

FEMALE, MALE AND GENOMIC MEASURES FOR USE IN GENETIC SELECTION TO IMPROVE LIFETIME WEANING RATE OF BRAHMAN CATTLE

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SUMMARY

Female and male measures with potential to be practical, early-in-life genetic indicators of female reproduction in Brahmans were chosen from earlier reports and compared, along with genomic measures, for multi-trait use to improve Brahman lifetime annual weaning rate (*LAWR*). Results suggested substantial genetic gains in *LAWR* may be possible in 10 years using these measures, but need confirming in other data. Female hip height and coat score and male preputial eversion and liveweight were measures that could warrant wider recording for *LAWR* improvement. Recording of pregnancy test outcomes from matings 1 and 2 should also be encouraged. A genomic EBV in combination with other measures added to the gain in *LAWR*, but needed an accuracy approaching 60% to be the most important contributor to gains in the combinations of measures studied.

INTRODUCTION

Low reproduction limits productivity in Brahmans, a major beef breed of tropical environments including in Australia (Johnston *et al.* 2013a). In a larger study, Barwick *et al.* (2013) examined the potential of numerous early-in-life measures for multi-trait use as selection criteria to improve female reproductive performance of Brahmans. This report focuses on lifetime annual weaning rate (*LAWR*) and on the multi-trait use of only the potentially most practical measures for recording in harsh tropical environments. The basis for comparing measures was the estimated genetic gain in *LAWR* from selection. *LAWR* aligns with the weaning rate trait of beef cattle breeding objectives (Barwick and Henzell 2005). Estimates of the changes expected in the individual criteria contributing to the gains in *LAWR* are also presented.

METHODS

Definitions. *LAWR* and the female and male measures studied were from an experiment with Brahmans in northern Australia. Environments and management were described by Barwick *et al.* (2009), Corbet *et al.* (2013) and Johnston *et al.* (2013a). Females were by 54 sires and male progeny of the females by a further 60 sires. Females calved first at 3 years and were culled if they failed to wean a calf in any two consecutive years. *LAWR* was the average weaning rate of cows based on the number of annual mating opportunities they experienced over 6 possible matings.

The female and male measures studied were chosen for their potential to be both indirect genetic criteria for *LAWR*, based on earlier bi-variate analyses, and practical to be recorded by industry. Female adaptive measures were coat colour and navel score at 9 m of age, coat score (*COAT*) at 12 m and rectal temperature at 13 m, from Prayaga *et al.* (2009) and Wolcott *et al.* (2013a); female 18- and 24-m measures were liveweight and hip height (*HH18*, *HH24*), scanned fat depth (*SFAT18*) and eye muscle area at 18 m, from Barwick *et al.* (2009) and Wolcott *et al.*

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(2013b); mating 1 and 2 measures were pregnancy-test outcomes from mating 1 (*PREG1*) and 2 (*PREG2*) at 28 and 40 m, days to 1st calving (*DCI*) at 37 m, and success at both weaning a calf from mating 1 and being pregnant from mating 2 (*WIP2*) at 40 m, from Johnston *et al.* (2013a, 2013b); male non-semen measures were flight time at 6 m, rectal temperature at 12 m, scrotal size at 12 and 18 m, liveweight (LWT15), hip height, scanned fat depth, scanned eye muscle area and body condition score at 15 m, sheath score and preputial eversion (EV) at 18 m, from Corbet *et al.* (2013) and Johnston *et al.* (2013b); and semen measures were sperm mass activity score, sperm progressive motility (MOT) and percent normal sperm at 18 m, from Corbet *et al.* (2013) and Johnston *et al.* (2013b). Genomic measures examined were genomic EBVs for *LAWR* of 30, 40 or 60% accuracy (GEN30, GEN40, GEN60) based on genotyping of males, and genomic EBVs for selected other measures of 40% accuracy. Female measures are shown in italics throughout this report; male measures are not italicised.

Evaluation of measures. Genetic gains were estimated assuming index selection across the four pathways of Rendel and Robertson (1950). Step-down analyses systematically eliminated measures that contributed least to the estimated gain in *LAWR* while retaining those contributing 5% or more of the gain. Analyses were conducted in blocks, with retained measures carried forward to be considered with other measures. Inbreeding and other contributors to long-term response were not considered. Estimates were adjusted to gains per 10 yrs for presentation and should be viewed as approximations of the selection gains in Brahmans that may be possible.

Parameters. These were based on bi-variate estimates from Barwick *et al.* (2009), Johnston *et al.* (2009), Prayaga *et al.* (2009), Corbet *et al.* (2013), Johnston *et al.* (2013a, 2013b) and Wolcott *et al.* (2013a, 2013b). For positive definite matrices it was necessary to reduce genetic correlations with *LAWR* to approximately 70% of their bi-variate values. This reduction was applied to all measures except genomic EBVs, which were retained at their assumed accuracies. Derivations of genomic EBV variances and genetic and phenotypic correlations involving genomic EBVs are described by Barwick *et al.* (2013). Zero environmental correlations were assumed, including between female and male measures. The genetic standard deviation for *LAWR* was 0.0877 (Johnston *et al.* 2013a).

Selection accuracies and correlated responses. Calculation of accuracies and correlated responses used MTIndex of J. van der Werf and assumed animals had a parent record, 20 half-sib records and their own record (depending whether selection was of sires or dams) for all measures.

Selection intensities. The selection described was for a Brahman population of 13000 cows and assumed a concerted selection effort could be made across the breed (Barwick *et al.* 2013). Sires to breed sires were the top 20 of 2000 (1%; $i = 2.665$), sires to breed dams the top 135 of 2000 (6.75%; $i = 1.9345$), dams to breed sires the top 800 of 8000 (10%; $i = 1.755$), and dams to breed dams the top 3800 of 4000 (95%; $i = 0.1086$). These levels were used to estimate genetic gains for comparing all combinations of measures. For the identified best combinations, estimated gains were also calculated assuming no selection of dams.

Generation intervals. The age structure assumed was derived from Brahman industry data and included cow calving age groups of from 3 to 13 years. Generation interval (L) was the average age of selected parents at the birth of progeny. For direct selection on *LAWR* (requiring outcomes from 6 matings) L 's for breeding sires and dams were 10.88 and 11.32 years. These were respectively 6.49 and 6.93 years for selection on *PREG2* or *WIP2*, 6.07 and 6.07 years for selection on *PREG1* or *DCI*, and 5.70 and 5.26 years for selection on any of the other measures considered. For selection on a combination of measures, L 's were decided by the last available measure.

RESULTS AND DISCUSSION

Results suggested substantial gains in *LAWR* may be possible in Brahmans from multi-trait selection on a best combination of practical, early-in-life measures. The estimated gains in *LAWR* in 10 years from this were 8 to 12% from sire selection and 12 to 15% (i.e. 0.12 to 0.15 calves weaned/cow) from selection of sires and dams (Table 1). Gains using combinations of measures were greater than using individual measures and greater than for direct selection. Gains from selection on individual genomic EBVs for *LAWR* were 0.066, 0.089 and 0.133 calves weaned/cow for GEN30, GEN40 and GEN60. Gains using an individual genomic EBV for a correlated trait were considerably less; and the gain using an individual fatness measure (*SFAT18*) was small.

Female *HH24* (and *HH18*) and *COAT* and male *EV* and *LWT15* were among the most important measures of combinations (Table 1) and may warrant wider industry recording. Greater *HH24* and lower *LWT15*, less preputial eversion and a sleeker coat were preferred for *LAWR*. *COAT* was also most important for reducing female age at puberty (Barwick *et al.* 2013). The estimated changes in individual criteria and in *LAWR* (Table 1) for measurement combinations 1) and 5), respectively, represented rates of gain of 0.08, 0.10, 0.03, 0.09 and 0.14 genetic standard deviations per year for *HH24*, *EV*, *LWT15*, *COAT* and *LAWR*, and 0.24, 0.12, 0.09 and 0.18

Table 1. Combinations of female, male and genomic measures giving the greatest estimated genetic gain in lifetime annual weaning rate (*LAWR*, calves weaned/cow) in Brahmans from selection of sires and dams, for differing categories of measures available^{1,2}. Also shown are the estimated 10 year gains in *LAWR* and the associated changes in each of the measures

Measures	Estimated change	Measures	Estimated change	Measures	Estimated change
<i>1) Female + male non-semen</i>		<i>2) Female + male</i>		<i>3) Female + male + GEN30</i>	
<i>HH24</i> (cm)	2.1	<i>HH24</i> (cm)	2.3	<i>HH24</i> (cm)	2.7
<i>EV</i> (mm)	-11.2	<i>EV</i> (mm)	-10.2	<i>EV</i> (mm)	-9.1
<i>LWT15</i> (kg)	-4.0	<i>MOT</i> (%)	12.6	<i>MOT</i> (%)	11.3
<i>COAT</i> (score)	-1.1	<i>LWT15</i> (kg)	-4.9	<i>GEN30</i> ³	0.035
		<i>COAT</i> (score)	-1.2	<i>LWT15</i> (kg)	-4.9
<i>LAWR</i> :	0.123	<i>LAWR</i> :	0.132	<i>LAWR</i> :	0.136
<i>4) Female + male + GEN40</i>		<i>5) Female + male + GEN60</i>			
<i>HH24</i> (cm)	2.8	<i>GEN60</i> ³	0.124		
<i>GEN40</i> ³	0.058	<i>HH24</i> (cm)	3.3		
<i>EV</i> (mm)	-9.3	<i>COAT</i> (score)	-1.1		
<i>MOT</i> (%)	11.6				
<i>LWT15</i> (kg)	-4.9				
<i>LAWR</i> :	0.143	<i>LAWR</i> :	0.154		

¹See earlier text for details of measures in each category. 'Female' & 'male' include relevant sub-categories.

²Combinations are the end result of step-down analyses of the estimated genetic gain. All lists show measures in their order of greatest importance to genetic gain. Female measures are italicised, male measures are not.

³GEN30, GEN40 and GEN60 are genomic EBVs for *LAWR* of 30, 40 and 60% accuracy, respectively. genetic standard deviations per year for GEN60, *HH24*, *COAT* and *LAWR*. Semen *MOT* added to gains when it was available. Adding *PREG1* and *PREG2* increased accuracies but not gains, as *L*'s were increased. Industry recording of *PREG1* and *PREG2* should be encouraged; pregnancy testing is commonly practiced and the marginal cost of the recording would be small. A genomic

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EBV for *LAWR* added to gains especially at an accuracy of 40% but needed an accuracy approaching 60% to be the most important measure of combinations (Table 1).

The results need confirming since they depend on many estimates and step-wise procedures are susceptible to bias. The results may apply only to Brahmans or perhaps to *Bos indicus*. The genetic relationships utilised for hip height and liveweight with *LAWR* in the Brahman (Wolcott *et al.* 2013b), in particular, need confirming. Measures were also considered separately between the sexes, which meant there was little opportunity for a measure to be important in both sexes. Where this separation can be relaxed, the gains may be greater.

CONCLUSIONS

Results need confirming but suggested substantial genetic gains in *LAWR* may be possible in Brahmans from selection on combinations of practical, early-in-life measures. Female *HH24* (or *HH18*) and *COAT* in females and male EV and LWT15 are measures that could warrant wider recording for this purpose. Recording of *PREG1* and *PREG2* should also be encouraged. A genomic EBV in combination with other measures added to gains, but would need to have an accuracy approaching 60% to be the most important individual contributor to gains in the combinations of measures studied.

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