Genetics of female reproduction traits

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Abstract

The genetics of heifer pubertal traits and their associations with female reproductive performance were estimated using records from 2,115 heifers representing 2 tropically adapted genotypes raised in northern Australia. Heifers were ultrasound scanned for ovarian activity every 4-6 weeks to determine the age at first observed corpus luteum (CL). Heifer live weight (WTCL) and ultrasound scanned fat depth (FATCL) were also recorded at this time. Heifers were mated at approximately 2 years of age and genetic and phenotypic relationships were estimated between days to calving (DC1), calving success (CS1) and age at first CL (AGECL). Results showed large genotype, location and birth month effects on age and fatness at first CL but not weight at first CL. Age at presence of the first CL (AGECL) was moderately to highly heritable: 0.57 and 0.52 for Brahmans and Tropical Composites, respectively. Other pubertal traits were also moderately heritable. Heritability estimates for DC1 and CS1, were 0.16 and 0.18 for Brahmans and 0.11 and 0.08 for Tropical Composites, respectively. DC1 and CS1 were genetically correlated with AGECL, particularly for Brahmans (0.87 and -0.58, respectively). Selection to improve first parity female reproductive performance is feasible in both genotypes, and for Brahmans AGECL could be used as an indirect selection criterion provided it can be measured cost effectively in industry. Associations with lifetime reproductive performance will be required before final recommendations can be made on recording and selection breeding schemes.

Introduction

Female reproductive performance (FRP) is an important component of profitable beef production and can be improved by genetic and non-genetic means. Several studies have shown breed differences in fertility exist for tropical genotypes in northern Australia (e.g. Mackinnon et al. 1989). Significant within breed genetic differences also exist for tropical beef cattle for female reproduction and related calf output traits (Davis 1993). However, female fertility traits are expressed relatively late in life, are sex limited, and are often difficult to measure and lowly heritable, thus making genetic improvement in these traits difficult. Worldwide, there are currently few female fertility traits recorded and analysed in beef genetic evaluation schemes, the exceptions being days to calving in Australia (Graser et al. 2005) and heifer pregnancy percentage in the US Red Angus. To achieve higher rates of genetic progress in these traits (and in the profit objective) requires measures that can be recorded earlier, that are heritable and that are correlated to the underlying profit trait. One trait that may influence maiden calving performance is age at puberty. Breed differences have been reported for age and weight at puberty (Martin et al. 1992) and Brahmans have been reported to be older at puberty than other breeds (Bolton et al. 1987, Hearnshaw et al. 1994). Several studies have shown age at puberty is heritable in beef cattle, particularly in Bos taurus breeds (e.g. Martin et al. 1992, Gregory et al. 1995), but limited studies exist for Bos indicus genotypes. Vargas et al. (1998) reported, from a small study, a heritability for age at puberty in Brahmans of 0.42. However relationships between age at puberty and subsequent measures of female fertility were inconclusive. Some studies show a favourable relationship between improved pregnancies and earlier age at puberty (Morris et al. 2000). However several others (e.g. Dow et al. 1982, Cundiff et al. 1986) have observed no relationship.

Ultrasonography can be used to measure ovarian activity, in particular follicular development and the occurrence of the CL, in livestock including cattle (Pierson and Ginther 1988; Griffin and Ginther 1992), and offers the ability to detect puberty in cattle. This paper reports results from a large breeding project aimed at improving profitability of cattle through improved reproductive performance in northern Australia. The initial aim of the study was to assess real time ultrasound ovarian scanning as a method to determine genetic

differences in pubertal traits of genotypes raised in a range of production environments in northern Australia, and to assess their potential use as measures for genetic selection. The main objective of this paper was to determine the genetic relationships between pubertal traits and FRP traits from first parity calving performance and the implications for genetic improvement of these traits.

Table 1. Distribution of numbers of heifers to each location by genotype and birth year

		Location				
Breed	Year	Swans	Belmont	Toorak	Brian Pastures	Total
BRAH	00		73			73
	01	188	111	65		364
	02	209	119	101		429
	03	42	124			166
	Total	439	427	166	0	**1032**
TCOMP	01		113	160	146	419
	02		140	184	272	596
	03		48		79	127
	Total	0	301	344	497	**1142**

Materials and Methods

Animals

Females used in this study were part of the Cooperative Research Centre (CRC) for Cattle and Beef Quality project 2.3 (Burrow et al. 2003). Two genotypes Brahman (BRAH) and Tropical Composites (TCOMP) were chosen to represent diverse genotypes of the sub-tropical and tropical regions of Northern Australia. The cattle were bred on 8 co-operator properties throughout Queensland and the Northern Territory. Calves were generated by artificial insemination and natural service on each of the properties. At each property of origin the calf sex, date of birth, dam ident and dam year of birth were recorded. Sire parentage was determined by DNA fingerprinting. Sires used by AI were used to genetically link across properties of origin within a genotype and also to generate progeny on several (approx 12) sires of known estimated breeding values for carcase traits from CRC1. At one location, BRAH and TCOMP heifers were raised from birth as contemporaries.

Heifer allocation and management

After weaning each year the entire calf crop from each of the property of origins were delivered to the control of the CRC. Calves were generated over 4 and 3 years for BRAH and TCOMP, respectively. Each year, heifers were allocated according to property of origin and sire (determined by DNA fingerprinting) to one of 4 research stations in Queensland (see Table 1). Heifers were allocated to Brian Pastures (Gayndah), Swans Lagoon (Ayr), Belmont (Rockhampton) and Toorak (Julia Creek) research stations. The distribution of numbers of BRAH was greater to the harsher environments compared to lower numbers allocated to the more benign locations. No BRAH were allocated to Brian Pastures. In contrast, the TCOMP were allocated with a greater distribution to more benign environments and lower numbers at the harsher environment (i.e. Belmont). No TCOMP were allocated to Swans Lagoon.

At each location all heifers from the same year of birth were managed as a single group (defined as a cohort). At each location the heifers were mated (by genotype) in large multiple sire groups for 12 weeks to the same breed of bull. The average age at the commencement of joining (JAGE) was approximately 25 months (i.e. to first calve as 3 year olds). The commencement date for mating differed slightly across locations within a year reflecting regional preferences for calving times. Calving was closely monitored at each location and the date of birth, sex of calf, and birth weight (at most locations) were recorded within 24 hours of birth. Dead calves were also recorded.

Measurements and trait definitions

First observed corpus luteum. Assessment of ovarian activity commenced in each cohort when average age was approximately 11-12 months. Assessments were conducted each 4-6 weeks, excluding the July-October period when 1.5-2.0 years of age, during which time assessment was each 8 weeks. Other than for the 2003 cohort, only heifers weighing in excess of 200 kg were assessed prior to 18 months of age. From this time (and for all 2003 heifers from 11 months of age), all non-pregnant heifers in a cohort were assessed at each muster. Prior to 2 years of age within the 2001 cohort, assessment was temporarily discontinued after a corpus luteum (CL) or a corpus albicans (CA) was recorded. Each ovary was viewed per rectum using linear-array ultrasound imaging (Aloka SSD-500 with 7.5 MHz rectal probe; or Honda HS-2000V with variable-frequency probe set at 10 MHz). The most advanced reproductive structure on the ovary was recorded. This was a CL (or CA) if present, and if not, diameter of the dominant follicle (mm) was measured. From mid-2003, the size of the dominant follicle on any ovary with a CL (or CA) was recorded.

At each ovarian scanning event at a location all heifers were weighed, ultrasound fat scanned at the P8 site and CS recorded. Prior to commencement of the study, all assessors across locations were trained to ensure consistency of scores.

Pubertal traits. For each heifer the date of her first observed CL was identified from her ovarian scanning data and used to calculate the age of the

heifer at that time (AGECL). The date at first observed CL was used to identify the heifer's weight (WTCL) and scanned P8 fat depth (FATCL) on or within 7 days (see Table 1). A binary variable relating to the presence (record=1) or absence (record=0) of a CL prior to the commencement of mating was assigned (PRIORCL).

Table 2. Trait means, standard deviations and ranges for BRAH

Trait	N	Mean	s.d.	Min.	Max.
AGECL (days)	1007	750.6	142.1	394	1211
WTCL (kg)	993	334.4	44.8	196	485
FATCL (mm)	951	4.47	2.19	1.0	15.0
PRIORCL (%)	1008	0.51	0.50	0	1
DC1	1020	346.4	49.8	279	423
CS1(%)	1020	0.71	0.45	0	1

Days to calving. Days to calving (DC1) was computed as the number of days from the commencement of the joining period until the subsequent calving date. Non-calvers were assigned a penalty DC1 record by computing a projected calving date (i.e. end of joining date + 42 days + 292 days average gestation length).

Calving success. Calving success (CS1) was simply recorded as a binary trait (1=calf born; 0=no calf born).

Statistical analyses

Fixed effect modelling

Significant fixed effects for each trait were identified using mixed model procedures in SAS (SAS Inst., Cary, NC) and were performed separately for each genotype. Models included the independent variables of birth month, cohort, origin, age of dam, and for TCOMP, sire and dam breed groups were also included to account for varying levels of heterosis in the different composite genotypes. Initial models included main effects and all first order interactions. Sire was included in all models as a random effect. Non-significant terms (P>0.05) were sequentially removed to yield the final models for each trait. Birth month was included to remove the effect of age and also seasonal effects. Within a location, adjacent birth months with few numbers were combined. Cohort included the effects of location and year (and mating group for the DC1 and CS2). Age of dam was recorded in years and when unknown was assumed to be the median for the origin.

Significant fixed effects were also identified for each trait using a combined dataset across genotypes. This entailed considering the significant effects identified above for each genotype along with additional terms for genotype and all first order interactions with genotype. Each model was reduced (P>0.05) to a final model for use in combined genotype analyses and for the estimation of least squares means for genotype, location and birth month.

Variance component estimation

Genetic variances and heritabilities for the 4 pubertal and 2 female reproductive performance traits were estimated in univariate analyses using restricted maximum likelihood (Gilmour et al. 1999). All traits were analysed using an animal model and included the set of fixed effects (identified above) and random effects of animal and residual. A relationship matrix including 3 generations of pedigree was used. There were 54 BRAH and 51 TCOMP sires with daughters recorded, and the number of sires with 20 or more daughters was 23 and 29 for BRAH and TCOMP, respectively. Genetic correlations were estimated in a series of bivariate analyses between pairs of traits.

Results and discussion

Summary statistics for pubertal traits are presented in Tables 2 and 3 for BRAH and TCOMP, respectively. Mean AGECL was 750.6 and 650.8 days for BRAH and TCOMP respectively. Both breeds showed considerable variation (18% CV). Differences in the raw means reflected breed, location, birth month and cohort effects. Trait means for DC1 (d), CS1 (%) and JAGE (d) were 346.4, 0.71 and 748 for BRAH and 318.9, 0.90 and 759 for TCOMP respectively.

1) Least squares means for pubertal and calving traits

Genotype effects

BRAH and TCOMP were not significantly different for WTCL (337 and 331 kg, respectively) but BRAH were on average 84 days older for AGECL,

Table 4. Least squares means for heifer pubertal and calving traits

	AGECL (days)	WTCL (kg)	FATCL (mm)	PRIORCL (%)	DC1 (d)	CS1
			Genotype			
BRAH	757	337	4.6	46	348	0.69
TCOMP_ST[1]	673	331	3.3	74	323	0.86
overall sed	*(17)*	*(6)*	*(0.3)*	*(5)*	*(4)*	*(0.04)*
			Location			
Brian Past.	652	334	2.9	79	322	0.90
Toorak	691	322	3.9	79	335	0.76
Belmont	711	354	4.3	61	328	0.84
Swans	804	323	4.5	42	356	0.62
overall sed	*(12)*	*(4)*	*(0.2)*	*(4)*	*(3)*	*(0.03)*
			Birth month[2]			
September	618	329	3.5	91	322	0.88
November	703	336	3.7	71	324	0.88
January	773	335	4.7	34	345	0.74
March	854	341	4.6	9	392	0.28
overall sed	*(20)*	*(8)*	*(0.4)*	*(7)*	*(7)*	*(0.06)*

[1] TCOMP_ST = sub-set of TCOMP representing only stabilised genotypes

[2] number of months reduced for ease of reporting

1.3 mm fatter and had significantly lower percentage PRIORCL, longer DC1 and lower CS1 compared to TCOMP (see Table 4). These results are consistent with several papers reporting increased age of puberty in Brahmans (e.g. Hearnshaw et al. 1994 Bolton et al. 1987). The reduced percentage of BRAH heifers showing a CL prior to mating clearly influenced the reproductive performance for the first calving (DC1 and CS1). However it is not possible to extrapolate genotype differences outside the range of environments in the experiment. TCOMP were purposely not allocated to the Swans location because it was perceived they would be very poorly adapted and survival (and reproductive performance) would have been compromised.

Table 5. Additive variances (Va) and heritabilites (h2) for BRAH

Trait	V_a	h^2	se
AGECL (days)	7375	0.57	0.12
WTCL (kg)	981	0.56	0.12
FATCL (mm)	2.41	0.55	0.13
PRIORCL	0.052	0.33	0.10
DC1	321.7	0.16	0.09
CS1	0.031	0.18	0.09

Table 6. Additive variances (Va) and heritabilities (h2) for TCOMP

Trait	V_a	h^2	se
AGECL (days)	5670	0.52	0.12
WTCL (kg)	789	0.46	0.11
FATCL (mm)	0.88	0.39	0.11
PRIORCL	0.022	0.13	0.07
DC1	170.0	0.11	0.06
CS1	0.0071	0.08	0.05

Location effects

Location had a large effect on AGECL. In particular, heifers at Swans were significantly older, tended to be fatter at first CL, had lower PRIORCL, and subsequently longer DC1 and lower CS1 but similar WTCL compared to the other locations. Hearnshaw et al. (1994) reported a large nutrition effect on age at puberty mainly through its effect on weight, where Brahmans could not increase growth under high nutrition relative to other genotypes. Ferrell (1982) showed that slower growth rate delayed age at puberty and subsequently reduced pregnancy compared to heifers that gained weight rapidly postweaning, suggesting that weight was more important than age in determining puberty. These results suggest that management to achieve minimum live weights (e.g. around 320kg) will decrease age at puberty and improve subsequent calf output (Rudder et al. 1985). However Mackinnon et al. (1989) hypothesized that once sexual maturity was reached there was little effect of increasing weight on subsequent fertility.

Birth month and season

Birth month, and associated seasonal effects, had a large effect on all traits. Late born heifers (e.g. March) had significantly increased AGECL and DC1, reduced PRIORCL and CS1 but increased FATCL compared to early born heifers (i.e. September). However there was little observed effect on WTCL. The AGECL of late born heifers was likely to be influenced by the effect of the distinct wet and dry seasons experience by these cattle in northern Australia and its effect on weight gain. Arije and Wiltbank (1971) reported seasonal pasture availability and birth month affected age at puberty in Hereford heifers. Bolton et al. (1987) reported large difference between spring and autumn calving season in the percentage of pubertal heifers at time of first joining and attributed the effect to the reduced growth rate of the autumn-born calves which slowed the rate of sexual development, particularly as Brahman content increased. Results from the current study may also include the effect of photoperiod of sexual development of the later born heifers.

2) Additive variances and heritabilities

All pubertal traits were moderately heritable with the exception of PRIORCL in TCOMP (see Tables 5 and 6). Heritabilities for AGECL were slightly higher than in the review of Martin et al. (1992), where a pooled estimate of 0.40 was reported. In general, additive variances from pubertal traits were larger for BRAH compared to TCOMP. These results indicate large differences between sires in their daughters' ages at first CL and also weight and fatness at first CL. The differences could be used to alter these traits if that was considered desirable. PRIORCL was heritable for BRAH (0.33) but less heritable for TCOMP (0.13). This result is likely to be related to the differences in the mean of the binary trait, with the BRAH trait average closer to 50%. DC1 and CS1 were more heritable for BRAH than TCOMP (0.16, 0.21 versus 0.11 and 0.06) and with larger additive variances. Heritabilities were higher than reviewed by Davis (1993) and may reflect the sampling of sires and the environments used in this study.

3) Genetic correlations among heifer pubertal traits

Moderate to strong positive correlations were estimated between each of the pubertal traits (see Table 7) showing animals that were older at first CL were also genetically heavier and fatter at the time of their first CL. Laster et al. (1979) also reported a positive genetic correlation between age at puberty and weight at puberty of 0.52. However the genetic correlations of AGECL with live weight and fat depth at an age constant basis were -0.34 and –0.30 (not shown in Table 7). Indicating animals with younger ages at puberty were genetically heavier and fatter at the same age.

Table 7: Correlations# between pubertal traits data combined across genotypes

Trait	AGECL	WTCL	FATCL	PRIORCL
AGECL		0.74 (0.06)	0.53 (0.10)	-0.99 (0.04)
WTCL	0.67		0.44 (0.11)	-0.81 (0.09)
FATCL	0.26	0.38		-0.66 (0.12)
PRIORCL	-0.55	-0.43	-0.23	

The occurrence of a CL at commencement of mating was highly negatively correlated with younger age at CL and with weight and fatness. Indicating those sires' daughters with higher age, weight and/or fatness at puberty are genetically less likely to have shown a CL prior to the commencement of their maiden mating.

3) Genetic correlations between DC1 and CS1 and with AGECL

For both genotypes, the genetic correlations between DC1 and CS1 were not significantly different from one, indicating they are very similar traits (see Table 8). However, DC1 contains additional information resulting from additive genetic differences in days to calving within the group of cows that calve, particularly for BRAH. Conversely, for TCOMP the additive variance for DC1 was mostly due to the inclusion of penalty records for cows that failed to calve.

AGECL was strongly genetically correlated with DC1 and CS1 in BRAH indicating that females that were younger at AGECL had genetically shorter DC1 and increased CS1, when mated for the first time at approximately 25 months. Although in the same direction, the correlations for TCOMP were smaller in magnitude (and with large SE), indicating AGECL was not as good a genetic predictor of calving performance traits in that genotype when heifers were first mated at 25 months. This is most likely because the average AGECL for TCOMP heifers was 108 days before the start of joining compared to BRAH whose average AGECL was 6 days after the start of joining. As a result, 79% of TCOMP had an observed CL prior to commencement of joining compared to 51% for BRAH. Morris et al. (2000) reported genetic correlations for first behavioural oestrus with calving date (same trait as days to calving) and pregnancy rate of 0.57 and -0.36, respectively in Angus cattle. Laster et al. (1979) reported a genetic correlation between age at puberty and heifer pregnancy of -0.42. Genotype differences in genetic parameter estimates from this study include the effects of the different production environments used in the study, in particular the effect of the harsher northern coastal location for BRAH.

Conclusions

Ultrasound ovarian scanning technology has been used to generate a trait (i.e. age at first CL) that was moderately to highly heritable in both genotypes and which was subsequently shown to be related to two calving performance traits. The technology and scanning protocols employed in this project have been able to deliver a very powerful means by which to estimate genetic differences in age at puberty (and associated traits) and genetic correlations with female reproductive performance traits.

The study has shown significant difference between genotypes, locations and birth months on AGECL. These differences could be used to develop management strategies to improve AGECL. For example calving times (i.e. start of mating and its duration) could be altered to reduce the number of calves born after January.

Genetic variation existed for pubertal traits with greater variance observed for BRAH. The two FRP traits examined in this study (DC1 and CS1) had considerable genetic basis under the production environments of this experiment and selection could improve these traits. Age at puberty was also highly heritable in both genotypes and, for BRAH, was strongly correlated with the reproductive performance traits and could be used as an indirect selection criterion. The challenge is to be able to measure the trait cost effectively in beef herds. For TCOMP, there was less genetic variation for the traits measured though significant sire differences existed. Age at puberty was heritable in TCOMP but was not strongly genetically correlated with the calving traits under the current mating management (i.e. first mating at 2 years). Future research will determine the relationship between AGECL and subsequent calving outcomes and lifetime reproductive performance in both genotypes. As well, possible genetic indicator traits for female fertility will be assessed as well as quantifying the correlated response to selection for improve FRP on steer profit traits (e.g. carcase weight, fatness, tenderness).

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Table 8. Genetic and phenotypic correlationsA for female reproductive performance traits in BRAH and TCOMP

Genotype	Traits	DC1	CS1	AGECL
BRAH				
	DC1 (d)		-0.93±0.05	0.87±0.19
	CS1 (%)	-0.92±0.01		-0.58±0.19
	AGECL (d)	0.40±0.03	-0.37±0.03	
TCOMP				
	DC1		-1.00±0.09	0.23±0.31
	CS1	-0.90±0.01		-0.24±0.34
	AGECL	0.05±0.03	-0.03±0.03	

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