

USING MATESEL TO AID SIRE ALLOCATION IN GENOMIC REFERENCE POPULATIONS – SOUTHERN MULTI-BREED AN EXAMPLE

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SUMMARY

The Southern Multi-breed project has been designed to generate data that will allow producers across Australia to directly compare bulls of different breeds via BREEDPLAN EBVs. The project incorporates six breeds (Angus, Hereford, Wagyu, Charolais, Shorthorn and Brahman) at five research sites across New South Wales. The following paper describes how the MateSel software was used to assist selection and allocation of sires within the project, to provide linkage across sites and years and minimise inbreeding within progeny.

INTRODUCTION

Genetic improvement is important to improve productivity and the competitive advantage of the Australian beef cattle industry (Swan *et al.* 2012). The BREEDPLAN genetic evaluation for the Australian beef industry delivered as breeds each having their own analysis. The Southern Multi-breed (SMB) project has been developed to form a multi-breed reference population for genetic evaluations and aims to generate data enabling direct comparisons between animals of different breeds. This multi-breed, multi-herd project includes the five most common temperate breeds (Angus, Hereford, Wagyu, Charolais, Shorthorn) along with Brahman to establish linkage to similar projects in Northern Australia (Repronomics; Johnston *et al.* 2017). By the end of the project, hard to measure phenotypes, including female reproduction (puberty, post-partum anoestrous) and genotypes will be collected on c. 2000 cows per year plus followers. Walmsley *et al.* (2021) presents a comprehensive summary of the SMB project.

The inclusion of DNA information into genetic evaluation, often termed genomic selection, has the potential to increase the rate of genetic improvement in many livestock species. Models that incorporate both genomic and pedigree information (single-step GBLUP) have already been implemented into Australia's BREEDPLAN genetic evaluation system for beef cattle (Johnston *et al.* 2018). To capture all of the potential value genomic selection presents, genomic reference populations should have a low average relationship between the reference animals and yet the relationship between the reference population and the animals being evaluated is high (Clark *et al.* 2012). Genetic and genomic evaluations have traditionally been limited to within single breed populations like Angus or Hereford (Boerner 2017). The collection of genotypes and phenotypes within the SMB will assist to underpin future BREEDPLAN multi-breed evaluations, and increase the accuracy of current genomic EBVs.

The most efficient design for a multi-site or multi-contemporary group (cg) projects is to have every sire represented in every cg, and the sires to be as diverse as possible. Physical restraints mean that this is difficult to achieve, as with comparisons across herds for the national evaluations, the ability to utilise information across research sites is reliant on genetic linkage across research sites,

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breeds and contemporary groups (Graser *et al.* 2005). Consequently, selection of the sires and base dams within the SMB project should capture the diversity within and across the breeds, with the resulting matings designed to maximise diversity within the population, and genetic linkage across research sites. This paper describes the genetic diversity of the SMB base herd and how the software program MateSel (Kinghorn 2011) was used in sire allocation.

BASE BREEDING HERD

The SMB herd is managed across five research sites across NSW and include; Glen Innes (New England), Grafton (North Coast), Trangie (Western), Tocal (Hunter) and EMAI (Outer Sydney). Approximately 1800-2000 base cows have been mated through a combination of AI and natural matings to bulls of their own breed over the last two years, these matings generating the base experimental females. A small crossbred joining program between Angus, Hereford and Brahman also occurred at the Grafton research site (Walmsley *et al.* 2021). Breed and cow allocation at each site (Figure 1) was based on breed representation, carrying capacity of the site, whilst accounting for dam source and sire line as per Walmsley *et al.* (2021). Angus cattle provide the link breed across the 5 sites, representing 223 unique sire families and incorporating the DPI herds at Glen Innes and Trangie (Walmsley and McKiernan 2011; Herd *et al.* 2014). The base cows also represent 197 Hereford, 99 Wagyu, 78 Brahman, 80 Charolais and 93 Shorthorn sire families.

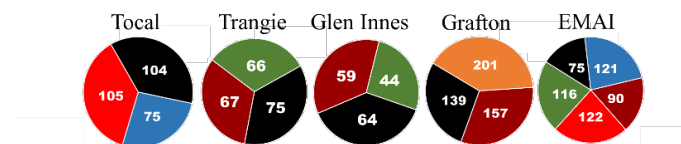


Figure 1: Number of cows for Angus (black), Brahman (orange), Charolais (blue, Hereford (maroon), Shorthorn (red) and Wagyu (green) represented at the five SMB research sites for the 2019 and 2020 matings

SIRE SELECTION

Sire selection was a balancing act between capturing the diversity of the breed and targeting high accuracy EBV bulls, such that the average accuracy of the progeny was as high as possible to allow the development of high accuracy across breed EBVs for animals. MateSel was used to aid selection within the industry nominated bulls, for the AI program, but ultimately final selection was heavily influenced by semen availability at the time of mating. The 2019/20 AI program used 171 bulls and incorporated 23 historic sires from previous Beef CRC projects (Upton *et al.* 2001, Figure 2), creating linkage to previous research herds and the different breed based Beef Information Nucleus projects through the use of project bulls and their sons for the southern breeds. Brahman bulls represented in the Repronomics project (14 bulls) (Johnston *et al.* 2017) and Beef CRC were also used as AI sires. Backup bulls are predicted to account for ~35% (AI success rate of ~50%) of the research animals. The selection of the 119 backup sires was done in conjunction with the AI sire selection, with herds and sires which were not represented in the AI sires favoured, within the limitations of the project budget.

MATE ALLOCATION

To avoid confounding between breed, site, year and sire effects, unique sire family lines needed to be spread across the fixed effects structure of the project, to maximise the ability to accurately remove the impact of environment. The aim was to generate the most genetically diverse progeny (low inbreeding) possible given the selected sires and dams, with sufficient linkage across sites via the sires.

MateSel is a software program for tactical implementation of breeding programs, based on an evolutionary algorithm (Kinghorn 2011). It accommodates the prevailing technical and logistical issues, including genetic gain, genetic diversity, trait distributions and the management of allele and genotype frequencies for individual genetic markers. Functions within the MateSel suite allows for the implementation of mating restrictions around the distribution of males for matings across groups of dams.

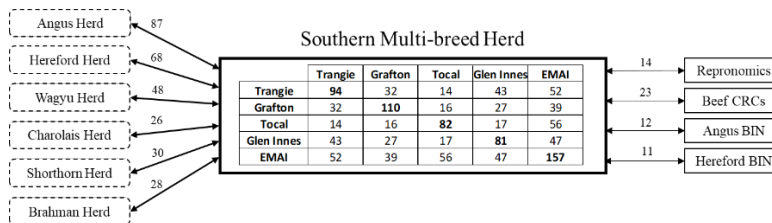


Figure 2: Number of Southern Multi-Breed bulls used at each research site (diagonal) as well as bulls in common (off diagonal). Bulls in common with other research herds and the industry herds represented by number above linking arrows

Methodology. The MateSel algorithm was provided with a complete set of selection candidates; AI sires and available dams, with index values (BREEDPLAN \$Index value) and 4 generations of pedigree information back from the candidate. The objective of the mate allocation was to generate high genetic diversity in the progeny born in the project, as per Clark *et al.* (2012), by targeting a low co-ancestry between parents and placing a negative weighting on inbreeding. MateSel was able to do this under the physical restraints of the project that included;

- 1) Sires are used enough to produce 6 to 8 daughters across the project
- 2) Genetic linkage via the use of sires across research sites, years, cow groups (eg. heifers/cows)
- 3) Sires linking across years (used at the same research site as previous years)
- 4) Minimum sire usage within a research site / year / dam age group to make sure guaranteed representation of the sire in the heifer progeny (assuming a 50% AI success rate, and 50:50 sex ratio of progeny)
- 5) Avoid high birth weight bulls being mated to heifers and first time calvers

The backup mating assignments followed the same AI mating rules, however, these allocations were also restrained by the sires’ physical location. Management restrictions meant that in some cases multi-sire backup groups needed to be allocated.

Outcomes. The final AI mate allocations were chosen when the smallest co-ancestry was achieved and all selected dams and sires had met usage requirements and no mating would produce a progeny with an inbreeding coefficient, based on pedigree, greater than 7% (> 10% in Wagyu, due to smaller genetic diversity of the breed). Slightly higher inbreeding thresholds were observed in the backup mating due to the physical restraints associated with bull allocations. The low level of co-ancestry within the mate allocations was achieved in conjunction with creating genetic links between sites via common sires as per. Figure 2. Alternatively, if the MateSel mate allocation had targeted the respective industry indexes, instead of genetic diversity, for Angus, Hereford and Wagyu the average level of inbreeding in the predicted progeny increased from 2.3% to 2.8%, 0.3% to 1.3% and 2.9% to 4.9%, for the three breeds respectively (Figure 3). Resulting in 12% of the predicted Wagyu progeny having an inbreeding coefficient of 10% or higher. Bulls used in the AI program were allocated between 4 and 24 matings / year (mean = 12), after two years of use have been allocated 8 to 33 matings ,with no less than 4 matings within a research site, year, dam age combination. Results from the 2019 mating reveal that the number of heifer progeny born per bull used across all matings ranged from 1 to 11 with an average of 3 heifer progeny.

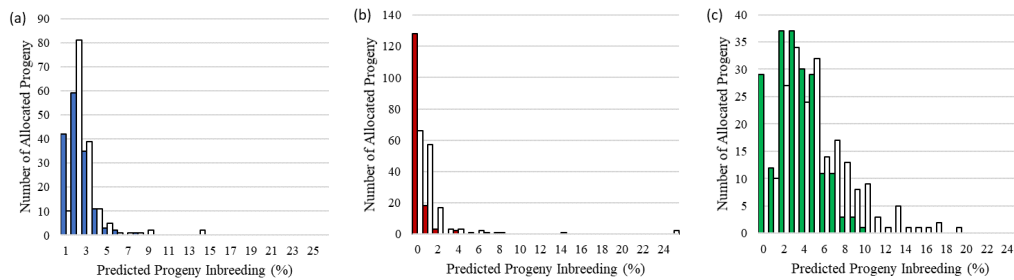


Figure 3: Comparison of the estimates of progeny inbreeding (%) when mating allocation was based on genetic diversity (coloured) or targeted index merit (white) for Angus (a), Herford (b), and Wagyu (c) using MateSel

CONCLUSIONS

MateSel has aided the allocation of the base dams and sires across the research sites within the SMB project so that the resulting progeny will reflect the genetic diversity in industry whilst maintaining genetic linkage across cohorts within the SMB project and industry herds. However, it should be acknowledged that the genetic diversity of the progeny and their genetic relationship to the national herd will not be fully understood until the planned genotyping of the progeny has occurred.

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