ADDRESSING SCUR PHENOTYPING CHALLENGES WITH THE SOUTHERN MULTI-BREED PROJECT

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SUMMARY

The genetic basis of polled or horned phenotypes in beef cattle is now well documented, however horned animals will continue to be born in the national herd for some time. Animal welfare will continue to be compromised due to the need to dehorn animals with horn buds. While scurs don't necessarily require removal, the inability to distinguish between horned or scurred animals at the age of dehorning mean they are dehorned nonetheless. Targeted breeding of polled herds in industry is increasing with genetic poll tests available, but without understanding the genetic basis of scurs, horn buds and thus dehorning practices will remain. The difficulty in identifying the genetic basis of scurs remains the lack of a reference population with accurate phenotypes, driven largely by the difficulty in phenotyping horns and scurs at usual dehorning age. This paper describes the challenges and preliminary results of a phenotyping project using the Southern Multibreed project herd, which will form a reference population with poll/horn/scur phenotypes, accompanied by full pedigree recording and genomics data.

INTRODUCTION

Carcase bruising from horns is estimated to cost the Australian meat industry $30 million per year (CSIRO 2014). These economic losses promote the accepted management practice of horn bud removal (i.e. dehorning) at an early age (less than 6 months) (Medugorac *et al.* 2012). However, dehorning can still lead to economic losses due to wound healing, translating into short term weight loss and increased mortality rates (Prayaga 2007; Bunter *et al.* 2013). Despite being commercially necessary, dehorning procedures are painful. The increasing importance of social license in agriculture and the impact dehorning has on animal welfare may see less acceptance of these practices in the future (Williams and Page 2014). The alternative to dehorning horned cattle is to breed polled cattle.

Horns in cattle form as a free-floating bud, which later fuses to the skull as a fixed bony extension, while scurs appear as small and only loosely attached horns, and polled cattle are naturally hornless (Seichter *et al.* 2012). While polled breeding is now targeted in industry, scurred animals will remain in the population until scur genetics are understood, requiring continued dehorning practices due to the inability to distinguish between horned or scurred cattle at the time of dehorning.

The genetic basis of polled cattle is now largely accepted as an autosomal dominant trait (Mariasegaram *et al.* 2010; Medugorac *et al.* 2012; Seichter *et al.* 2012; Rothammer *et al.* 2014; Utsunomiya *et al.* 2019) with two alleles (Celtic P_C, and Friesian P_F) forming the basis for genetic testing enabling direct selection for polledness. The genetic basis for horns is the absence of any polled alleles, while the genetic basis of scurs appears to be more complex. The inheritance model initially proposed was that scurs is a sex-influenced trait characterized by two alleles, Sc (scurs)

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and sc (no scurs), where one Sc in males results in scurs, while females require two Sc alleles to be scurred (White and Ibsen 1936). Due to growth in the same head position, horns mask the expression of scurs; it is proposed that homozygous polled alleles also inhibit scur growth, unless the animal also possesses homozygous scur alleles (Sc/Sc) (Long and Gregory 1978). More recent studies have offered varied and contradicting conclusions on scur genetics, including as autosomal recessive and not sex-influenced (Capitan *et al.* 2009), mapped to bovine chromosome 19 (Asai *et al.* 2004), autosomal dominant inheritance mapped to chromosome 4 (Capitan *et al.* 2011), and oligogenic and age-dependent penetrance (Gehrke *et al.* 2020). Additionally, studies have shown the diversity in scur phenotypes, with small scabs and scaly patches, to tiny loose buds, to long pendulous loose horns, along with differences in head shape and bumps (Capitan *et al.* 2011; Gehrke *et al.* 2020).

One dimension of the complexity of scur studies lies in the difficulty of obtaining accurate phenotypes, given the variation due to age and breed, and the need to adjust management to enable recording prior to dehorning to avoid misclassification. Furthermore, the number of scurred animals in the population is relatively unclear for similar reasons. Observations from the Australian microsatellite haplotype poll test showed scur phenotype rates of approximately 5% (Connors *et al.* 2018); however phenotypes were industry supplied and subject to bias (Connors *et al.* 2019). Most studies on scurs have been performed in the absence of poll genetic testing, which can clarify an animal's horn genetics in addition to its phenotype. Additionally, obtaining large numbers of phenotypes has been performed within dairy breeds rather than beef breeds, likely due to the differences in management practices. Here, preliminary findings of a beef cattle poll/horn/scur phenotyping study using the Southern Multibreed Project (Walmsley *et al.* 2021) as a reference population are presented. While this study is preliminary, this paper will set the scene for the establishment of a reference dataset of multibreed populations with full pedigree recording, poll genetic testing, SNP genotypes, and phenotypes at marking and when older, for generations.

MATERIALS AND METHODS

The Southern Multibreed Project has cattle populations at five sites across NSW, including Trangie Agricultural Research Centre (TARC), Grafton Primary Industries Institute, Glen Innes Agricultural Research & Advisory Station, Elizabeth Macarthur Agricultural Institute, and Tocal Agricultural Centre. Each site has varied cattle populations in number and breed, which includes Brahman, Charolais, Shorthorn, Angus, Hereford, and Wagyu, and some Brahman-Hereford and Brahman-Angus F1 crossbreds. Calves at each site were marked at age 8-12 weeks, along with horned/polled/scurred phenotypes, sex, and breed recorded. Phenotypes were classified as the following:

(i)   smooth poll cone = no buds, smooth poll, pointed cone shape of skull;
(ii)   poll broad cone = no buds, smooth poll, broad cone shape of skull;
(iii)   poll = no buds, smooth poll, flatter shape of skull (i.e. no cone);
(iv)   poll frontal bumps = no buds, poll, bumps felt on skull;
(v)   buds = small keratin buds present (diameter measured);
(vi)   horns = small keratin horns present, >3cm length (diameter measured);
(vii)   scurs = scaly, scabby patches, no keratin (diameter measured).

Each animal was photographed and the skull was palpated for head shape and to ensure buds were felt beneath longer coats; horns were already of considerable length such that they are seen through the coat. Buds, horns and scurs were measured in diameter at the skull. Data was recorded manually on-site, entered into Excel afterwards, and cross-checked with project records.

RESULTS AND DISCUSSION

The number of animals phenotyped in this study was 1309, consisting of 646 male and 663 female calves. The phenotypes recorded are summarised in Table 1, and examples of the phenotypes

are pictured in Figure 1. Simply, the number of polled animals was 985, buds/horned was 298, and 26 scurs. The majority of the scurred phenotypes were observed in crossbred calves, which may indicate an effect of the indicus lines on scur development. All but four Wagyu calves had buds or horns, and all Angus calves were polled. Differences in horn growth between sexes is difficult to determine at this early stage, though of note are the number of horned calves compared to budded calves for Wagyu and Hereford, with more males phenotyped as horned (i.e. longer growth) suggesting males grow horns quicker than females, and agreeing with current anecdotes of the horn growth-promoting effects of testosterone. The number of scurs in males and females appears to be similar, showing no agreement with current theory of sex-influenced genetics. It is important to note possible scabby patches phenotyped as scurs may have grown into buds over time, testament of the difficulty in phenotyping. Further observation of these calves will be performed at weaning to determine any late scur/bud growth in poll phenotyped animals. With poll genomic testing now common, testing calves at birth may enable informed disbudding choices, by only disbudding genetically horned calves, which would leave scur phenotypes to grow over time.

Table 1. Summary of phenotypes for each breed and sex

Breed	Sex	Phenotypes							
		Smooth Poll Cone	Poll Broad Cone	Poll	Poll Frontal Bumps	Buds	Horns	Scurs	Total
Angus	F	201		6	1				392
	M	173	9	2					
Brahman	F	6		1		4	8	2	41
	M	4		3		7	3	3	
Charolais	F	26	14	2	2	12	1		115
	M	9	19	10	5	15			
Hereford	F	109	9	12	1	15	3	1	299
	M	68	11	22	18	12	14	4	
Shorthorn	F	82	4	1	2	2			182
	M	62	13	4	4	5	3		
Wagyu	F	2			2	83	5		184
	M					61	31		
Cross	F	23		1	4	3	4	9	96
	M	21		7	10	7		7	
Total		786	79	71	49	226	72	26	1309

Figure 1. Phenotype examples. (a) smooth poll cone, (b) scur, (c) buds, and (d) horns

CONCLUSIONS

This study describes the preliminary findings of phenotype collection for potential scur research. The population had good distribution of phenotypes across breed and sex. Genotypes on calves and parents, including poll genotype, will be available later in the year where concordance of genotypes

and phenotype can be analysed. Use of the Southern Multibreed project as a reference population will provide generations of phenotype, genotype, and pedigree across multiple breeds, for further analysis of the complex scurs trait.

ACKNOWLEDGEMENTS

REFERENCES
Asai M., Berryere T.G., Schmutz S.M. (2004) *Anim Genet* **35:** 34.

Bunter K.L., Johnston D.J., Wolcott M.L., Fordyce G. (2013) *Animal Production Science* **54:** 25.

Capitan A., Grohs C., Gautier M., Eggen A. (2009) *Bmc Genetics* **10:**

Capitan A., Grohs C., Weiss B., Rossignol M.N., Reversé P., Eggen A. (2011) *PLoS One* **6:** e22242.

Connors N.K., Banks R.G., Johnston D.J. (2019) *Proceedings of the 23rd Conference of the Association for the Advancement of Animal Breeding and Genetics* 330.

Connors N.K., Tier B., Johnston D.J. (2018) Current status of Australia's diagnostic poll haplotype test. In 'Proc. World Congr. Genet. App. Livest. Breed. Volume 11 pp. 344.

CSIRO (2014) Annual Report 2013-2014. New Millenium Print. Available at www.csiro.au/annualreport2014.

Gehrke L.J., Capitan A., Scheper C., König S., Upadhyay M., Heidrich K., Russ I., Seichter D., Tetens J., Medugorac I., Thaller G. (2020) *Genetics Selection Evolution* **52:** 6.

Long C.R., Gregory K.E. (1978) *Journal of Heredity* **69:** 395.

Mariasegaram M., Reverter A., Barris W., Lehnert S.A., Dalrymple B., Prayaga K. (2010) *Bmc Genomics* **11:**

Medugorac I., Seichter D., Graf A., Russ I., Blum H., Göpel K.H., Rothammer S., Förster M., Krebs S. (2012) *PLoS One,* **7:** e39477.

Prayaga K.C. (2007) *Australian Journal of Agricultural Research* **58:** 1.

Rothammer S., Capitan A., Mullaart E., Seichter D., Russ I., Medugorac I. (2014) *Genetics, selection, evolution : GSE* **46:** 44.

Seichter D., Russ I., Rothammer S., Eder J., Forster M., Medugorac I. (2012) *Animal Genetics* **43:** 595.

Utsunomiya Y.T., Torrecilha R.B.P., Milanesi M., Paulan S.C., Utsunomiya A.T.H., Garcia J.F. (2019) *Anim Genet* **50:** 187.

Walmsley B.J., Donoghue K.A., Johnston D.J., Clark S.A., Siddell J.P., Walkom S.F., Granleese T., Arthur P.F. (2021) *Proc. Assoc. Advmt. Anim. Breed. Genet. 24: These Proceedings.*

White W.T., Ibsen H.L. (1936) *J Genet.* **32:** 33.

Williams S., Page S. (2014) B.AWW.0189 Final Report: Literature review of pain and welfare impacts associated with on-farm cattle husbandry procedures. Meat & Livestock Australia Limited, North Sydney, NSW.