

## GENETIC VARIATION IN ADAPTIVE TRAITS OF CATTLE IN NORTH AUSTRALIA

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### SUMMARY

Adaptation to environmental stressors is of particular importance for cattle breeders in tropical regions of northern Australia. Various studies have estimated the genetic parameters for adaptive traits measured in northern Australian cattle herds, but most were specific to regions and breeds. The current study assesses adaptability measures of both Brahman and Composite cattle ( $n=2071$ ) raised in four distinct environments of northern Australia. Heritabilities for tick score, worm egg count, buffalo-fly lesion score, rectal temperature, coat score, flight time, navel score and colour score ranged from 0.12 to 0.70. The heritability of most traits indicated potential to genetically improve these traits in both Composite and Brahman populations.

### INTRODUCTION

Adaptation of cattle to their immediate environment is important for efficient beef production because of the lower physiological stress on the animal. In tropical northern Australia, cattle are expected to survive, grow and reproduce whilst enduring environmental stressors such as parasites, hot, humid conditions and seasonally poor nutrition. To counter these stressors, breeds with natural resistance (e.g. *Bos indicus*) were successfully introduced over recent decades. However, their lower fertility rates and poorer meat quality attributes has led to the use of alternative breeding strategies such as the development of Tropical Composite breeds combining the complimentary attributes of breeds originating from India, Africa, Britain and Europe. Various studies have outlined the genetic parameters of adaptive traits in north Australian composite (e.g. Burrow 2001) and crossbred (e.g. Prayaga and Henshall 2005) cattle populations. However, these studies were region specific and not representative of cattle populations across northern Australia. In a Beef CRC (Cooperative Research Centre) project designed to understand the genetic links between beef quality and components of herd profitability in northern Australia, a full range of productive, reproductive and adaptive traits were recorded. In the current study, adaptability measures of Brahman and Tropical Composite cattle were assessed at four environmentally different locations in central and northern Queensland. Heritability of these measures was estimated for both genotypes.

### MATERIALS AND METHODS

**Animals.** Data were obtained from heifers of two genotypes (966 Brahmans and 1105 Composites) bred for the Beef CRC Project 2.3 (Burrow and Bindon 2005). The Composites comprised admixes of Belmont Red, Charbray, Santa Gertrudis and Senepol breeds. The heifers were bred on 8 properties in Queensland and Northern Territory using AI and natural service. The AI sires used ensured genetic linkage across years and properties of origin within genotype. Heifers were generated over 4 years for Brahmans and 3 years for Composites. At weaning, heifers were allocated according

to sire and property of origin and transported to one of 4 research stations in Queensland. Brahmans were allocated to Belmont (Rockhampton), Swans Lagoon (Ayr) and Toorak (Julia Creek) while Composites were allocated to Brian Pastures (Gayndah), Belmont and Toorak. Brahmans and Composites were raised from birth as contemporaries only at Belmont. At each location all heifers weaned in the same year were managed as a single group (defined as a cohort) until mated as 2 year olds when they joined other cohorts in large multiple sire mating groups.

**Traits.** Specific traits studied are defined in Table 1 and were chosen based on their biological significance and the availability of sufficient records. Because of fluctuations in field parasite challenges, TICK and FLY were recorded when the heifers were mature cows while the other traits were recorded between 200 and 400 days of age.

**Table 1. Abbreviations and definitions of adaptive traits recorded**

Abbreviation	Definition
TICK	Tick score: 0 (no ticks), 1 (10 or fewer ticks), 2 (11 to 30 ticks), 3 (31 to 80 ticks), 4 (81 to 150 ticks), and 5 (more than 150 ticks per side) at ~3 yrs of age
EPG	Number of helminth eggs per gram of faeces recorded in spring at ~ 260 days of age when parasite challenge was highest
FLY	Buffalo fly lesion score: 1 (no visible lesions), 2 (one lesion $\leq$ 7 cm), 3 (4 to 6 lesions), 4 (multiple lesions on three sites such as neck, belly and withers), 5 (extensive lesions over most of the hide area); scored at ~3.5 yrs
TEMP	Rectal temperatures of animals recorded at ~ 400 days of age mid-summer when ambient temperature was $> 30^{\circ}\text{C}$
COAT	Coat score: 1 (extremely short and sleek coat) to 7 (very woolly coat); recorded mid-summer at ~ 360 days
FLIGHT	Flight time at ~ 300 days of age; electronically recorded time in seconds taken for an animal to cover a fixed distance (1.7 m) after leaving the weigh scales
NAVEL	Navel score: the amount of navel skin, scored 1 (very pendulous) to 9 (extremely tight against the underline) at ~ 260 days
COLOUR	Coat colour score: subjectively scored on a "grey-scale" from 1 (light) to 6 (dark); scored at ~ 260 days

**Statistical analyses.** Significant fixed effects were identified separately for each genotype using mixed model procedures in SAS (1991). Models included the effects of origin (one of 8 properties), cohort (combined effects of year weaned and location), dam age and calf month of birth (to account for age and season effects), and for Composites, sire and dam breed groups were included to account for varying levels of heterosis. Initial models included main effects and all two way interactions with sire as a random effect. For TEMP, time of recording was included to account for differences in ambient air temperature during the day. Non-significant terms were sequentially removed to yield the final models used for each trait. Similarly, significant fixed effects were identified for each trait using a combined dataset across genotypes with additional terms of genotype and all first order interactions considered. Phenotypic variances and trait heritabilities were estimated in univariate analyses using ASReml (Gilmour *et al.* 2005). Traits were analysed using an animal model which included the final

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fixed effects models identified above and random effects of animal and residual. There were 7910 animals in the pedigree file. TICK, FLY and FLIGHT were log transformed and EPG were cube-root transformed for variance component analyses to approximate normal distribution. The COAT trait, scored from 1 to 7 with plus and minus scores, was converted to a 21 point scale for variance component analyses to give a continuous gradation in COAT from sleek to woolly.

### RESULTS AND DISCUSSION

Genotype means for adaptive traits are presented (Table 2) for the heifers at Belmont where both breeds were raised as contemporaries for a valid breed comparison. Breed was a significant ( $P < 0.05$ ) source of variation for all traits measured and generally indicates an adaptive advantage to Brahmans. Despite significant breed differences, FLY means show that both breeds were not impervious to buffalo-fly irritation, and TEMP means indicate the ability of Composites to endure Belmont summer temperatures. FLIGHT was higher for Brahmans than Composites suggesting that Brahmans were more docile. The flight time of animals in the current study may have been affected by intensive pre-weaning handling when the heifers were yarded daily with their dams during AI programs. If so, the data indicate that the Brahmans adapted more favourably to continual human proximity.

**Table 2. Genotype least squares means for adaptive traits of heifers at Belmont**

Trait	Brahman		Composite	
	No. records	Mean (se)	No. records	Mean (se)
TICK	296	1.3 (0.12)	242	2.2 (0.11)
EPG	345	290 (63.4)	292	700 (57.5)
FLY	397	1.6 (0.05)	283	1.8 (0.07)
TEMP	227	39.3 (0.04)	157	39.4 (0.05)
COAT	345	1.7 (0.09)	293	2.3 (0.09)
FLIGHT	345	1.96 (0.048)	293	1.60 (0.054)
NAVEL	348	4.0 (0.18)	291	7.2 (0.15)
COLOUR	348	2.9 (0.08)	294	4.0 (0.08)

Phenotypic variance and heritability of the traits are summarised in Table 3. There was evidence of breed differences in phenotypic variance for some traits but the estimates of trait heritability were generally similar between genotypes and indicated potential for genetic improvement of most traits. TICK and FLY, traits which scored the prevalence of external parasites, had the lowest heritability possibly indicating that the subjective scoring systems for these traits are less reliable than the actual counts used in earlier studies (e.g. Burrow 2001). NAVEL and COLOUR are important breed characteristics but their relationship with tropical adaptation not fully understood. Excessively pendulous navel skin may pose reproductive and health problems in males (McGowan *et al.* 2002), while insufficient navel skin and hair colour may represent a lack of breed character in some breeds. The scored hide traits (COAT, NAVEL and COLOUR) were simple to measure and moderately to highly heritable. If these easily measured traits are genetically associated with adaptive traits more

difficult to measure (e.g. TEMP and EPG), then improvement of the latter could be made by indirect selection. Further analysis will be conducted to evaluate the genetic correlations among these adaptive traits and other production traits.

**Table 3. Phenotypic variance ( $V_p$ ) and direct heritability ( $h^2$ ) for genotypes at all locations**

Trait	Brahman			Composite			Breeds pooled		
	<i>n</i>	$V_p$	$h^2$ (se)	<i>n</i>	$V_p$	$h^2$ (se)	<i>n</i>	$V_p$	$h^2$ (se)
TICK*	659	0.018	0.15 (0.10)	242	-	-	901	0.018	0.13 (0.08)
EPG*	663	4.08	0.40 (0.12)	1090	3.48	0.28 (0.09)	1753	3.72	0.33 (0.07)
FLY*	913	0.033	0.14 (0.08)	1053	0.018	0.05 (0.05)	1966	0.025	0.12 (0.05)
TEMP	764	0.13	0.22 (0.10)	301	-	-	1064	0.15	0.21 (0.09)
COAT	828	2.19	0.63 (0.14)	947	5.62	0.64 (0.13)	1775	4.01	0.62 (0.09)
FLIGHT*	961	0.021	0.17 (0.07)	1100	0.015	0.31 (0.09)	2061	0.018	0.24 (0.06)
NAVEL	673	1.19	0.35 (0.12)	920	0.68	0.22 (0.11)	1593	0.91	0.33 (0.08)
COLOUR	966	0.71	0.61 (0.12)	1105	0.88	0.84 (0.14)	2071	0.79	0.70 (0.09)

\*Estimates on transformed data; *n*, number of records; genetic parameters not estimated where  $n < 600$

## CONCLUSION

Despite significant breed differences in the adaptive traits measured, the heritability of the traits indicates the potential for genetic improvement within both the Composite and Brahman populations.

## ACKNOWLEDGEMENTS

We gratefully acknowledge the contributions of Warren Sim, Paul Williams, Matt Wolcott, Mick Sullivan, Andrew McCann and research station staff for collecting and collating the data.

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