at puberty was calculated as the date of detection of a heifer's first CL minus their date of birth.

3.3 Scanning in lactating first calf females to determine lactation anoestrous interval

Scanning for ovarian function in lactating first calf females was carried out following the protocols described by Johnston *et al.* (2014) in the Beef CRC. Scanning was repeated at approximately 1 month intervals from an initial scan, at the start of the mating period in October. The final scan occurred in February – March of the following years, with 4 opportunities for lactating first calf females to return a positive result for the presence of a CL. Lactation anoestrous interval was calculated as the date at which a CL is detected, minus bull in date in October / November. As LAI is a trait of lactating females only, the numbers of females eligible for scanning for the trait is a factor of weaning rates from their maiden mating, which in Brahman cattle is well documented to be lower than that observed in temperate beef breeds.

In the first year of the project, lactating 2014 weaned heifers were scanned to estimate LAI and only 60 females met the criteria for recording the trait. This was the result of management decisions made before the commencement of the project to cull a proportion of late calving 2014 weaned first calf females. For 2015 and 2016 weaned females these numbers improved, with 99 and 107 females producing valid records for the trait respectively.

3.4 Genotyping

A key component of the project was to genotype all males and females evaluated for reproduction traits. Hair samples were collected at weaning for all 2016, 2017 and 2018 weaned bulls and heifers. These were submitted to the Australian Brahman Breeders Association and have been processed by NeoGen (previously University of Queensland Animal Genetics Laboratory) using the 50K TropBeef chip. All genotypes have now been included in the Brahman BREEDPLAN analysis.

There were 252, 262 and 251 Male and 246, 252 and 267 female genotypes (for 2016, 2017 and 2018 weaned calves) added to the Brahman evaluation as a result of this project. As the male and female reproduction phenotypes recorded as part of this project were submitted for BREEDPLAN analysis, this genomic information maximises the advantage of the intensive recording conducted at Kaiuroo, at the breed level.

3.5 Statistical analysis

The key analyses undertaken for this project are those conducted as part of routine BREEDPLAN runs. The analytical methods applied to generate BREEDPLAN estimated breeding values (EBVs) are well documented, with Graser *et al.* (2005) describing the statistical methods underlying the evaluation, and Johnston *et al.* (2018) describing the methods and outcomes for incorporation of genomic information into BREEDPLAN's estimation of breeding values. To highlight the impact of the recording which has been undertaken for the project, EBVs were logged for key animals prior to and following the submission of the data to BREEDPLAN. Contrasting EBVs and their accuracies pre- and post-inclusion of the Kaiuroo data provides a demonstration of the impact of the recording undertaken for this project. This comparison required no analysis of BREEDPLAN data beyond that undertaken for routine runs to generate publically available EBVs.

To confirm the suitability of the data collected at Kaiuroo to be included in the BREEDPLAN evaluation, univariate models were built for each of the traits submitted to estimate variance components and heritabilities. These models were built in accordance with the protocols described by Graser *et al.* (2005), fitting the BREEDPLAN contemporary group for animals at their last submitted record, prior to recording of the reproduction traits collected for this project. Estimates of heritability for such small

datasets (244 – 643 records / trait) can be unreliable, but provide some confidence in the quality of the data if they are consistent with published results for the same trait, estimated in larger datasets. To understand the genetic relationship between the reproduction traits recorded as part of this project, a small number of bivariate analyses were undertaken using the ASReml analysis package, with analyses run to estimate the genetic correlation between PNS and AP, PNS and LAI, and AP and LAI. As with the heritabilities described above, these genetic correlations allow comparison of results obtained as part of the Kaiuroo MDC with results from prior, larger experiments, and provide a metric for the quality of data being contributed to the Brahman BREEDPLAN evaluation by this project.

4 Results

4.1 BBSE records for 2016, 2017 and 2018 weaned bulls

Table 4.1.1 presents descriptive statistics for BBSE and sperm morphology traits evaluated in the 2016, 2017 and 2018 weaned Kaiuroo bulls. BREEDPLAN has recently begun analysis and publication of EBVs for percent normal sperm (PNS) in the Brahman evaluation. The vast majority of records included in the analysis to date are from data collected as part of Beef CRC research. Since the end of the CRC, few new records for the trait have entered the analysis. The PNS data collected as part of this project represent records from industry which are, by design, linked to the female reproduction phenotypes collected as part of this project, as well as those from the Brahman BIN, the Repronomics projects, and the contemporary Brahman seedstock population.

Table 4.1.1. Descriptive statistics (STAT) for percent normal sperm (PNS) and component sperm abnormality traits* for 2016, 2017 and 2018 weaned Kaiuroo bulls.

YEAR	STAT	PNS	PD	MP	TH	PY	KA	VT	SA
2016 (N = 196)	Mean	73.9	3.7	10.0	4.2	0.1	1.1	5.5	1.8
	sd	12.6	4.6	7.8	4.6	0.2	3.0	5.7	3.7
	Min	31	0	0	0	0	0	0	0
	Max	98	28	59	29	1	32	51	29
2017 (N = 168)	Mean	76.1	5.1	10.6	4.7	0.1	0.4	2.7	1.1
	sd	16.9	11.3	9.6	6.4	0.5	0.8	3.9	2.0
	Min	19	0	0	0	0	0	0	0
	Max	96	59	51	48	5	4	30	10
2018 (N = 179)	Mean	72.9	5.7	11.7	8.5	0.1	1.1	6.3	0.4
	sd	14.3	10.1	9.0	9.5	0.4	2.4	7.5	1.7
	Min	23	0	0	0	0	0	0	0
	Max	99	68	68	53	2	26	53	16
Overall (N = 543)	Mean	74.2	4.6	10.7	5.8	0.1	0.9	5.0	1.1
	sd	14.6	8.5	8.8	7.4	0.4	2.3	6.1	2.8
	Min	19	1	1	1	1	1	1	1
	Max	99	68	68	53	5	32	53	29

* See Table 3.1.1 for a description of acronyms used for sperm abnormality traits.

Means and variation for percent normal sperm were quite consistent with results presented by Corbet *et al.* (2013) for the 24 month old Brahman bulls recorded in the Beef CRC (PNS = 71 ± 23%). Results for the component sperm abnormality traits PD, MP and TH were similar to those reported by Wolcott *et al.* (2018) in describing the genetics of sperm abnormality traits recorded in 24 month old Brahman bulls in the Beef CRC (7.7 ± 15.6, 11.3 ± 12.3 and 5.6 ± 9.0 % respectively). That publication also

observed that the remaining traits (PY, KA, VT and SA) displayed low proportions of non-zero results, which was also consistent with results observed in the bulls sampled at Kaiuroo for the current study.

4.2 Ultrasound scanning data for age at puberty in 2016, 2017 and 2018 weaned heifers

Figure 4.2.1 presents the cumulative proportion of heifers which reached puberty (first observed CL) at each scanning time, by weaning year group (2016, 2017 and 2018) up to the final scan, as they entered their first mating, in October of each year.

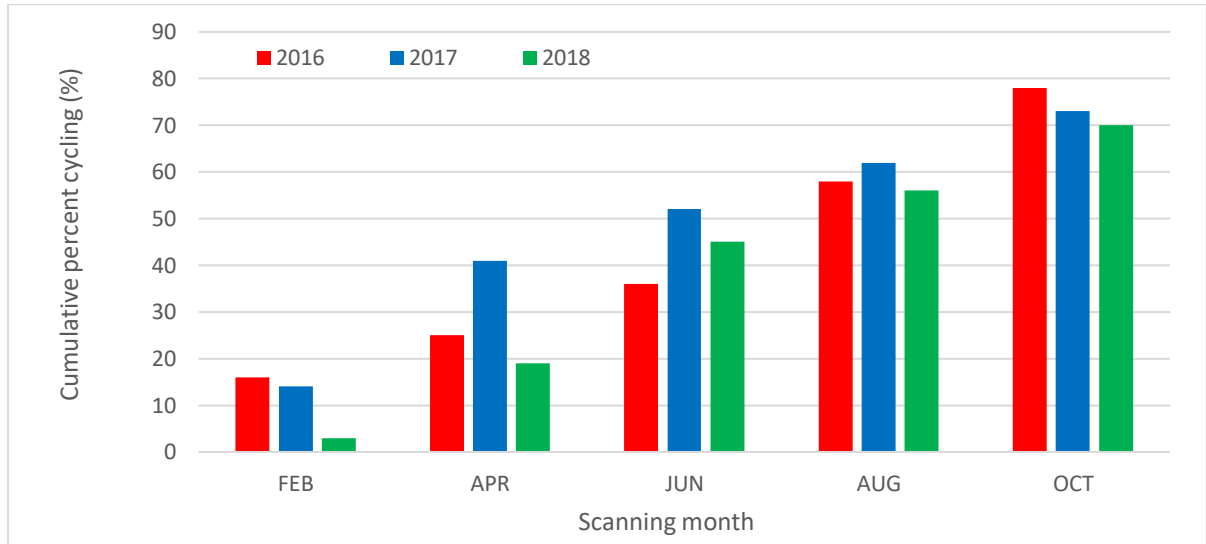


Figure 4.2.1. Proportion of Kaiuroo heifers which displayed a CL at each ovarian scan, by year of weaning (2016, 2017 and 2018).

The slightly declining trend in the proportion of heifers pubertal into mating in 2016, 2017 and 2018 weaned females (78, 73 and 70% respectively) reflects variation in seasonal conditions and may have been impacted by a management decision to move towards a reduction of the mating period for young females to three months (though this was not fully implemented over the course of this project).

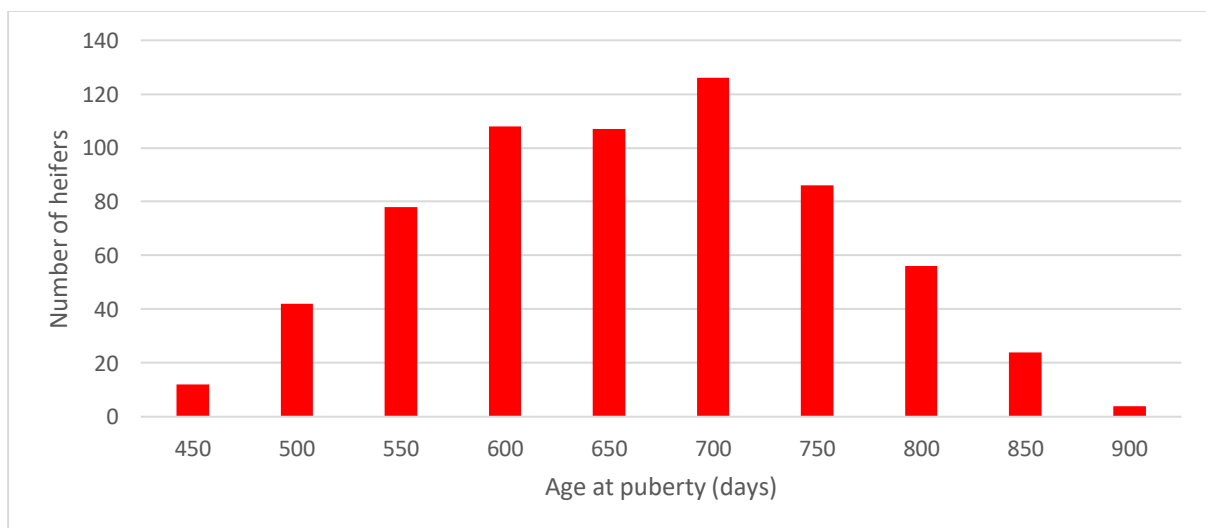


Figure 4.2.2. Distribution of age at puberty for 2016, 2017 and 2018 weaned heifers at Kaiuroo.

Figure 4.2.2 presents the distribution of ages at puberty for the combined dataset. Mean age at puberty across the three years of the project was 635.1 ± 96.5 days. This was significantly lower than the result observed for Brahmans in the Beef CRC (750 ± 142 days). The difference is likely to be associated with superior genetic AP in the Kaiuroo herd as well as (and probably more importantly) significantly higher mean weight and condition into mating for Kaiuroo heifers (370kg liveweight and 5mm P8 fat) than their CRC counterparts (320kg liveweight and 3mm P8 fat). The results for age at puberty reported in the Repronomics™ project (Johnston *et al.* 2019) for Brahman and Droughtmaster heifers recorded at the Spyglass research station (age at puberty = 657.2 ± 143.3 days) were quite consistent with those observed at Kaiuroo.

4.3 Ultrasound scanning data for lactation anoestrous interval in 2014, 2015 and 2016 weaned heifers

Average adjusted lactation anoestrus interval (LAI) across the 2014, 2015 and 2016 weaned lactating first calf females was 83.5 ± 36.1 days, and ranged from 0 to 193 days. Figure 4.3.1 illustrates the distribution of LAI results, describing an essentially normally distributed trait. The higher than expected frequency of records in the 160 – 200 day category are for animals which failed to show a CL during the scanning period or to conceive a calf from that mating, which received a penalty of the maximum LAI for their contemporary group plus 42 days (two cycles).

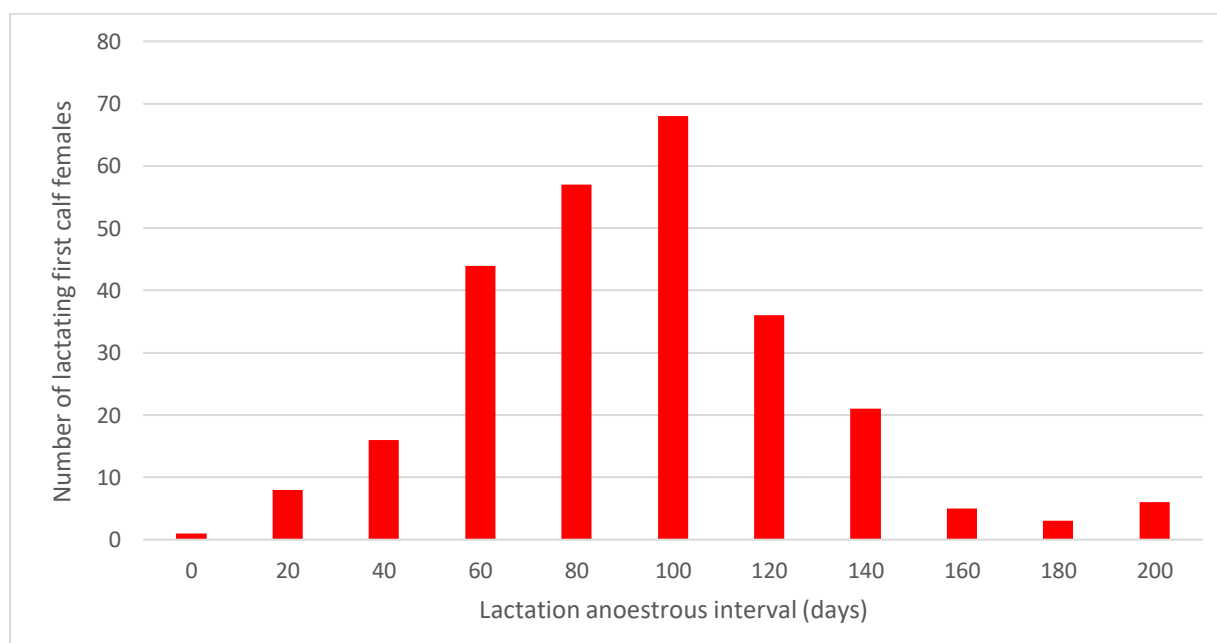


Figure 4.3.1. Distribution of lactation anoestrous interval for 2014, 2015 and 2016 weaned lactating first calf females at Kaiuroo.

These results were substantially lower than those reported by Johnston *et al.* (2014a) for Brahman, lactating first calf females in the Beef CRC (LAI = 133.7 ± 109.5 days), but were more consistent with those for the Brahman and Droughtmaster Spyglass heifers reported for the Repronomics™ project by Johnston *et al.* (2019) (LAI = 83.5 ± 84.4 days). Differences in the variation in lactation anoestrus interval observed at Kaiuroo (s.d. = 36.1 days) and for the Beef CRC and Repronomics™ projects (s.d. = 109.5 and 84.4 days respectively) will be associated with protocols for projects conducted on research stations which allowed scanning beyond the end of mating for females which failed to record a CL by that time. This increased maximum LAI significantly (up to 411 days for the Beef CRC and 360 days in the Repronomics project), and will explain the majority of the difference between Kaiuroo and research station based results.

4.4 Genetic parameters for male and female reproduction traits recorded at Kaiuroo

Estimation of genetic parameters for small datasets (less than 5000 records) is not generally recommended, or considered particularly reliable. If heritabilities are consistent with expectations, however, it does provide some confidence in the data collected. Similarly, genetic correlations which support the current understanding of interactions between traits, at the genetic level, provide confidence that the records collected for this project will contribute to better selection opportunities for Brahman breeders. Table 4.4.1 presents variance components and heritabilities for the male (PNS) and female (AP and LAI) reproduction traits submitted to BREEDPLAN by the Kaiuroo MDC project.

Table 4.4.1. Additive (V_a), residual (V_r) and phenotypic (V_p) variances and heritabilities (h^2) for male percent normal sperm (PNS) and female age at puberty and lactation anoestrus interval (AP and LAI) reproduction traits submitted to BREEDPLAN as part of the Kaiuroo MDC project.

TRAIT	N	V_a	V_r	V_p	h^2	se
PNS	543	33.3	167.0	200.3	0.17	0.12
AP	643	5855.9	4575.6	10431.5	0.56	0.13
LAI	244	465.1	735.0	1200.1	0.39	0.27

The heritability for PNS was consistent with those reported by Corbet *et al.* (2013) for bulls at 18 and 24 months of age ($h^2 = 0.25 \pm 0.09$ and 0.15 ± 0.06 % respectively). Beef CRC studies also described genetic parameters for heifer age at puberty (Johnston *et al.* 2009) and lactation anoestrus interval (Johnston *et al.* 2014a), which included heritabilities of 0.57 ± 0.12 and 0.51 ± 0.18 respectively. These were also close to the results reported here for Kaiuroo females, which provides confidence that the records will provide a similar basis for selection to improve reproduction for Brahman breeders as those from the Beef CRC and Repronomics™ projects, which currently make up the vast majority of intensively recorded reproduction data in the Brahman evaluation.

Table 4.4.2 presents genetic correlations between the three reproduction traits submitted to BREEDPLAN from the Kaiuroo MDC project. As observed for the heritabilities, the genetic relationship of PNS with LAI described by Johnston *et al.* (2014b) was identical to results presented here ($R_g = -0.52$), and the genetic correlation of AP with LAI ($R_g = 0.31$) was also pleasingly consistent with results from the current study. The genetic relationship of PNS with AP presented by Johnston *et al.* (2014b) ($R_g = -0.48$) was stronger than that observed for the Kaiuroo bulls and heifers, though the association of higher PNS with lower AP remained present. Standard errors for all of these estimates are very high, but the trend for the results from this study to be consistent with those from previous research provides additional confidence in the data being submitted to BREEDPLAN.

Table 4.2.2. Genetic correlations (and standard errors) between intensively recorded reproduction traits collected as part of the Kaiuroo MDC project.

TRAIT	Age at puberty	Lactation anoestrus interval
Percent normal Sperm (%)	-0.03 (0.32)	-0.52 (0.48)
Age at puberty (days)		0.62 (0.36)

4.5 Impact of Kaiuroo phenotyping on BREEDPLAN reproduction EBVs

With the majority of data collected as part of the Kaiuroo MDC project submitted to the BREEDPLAN analysis at the same time (September 2019), it is possible to gauge the impact of these records on EBVs, and their accuracies, by contrasting September 2019 (post-inclusion) with August 2019 (pre-inclusion) results. It has to be noted that the differences in EBVs and their accuracies between the two runs are not solely the result of Kaiuroo MDC project phenotypes. Results submitted by other breeders and research projects will have had an effect via their relationship to Kaiuroo animals, as will data submitted on other animals from within the herd. More significantly, genotypes were submitted annually for 2016, 2017 and 2018 weaned animals, and these will have all been impacting the BREEDPLAN evaluation prior to August 2019. This means that the differences presented in the following tables describe the impact of the phenotypes collected as part of this project alone. These will be smaller than the impact of genotyping and phenotyping combined, but without conducting research runs of BREEDPLAN to specifically include and exclude project data from the analysis, this is as close as we can get to isolating the impact of Kaiuroo MDC recording on the EBVs made available to industry.

Table 4.5.1 shows the average accuracy of these EBVs for Kaiuroo bulls and heifers (combined) based on data available in August of 2019 (prior to the inclusion of ovarian scanning data) and records available for the September 2019 analysis. Following the addition of Kaiuroo MDC phenotypes to the analysis, the accuracy of DTC, AP, LAI and PNS EBVs showed significant improvement for animals for which data was recorded for each trait (highlighted in **bold**). On average, days to calving EBV accuracy increased by 8.1 percent, from 41.0 to 49.1%. This was contributed to via the correlated responses from age at puberty, which improved in accuracy from 24.1 to 53.8%, and lactation anoestrous interval, increasing from 27.5 to 43.8% EBV accuracy. Similarly, accuracy of PNS EBVs for 2016 – 2018 weaned bulls increased from 22.3 to 38.2% as a result of the phenotypes and genotypes collected as part of this project.

Table 4.5.1. Mean accuracy of days to calving (DTC), age at puberty (AP), lactation anoestrous interval (LAI) and percent normal sperm (PNS) EBVs for 2010 - 2018 weaned Kaiuroo animals, from August (AUG) and September (SEP) 2019 (pre- and post-inclusion of MDC project data).

Year of Birth	Number of progeny	DTC		AP ¹		LAI ¹		PNS	
		AUG	SEP	AUG	SEP	AUG	SEP	AUG	SEP
2010	631	42.4	45.6	25.9	40.9	31.3	38.4	17.6	27.5
2011	485	42.3	46.8	24.8	43.5	30.2	39.3	18.0	29.0
2012	524	41.1	45.4	24.6	41.6	29.9	38.2	16.2	27.1
2013	436	43.1	48.1	25.5	45.9	31.1	41.2	17.8	31.2
2014	340	41.0	46.0	22.9	43.9	28.2	38.8	16.4	30.3
2015	317	40.7	48.6	21.8	44.0	27.3	45.9	15.4	30.6
2016	523	41.2	52.1	23.4	58.6	27.1	46.8	19.8	38.1
2017	494	39.8	47.7	22.0	56.4	26.0	37.7	21.5	39.4
2018	435	41.9	47.6	26.8	46.3	30.2	39.2	25.5	37.0

¹ AP and LAI EBVs are not published by BREEDPLAN, but contribute to the estimation of DTC EBVs and their accuracy.

Table 4.5.1 also provides an illustration of how increases in EBV accuracy feed through to previous and subsequent cohorts in the Kaiuroo herd due to their relationships with the 2016 – 2018 heifers and bulls evaluated for this project. The size of the effect is dependent on the level of relatedness of those animals to the phenotyped and genotyped reference animals, and this effect will also be seen for any related animals in the wider Brahman evaluation. These improvements in EBV accuracy for hard to measure male and female reproduction traits were a key objective of the project, and are a direct result of the intensive phenotyping and genotyping carried out at Kaiuroo over the last 3 years.

Table 4.5.2 shows the changes in EBV accuracy for reproduction traits for sires of the females and bulls evaluated as part of the Kaiuroo MDC from 2016 – 2018, and which have progeny outside of the Kaiuroo herd. This is an important group of animals, having been evaluated as part of the Kaiuroo project, and contributing to the genetics of the Brahman breed beyond the Kaiuroo herd. The 25 sires presented in Table 4.5.2 have a total of 1939 progeny outside of the Kaiuroo herd, a proportion of which will be among young bulls used in industry from 2018. All sires show an improvement in the EBV accuracies as a result of the genotyping and phenotyping conducted as part of this project. Increases in DTC accuracy tend to be modest, reflecting the low heritability of the trait and a genetic correlation with other traits in the evaluation substantially less than 1. There is also a proportion of bulls in this group which had accurate DTC EBVs prior to the inclusion of data from this project, and changes in accuracy for those animals has been predictably low.

Table 4.5.2. EBV accuracies for days to calving (DTC), age at puberty (AP), lactation anoestrous interval (LAI) and percent normal sperm (PNS), for sires of Kaiuroo females and bulls with progeny bred within (KAI PROG) and used outside the Kaiuroo herd (Ex-KAI). EBV accuracies are presented from August and September 2019 (pre- and post-inclusion of Kaiuroo MDC project data)

Society ID	KAI PROG	Ex-KAI	Aug. 2019 EBV accuracy				Sept. 2019 EBV accuracy			
			DTC	AP ¹	LAI ¹	PNS	DTC	AP ¹	LAI ¹	PNS
CBV06-3751M	8	277	91	69	77	85	92	77	82	86
CBV10-7694M	15	274	82	90	66	76	87	90	78	80
CBV06-4269M	9	228	90	84	76	81	91	85	80	81
ELR9484M	10	165	56	39	37	64	58	40	39	64
CBV11-9116M	20	127	76	51	62	63	80	58	68	63
ELR10006M	18	110	54	33	36	59	55	42	42	59
FHS2071M	12	102	67	43	51	14	71	73	54	58
NCC2581M	7	83	49	63	31	15	55	64	46	50
LMC700/7M	10	81	50	67	30	14	61	68	58	50
NCC369M	3	68	69	61	51	13	69	62	52	20
NCC2663M	25	65	63	86	43	21	74	87	74	57
ELR9074M	10	58	58	68	34	34	64	72	56	47
NCC2904M	7	49	40	31	27	19	54	71	36	35
JDH28/4M	12	44	55	73	34	19	61	73	54	51
ALC12-0065M	144	44	69	44	52	61	77	92	62	79
TTS086040M	17	42	78	79	61	25	83	83	79	62
KAI147250M	5	32	50	38	28	19	58	54	51	28
VSH390-0M	16	30	61	78	37	17	73	80	74	50
JDH776/6M	8	26	61	73	47	32	65	73	60	35
ALC13-0375M	81	10	64	43	51	59	66	49	54	59
TTS106546M	18	7	66	53	50	25	75	78	70	47
VSH383-0M	17	6	61	83	41	16	73	83	75	45
TTS106499M	11	5	67	68	51	28	69	74	56	48
EFS4083M	12	4	54	77	33	14	65	77	64	51
TTS116579M	10	2	64	57	41	19	75	69	75	38

¹ AP and LAI EBVs are not published by BREEDPLAN, but contribute to days to calving EBVs and their accuracy.

For these sires, changes in DTC accuracy were predictably modest (averaging 6.2%, from 63.8 to 70.0%). Changes in the accuracy of PNS EBVs for this group were more significant, going from an average of 35.7 to 53.7%. This reflects the lower level of recording for the trait in industry, and improving the accuracy of male reproduction EBVs in the Brahman evaluation was a key objective of this project. Similarly, the accuracy of AP and LAI EBVs were also higher, going from an average of 62.0 and 35.7% prior to the inclusion of Kaiuroo MDC data to 71.0 and 61.6% respectively.

Bulls with progeny outside the Kaiuroo herd, and with phenotypes and genotypes from beyond the project contributing to the estimation of their genetic merit, will display the lowest change from the intensive phenotyping which has been undertaken for this project. The data contributed from the Kaiuroo MDC will, however, have favourable consequences for the accuracy of other bulls, in the wider Brahman evaluation, due to relationships in the G-matrix (and conventional pedigree) which are described in the recently introduced Brahman single-step BREEDPLAN evaluation. This is a very clear demonstration of the way in which careful recording in an industry herd can contribute to the usefulness of genomic selection for the whole breed, and establishes an important option for the breed and industry in developing broader strategy for utilising genomic technology.

Table 4.5.3. EBVs for days to calving (DTC), age at puberty (AP), lactation anoestrous interval (LAI) and percent normal sperm (PNS), for sires of Kaiuroo females and bulls with progeny bred within (KAI PROG) and used outside the Kaiuroo herd (Ex-KAI). EBVs are presented from August and September 2019 (pre- and post-inclusion of Kaiuroo MDC project phenotypes)

Society ID	KAI PROG	Ex-KAI	Aug. 2019 EBVs				Sept. 2019 EBVs			
			DTC	AP ¹	LAI ¹	PNS	DTC	AP ¹	LAI ¹	PNS
CBV06-3751M	10	277	-5.7	-88	-34	5.0	-5.0	-94	-33	5.3
CBV10-7694M	19	274	-5.6	-11	-57	2.0	-4.4	-10	-50	2.7
CBV06-4269M	9	228	-15.9	-79	-88	13.8	-14.9	-89	-110	13.9
ELR9484M	18	165	-3.7	10	18	1.3	-4.0	8	17	1.3
CBV11-9116M	22	127	-15.4	-111	-81	-9.5	-16.5	-120	-92	-9.6
ELR10006M	18	110	4.9	41	42	-3.6	7.8	53	51	-3.6
FHS2071M	16	102	1.2	7	6	-0.4	4.5	77	12	3.4
NCC2581M	8	83	9.5	88	47	-0.9	10.9	80	55	-0.4
LMC700/7M	14	81	-2.0	138	30	3.4	4.7	140	37	5.3
NCC369M	3	68	5.5	-68	19	-1.9	5.3	-73	17	-0.8
NCC2663M	27	65	3.5	27	6	-2.1	6.4	26	27	-2.5
ELR9074M	9	58	0.0	-45	6	4.7	-0.2	-44	6	2.6
ALC12-0065M	262	44	-9.3	-86	-26	4.8	-13.1	-162	-51	6.1
NCC2904M	9	49	8.4	42	23	-1.3	7.1	7	18	0.7
JDH28/4M	14	44	8.6	41	25	1.2	9.5	49	36	5.1
TTS086040M	85	42	8.6	68	17	-2.4	10.0	55	39	-2.6
KAI147250M	14	32	-7.4	-31	-1	0.3	-8.7	-51	-7	-2.6
VSH390-0M	20	30	11.2	61	39	0.0	6.2	60	-5	-3.8
JDH776/6M	10	26	-1.5	18	-19	-2.6	0.7	27	1	-2.3
ALC13-0375M	132	10	-5.8	-50	-33	5.5	-6.3	-55	-41	6.1
TTS106546M	52	7	-4.9	-14	-35	-6.1	-0.8	22	-13	-3.2
VSH383-0M	19	6	7.5	56	21	0.6	4.9	61	-6	-1.2
TTS106499M	44	5	7.8	27	13	-0.8	8.8	49	32	0.9
EFS4083M	16	4	-2.2	-39	6	-0.2	-4.0	-40	-12	2.0
TTS116579M	61	2	-8.6	-47	-8	0.3	-10.2	-83	-7	-4.3

¹ AP and LAI EBVs are not published by BREEDPLAN, but contribute to days to calving EBVs and their accuracy.

Table 4.5.3 contrasts EBVs prior to and following the inclusion of phenotypes collected as part of the project for sires with progeny outside of the Kaiuroo herd. Given the higher accuracies presented in Table 4.5.2, the generally small changes in DTC EBVs are consistent with expectations. The intensive phenotyping undertaken by the project has, however, confirmed the genetic superiority of ALC12-0065M for all reproduction traits evaluated, with DTC going from -9.3 to -13.1, and PNS improving from 4.8 to 6.1%, in what was an already accurately described sire. LMC700/7M has 91 progeny across 17 seedstock herds. His significant change in DTC EBV, (-2.0 to +4.7) accompanied by a 11% increase

in accuracy resulting from the intensive phenotyping conducted as part of this project, is important information for breeders and bull buyers seeking to improve female reproduction by selection.

Table 4.5.4 Presents the changes in accuracy for sires of progeny intensively phenotyped as part of the Kaiuroo MDC project, which currently have progeny within the Kaiuroo herd only. The recording carried out as part of this project will see the improvements in accuracy in reproduction EBVs spread to related animals via genomic relationships in the single-step evaluation, as is the case for bulls with progeny outside of the herd. As recording at Kaiuroo will be the dominant source of accuracy for animals in this group, those prior to submission of Kaiuroo MDC project phenotypes were lower than those for sires with progeny outside the herd, and the difference between pre- and post- data submission accuracies was greater. On average, sires in this category improved DTC accuracy by 7.0%, while AP, LAI and PNS accuracies increased by an average of 44.8, 23.6 and 29.1% respectively. The increase in PNS accuracy was a key contribution this project was designed to make to the Brahman evaluation, and the improved description of genetic merit for reproduction in young Brahman bulls, from the sperm morphology data and analyses, is a valuable industry outcome.

Table 4.5.5 presents EBVs prior to and following the inclusion of data from the Kaiuroo MDC project. Theory predicts that as new data is added to a genetic evaluation, and breeding values are estimated with more accuracy, average changes in EBVs for a group of animals should be small. This was the case for the (predominantly) young sires described in Table 4.5.5, with average changes from August to September BREEDPLAN runs of +0.5, +1.1, +5.8 days and -0.4% in DTC, AP, LAI and PNS EBVs respectively. The young, home grown, sire KAI147349M went from -2.4 to -8.0 for DTC, which was contributed to by favourable AP (-47.4 days) and LAI (-32.8 days) EBVs. It was only as a result of the intensive recording of AP and LAI undertaken in this project that this bull, and many like him in the tables below, was able to be deviated from his mid parent results of +54.5 and -18.3 days for AP and LAI respectively.

Table 4.5.4. EBV accuracies for days to calving (DTC), age at puberty (AP), lactation anoestrous interval (LAI) and percent normal sperm (PNS), for sires of genotyped and phenotyped Kaiuroo females and bulls with progeny within the Kaiuroo herd only (KAI PROG). EBVs are presented from August and September 2019 (pre- and post-inclusion of Kaiuroo MDC project phenotypes)

Society ID	Birth Year	KAI PROG	Sep. 2018 EBV accuracy				Sept. 2019 EBV accuracy			
			DTC	AP ¹	LAI ¹	PNS	DTC	AP ¹	LAI ¹	PNS
TTS127022M	2011	55	62	26	28	19	72	87	64	67
NCC1530M	2009	44	79	46	59	26	86	88	86	73
KAI137133M	2013	42	54	24	29	27	64	79	46	65
KAI147317M	2014	38	54	26	33	21	62	71	47	52
TTS106549M	2010	35	64	25	28	17	74	89	66	63
NCC1725M	2010	30	72	41	52	24	81	83	80	57
KAI147328M	2014	29	53	24	28	21	62	77	46	62
TTS106445M	2009	29	71	35	47	20	80	81	81	63
TTS127024M	2012	29	67	35	42	23	79	81	82	56
TTS127018M	2012	26	56	30	34	24	69	79	64	62
KAI147246M	2014	23	53	26	29	19	64	78	50	48
TTS127008M	2012	18	51	27	30	18	64	85	50	54
TTS106545M	2010	17	56	28	33	18	67	83	53	54
TTS126903M	2012	17	63	26	36	17	74	76	76	50
TTS116738M	2011	16	63	27	32	25	66	79	55	59
TTS127013M	2012	15	55	29	35	20	65	76	53	51
KAI137122M	2013	15	63	28	32	23	71	76	69	61
TTS065432M	2006	14	60	21	27	17	67	78	62	34
KAI147323M	2014	13	51	26	33	23	58	70	43	63
KAI147349M	2014	13	53	23	27	20	61	74	45	59
TTS126900M	2012	13	59	24	29	15	67	78	63	43
KAI137082M	2013	13	62	18	22	22	68	78	61	47
KAI147287M	2014	12	50	27	35	22	60	75	45	58
TTS127020M	2012	12	52	21	26	20	62	74	48	41
KAI137185M	2013	12	63	28	32	22	70	77	67	62
KAI147330M	2014	11	55	32	36	25	62	72	50	55
TTS116708M	2011	11	64	31	38	23	68	76	62	56
TTS127021M	2012	10	58	31	36	24	64	69	59	57
WRM1001M	2015	10	32	20	19	15	40	29	25	19
TTS116689M	2011	8	61	28	33	29	62	72	49	50
TTS127014M	2012	7	57	23	29	19	67	74	59	39
KAI147289M	2014	7	47	27	29	22	53	61	40	56
TTS126785M	2012	7	55	24	30	18	60	55	53	54
TTS137051M	2013	7	60	31	37	21	66	77	59	43
TTS137054M	2013	7	59	25	32	20	60	72	46	48
KAI137193M	2013	7	48	24	31	16	52	42	38	25
KAI147247M	2014	6	50	19	24	18	60	74	46	50
TTS126815M	2012	6	53	25	31	15	65	46	67	24
TTS127017M	2012	6	57	24	33	23	63	64	59	50
KAI157526M	2015	6	50	31	34	24	55	51	48	38
KAI147214M	2014	5	45	24	29	18	55	66	41	36
KAI137129M	2013	5	50	16	19	19	59	69	49	28
TTS126806M	2012	5	60	33	42	23	69	59	69	43
TTS127010M	2011	5	57	37	40	26	58	67	47	32

¹ AP and LAI EBVs are not published by BREEDPLAN, but contribute to days to calving EBVs and their accuracy.

Table 4.5.5. EBVs for days to calving (DTC), age at puberty (AP), lactation anoestrous interval (LAI) and percent normal sperm (PNS), for sires of Kaiuroo females and bulls with progeny bred within the Kaiuroo herd (KAI PROG). EBVs are presented from August and September 2019 (pre- and post-inclusion of Kaiuroo MDC project data)

Society ID	Birth Year	KAI PROG	Aug. 2019 EBVs				Sept. 2019 EBVs			
			DTC	AP ¹	LAI ¹	PNS	DTC	AP ¹	LAI ¹	PNS
TTS127022M	2011	55	6.3	-2	14	2.4	0.7	-56	-5	3.4
NCC1530M	2009	44	0.2	52	-21	-0.3	1.9	46	-9	-0.2
KAI137133M	2013	42	-1.1	-1	-3	-0.1	2.5	36	15	-0.8
KAI147317M	2014	38	0.8	5	-5	1.0	1.1	-4	12	3.1
TTS106549M	2010	35	10.8	72	41	0.3	11.0	92	41	1.7
NCC1725M	2010	30	-0.4	36	-12	-3.1	3.4	72	12	-5.3
KAI147328M	2014	29	-9.3	-37	-34	-0.1	-7.3	-42	-16	-6.5
TTS106445M	2009	29	4.8	55	8	0.6	5.1	62	24	-3.0
TTS127024M	2012	29	-2.3	-68	-32	-1.8	1.3	-58	13	-0.5
TTS127018M	2012	26	2.6	38	17	-4.5	2.6	66	17	0.3
KAI147246M	2014	23	1.1	40	14	-0.2	3.5	51	16	0.5
TTS127008M	2012	18	10.2	60	31	0.2	9.4	70	28	2.3
TTS106545M	2010	17	8.9	38	24	1.3	6.3	7	14	0.8
TTS126903M	2012	17	3.3	15	-15	0.7	1.9	18	-24	1.4
TTS116738M	2011	16	-2.3	-1	-12	0.3	0.0	6	3	1.9
TTS127013M	2012	15	1.5	2	14	0.3	0.4	-12	6	-3.6
KAI137122M	2013	15	3.1	28	-6	1.0	5.8	36	18	0.9
TTS065432M	2006	14	-1.0	-66	18	1.9	-5.7	-63	-21	1.5
KAI147323M	2014	13	2.0	31	3	1.1	5.2	72	20	-2.7
KAI147349M	2014	13	-2.8	51	-20	-1.8	-8.0	-47	-33	-5.0
TTS126900M	2012	13	-1.3	-2	-6	0.5	-1.6	-6	-4	-2.0
KAI137082M	2013	13	-5.2	6	-26	0.5	-3.1	9	-4	-1.3
KAI147287M	2014	12	6.2	11	3	-0.3	9.9	54	27	-4.2
TTS127020M	2012	12	1.5	-4	22	0.6	-2.6	-68	2	-2.1
KAI137185M	2013	12	-2.1	32	-23	0.3	0.6	41	0	5.0
KAI147330M	2014	11	-5.6	49	-16	0.2	-3.6	59	-1	1.0
TTS116708M	2011	11	-1.2	-1	-24	3.1	0.4	2	-7	-0.2
TTS127021M	2012	10	2.9	13	-20	-4.5	5.5	33	1	-3.5
WRM1001M	2015	10	-1.5	-30	-11	2.7	0.6	-35	-6	2.3
TTS116689M	2011	8	-3.3	-1	-9	-2.0	-1.4	-5	6	-7.8
TTS127014M	2012	7	11.8	45	40	0.7	14.0	94	44	1.8
KAI147289M	2014	7	-1.3	38	-8	-0.5	-1.8	21	-5	-2.2
TTS126785M	2012	7	5.7	52	-2	-1.6	7.8	66	18	-1.0
TTS137051M	2013	7	-0.7	16	-7	-0.5	-0.5	20	9	1.0
TTS137054M	2013	7	3.2	74	12	-1.6	4.3	76	28	0.0
KAI137193M	2013	7	10.6	61	39	-1.9	10.5	69	31	-1.4
KAI147247M	2014	6	2.5	30	13	2.6	3.5	55	14	2.4
TTS126815M	2012	6	-2.5	2	-3	2.3	-1.7	4	0	2.3
TTS127017M	2012	6	7.4	22	1	-2.0	8.1	26	19	-1.7
KAI157526M	2015	6	-6.7	-36	-25	-2.6	-5.9	-16	-16	-4.4
KAI147214M	2014	5	2.4	-5	-3	0.6	1.8	-22	-8	3.4
KAI137129M	2013	5	2.8	-6	3	-0.3	0.0	2	-14	-0.5
TTS126806M	2012	5	1.4	12	-14	1.3	3.6	-3	10	0.4
TTS127010M	2011	5	1.6	35	-6	-0.8	2.9	38	6	-0.9

¹ AP and LAI EBVs are not published by BREEDPLAN, but contribute to days to calving EBVs and their accuracy.

4.6 Extension of Kaiuroo MDC results to industry

While not a defined objective of the project, significant efforts have been made to share the favourable outcomes of the project with seedstock breeders and the wider, northern beef industry. Appendices 1 – 4 present copies of articles on Beef Central and in the MLA Feedback magazine detailing the work undertaken as part of the Kaiuroo MDC project. A key element of this material is the discussion of the impact the research has had on breeding objectives within the Kaiuroo herd. The bulk of the material includes information made available to visitors during the 'BEEF 2018' tour, where AGBU scientists presented material which described the research undertaken as part of the Kaiuroo MDC project, and more broadly covered developments in genetic evaluation relevant to northern breeders.

5 Discussion

The aims of this project were to genotype and collect records on hard to measure male and female reproduction traits in Brahman seedstock cattle which would improve the accuracy of EBVs describing these economically important traits in the breed's single-step BREEDPLAN evaluation. This has been done successfully, with 1530 animals genotyped and 1430 phenotyped for AP, LAI or PNS. These data have all been submitted for BREEDPLAN analysis, and the resulting improvements in EBVs describing reproductive performance have been shown to impact selection candidates within the Kaiuroo herd, as well as 2033 progeny outside of the herd in which the intensive recording and genotyping was conducted for this project. These outcomes present clear and valuable opportunities for Brahman breeders to make better informed selection decisions if they aim to improve reproductive performance in their herds.

5.1 Resourcing, costs and returns associated with intensive phenotyping to describe male and female reproductive performance

If ovarian scanning is to contribute to the genetic evaluation of reproduction traits for tropical beef breeds, there is a need to address the availability of expertise to perform this work. Currently, the only technicians who possess the skills to undertake large scale ultrasound imaging for ovarian function are employed by research agencies and industry service providers (Central Queensland University, Queensland Alliance for Agriculture and Food Innovation, and the Agricultural Business Research Institute sponsored Tropical Beef Technology Services). It was only because the current project was undertaken as industry funded research that personnel were available from these institutions (specifically TBTS) to undertake the data collection for this study. If large (or even modest) scale collection of ovarian scanned data were to be targeted as a means of increasing the accuracy of genetic evaluation for reproduction traits in tropical beef breeds, the lack of commercial service providers will need to be addressed.

Other MLA funded research projects (Enabling genetic improvement of reproduction in tropical beef cattle: B.NBP.0759, and the heifer puberty component of the Trans-Tasman Beef Cow Productivity Project: P.PSH.0869) have both examined alternative technologies to identify oestrus in beef heifers. These present opportunities to avoid the bottle-neck of commercial service providers in this area, but do have limitations of their own which will need to be addressed and overcome if their application is to be undertaken on a scale which would yield useful quantities of data for genetic evaluation.

The cost of serial ultrasound scanning to detect ovarian function in heifers or lactating first calf females is also a consideration. For this study, heifers were scanned 5 times each before their first natural mating and lactating first calf females 4 times through the course of their first mating. This represents a cost of approximately \$25/heifer to detect age at puberty and \$20/lactating first calf female to

collect this data. This does not include the additional operational costs associated with undertaking this work, or the costs associated with data analysis to generate results for genetic evaluation.

The collection of samples and analysis to generate bull sperm morphology results is also an expensive undertaking, costing approximately \$20/bull to collect a sample and produce a crush-side analysis of mass activity and motility, and an additional \$20/bull to conduct sperm morphology analysis in a laboratory. Again, these figures do not include the costs associated with additional handling of animals and data analysis to produce results which can be submitted for genetic evaluation. As Bull Breeding Soundness Evaluations have become a reasonably standard exercise for sellers of tropically adapted bulls, it is likely that some, or even the majority of costs associated with sperm morphology testing could be off-set against existing management procedures.

If a breeder wished to collect intensively recorded phenotypes to describe reproductive performance in 500 males and females (500 heifers and the lactating proportion of first calvers), and to genotype all recorded animals, marginal annual outlay would be in the vicinity of \$12,500 for heifer age at puberty scanning, \$7,000 for LAI scanning, \$20,000 for BBSE and percent normal sperm analysis in young bulls and \$53,000 to genotype both males and females. This means a marginal annual cost of almost \$100,000 per year to generate high accuracy reproduction phenotypes for 500 males and 500 females. Again, it is stressed that the additional handling required and associated labour inputs are not factored into this amount, nor are the other costs associated with the management of a successful seedstock herd. The return on this investment will be dependant on the increase in EBV accuracy resulting from the recording program put in place (as illustrated in Tables 4.5.2 and 4.5.4 for this project), and the degree to which the higher accuracy and genetically superior animals identified are selected as parents for subsequent generations. It is emphasised that the phenotyping regime put in place at Kaiuroo was less comprehensive than that applied in research herds, where scanning of females (both heifers and lactating first calvers) through, and beyond their first mating provides greater accuracy in describing AP and LAI, and which is key to maintaining the quality of the evaluation for tropical breeds.

5.2 Meeting project objectives

5.2.1 Objective 1.

The project aimed to collect genotypes and high quality phenotypes, for traits contributing to male and female reproductive performance in Brahman cattle, on approximately 500 animals (bulls and heifers equally) in each of 3 successive calf crops, in a Brahman stud that is well genetically linked to the overall Brahman breed in Australia, and to research herds.

Genotypes were collected and submitted to the Brahman BREEDPLAN evaluation for 252, 262 and 251 male and 246, 252 and 267 female 2016, 2017 and 2018 weaned calves. After data cleaning and editing, and the inevitable challenges of collecting research data under commercial conditions, 643 age at puberty, 244 lactation anoestrus interval and 543 percent normal sperm records were also submitted for analysis to the Brahman evaluation.

5.2.2 Objective 2.

These records will contribute in realtime to the reference population for Brahman single step BREEDPLAN, and help ensure that genomic breeding values for reproduction traits in Brahman cattle are at useful levels of accuracy, and hence that genomic testing in Brahman cattle is as reliable as practically possible.

For 72 sires of Kaiuroo progeny evaluated as part of this project, EBV accuracies for days to calving, age at puberty, lactation anoestrus interval and percent normal sperm increased from 59.9 to 66.1, 40.4 to 70.9, 38.1 to 57.5 and 26.1 to 50.9 percent respectively. This group of sires included 26 bulls with a combined 2033 progeny in 89 herds outside of Kaiuroo. These improvements to the accuracy of BREEDPLAN EBVs describing reproductive performance present clear opportunities for Brahman breeders to make better informed selection decisions to improve reproduction in their herds.

6 Conclusions/recommendations

As our understanding of genetic evaluation in the genomic era has improved, it has become clear that there is an on-going need for traits which are given priority in the breeding objective to be well recorded in animals which have genotypes included in the analysis. For tropical beef breeds, reproductive performance is a major driver of profitability, and the need for genotyping and intensive phenotyping to ensure the traits are well described across the range of genetics present in the breeds will be on-going. Industry-supported projects like this one are one means of achieving this. The challenges of conducting intensive phenotyping under commercial conditions cannot be understated, however, and there will always be a need for research projects to be carried out under more controlled conditions than is possible in commercial herds, to underpin the genetic evaluations for these breeds.

7 Key messages

This project set out to economically expand the efficacy of the single-step BREEDPLAN evaluation for the Brahman breed to allow better informed selection decisions associated with improving reproduction traits that have been shown to be key drivers of profitability for northern Australia's beef breeders. The following points summarise the key takeaways from this project.

Primarily, this project:

- Provided no new knowledge associated with factors impacting productivity for the beef industry.
- Is a useful case study for demonstrating the opportunities available to northern seedstock breeders to better describe male and female reproduction in their herds.
- Demonstrates the value of careful recording in terms of increasing the usefulness of genomic selection, and so is a case study for breed and/or industry investment in genomic reference populations.
- Effectively illustrates what can be achieved when this understanding is applied to the development of breeding objectives and the application of a structure breeding program to improve reproductive performance.
- Has opened up discussions with TBTS experts to develop an extension model built around the results of this project, and how this new information can be applied in the Kaiuroo herd to drive genetic improvement in male and female reproduction and genetic profitability in the herd.
- Has provided opportunities that will be pursued as work undertaken in the AGBU core beef project, with expectations that the material will feature in TBTS extension products in 2020.

Secondarily, this project:

- Confirmed the efficacy of ovarian scanning for age at puberty and lactation anoestrus interval.
- Proved that sperm morphology testing in males could be used as tools to describe genetic reproduction in tropical beef herds.

8 Bibliography

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9 Appendix

9.1 Appendix 1: Beef central article by Wayne Upton – 10th July 2018.



Kaiuroo project

In 2017, an MLA Donor Company-supported project was initiated which aimed to undertake intensive phenotyping for male and female reproductive performance, as well as genotyping of all animals evaluated for those traits, in a seedstock herd with good genetic links to industry and current research herds.

This study was proposed, and is part funded, by the managers and principal of the Kaiuroo Aggregation in Central Queensland, with assistance in the design and analysis provided by researchers from the Animal Genetics and Breeding Unit (Dr Matt Wolcott).

The male component of this work, which will see all bulls sampled to assess sperm morphology traits, is of particular importance, as the Repronomics project is evaluating all male progeny as steers to examine finishing and carcass traits. This means that the Kaiuroo MDC project will be the only source of sperm morphology phenotypes available from a designed research project for the Brahman breed since the end of the Beef CRC in 2012.

The motivation for Kaiuroo management to initiate the project came from an appreciation of the importance of female and male reproduction as a driver of profitability for breeders of Brahman cattle, a desire to better understand the genetics of these traits in their own herd, and to contribute to the quality and breadth of genetic description of reproductive performance in bulls and females at the breed level.

While undertaking the intensive recording required by the Kaiuroo MDC project, there has also been a significant effort made to introduce superior genetics for reproduction into the Kaiuroo stud herd.

"We saw genetic improvement as vital to our drive to improve productivity and profitability of our organic commercial operation," says Jennifer McCamley, of the Kaiuroo Aggregation management team.

"Our 2017 drop calves were the first generated by the newly focused breeding program, and those progeny display significantly lower days to calving and higher 600 days weight EBVs, as well as higher JapOX \$Indexes than those of previous generations," she said.

Ms McCamley said she recognised that selection based on profitability would produce the optimal genetics for the Kaiuroo breeding program and bull buyers, and that single trait selection was not the way to go as there were a number of contributors to the profitability of a bulls progeny (both male and female).



Jennifer McCamley and Tom Emmery of the Kaiuroo management team



Matt Wolcott

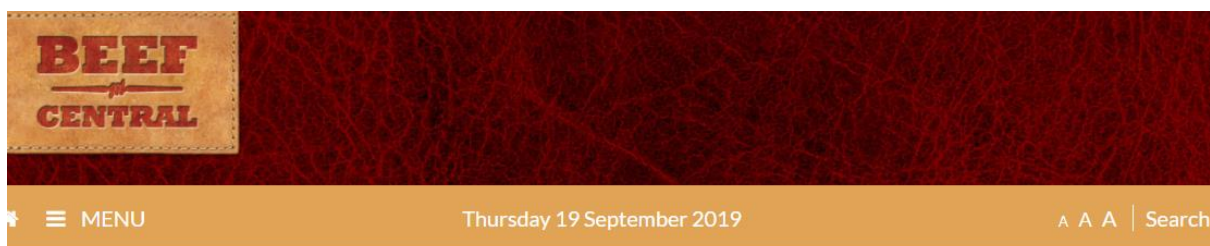
In conjunction with AGBU's Dr Matt Wolcott, Kaiuroo management have developed their own custom selection index, which aims to use a balanced approach to improve the genetics of reproduction, growth and carcass traits to increase the profitability of Kaiuroo bulls, as sires of commercial breeding females required to reproduce and survive under the harsh conditions which prevail in northern Australia.

Dr Wolcott said it had been enlightening to work with Jennifer and her dedicated team at Kaiuroo.

"They should be congratulated on their forward-thinking initiative to set up this project," he said.

Source: <https://www.beefcentral.com/genetics/weekly-genetics-review-selecting-for-fertility-to-boost-profits-in-the-north/>.

9.2 Appendix 2: Beef central article by Alex McDonald 17th April 2018.



GENETICS

Weekly genetics review: Genetic technologies on show at Beef 2018

Genetics editor Alex McDonald, April 17, 2018



Farm tours

A feature of Beef Australia 2018 are the Westpac-sponsored property tours which include half-day or one-day tours to 11 beef properties in Central Queensland over the five days. Several of these tours will demonstrate the application of genetic technologies to breeding programs.

Platinum tours will involve small groups flying to and from the property and travel to the remainder of the full day and half-day tours will be by coach. Tours may be booked out so it is important to book ahead on the [Beef 2018 website](#).

Kaiuroo Station: Monday May 7 (Platinum Tour)

Kaiuroo Station is an amalgamation of five neighbouring properties nestled next to the MacKenzie River, which runs registered Grey and Red Brahman herds. It is managed by Jennifer McCamley and Tom Emmerly of Ag Resource Management. Jennifer and Tom will showcase their innovative approach, which combines the best practical procedures with the very latest science in Brahman seedstock.



Kaiuroo operates under Certified Organic production principles

They will present how profitability in their commercial herd has defined their objectives, and reveal how they have used a genotyping program to describe the genetic merits of animals in the seedstock herds

The Kaiuroo registered herd is currently involved in a MLA Donor Company (MDC) funded project. The project aims to measure phenotypes for male and female reproductive performance as a part of the Brahman Breedplan analysis of their seedstock herd.

Dr David Johnston and **Dr Matt Wolcott** from Animal Genetics & Breeding Unit will present the MDC project objectives, early outcomes, and the latest developments in the genetic evaluation for tropical beef breeds on the tour. **Paul Williams** from Tropical Beef Technology Services will demonstrate

ovarian scanning as well as presenting key updates from the Brahman Beef Information Nucleus (BIN) project.

Source: <https://www.beefcentral.com/genetics/weekly-genetics-review-genetic-technologies-on-show-at-beef-2018/>.

9.3 Appendix 3: MLA Feedback Magazine article – July 2018

ON FARM
NORTHERN CATTLE

GENETICS 

Up to the challenge

Visitors to Beef Australia 2018 were offered a farm tour with a difference – the chance to fly into 'Kaiuroo' and see the management strategies employed by managers Jennifer McCamley and Tom Emmerly first-hand.



SNAPSHOT: Jennifer McCamley and Tom Emmerly, Kaiuroo aggregation, Central Queensland 



Enterprise:
Brahman stud and commercial breeding and finishing for organic market

Livestock:
900 breeders, 3,000 commercial cattle

Pasture:
Natives, Buffel, irrigated leucaena undersown with Rhodes and Gatton panic

Soil:
50% native tablelands, 25% deep alluvial river flats, 25% brigalow scrub soils

Rainfall:
650mm

ON FARM
NORTHERN CATTLE

During the past four years, Jennifer McCamley (pictured opposite) and Tom Emmerly, of Ag Resources Management, have nursed the Kaiuroo aggregation through the worst droughts and floods in living memory.

Three once-in-100-year events occurred in the past four years – the driest year, the highest rainfall in a 12-hour period and the highest flood level ever recorded. This was followed up by more flooding in March.

"Everywhere you look there is something damaged or not operational," Jennifer said.

Despite the environmental challenges, a commitment to good genetic selection, effective breeder management and pasture improvement is seeing them lift the productivity of the Kaiuroo Brahman stud and organic beef enterprise.

The enterprise is run on an aggregation of five conjoined central Queensland properties owned by the Rohatyn Group. The country ranges from prime river delta (at the junction of the Mackenzie and Isaac river systems) where young stock are finished on irrigated leucaena, to harsh tablelands where mature breeders are managed for optimum pregnancy rates.

Tom and Jennifer explained their management strategies to Beef Australia visitors. These included the following:

Breeder focus

"One of the best decisions we've made is to manage our commercial herd joinings according to seasonal conditions, rather than to a calendar," Tom said.

"Bulls are only put out after it's rained – in the past few years that's been as late as January and February – and we manage our mobs according to foetal ageing determined at pregnancy testing."

Cows are drafted into early or late pregnancies and empties.

"If cows are too late getting back in calf, the option is to segregate them or sell them as pregnancy tested in calf cows," Tom said.

"The benefit has been far less age and weight variation in the calves and the cows are much more even in terms of body condition score.

"It also helps us manage our breeder condition and to control supplementation of lactating cows with calves of similar ages."

Tom and Jennifer supply cattle each month to Australian Organic Meats and have the benefit of almost 650ha of irrigated leucaena, undersown with Rhodes grass and Gatton panic, for finishing.

If conditions tighten, Jennifer said early weaning is their relief valve that ensures cows generally don't slip below condition score 3.

Genetic selection

Jennifer, the daughter of Sir Graham McCamley of Tartrus Stud, grew up understanding performance recording, genetic and, later, genomic selection.

Her commitment to improving the quality and quantity of performance data available for Brahmans has continued with the Kaiuroo Stud. The stud has become involved in an MLA Donor Company-funded project with the Animal Genetics Breeding Unit to enhance Brahman fertility traits described in BREEDPLAN.

"All our registered bulls and heifers are involved in the program and are being genotyped," she said.

"Bulls are recorded for sperm morphology, and heifers and lactating first-calf females are scanned to determine age of puberty and lactation anoestrus.

"The strong linkages of the Kaiuroo Stud to significant Brahman sire lines means this work will have real and positive ramifications at the breed level."

Culling is another aspect of the genetic improvement strategy for the commercial herd.

"The first cull of the heifers occurs before joining, with the focus being on temperament and structure. Any animal that does not make the grade is spayed and fattened on leucaena ready to be sold. After pregnancy testing, the empties go to the organic market," Jennifer said.

Sires selected to join to the commercial herd also have to meet a set of criteria.

"Importance is placed on calm temperament, structure, reproduction, growth and meat quality, and Brahman BREEDPLAN is a critical tool for us in this selection process," Jennifer said.

Technology

Kaiuroo has the benefit of investment by the Rohatyn Group in state-of-the-art flood irrigation, live-entry data-recording systems for all herds, and modern cattle-handling facilities with hydraulic gates and crush operations.

Jennifer believes safe, efficient stockyards are essential.

"We're working towards putting more safety features in our yards but we're also committed to training our staff in low-stress stock-handling methods," she said.

"It's really important to have quiet cattle that are happy to move about the yards calmly – it pays dividends right through the value chain." ■

LESSONS LEARNED

- > Foetal ageing is an effective management tool to improve productivity and profitability.
- > Quiet cattle pay dividends from producer to consumer.
- > BREEDPLAN is becoming a more effective genetic selection tool as more high quality phenotypes and genomic information enter the analysis.

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BREEDPLAN:
breedplan.une.edu.au
Tips on growing leucaena:
mla.com.au/planting-leucaena
Calf survival checklist:
mla.com.au/calf-survival-checklist

9.4 Appendix 4: YouTube video produced by Kaiuroo management including material recorded during Beef 2018 tour - 7th May 2018.



Kaiuroo, with assistance from the [Animal Genetics and Breeding Unit](#) (University of New England, Armidale, Australia), aims to contribute to the quality and breadth of genetic description of reproductive performance in bulls and females at the breed level.

Source: <https://youtu.be/9QGJ8mwjveE>.