CSIRO PUBLISHING

RESEARCH ARTICLE
https://doi.org/10.1071/AN25246

ANIMAL PRODUCTION SCIENCE

Gestation length is highly heritable and could indirectly reduce birthweight without impacting the weaning weight of Australian tropically adapted *Bos indicus* beef cattle

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Handling Editor:
Sue Hatcher

Received: 16 July 2025
Accepted: 24 November 2025
Published: 15 December 2025

Cite this: Moore KL *et al.* (2025) Gestation length is highly heritable and could indirectly reduce birthweight without impacting the weaning weight of Australian tropically adapted *Bos indicus* beef cattle. *Animal Production Science* **65**, AN25246. doi:10.1071/AN25246

ABSTRACT

Context. Gestation length is an important trait in beef cattle, because it is associated with calf birthweight and dystocia. This paper presents the first genetic parameters for gestation length in Australian tropical breeds, and the genetic relationships with birth and weaning weight. **Aims.** We investigated the genetic and non-genetic effects of gestation length, birthweight and weaning weight for three tropical beef breeds (Brahman, Droughtmaster and Santa Gertrudis) in northern Australia. Genotype by environment interactions were assessed for each trait. **Methods.** Animals were born between 2014 and 2022 from two herds, and after edits, there were 2346, 7044 and 6248 records for gestation length, birthweight and weaning weight, respectively. Animals were by 245 sires, with an average half-sibling family size of 29. Genetic parameters were estimated from pooled breed and breed-specific datasets. To assess genotype by environment interactions, traits at each herd were considered separate traits and bivariate analysis was undertaken. **Results.** Breed, cohort and calf sex were the only non-genetic factors influencing gestation length; males were estimated to have longer gestation lengths of 3.1, 2.4 and 1.9 days for Brahman, Santa Gertrudis and Droughtmaster breeds, respectively. Gestation length was under high genetic influence, with a direct heritability of 0.79 (0.05). Birthweight and weaning weight direct heritability estimates were 0.52 (0.04) and 0.40 (0.04), respectively. Maternal heritability estimates for birth and weaning were 0.10 (0.02) and 0.15 (0.03), respectively. A positive genetic correlation of 0.30 (0.09) was estimated between gestation length and birthweight, whereas no significant genetic relationship was estimated between gestation length and weaning weight. No genotype by environment interactions were detected for gestation length, birthweight and weaning weight. **Conclusions.** Gestation length for three tropically adapted breeds in northern Australia was highly heritable and showed no genotype by environment interaction. Genetic selection of sires for gestation length will reduce gestation length, and indirectly reduce birthweight and calving difficulties without any unexpected correlated effects on weaning weight. **Implications.** Selection for decreased gestation length can indirectly reduce calf birthweight without impacting weaning weight.

Keywords: across breed EBVs, genetic correlation, genotype by environment interaction, gestation length, heritability, indirect selection, reproduction, variance components.

Introduction

Gestation length is a simple trait by definition, being the number of days between conception and birth. However, an accurate date of conception is generally only possible from artificial insemination (AI) matings. The low use of AI in the national beef herd limits the number of gestation length records available for genetic evaluation. Decreasing gestation length may reduce calving difficulties and enable more cows to maintain an annual calving pattern (Paschal *et al.* 1991; Chud *et al.* 2014; Jeyaruban *et al.* 2016; Wolcott *et al.* 2016).

Gestation length genetic parameters for some Australian temperate beef breeds have been estimated (Jeyaruban *et al.* 2016); however, there are no estimates for tropical breeds in Australia, and very few estimates of genetic parameters for gestation length in tropical breeds in other countries (Chud *et al.* 2014). Most literature on gestation length in tropical breeds has been limited to reporting the non-genetic factors influencing the trait (Plasse *et al.* 1968; Paschal *et al.* 1991; Corbet *et al.* 1997; Messine *et al.* 2007). Breed differences in gestation length have been reported, with tropical breeds consistently having longer gestation lengths than temperate breeds (Corbet *et al.* 1997; Sartori and Barros 2011).

The objectives of this study were to assess the non-genetic and genetic effects of gestation length, birthweight and weaning weight, and estimate the genetic variances and genetic relationships between the three traits in a dataset of pooled tropical breeds located in northern Australia. Data were recorded at two locations, and genotype by environment interaction between these locations was also investigated.

Materials and methods

Animal data

The data in this study were a subset of a research project, '*Repronomics*' (MLA projects B.NBP.0759 and P.PSH.1221), targeting female reproduction of three tropically adapted purebred beef breeds in northern Australia. Project details and overall project design are described by Johnston *et al.* (2017), with animals managed according to the Code of Practice for the care and use of animals for experimental purposes, and approved by the Animal Ethics Committee of the Queensland Department of Primary Industries (SA2013/10/445). Data included Brahman, Droughtmaster and Santa Gertrudis cattle from two Queensland Department of Primary Industries research herds: Spyglass Beef Research Facility, 110 km north of Charters Towers, Queensland (19°23′57″S; 145°44′53″E) and Brian Pastures Research Facility, 18 km east south-east of Gayndah, Queensland (25°39′13.60″S; 151°44′0.92″E). Spyglass is a tropical semi-arid environment with summer dominant rainfall (long-term average of 610 mm) and predominantly native pastures, with some introduced species. Brian Pastures is a sub-tropical environment of South East Queensland's sub-coastal spear-grass region, with a long-term average annual rainfall of 730 mm, consisting mainly of native pastures with some improved grass species and legumes.

All three breeds were represented at Brian Pastures, but only Brahman and Droughtmaster were at Spyglass. Brahman, Droughtmaster and Santa Gertrudis sires were selected to represent the national breed population, especially if the sire was influential and had limited female reproduction information available. AI and natural mated sires were used across herds and years to provide genetic linkage. Sires were mated to cows of the same breed. However, some Droughtmaster and Santa Gertrudis sires at the Brian Pastures herd were mated to base Tropical Composite cows from the previous Beef CRC genetics project (Barwick *et al.* 2009). Progeny from these matings was considered the same breed as the sire, and hybrid vigour was not fitted, although dam breed was considered in statistical models, as described later. Most base cows were born in 2010 and 2011, but the cows' years of birth ranged from 2001 to 2013. Female calves produced during the project (2014–2019) were retained in the cow herd and were the dams of future generations; for example, 2014-born females were dams of some of the 2017-born calves. All cows remained in the herd of birth and were culled only if they failed to wean a calf. Cows from their second lactation onwards were mated using a two-round fixed-time AI program, with 30 days between the AI rounds. Back-up bulls were used after the AI programs and were combined with the natural mating groups at each location. In the first year of the project (2014), all calves were the result of natural mating regardless of the parity status of the cow. Natural mating groups comprised multiple sires joined to maiden heifers and first-lactation cows over a 12-week period. All cows at each location were managed the same way, and breeds were run together at all times, apart from the natural mating groups, when the three sire breeds were run separately.

At calving, cows were checked daily to record the date of birth, and birthweight was recorded using electronic scales. Gestation length was calculated for AI matings as the number of days between the AI date and birth date. Calving ease was recorded, but very few calving difficulties occurred and were not considered in this study. A tail hair sample from each calf was also obtained for subsequent DNA parentage determination. At approximately 3 months of age, all calves at each location were mustered and processed through cattle handling facilities, and male calves were castrated. Calves were weaned at approximately 6 months of age (average 181.5 days), and weaning liveweight was recorded using digital scales.

Data analysis

Birth and weaning weight records ($N = 7707$) were collected on animals born between 2014 and 2022. Gestation length ($N = 2536$) records were collected on animals born between 2015 and 2022. Records were removed if they were from multiple births, were not purebred (except for the planned matings with Tropical Composite dams) due to AI straw mix-ups or mating group errors and if sex, date of birth, sire, dam or the age of dam were unknown. Birthweights <16 kg were suspected premature births and removed as outliers. The final dataset contained 2346 gestation length records from 112 sires (Table 1). The average sire family group was 20.9 progeny, ranging from 1 to 48. After edits, 7044 records remained for birthweight, and 6248 had a weaning weight recorded. Birthweight records were from 245 sires, with the average sire family group size of 28.8, ranging from 1 to 155.

Table 1. Summary statistics, number of sires, and mean and range of progeny per sire for gestation length (days), birthweight (kg), weaning weight (kg) and weaning age (days) of tropical beef breed calves born 2014–2022.

Trait	*N*	Mean	s.d.	Minimum	Maximum	No. of sires	No. of progeny per sire	
							Mean	Range
Gestation length (days)	2346	289.4	6.0	271	305	112	20.9	1–48
Birthweight (kg)	7044	33.9	5.5	18	58	245	28.8	1–155
Weaning weight (kg)	6248	194.3	34.2	78	343	242	25.8	1–141
Weaning age (days)	6248	181.5	24.7	97	244			

Significant non-genetic factors were determined using the PROC MIXED procedure in SAS (SAS Institute 2007), with sire fitted as a random effect in all models. Unless otherwise stated, all model terms were included as fixed class effects. There was confounding between cow age and breed type (Brahman, Droughtmaster, Santa Gertrudis and Tropical Composite base cows); therefore, cow age was grouped into three age classes based on cow birth year: 2001–2005, 2006–2009 and 2010–2019, and then concatenated into a cow-group term (i.e. herd, cow breed type, cow herd of origin and cow age group). The calf cohort for gestation length was defined as a concatenation effect of AI herd, birth herd, project herd and birth year. In most cases, the calf cohort's AI, birth and project herd were the same. However, in 2016, some of Spyglass's calves were conceived at Spyglass, relocated due to drought conditions and subsequently calved at Brian Pastures. The cows were then re-mated at Brian Pastures before cows and calves were transferred back to Spyglass, where the next cohort of calves was subsequently born.

Within each breed, non-significant effects ($P > 0.05$) were eliminated using a step-wise reduction to determine the significant effects for each trait. The final model was then determined from a pooled dataset with all three breeds; the initial model effects were the within-breed significant effects, with additional terms for the breed, and potential interactions between the breed and the other effects in the model.

The initial model for gestation length included the calf cohort (a concatenation of the AI herd, birth herd, project herd and birth year), cow lactation status (wet or dry), calf sex (male or female), cow group (a concatenation of cow herd, cow breed type, cow herd of origin and cow age group) nested within calf cohort and all first-order interactions. The birthweight initial model included birth cohort (herd and year of birth), calf sex (male or female), birth month (calendar birth month), cow group (a concatenation of cow herd, cow breed type, cow herd of origin and cow age group) nested within the birth cohort and all first-order interactions. For weaning weight, the initial model was the same as birthweight, with weaning age also fitted as a linear and quadratic covariate effect.

After model reduction, the significant fixed effects for gestation length were sire breed, calf sex, calf cohort and sire breed × calf sex. The final fixed effects for birthweight were sire breed, calf sex, birth cohort, birth month, cow group nested in the birth cohort and birth cohort × birth month. The final fixed effects for weaning weight were sire breed, calf sex, birth cohort, birth month, cow group nested in birth cohort, birth cohort × birth month, birth cohort × calf sex, sire breed × birth month, and the linear and quadratic weaning age. Least squares means for breed and sex were obtained from the models described above in the pooled breeds dataset. Cow group and sire breed were confounded; therefore, the cow group term was excluded to obtain sire breed least squares means for birth and weaning weight. Furthermore, to obtain estimable least squares means for birthweight, the interaction of birth cohort × birth month was removed. To obtain project herd least squares means, the models were re-run to include the project herd, and the calf cohort was then nested within the project herd to avoid confounding terms.

Genetic parameters were estimated using univariate mixed linear models in ASReml software (Gilmour *et al.* 2009) and the pooled breed dataset. The fixed effects fitted in the model to estimate genetic parameters were those found to be significant from the methodology described above. An animal model was used for all traits, with maternal and maternal permanent environment effects fitted for all three traits. A log-likelihood ratio test was used to determine the significance of random effects to identify the most parsimonious model. The data structure for estimating maternal effects included six cohorts (2017–2022), where birth and weaning weight data were available for both the calf and the dam. However, for gestation length, there were only 162 gestation length records over three cohorts (2020–2022), where both the calf and dam were recorded for gestation length. The lower number of calves with a dam recorded for gestation length was due to project-born females being naturally mated for their first two matings. Dams had, on average, 2.1, 2.3 and 2.3 calves recorded for gestation length, birthweight and weaning weight, respectively, with some dams having nine recorded calves. Up to three generations of pedigree were extracted from the breed society databases into a combined breed pedigree file. Generally, all project calves had sires and dams that were known, but the pedigree depth for some dams was limited. A series of bivariate models was used to estimate the genetic and phenotypic correlations between gestation length, birthweight and weaning weight in the pooled dataset.

To quantify the breed effect on variance component estimates, all univariate and bivariate models were rerun with sire breed and cow group excluded from the model and the pooled breed dataset. Across-breed estimated breeding values (EBVs) were obtained from ASReml animal solutions from the model with sire breed and cow group excluded, and the genetic merit of sires was compared for all three traits. Univariate variance components were also estimated in breed-specific datasets.

To test genotype × environment interactions, gestation length, birthweight and weaning weight from the two herds were considered separate traits in bivariate models from the pooled breed dataset, with sire breed and cow group (and interaction terms including sire breed) fitted to estimate the genetic correlation across herds. Santa Gertrudis animals were removed for all analyses, because the breed was located in only one herd.

Results and discussion

Data summary

Table 1 summarises the raw data. The average gestation length was 289.4 days with a 34-day spread. The average birth weight of calves was 33.9 kg, and calves were weaned at an average of 181.5 days and weighed 194.3 kg.

Least squares means for sire breed and location for all traits

Table 2 presents the least squares means for sire breed and location. The least squares means showed significant differences in breed and location for birth and weaning weight. There were significant differences between the three breeds for gestation length ($P < 0.05$); Brahman gestation lengths were 6.4 days longer than Santa Gertrudis, with least squares means of 291.5, 288.2 and 285.1 days for Brahman, Droughtmaster and Santa Gertrudis, respectively. The gestation length reported for Brahman cattle was longer than the 287 days reported by Corbet *et al.* (1997) in Australian Brahman, but similar to Plasse *et al.* (1968), who reported gestation lengths between 291 and 293 days for American Brahman. Messine *et al.* (2007) reported average gestation lengths of 293.4 days for Zebu cattle in Cameroon, and Chud *et al.* (2014) found Brazilian Nellore cattle had average gestation lengths of 296.6 days. Paschal *et al.* (1991) also reported similar gestation lengths for Grey and Red Brahman crossed with Hereford (290–291 days), and showed that *Bos indicus*-sired cattle had gestation lengths between 7 and 12 days longer than *Bos taurus*-sired cattle. Apart from a preliminary analysis of an earlier subset of the current data (Johnston and Grant 2017), no other gestation length data have been reported in the literature for purebred Droughtmaster and Santa Gertrudis cattle. Corbet *et al.* (1997) reported average gestation lengths of 282 days for Santa Gertrudis × Brahman cattle. They showed that when mated to Brahman cows, British *Bos taurus* sire breeds had shorter gestation lengths than European *Bos taurus* sire breeds and *Bos indicus* sire breeds, which were similar. Jeyaruban *et al.* (2016) also reported differences between British and European *Bos taurus* beef breeds, with average gestation lengths ranging from 280.8 to 284.8 days for British *Bos taurus* breeds, and 286.1 to 288.7 days for European *Bos taurus* breeds.

There were significant differences between the three breeds for both birth and weaning weights ($P < 0.05$). Brahman calves were the lightest at birth (33.3 kg) and weaning (191.3 kg), and Santa Gertrudis calves the heaviest at birth (36.6 kg) and weaning (200.0 kg; Table 2). There were significant location differences, with calves born at Brian Pastures being 2.3 kg heavier at birth and 7.0 kg heavier at weaning than Spyglass calves.

Table 2. Sire breed and location least squares means and standard errors for gestation length (days), birthweight (kg) and weaning weight (kg) for tropical beef breed calves born 2014–2022.

Trait	Data subset	Sire breed			Location[A]	
		Brahman	Droughtmaster	Santa Gertrudis	Brian Pastures	Spyglass
Gestation length (days)	*N*	1255	773	318	604	1424
	Least squares mean	291.5a	288.2b	285.1c	289.7a	289.9a
	s.e.	0.22	0.24	0.50	0.26	0.19
Birthweight (kg)	*N*	3355	2620	1069	1965	4010
	Least squares mean	33.3a	34.7b	36.6c	35.2a	32.9b
	s.e.	0.21	0.24	0.37	0.21	0.18
Weaning weight (kg)	*N*	2959	2366	923	1688	3637
	Least squares mean	191.3a	197.6b	200.0c	194.8a	187.8b
	s.e.	1.38	1.49	2.47	2.72	1.90

Different lowercase letters (a–c) within sire breed and project herd represent least squares means significantly different based on 95% confidence intervals.

[A] Only Brahman and Droughtmaster were considered in herd location, as Santa Gertrudis was only present at Brian Pastures.

Non-genetic factors of gestation length

Very few non-genetic factors were found to be significant for gestation length. This suggests that genetic factors predominantly control the trait, and very high heritability estimates have confirmed this. Calf sex was significant for all three breeds. The calf cohort was significant for Brahman, but this was not observed for Droughtmaster and Santa Gertrudis. Johnston and Grant (2017) reported the same significant factors from a preliminary study considering the first 2 years of the project data. Fig. 1 presents the least squares means for calf sex for each breed. In all breeds, the least squares means showed that male calves had longer gestation lengths, with the difference between males and females being 3.1, 1.9 and 2.4 days for Brahman, Droughtmaster and Santa Gertrudis calves, respectively. The effect of sex on gestation length reported in the literature has ranged from 1.9 days in purebred Brahman (Plasse *et al.* 1968) to 5 days for Grey Brahman × Hereford cattle (Paschal *et al.* 1991). Our results agree with the literature, where only the calf sex and sire have consistently been reported as significant fixed effects for gestation length, with other factors, such as location, cow parity and age, tending not to be significant (Plasse *et al.* 1968; Paschal *et al.* 1991; Corbet *et al.* 1997; Messine *et al.* 2007; Johnston and Grant 2017).

Variance component estimation

Gestation length was highly heritable (Table 3), with a direct heritability estimate of 0.79 (0.05) from the pooled breeds dataset with breed fitted in the model. The gestation length log-likelihood ratio test showed that fitting maternal effects resulted in a less parsimonious model; thus, only the animal effect was fitted in the gestation length model. The current data structure likely impacted the partitioning of the direct and maternal components. Birth and weaning weight had direct heritability estimates of 0.52 (0.04) and 0.40 (0.04), respectively. Maternal heritability was estimated to be 0.10 (0.02) and 0.15 (0.03) for birthweight and weaning weight, respectively. These parameter estimates were supported by within-breed estimates, albeit with lower numbers of records and higher standard errors. Within-breed variance component estimates were similar and not significantly different to estimates from the pooled breeds dataset when breed was fitted in the model.

When breed effects were not fitted in the pooled breed dataset, estimates of the variance components were impacted. Although not significant, the additive variance increased, whereas the residual variance decreased for gestation length and weaning weight. This resulted in inflated direct heritability estimates, with direct heritability estimates going from 0.79 (0.05) to 0.87 (0.05) for gestation length, and from 0.40 (0.04) to 0.46 (0.04) for weaning weight. The maternal heritability for weaning weight was unaffected. Ignoring breed effects for birthweight also increased genetic variances and decreased residual variance estimates, but the direct heritability was not inflated for birthweight. Instead, the maternal heritability increased from 0.10 (0.02) to 0.12 (0.02). These findings demonstrate that when breed effects

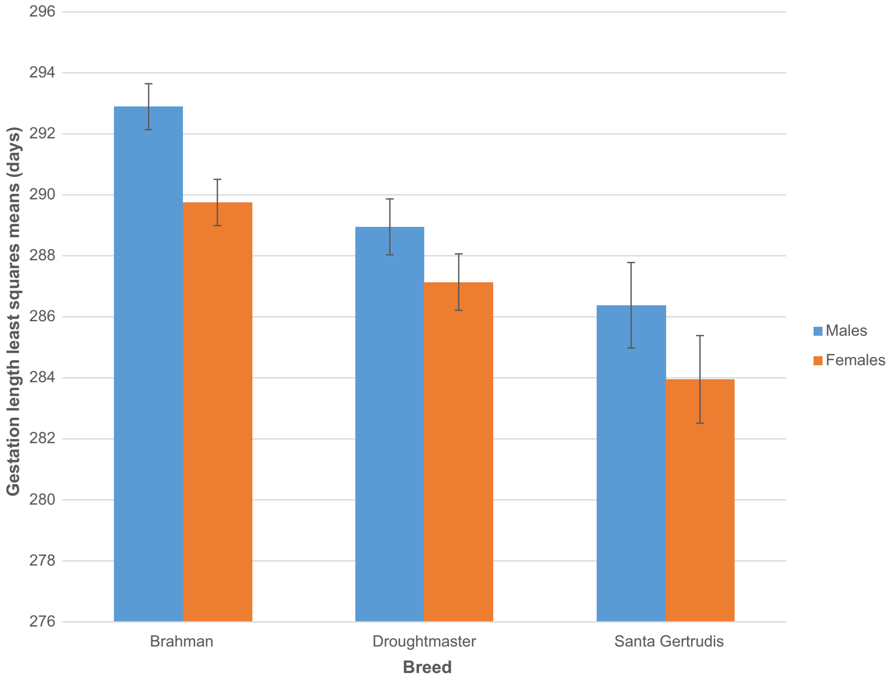

Fig. 1. Breed by sex least squares means and standard errors for gestation length (days) for tropical beef breed calves born 2014–2022.

Table 3. Univariate variance component and heritability estimates (standard errors in brackets) for gestation length (days), birthweight (kg) and weaning weight (kg) of tropical beef breeds.

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

Va, additive genetic variance; Vm, maternal genetic variance; Vpe, permanent environment variance; Ve, residual variance; Vp, phenotypic variance; h_d^2, direct heritability; h_m^2, maternal heritability.

^{A}Indicates the most parsimonious model after testing random effects for significance using log-likelihood ratio test; within-breed models were the most parsimonious pooled breed model.

are not correctly modelled (i.e. ignored), the genetic (direct and/or maternal) variance estimates capture the breed effects, which reduces the residual variance, resulting in inflated heritability estimates.

These gestation length heritability estimates are the first estimates reported in Australian tropical beef breeds, with very few genetic parameter estimates reported for *Bos indicus* breeds in general. The high gestation length heritability and genetic variance estimates indicate that selection may be a very effective way to improve the gestation length of tropical beef breeds. In five *Bos taurus* breeds, Jeyaruban *et al.* (2016) estimated gestation length to be highly heritable with direct heritabilities of between 0.42 (0.03) and 0.52 (0.02), and maternal heritabilities between 0.03 (0.02) and 0.09 (0.01). For birthweight, Jeyaruban *et al.* (2016) estimated direct and maternal heritabilities between 0.35 (0.02) and 0.46 (0.01), and between 0.08 (0.01) and 0.11 (0.02), respectively. The gestation length heritability and phenotypic variance (28.4) estimated from this study were higher than the *Bos taurus* breeds (20.71–23.98) reported by Jeyaruban *et al.* (2016). Chud *et al.* (2014) also estimated a larger gestation length phenotypic variance of 32.2 from an industry dataset of Nellore cattle in Brazil. In the same study, the direct and maternal birthweight heritability of Nellore cattle was estimated to be 0.40 (0.03) and 0.07 (0.02), respectively. The heritability estimates in the current study may be higher than those observed from industry data, because the dataset used in this study was collected as part of a designed experiment with high-quality data recording, especially having very accurate dates of birth.

Generally, differences in animal age within a cohort are random. However, for AI-born calves (conceived on the same day), the age difference is not random, but is strongly influenced by the sire's genetics for gestation length. This may have implications for the experimental design of projects, especially when multi-breeds are considered. When age is not fitted into the model, the variance explained by age should be partitioned as residual variance. However, Moore *et al.* (2023) demonstrated that when calf age was confounded with sire (i.e. due to variation in sire gestation length genetic merit) and not modelled correctly, the additive variances and heritability estimates increased significantly for live weight at 3 months. Therefore, the strong genetic heritability of gestation length has implications for the experimental design of projects involving AI mating, and demonstrates the importance of accurately recording the date of birth to account for age in subsequent analyses to avoid breed effects being partitioned as part of the additive variance and heritability estimates.

A moderate positive direct genetic correlation (Table 4) of 0.30 (0.09) was estimated between gestation length and birthweight, and a strong positive genetic correlation (r_g = 0.64 (0.06)) was estimated between birth and weaning weight. However, the genetic correlation between gestation length and weaning weight (r_g = −0.09 (0.10)) was not significantly different from 0. The lack of genetic relationship between gestation length and weaning weight was also reported by Chud *et al.* (2014), with genetic correlation estimates of 0.19 between gestation length and birthweight, and 0.02 between gestation length and weaning weight. Jeyaruban *et al.* (2016) estimated genetic correlations between 0.15 and 0.45 for gestation length with birthweight, but did not include weaning weight in their study. These genetic correlations suggest that the genes underlying the relationship between gestation length and birthweight are not the same genes that influence an animal's subsequent growth. The genetic correlation between the direct and maternal components of birthweight and weaning weight was estimated to be −0.18 (0.10) and −0.06 (0.11), respectively. Jeyaruban *et al.* (2016) reported similar estimates for birthweight in temperate breeds. The genetic correlation estimates between direct gestation length and maternal birth and weaning weight were not significantly different from 0. This was also the case for the other trait combinations that compared direct and maternal genetic correlations. A positive correlation of 0.36 (0.11) was estimated between maternal birth weight and maternal weaning weight. Correlation estimates when the breed was excluded from the model were similar and not significantly different from correlation estimates when the breed was fitted.

Table 4. Phenotypic (below diagonal) and genetic (above diagonal) correlation estimates for direct and maternal components of gestation length, birthweight and weaning weight of tropical beef breeds.

Trait	GLd	BWTd	WWTd	BWTm	WWTm
Pooled (breed fitted in model)					
GLd		**0.30 (0.09)**	−0.09 (0.10)	0.17 (0.12)	0.10 (0.10)
BWTd	**0.30 (0.03)**		**0.64 (0.06)**	−0.18 (0.10)	0.04 (0.10)
WWTd	0.02 (0.03)	**0.38 (0.02)**		−0.07 (0.12)	−0.06 (0.11)
BWTm					**0.36 (0.11)**
Pooled (breed excluded from model)					
GLd		0.12 (0.08)	−0.17 (0.09)	**0.26 (0.10)**	0.14 (0.09)
BWTd	**0.24 (0.03)**		**0.69 (0.05)**	**−0.26 (0.10)**	−0.05 (0.09)
WWTd	−0.02 (0.04)	**0.40 (0.02)**		−0.16 (0.10)	**−0.21 (0.09)**
BWTm					**0.37 (0.09)**

For each trait, the most parsimonious pooled breed model was fitted. Data are shown as correlation estimates with s.e. in parentheses. Significant correlations are shown in bold. BWT, birthweight (kg); d, direct components of gestation length; GL, gestation length (days); m, maternal components of gestation length; WWT, weaning weight (kg).

Genotype by environment interaction

The genotype by environment interaction across the two locations was investigated using bivariate analysis when the records at each location were considered different traits. For each trait, the estimated direct genetic correlations were not significant from one (Table 5). The estimated maternal genetic correlations for all three analyses exceeded the upper bounds with large standard errors (results not shown). These results show no evidence of significant genotype by environment interaction between the two locations considered in this study. Phenotypic and additive genetic variances were similar between the locations, and sires are expected to rank the same across herds. Therefore, these results show that it is suitable to consider both locations as one trait and include them in a single genetic evaluation.

Sire estimated breeding values

Animal solutions (EBVs) from across-breed analyses for gestation length, birthweight and weaning weight were produced for 3468, 2717 and 1077 Brahman, Droughtmaster and Santa Gertrudis animals, respectively. Figs 2, 3 and 4 present the EBVs for 112, 245 and 242 sires, with ≥10 progeny

Table 5. Variance component, heritabilities and genetic correlation estimates across project herds (standard errors in brackets) for gestation length, birthweight (BWT, kg) and weaning weight (WWT, kg) of Brahman and Droughtmaster in two separate environments.

	Brian pastures							Spyglass							
	Va	Vm	Vpe	Ve	Vp	h^2	h_m^2	Va	Vm	Vpe	Ve	Vp	h^2	h_m^2	Direct Rg
GL	25.4			3.2	28.6	0.89 (0.09)		22.2			6.5	28.6	0.77 (0.06)		0.98 (0.05)
BWT	14.6	3.5		6.7	24.9	0.59 (0.07)	0.14 (0.04)	12.7	2.5		7.3	22.5	0.56 (0.05)	0.11 (0.03)	0.99 (0.05)
WWT	167.2	69.9	9.4	132.2	378.7	0.44 (0.08)	0.18 (0.06)	164.8	56.5	54.1	123.4	398.8	0.41 (0.05)	0.14 (0.04)	0.87 (0.09)

Data are shown as correlation estimates with s.e. in parentheses. BWT, birthweight (kg); GL, gestation length (days); WWT, weaning weight (kg); Va, additive genetic variance; Vm, maternal genetic variance; Vpe, permanent environment variance; Ve, residual variance; Vp, phenotypic variance; h^2, direct heritability; h_m^2, maternal heritability; Rg, direct genetic correlation; maternal genetic correlations for BWT and WWT exceeded the upper bounds.

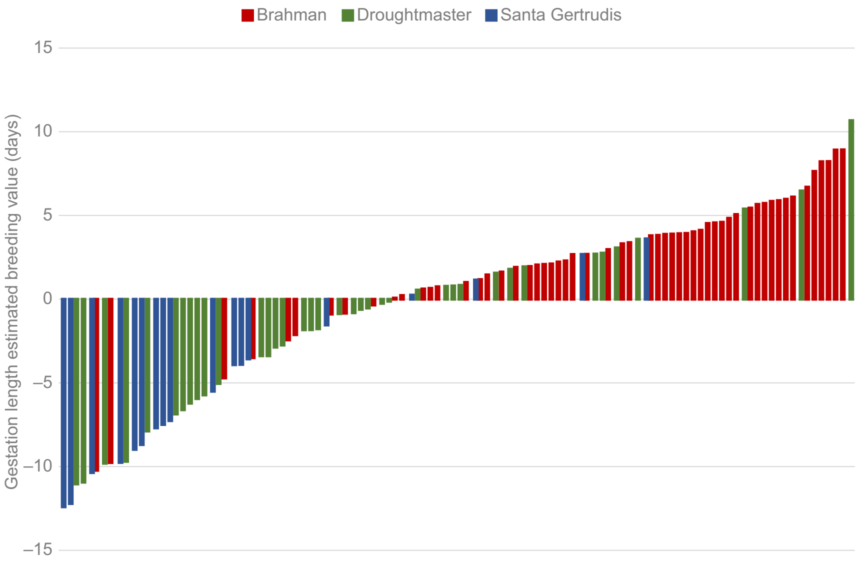

Fig. 2. Across-breed gestation length estimated breeding values for Brahman, Droughtmaster and Santa Gertrudis sires.

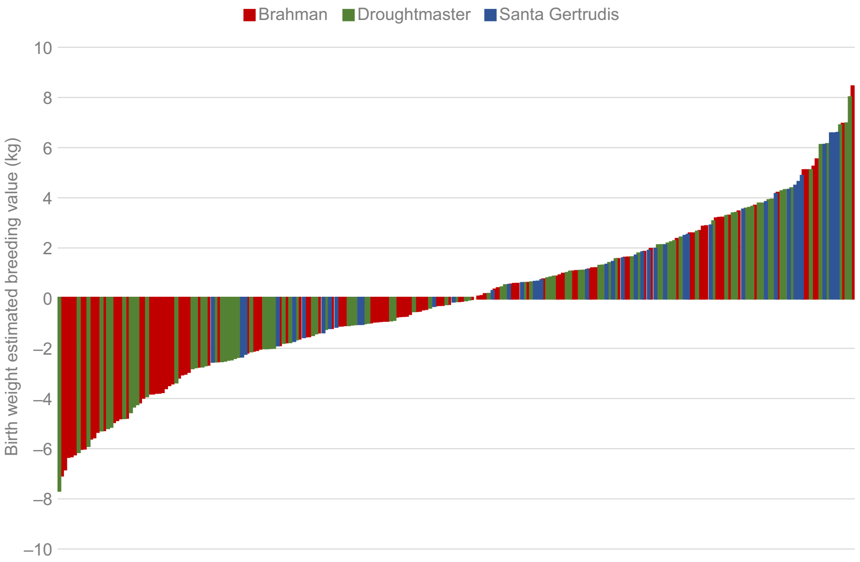

Fig. 3. Across-breed birthweight estimated breeding values for Brahman, Droughtmaster and Santa Gertrudis sires.

recorded for gestation length, birthweight and weaning weight, respectively. On average, Brahman animals had the larger (i.e. longer) gestation length EBVs, with average gestation length EBVs of 1.0, –0.6 and –2.3 days for Brahman, Droughtmaster and Santa Gertrudis animals, respectively. Brahman sires had the larger (i.e. longer) gestation length

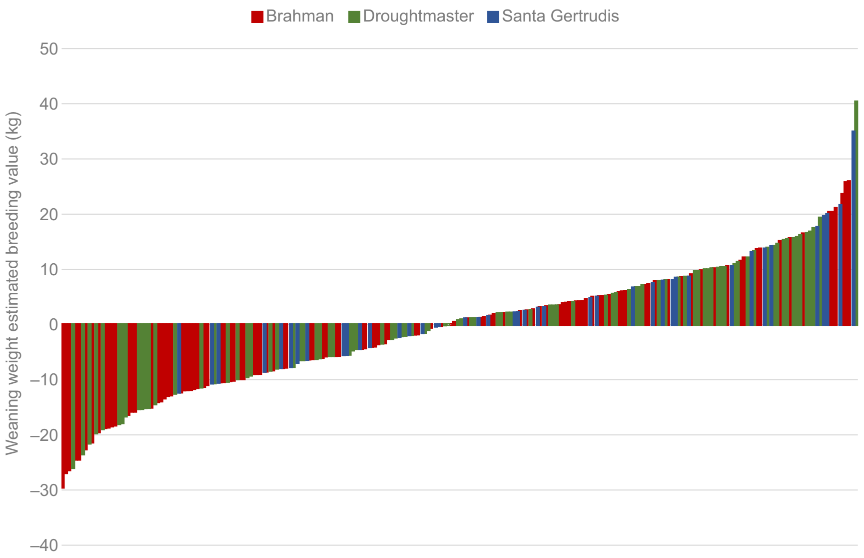

Fig. 4. Across-breed weaning weight estimated breeding values for Brahman, Droughtmaster and Santa Gertrudis sires.

EBVs, with average gestation length EBVs of 2.7, –2.2 and –6.2 days for Brahman, Droughtmaster and Santa Gertrudis sires with ≥10 progeny recorded, respectively. The difference between extreme sires for gestation length EBVs was 19.1, 21.7 and 16.0 days for Brahman, Droughtmaster and Santa Gertrudis sires, respectively. The large spread of EBVs indicates that genetic selection for gestation length is likely to be effective in reducing gestation length.

Brahman animals had lower (i.e. lighter) birthweight EBVs, with average birthweight EBVs of –1.2, 0.0 and 1.3 kg for Brahman, Droughtmaster and Santa Gertrudis calves, respectively. Brahman sires tended to have lower (i.e. lighter) birthweight EBVs, with average birthweight EBVs of –0.9, 0.0 and 1.6 kg for Brahman, Droughtmaster and Santa Gertrudis sires with ≥10 progeny recorded, respectively. Santa Gertrudis sires tended to have higher birthweight EBVs, whereas Droughtmaster were more evenly represented across the whole distribution. The difference between extreme sires for birthweight EBVs was 15.5, 15.7 and 9.1 days for Brahman, Droughtmaster and Santa Gertrudis sires, respectively.

Average weaning weight EBVs were –4.0, 0.3 and 2.1 kg for Brahman, Droughtmaster and Santa Gertrudis animals, respectively. For weaning weight EBVs, the sire breeds were more evenly distributed. However, Santa Gertrudis sires tended to have higher (i.e. heavier) weaning weight EBVs. Average weaning weight EBVs were –3.6, 0.9 and 4.6 kg for Brahman, Droughtmaster and Santa Gertrudis sires, with ≥10 progeny recorded, respectively. Again, Droughtmaster sires were more evenly represented across the whole distribution. The difference between extreme sires for weaning weight EBVs was 55.4, 66.3 and 47.2 days for Brahman, Droughtmaster and Santa Gertrudis sires, respectively.

The EBV spread for all traits was smaller for Santa Gertrudis compared with the other breeds. This may be due to Santa Gertrudis having fewer sires in the analysis.

Conclusions

This study provided the first gestation length genetic parameter estimates in Australian tropical beef breeds, and found that gestation length was highly heritable with no evidence of genotype by environment interactions across the two locations. Breed effects were identified, with Brahman tending to have longer gestation lengths, and lighter birth and weaning weights; Santa Gertrudis had shorter gestation lengths, and heavier birth and weaning weights; and Droughtmaster had sires distributed evenly across the distribution. Gestation length had a moderate positive genetic correlation with birthweight. but not with weaning weight. This suggests that the genes underlying the relationship between gestation length and birthweight are not the same genes that influence later growth. Thus, genetic selection for gestation length could be used to change gestation length and reduce birthweight without correlated effects on weaning weight.

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Data availability. The data that support this study were obtained from MLA by permission/licence. Data will be shared upon reasonable request to the corresponding author with permission from MLA.

Conflicts of interest. The authors declare that they have no conflicts of interest.

Declaration of funding. The authors acknowledge funding from MLA and MLA donor company (projects B.NBP.0759 and P.PSH.1221).

Acknowledgements. The authors acknowledge funding from MLA (projects B.NBP.0759 and P.PSH.1221) and the contributions of the project collaborator institutions: AGBU, Queensland Department of Primary Industries, Northern Territory Department of Primarily Industries and Fisheries, University of Queensland and QAAFI. We especially thank the efforts of the Queensland Department of Primary Industries research station managers at Spyglass and Brian Pastures, with their staff and the team of technicians involved in animal management and data collection at the research stations: Tracy Longhurst, Joanne Campbell, Nicholas Brazier, Kerry Goodwin, Jarud Muller, Stacey Haucke, Leanne Hardwick, Nicole Limburg, Andrew Lewis, Callum Olver, Melissah Dayman, Brad Hough, Ian Dunbar and Hannah Vicary. Thanks to the database specialists, Jim Cook and Tracy Longhurst. Finally, we acknowledge the three breed societies and their members for access to their performance and pedigree database with the extract provided by ABRI.

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