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DIGITAL TWIN: MODELLING BREEDING PROGRAM APPROACHES IN AUSTRALIAN WAGYU

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SUMMARY

We developed a 'digital twin' of AACo's Wagyu seedstock breeding program utilising the genomicSimulation software. We aimed to find the optimal selection pressure and reproductive technology to rapidly meet the objective of a completely polled herd while optimising genetic gain for key traits and managing inbreeding. Our results demonstrated that a polled Wagyu herd could be achieved within 8 years using a combination of invitro fertilisation (IVF) and natural service (NS) in a breeding program which applied 100% weighting to polled. However, we demonstrated that applying this level of selection pressure came at a significant cost to genetic progress for other traits. A 60% weighting to polled selection was able to achieve a polled herd within 10 years whilst meeting the other objectives.

INTRODUCTION

Breeding programs in beef cattle are challenging to evaluate in a timely manner. Whilst genomic technologies allow breeding decisions to be made earlier-in-life and has accelerated the rate of genetic gain in AACo's herd, substantial risk is still attached to breeding programs. Therefore, we sought to create a 'digital twin' of AACo's breeding program using the genomicSimulation software (Villiers *et al*. 2022). This software allowed for proposed breeding programs utilising different: scenarios, selection pressures, technologies and target traits to be fully tested before implementation. The digital twin is a detailed representation of AACo's Wagyu breeding program where the aim is to develop a polled pure-bred Wagyu herd. Selection for polled was balanced with selection for a Wagyu production index (WAGIN). Inbreeding, measured as Runs of Homozygosity (ROH), was also evaluated. The 'twin' aimed to find the optimal breeding program to achieve a completely polled herd in the shortest time using a combination of natural service (NS), invitro fertilisation (IVF) and artificial insemination (AI).

MATERIALS AND METHODS

Genomic resources. The founding population for the digital twin was a group of 2,500 genotyped animals, each with a Bovine TropBeef (50K) SNP array imputed to 770K. SNP effects for the modelled production traits were taken directly from AACo's internal prediction pipeline. These SNP effects are updated as required, an assumption that was also carried into the digital twin. The WAGIN production index is comprised of several production traits and is specifically designed for selection of Wagyu sires. The poll allele within the Wagyu population was modelled as a single additional SNP at the map location of the known Celtic mutation; chromosome 1: 2429319 bp (Randhawa *et al.* 2020). The effect of the poll allele was set to 1 and the effect of the horn allele to 0.

Computational resources. The digital twin simulations utilised the genomicSimulation package in R (version 0.2.4.003) (Villiers *et al.* 2022). GenomicSimulation was designed for the simulated stochastic crossing and selection of real genotypes, which combined with known SNP effects allowed for the calculation of genomic breeding values (GBVs) of individual animals. Simulation was conducted in a unix environment using the resources of the University of Queensland's HPC.

Breeding program assumptions. The digital twin was used to model three different breeding programs: NS, AI and IVF, and investigated the outcomes of placing different selection emphasis on polled vs WAGIN. NS assumed that all heifers and mature cows were mated using natural service with a pregnancy rate of 85%. Bulls were joined at 3% of the female herd, with offspring per bull being capped at 20% of all calves. Females were replaced at 25% per annum, replacement heifers being selected on estimated genetic merit. Bull selection was conducted in two steps, firstly 36% were randomly culled, remaining candidates were then selected on genetic merit to meet a 33% annual replacement rate. Virgin bulls were mated to heifers only, after which they were placed within a common pool of mature bulls. The AI scenario assumed that all heifers were AI'd as yearlings, with 50% of AI resulting in pregnancy, the remainder of the available females were mated using natural service. Two different IVF scenarios were modelled, IVF5 assuming 5 embryos per donor and IVF10 assuming 10. Both selected 350 mature cows as recipients for embryo's donated by either the 65 (IVF5) or 35 (IVF10) heifers of highest genetic merit, all remained females were natural mated. The selection of sires, donors and replacement heifers was subject to different levels of selection intensity for polled (polled weight): 0, 0.4, 0.6 and 1. Polled weight was balanced against production traits, expressed using WAGIN. Selection candidates were ranked by combining rescaled GBVs for polled and WAGIN.

Inbreeding. Inbreeding was defined using runs of homozygosity (ROH). ROHs are long continuous segments in the genome which, due to their length, are assumed to come from a common ancestor (Meyermans *et al.* 2020). ROHs were detected using the sliding window approach in PLINK 1.9 (Chang *et al.* 2015). Both the GBVs and ROHs values presented were the mean value of 25 replicates per generation, necessary due to individual matings in natural service scenarios not being predetermined.

RESULTS AND DISCUSSION

A range of different 'poll weights' were tested within the digital twin, ranging from 0, indicating no selection pressure for polled, to 1, indicating 100% selection pressure on polled, ignoring production traits. We have chosen to present only a subset of these poll weights in the analysis. The Polled Frequency presented in Figure 1. are the combined sum of PP and HP animals divided by number of animals times 2. All breeding programs, even NS were able to achieve a 100% Polled Frequency when applying 100% weighting to Polled. However, our results clearly demonstrated that applying only a 60% weighting to polled would achieve a similar result. This is due to the low number of polled animals available in the base population. Within this herd, there is simply no point in applying selection pressure beyond 60% for polled. Unsurprisingly, programs using intensive breeding tools such as AI and IVF were able to achieve a polled herd in less time. The results of the Polled Frequency analysis carry implications for the WAGIN gain results in Figure 2. As expected, applying 100% selection intensity for Polled meant that genetic gain for WAGIN was zero for 10 years, until a completely polled herd was achieved. Conversely, genetic gain for WAGIN under a 60% selection intensity for polled was still reasonable under all breed programs.

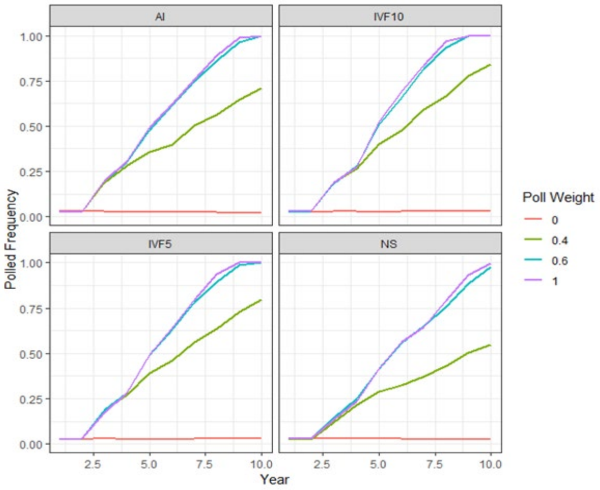

Figure 1. Genetic gain for Polled Frequency

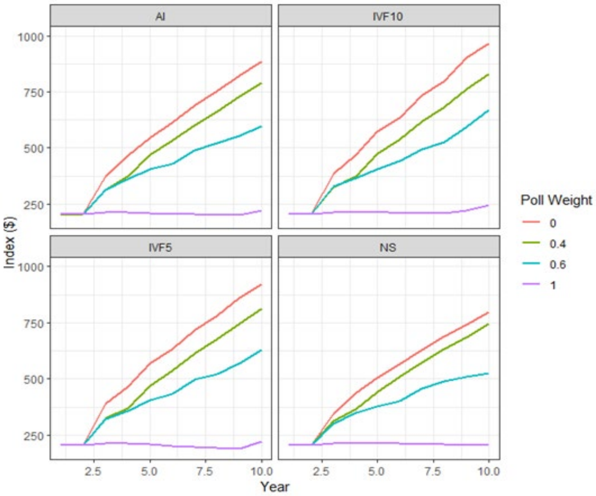

Figure 2. Genetic gain for WAGIN

IVF and AI assisted breeding were, as expected, able to provide superior rates of genetic gain. The opportunity cost of the forgone genetic gain for WAGIN is difficult to determine. It must account for the value of the genetic gain for production traits in real terms and balance this against the value of increased polled frequency. Such analysis is beyond the scope of this paper but must assign a monetary value to polled through factors including decreased mortality from dehorning, market access from improved animal welfare.

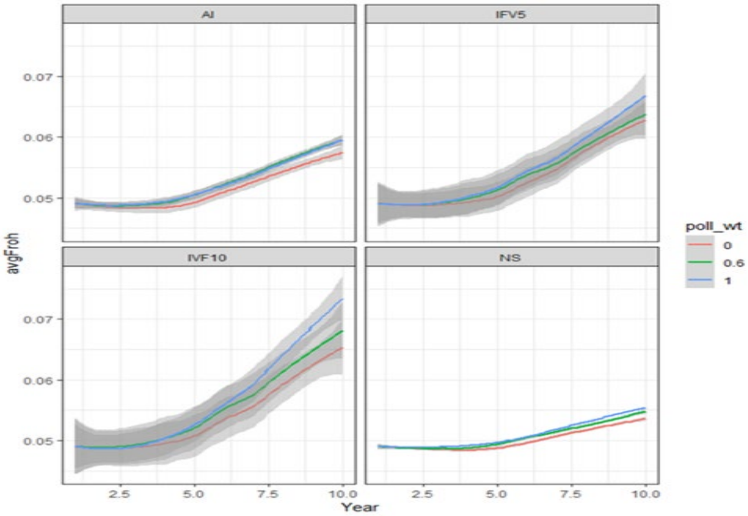

Figure 3. Inbreeding rate for different breeding program scenarios

Another important factor when considering the cost benefit analysis of the respective breeding programs is the projected level of inbreeding. Our previous results clearly demonstrated the superiority of IVF and AI programs in achieving the breed objectives, but this is accompanied by a higher level of inbreeding (Figure 3). Compared to the NS breeding program where ~5.5% of the genome was found within ROHs, the IVF10 program resulted in ~6.5-7.4% within ROHs (Figure 3). Whilst inbreeding depression could not be modelled in this scenario, it has been observed in dairy cattle previously (Pryce *et al*. 2014) that a 1% increase in inbreeding was associated with 1-1.5% reduced milk, fat and protein yields as well as declining fertility. Increasing selection weight on polled did increase inbreeding, however the type of breeding program was found to be more impactful. For example, the inbreeding in the NS program at polled weight = 1 was lower than the AI program at polled weight = 0. This is a direct function of the small effective population size of polled animals available for selection as well the limited number of animals inducted as AI sires and IVF donors. The use of technologies like AI and IVF, which accelerate the rate of genetic gain for target traits, are not without drawbacks.

CONCLUSION

The results of the simulations indicated that AACo achieving a polled Wagyu herd is possible within a 10-year time frame. However, selection for polled must be finely balanced against selection for WAGIN. We concluded that polled weight in the breeding program should not exceed 0.6, doing so does not increase the proportion of polled animals in the herd and would only serve to compromise genetic gain for WAGIN. AI and IVF breeding programs performed better than NS in achieving the breeding objectives sooner but did result in higher rates of inbreeding. Maintaining genetic diversity is especially important for Wagyu breeding programs, thus upcoming iterations of the digital twin analyses will incorporate optimal contribution selection and be able to balance multiple traits with rates of inbreeding.

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