QUANTIFYING THE LINKAGE BETWEEN GENETICS REPRESENTED IN THE SOUTHERN MULTI-BREED PROJECT AND THE WIDER BEEF POPULATIONS

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SUMMARY

Southern Multi-Breed (SMB) is a landmark five-year project, collecting high-quality phenotypes and genotypes on animals from six breeds, managed in multi-breed groups at five NSW Department of Primary Industries research herds. Data collected will enhance genetic evaluations and facilitate the development of a multi-breed genetic evaluation. The project design focussed on selecting foundation cows and sires to represent the breed's populations. This paper aimed to quantify the linkage between the genetics represented in the SMB project and the breed populations. Within each breed, the average relationship coefficient of each animal to SMB foundation cows and sires and all animals in the breed was calculated and plotted to form a visual metric of the linkage. Regression slopes between 1.11 and 1.37 and correlations between 0.86 and 0.99 were calculated from the plots. The visual and quantitative metrics indicated that the genetics in SMB represent the breed populations. Therefore, the reference data collected as part of SMB will benefit the broader industry.

INTRODUCTION

The potential benefits of genomic selection are directly impacted by the size of the reference population, trait heritability, and effective population size (Goddard and Hayes 2009), relatedness amongst the reference animals, and relatedness to selection candidates (Pszczola *et al.* 2011). Therefore, when designing reference data projects, multiple design principles must be balanced to maximise the value of the collected data.

Southern Multi-Breed (SMB) is a landmark five-year reference data project involving six beef cattle breeds. Calves are born and managed in mixed-breed groups across five NSW Department of Primary Industries (DPI) sites (Walmsley *et al.* 2021). Progeny is intensively performance recorded for BREEDPLAN traits and other traits of economic importance (Donoghue *et al.* 2001, Walmsley *et al.* 2023). The over-arching goal of SMB is to collect high-quality reference data - particularly for hard to measure traits - to enhance genetic evaluations and facilitate the development of a multi-breed genetic evaluation. As such, the design of the SMB project is of critical importance, not just to ensure fair head-to-head across breed comparisons but also to ensure that the generated reference data genetically represents the breed populations. Moore *et al.* (2022) presented a metric to describe and compare the relatedness of reference populations to a whole breed. A key element of the SMB project design was the selection of foundation cows and sires to maximise relationships between SMB and the wider breed. This paper aims to assess if the choice of foundation cows and sires has been effective in ensuring that SMB data is genetically linked to the whole population within the respective breeds.

MATERIALS AND METHODS

Commencing in 2020, three cohorts of SMB progeny have now been born across five DPI

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locations (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) from six purebred breeds (Angus, Brahman, Charolais, Hereford, Shorthorn and Wagyu). In addition to the purebred matings, at Grafton, a small amount of cross-breeding involving Brahman reciprocal matings to Angus and Hereford also occurred. Walmsley *et al*. (2021; 2023) provide details about the SMB project design, and Walkom *et al*. (2021) outline the mating strategy within the project. At the commencement of SMB, foundation cows were purchased from industry seedstock herds. These were identified as herds that BREEDPLAN recorded and were influential in the breed (either using a wide range of sires or selling their genetics to other seedstock herds). Groups of cows were sourced from these herds. All cows were BREEDPLAN performance recorded with pedigree information and were selected to be representative of the national population (assessed via 400-day weight and reproduction EBVs), but especially if their sires were current influential sires (i.e. a large number of progeny). Angus foundation cows were also retained from the NSW DPI muscling (McKiernan and Robards 1997) and feed efficiency selection (Arthur 1997) herds. Female progeny are retained in the project, with foundation cows exiting the project as the number of project-born females increases. Project sires were also BREEDPLAN performance recorded with pedigree information. Natural mate sires were purchased from industry herds, and nominations were sought by the industry for artificial insemination sires. In both sire mating types, sires were selected to represent the breed, with an emphasis on using current or immerging influential sires. This involved studying the pedigrees to identify sire lines not already represented in the SMB foundation animals and undertaking MateSel (Kinghorn 2011) analysis to identify new and important genetics to include in the project. Several sires were also used that provide genetic links with other reference data projects (past and present, i.e. Repronomics, Beef CRC and existing within-breed reference data projects). Sires were used across sites and years, with new sires also purchased each mating. This study considered the cows and sires that produced the first two cohorts of calves, with Donoghue *et al*. (2021) providing details on the first two cohorts of calves produced.

Moore *et al*. (2022) described a methodology to assess how related reference populations are to a wider population. This method was used to assess how the SMB foundation cows and sires are related to the breed population for five of the six breeds represented in the project. All known pedigree information was available for breeds A, B, C and E, but pedigree was only available for a subset of breed D. Of the 267 breed D foundation animals, 116 foundation cows and sires were present in the available pedigree subset, and these animals were considered in the current study. No pedigree was available for the breed not included in this study. A whole breed numerator relationship matrix was constructed for each breed in the study based on the breed's recorded pedigree. The average relationship coefficient for each animal in the breed was calculated with 1) SMB foundation cows and sires and 2) all animals within the breed. A visual metric (Figure 1) was produced for each breed, where the average relatedness to SMB animals (y-axis) was plotted against the average relatedness to all animals (x-axis) in the breed. The regression slope and Pearson correlation coefficient were also calculated for each plot to quantify the relationships between SMB and the whole breed population.

RESULTS AND DISCUSSION

Table 1 summarises by breed the 1,149 foundation cows and 277 sires. Cows were from similar age structures and sourced from 5 to 13 herds per breed. The number of foundation cows per breed varied depending on the number of sites the breeds were present at. Breed C had the largest number of cows (n=370) due to being present at four of the sites. Breeds B, D and E were located at two or three project sites, while breed A was located at only one site. The number of sires per breed depended on the number of cows and sites the breeds were present at, and mating was from natural mating or artificial insemination.

Figure 1 describes how animals in the breed were related to SMB foundation cows and sires and the breed population. The average relatedness to all animals in the breed ranged between 0.0 and 0.05. The exception was breed E, where the average relatedness to all animals was much higher (0.0 to 0.2), reflecting breed E's reduced diversity due to being founded from a limited number of animals. These plots demonstrate that the genetics represented in SMB are well linked to the breed population for all five breeds considered in this study. The shapes of the plots indicate that the animals with higher average relationship coefficients to all animals in the breed also demonstrated higher average relationship coefficients to SMB animals. Data points in the plots generally followed the 1:1 line marked, although they tended to be slightly above the line. The 1:1 line is the expected relationship between both axes when the reference population is the same as the whole population (Moore *et al*. 2022).

Table 1. A summary of the SMB project foundation cows and sires

Breed	A	B	C	D	E
Number of site locations	1	2	4	2	3
Number of foundation cows	166	182	370	219	212
Number of herds	7	5	13	10	9
Year of birth range	2008-18	2009-19	2009-18	2010-17	2010-18
Number of project sires	41	36	89	48	63

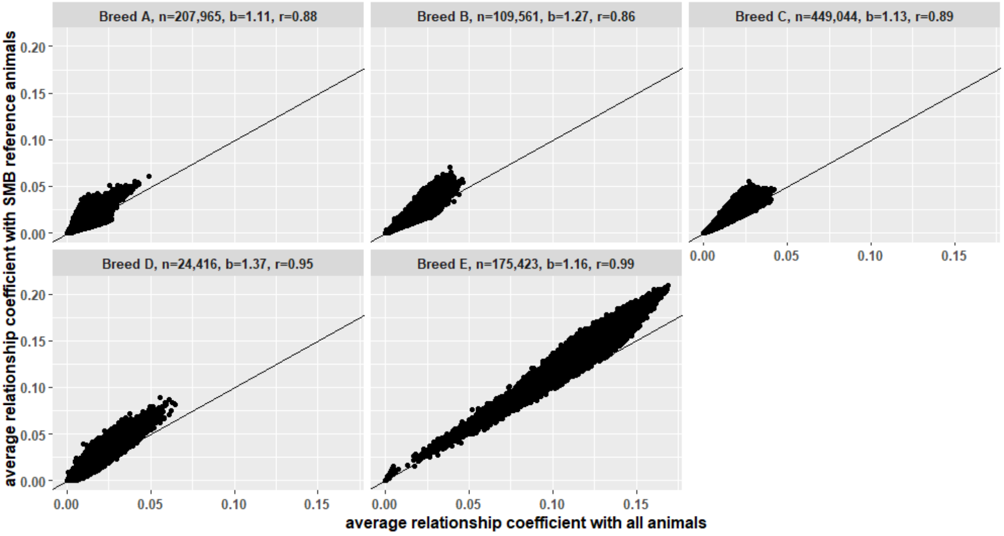

Figure 1. The average relatedness to all animals (x-axis) compared with animals in the SMB reference population (y-axis), regression coefficient (b) and correlation (r) for all animals born after 2010 (n) in five of the breeds represented in SMB

Regression slopes were estimated to be 1.11, 1.27, 1.13, 1.36 and 1.16, respectively, for breeds A, B, C, D and E. Moore et al. (2022) reported that a regression slope close to 1 was considered optimum. For each breed, the regression slope was slightly greater than 1. A regression slope above 1 indicates that the reference population (in this case, SMB founder cows and sires) contains a higher proportion of animals with high relatedness to all animals. The above 1 regression coefficients found align with the strategy to target high-impact and diverse genetics when sourcing foundation cows and sires and suggest that when selecting future project sires, more emphasis can be placed on increasing diversity as high-impact animals are currently represented. These regression slope values were comparable to those found for the live weight reference populations assessed by Moore *et al.* (2022). Live weight is generally one of the better-recorded traits, but only between 30 and 74% of the breed population was recorded for live weight. Selection strategies for SMB cows and sires required that animals were BREEDPLAN recorded. Similar regression slopes for the SMB foundation animals and the breed's live weight references appear sensible. Pearson correlations of 0.88, 0.86, 0.89, 0.95 and 0.99 were estimated for breeds A, B, C, D and E, respectively. These correlations indicate a very strong relationship between the relatedness of SMB and the breed population. This correlation was especially high for breeds D and E, and this could suggest that foundation animals contain a more even representation of different relatedness levels to the whole breed. Lower correlations can be seen in the plots (particularly for breeds A and B) where animals that were the highest related to all animals showed a narrower range in relatedness values to SMB, i.e. the width of the cluster was smaller for higher related animals, and this aligns with the strategy of targeting cows with influential sires, and current or emerging influential sires themselves.

CONCLUSIONS

SMB is a landmark project collecting reference data to enable across-breed comparisons and provide valuable reference data for within-breed genomic evaluations. As part of the project design, foundation cows and sires were identified to be representative of the breed. This study confirmed that these foundation cows and sires used in SMB are related to the breed population. Therefore, the reference data collected will benefit the development of multi-breed genetic evaluations and within-breed genomic selection programs.

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