ANIMAL SCIENCE IN AUSTRALIA

Proceedings of the Australian Association of Animal Sciences

Volume 34

Anchoring knowledge – exploring the animal science ecosystem

34th Biennial Conference

Pullman Cairns International Hotel, Cairns, Queensland
5–7 July 2022

Poll genotype or phenotype are not associated with growth performance in tropical beef breeds

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Increasingly the northern beef industry is selecting for more polled animals. However, a common industry perception is this selection will be associated with decreased performance. Single trait selection for any trait can lead to genetically inferior animals and this could occur if selection was only to occur for polled. From a selection viewpoint it is important to establish if the polled locus is genetically linked to other economically important traits. The recording and design of the Repronomics project (Johnston *et al.* 2017) provides a unique dataset to examine the association between polled status (both genotypic and phenotypic) and early growth traits. This was achieved by analysing the effects of polled status within large half sib-families where the polled gene is segregating in 3 tropically adapted beef breeds (*viz.* Brahman, Droughtmaster and Santa Gertrudis).

Data analysed was a subset of the Repronomics project (N = 3,493) representing 2016–2020 calf drops from the Department of Agriculture and Fisheries (DAF) research herds (*viz.* Brian Pastures and Spyglass Research Facilities) that had both DNA polled/horn genotype (i.e. GENO = HH, PH, PP) and horn status phenotype (i.e. HORN = horned, polled, scurred) recorded at branding (approximately 3-4 months of age). Horns and scurs were removed and males castrated at the branding event. Growth traits analysed included birth weight, branding weight, post-branding weight gain, weaning weight, 400 d weight and postweaning average daily gain. At weaning all heifers and steers were split and managed in separated groups.

Statistical analyses were performed using SAS (SAS Institute Inc. Cary, NC, USA). For each trait the base model included fixed effects associated with the experimental design: cohort (i.e. location, year), dam age, birth month and sex. The base model was run including the effect of GENO (3 levels) and a separate model including the effect of HORN (3 levels). Each model included a term for sire nested within the effects of GENO and HORN as a random effect. This term was used in the denominator (instead of error term) as a test of significance for the GENO and HORN effects.

Table 1. Significance and least squares means for GENO, HORN and SEX effects on early growth traits in tropical beef breeds

Effect	Level	Least squares means					
		Birth weight (kg)	Branding weight (kg)	Post branding gain (kg)	Weaning weight (kg)	Postweaning ADG (kg/d)	400 d weight (kg)
GENO	HH	33.7	124.7	57.6	182.2	0.38	282.7
	PH	33.7	125.1	59.6	185.1	0.39	286.4
	PP	34.7	123.8	60.8	184.0	0.39	289.0
	P-value	0.30	0.85	**0.06**	0.31	0.53	0.26
HORN	HORNED	33.6	124.1	57.7	181.9	0.38	281.9
	POLLED	33.7	122.8	59.6	182.4	0.39	284.2
	SCURRED	33.4	126.6	59.7	185.9	0.38	286.0
	P-value	0.87	0.22	0.14	0.29	0.71	0.40
SEX	Heifer	32.7	119.4	58.5	177.9	-	-
	Bull/Steer	35.4	129.7	60.1	189.6	-	-
	P-value	**<0.0001**	**<0.0001**	**<0.0001**	**<0.0001**	-	-

Table 1 presents test of significance and least squares means estimates for the effects of GENO and HORN, and for comparison, the effect of sex. The GENO and HORN effects were not significantly associated with early growth traits in our data. The only exception was post branding weight gain (to weaning), where the GENO effect was trending towards significant ($P < 0.06$) and to a lesser extent for the HORN effect ($P = 0.14$). The LSM shows animals with HH genotype had a 2–3 kg lower post-branding weight gain compared to PH and PP animals. Large differences were observed between the sexes for all traits and LSMs showed birth and branding weights of (entire) males were heavier than heifers but the differences were reduced post branding suggesting effect of castration and/or lower hormone production reduced steer performance compared to the heifers. Further analyses can be undertaken using the same data to investigate possible effects on other traits and there is potential to examine the genomic structure on these data using high density SNP panels and whole genome sequence data.

This study has shown that selection can occur for either genotypic or phenotypic polled status without influencing growth performance however the genetic merit of selection candidates should be assessed separately using growth EBVs.

Reference

Johnston DJ *et al.* (2017) The Repronomics Project – Enabling Genetic Improvement in Reproduction in Northern Australia. In 'Proceedings of the 22nd AAABG Conference', Townsville, Qld, Australia. **22**, 385–388.