INITIATING THE SOUTHERN MULTI-BREED RESOURCE POPULATION

B.J. Walmsley[1,2], K.A. Donoghue[3], D.J. Johnston[1], S.A. Clark[4], J.P. Siddell[2], S.F. Walkom[1], T. Granleese[5] and P.F. Arthur[6]

[1]Animal Genetics and Breeding Unit[*], University of New England, Armidale, NSW, 2351
[2]NSW Department of Primary Industries, Livestock Industries Centre, Armidale, NSW, 2351
[3]NSW Department of Primary Industries, Agricultural Research Centre, Trangie, NSW, 2823
[4]School of Environmental and Rural Science, University of New England, Armidale, NSW, 2351
[5]NSW Department of Primary Industries, Grafton Primary Industries Institute, Grafton, NSW, 2460
[6]NSW Department of Primary Industries, Elizabeth MacArthur Agricultural Institute, Menangle, NSW, 2568

SUMMARY

This paper describes the first year of a large 5-year breeding project being conducted across New South Wales involving five temperate beef breeds and the Brahman breed. Artificial insemination and back-up matings were designed to produce progeny that are representative of the genetic diversity in the national herd of each breed. Sires and dams were selected with a focus on high accuracies for the 400-day weight estimated breeding value (EBV) and reproduction EBVs. The project progeny will be managed in mixed-breed groups and intensively recorded head-to-head for current BREEDPLAN and new economically important traits such as early-in-life female reproduction and worm egg counts. All animals will have high density SNP genotypes taken to contribute to the breeds' genomic reference populations and for inclusion in BREEDPLAN genomic evaluations. The project design will facilitate development of genomic EBVs to allow across-breed comparisons, assist in increasing selection accuracy, particularly for young bulls, allow genotype by environment (*GxE*) investigations, and the potential development of new traits.

INTRODUCTION

Significant profitability gains have been generated in temperate Australian beef breeds through selection using EBVs and indexes (Swan et al. 2011). Currently, the EBVs, and the selection indexes they drive, are generated from within-breed genetic evaluations (Graser *et al.* 2005), limiting the capacity to compare animals across breeds. To overcome this, breeds must be managed, and performance recorded for these traits, on a head-to-head basis to facilitate the development of EBVs that allow for across-breed comparisons. Reproduction is one such trait that is of importance in indexes producing replacement heifers, but it has been poorly recorded (Gudex and Millen 2019). Recent studies (Wolcott *et al.* 2019; 2021) have also found only c.50% of heifers in key Hereford and Angus seedstock herds were pubertal prior to synchronisation for fixed time artificial insemination (AI). These findings suggest that given the increasing prevalence of AI, there is a need to monitor the capacity of temperate breed heifers to conceive early in their first mating season as a trait for inclusion in genetic evaluations. A new project (MLA *P.PSH.1261*) is being conducted over the next 5 years (2020 to 2025), known as the Multi-Breed Genomic Beef Cattle Resource or Southern Multi-Breed (SMB) project which aims to address these issues. This project will extensively phenotype progeny from temperate beef breeds and Brahmans, managed in mixed-breed groups at sites across NSW for existing BREEDPLAN and new economically

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important traits, such as early-in-life reproduction. The project has been designed to have links to past and current genetic research in Australia including the Repronomics[TM] project (Johnston *et al*. 2017). The project will genotype all sires, dams and progeny to capture the benefits of genomic evaluations (Johnston *et al*. 2018), particularly for hard-to-measure and new traits. This paper provides a brief description of the experimental design and current progress of the project.

LOCATIONS AND BREEDS

The research project is being conducted on New South Wales Department of Primary Industries (NSW DPI) and University of New England (UNE) research facilities. To reflect the diversity of production environments in southern Australia across years, the breeding herds are located on 5 NSW DPI research properties dispersed across NSW (Trangie Agricultural Research Centre, Trangie; Grafton Primary Industries Institute, Grafton; Tocal Agricultural Centre, Tocal; Glen Innes Agricultural Research and Advisory Station, Glen Innes; Elizabeth MacArthur Agricultural Institute (EMAI); Menangle). All steer progeny will be backgrounded prior to feedlot entry at 2 NSW DPI research properties (EMAI; Duck Creek Agricultural Field Station, Ballina) with feedlot finishing occurring at the UNE research feedlot, "Tullimba" (Kingstown). The project includes the 5 numerically largest temperate breeds (*viz.* Angus, Charolais, Hereford, Shorthorn and Wagyu) in southern Australia and the Brahman breed, which is commercially important in the sub-tropical regions of NSW and creates linkage to the Repronomics project. At all locations, the breeds are being managed and recorded in mixed groups.

FEMALE SELECTION

Base females were purchased from key industry seedstock herds. Angus females from the BREEDPLAN recorded NSW DPI muscling (Walmsley and McKiernan 2011) and feed efficiency selection (Herd *et al*. 2014) herds were also retained. All females were only purchased if they were pedigree and performance recorded in BREEDPLAN. The objective was to capture, as closely as possible, the genetic diversity of that breed's national herd, with a focus on dams from sire lines of high current impact. There was also a focus on selecting females with high accuracy and diversity for the 400-day weight and reproduction EBVs; days-to-calving (Angus, Brahman, Hereford and Shorthorn) or scrotal size (Charolais and Wagyu). A visual inspection of females was conducted to assess structural soundness and maximise the chances they would produce 2 calves in the project. Females were allocated to research sites based on the site's carrying capacity, the availability of females, the breed's relevance to the local environment (e.g. Brahman cows are only present in the sub-tropical environment at Grafton) and the numbers of each breed required to provide meaningful comparisons. Angus females are used to link sites because not all breeds can be accommodated at all sites. Table 1 contains the number of base females at each research site.

Table 1 Allocation of base females to the five NSW DPI research sites

Site	Angus	Brahman	Charolais	Hereford	Shorthorn	Wagyu	Total
Trangie	75			67		66	208
Grafton	139	201		157			497
Tocal	104		75		105		282
Glen Innes	64			59		44	167
EMAI	105		121	90	122	116	554
Total	490	201	144	373	227	226	1661

SIRE SELECTION

Sires selected included both AI sires nominated by industry and those selected to provide direct linkage to past research, such as the Beef CRC and Beef Information Nucleus projects. In addition, natural mate back-up bulls were purchased by NSW DPI from key industry seedstock herds or Repronomics project (Johnston *et al*. 2017) bulls were purchased from the Queensland Department of Agriculture and Fisheries. All bulls were pedigree and performance recorded in BREEDPLAN. Sire purchasing was a key design feature of the project to achieve representation of each breed's genetic diversity. There was a preference toward sire lines of influence that will shape the future makeup of the breed. Although not a primary objective, poll status was also taken into consideration. Straightbred matings will primarily occur with a small numbers of crossbreed matings at Grafton involving Brahman reciprocal matings to Angus and Herefords (i.e. BxA, AxB, BxH and HxB). Currently, ~290 sires have been used during the AI programs or as back-up sires in 2019 and 2020 with either calves weaned, or successful pregnancies diagnosed. Walkom *et al*. (2021) provide a brief description of the MateSel procedure used for allocating matings based on coancestry to limit inbreeding, with a small amount of emphasis placed on the index.

PROGENY GENERATED

The project aims to generate up to 8,000 progeny managed in mixed-breed contemporary groups. Currently, the project has generated ~1400 calves from the 2019 matings with ~1500 diagnosed pregnancies from the 2020 matings. All progeny will be retained within the project and recorded until the steers are slaughtered or the females are surplus to requirement. The female progeny will be retained and grown out at each research site prior to joining the breeding herd as maidens at ~15 months of age with natural matings to sires of their own breed. These females will also be naturally mated to sires of their own breed as first-lactation cows and will be retained in their respective herds for a minimum of 3 matings. The male progeny will be castrated at marking and following weaning will be transported to 2 research sites (EMAI, Duck Creek) to undertake backgrounding until they reach feedlot entry weights. The steers will then be feedlot finished for a minimum of 100 days at the UNE Tullimba feedlot prior to slaughter.

KEY TRAIT RECORDING

All calves generated by the project will be recorded intensively from birth to the end of backgrounding (steers)/grow-out (heifers). Recording will include accurate recording of birth date, birth weight, calving ease and survival, gestation length (AI calves only), weaning weight, flight time, docility score, yearling weight, and structure. Other traits, such as worm egg count, will be recorded regularly beginning at weaning and continuing until the steers enter Tullimba feedlot and the heifers wean their first calf. Horn/poll assessments will be conducted on all calves at marking, with monitoring continuing while animals are involved in the project (Connors *et al*. 2021). Following weaning, the heifer progeny will have regular ovarian assessments conducted using real-time ultrasound performed by highly skilled ultrasonographers to determine follicle development, and, in particular, identify the presence of a corpus luteum as a measure of puberty. All first-lactation cows will be regularly scanned after calving to determine their return to oestrous. Females will have live weight, hip height, body condition score, eye muscle and subcutaneous fat depth recorded prior to mating and at weaning each year, and will be assessed for calving ease, teat and udder score at calving. Steer progeny will have weight and scan traits, as well as net feed intake, recorded while in Tullimba, with full abattoir, meat quality and consumer testing undertaken following slaughter. All BREEDPLAN traits will be quality checked and loaded into ABRI's southern multi-breed research database.

ANIMAL GENOTYPING

The implementation of single-step GBLUP (Johnston *et al*. 2018) represents a major evolution of the BREEDPLAN genetic evaluation system. To capture the benefits of these developments and extract full value from the investment in this project, all animals will be genotyped in alignment with BREEDPLAN (Connors and Ferdosi 2019). All base females have been DNA sampled and will be genotyped as a minimum with a 50K SNP chip. All current back-up and AI sires have been DNA sampled for genotyping. A group of 51 AI sires across all breeds have been selected based on the number of calves they produced from the 2019 AI program for full genomic sequencing at 10x coverage for inclusion in the 1000 Bull Genomes Project (Hayes and Daetwyler 2019). All SNP data will be quality checked, stored on a project database and loaded into ABRI's southern multi-breed research database.

CONCLUSIONS

The project is currently in the first 12 months of operation with all base females having been purchased and allocated to research sites. These females have undergone AI and back-up mating programs in 2019 and 2020 to ~290 different sires across the six breeds. The intensive recording of project-generated progeny is underway with the first ~1400 calves recorded at calving in 2020 and weaning in 2021. The recording of breeds on a head-to-head basis represents a significant industry and government investment which will allow genetics to be compared across environments and provide a resource to benchmark reproduction and other traits across-breeds, including hard-to-measure traits. As such, the project will enable stronger selection for those traits contributing to value chain profit.

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