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GENOTYPING STRATEGIES OF SELECTION CANDIDATES IN SHEEP BREEDING PROGRAMS

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SUMMARY

Genotyping strategies for both ram and ewe selection candidates were investigated to maximise the benefit of genomic selection while minimising genotyping costs. Through stochastic simulation we investigated both early and late-stage genomic selection of rams using a selection index that contained an early in life measurement (post-weaning weight) and a hard to measure trait (intra-muscular fat) that was not measured on selection candidates. We also simulated genotyping strategies for female selection candidates in breeding programs using natural mating, multiple ovulation and embryo transfer (MOET) or juvenile *in vitro* fertilisation and embryo transfer (JIVET). Our results showed that genomic selection of rams lifted genetic gain by 40%. Genomic testing the top 20% of ram selection candidates achieved 80% of the maximum benefit using late-stage genomic selection, while testing 47% of the top ranked rams implementing early-stage genomic selection was required to achieve 80% of the benefit. Genetic gain lifted by a maximum of 15-65% for genomic testing in (only) ewe selection candidates. To achieve 80% of the maximum benefit of genomic selection, 65%, 35% and 45% of ewe selection candidates required genomic testing each year for natural, MOET and JIVET breeding programs, respectively. Genotyping ram selection candidates provided the best value for money.

INTRODUCTION

Limited research has been published about strategies to genotype selection candidates while minimising costs. Van der Werf *et al.* (2014) and Horton *et al.* (2015) proposed that genotyping 20% of ram selection candidates will return 80% of the maximum potential benefit (i.e. compared with testing all rams) and assuming 2-stage genomic selection. Van der Werf *et al.* (2014) also discussed multiple trait indexes with unfavourable correlations between early measured traits and late-in-life- or hard-to-measure traits and agreed with Sise and Amer (2009) that more candidates would need to be tested by genomic methods compared with simple single-trait indices. There is little published data investigating genotyping methods of the optimisation of ewe selection candidates, particularly when using female reproductive technologies.

This paper aims to investigate genotyping strategies for early-stage and late-stage selection for ram selection candidates using a multi-trait index with a hard-to-measure trait to maximise genetic progress while minimising testing costs. This paper also investigates genotyping strategies in ewes.

MATERIALS AND METHODS

Stochastic simulation was used to model closed breeding schemes for 500 sheep. For each scenario we generated a base population of unrelated animals, and subsequently established a 15-year breeding program with overlapping generations. We simulated an early-in-life measured trait (post-weaning weight - PWT) and a trait that did not get measured (intra-muscular fat - IMF). Heritabilities, genetic and phenotypic (co)variances for the parameters were used from Swan *et al.* (2015). Each year, individual animals had breeding values estimated (EBV) via pedigrees based on multi-trait Best Linear Unbiased Prediction (BLUP) using ASReml software (Gilmour et al. 2009).

For each breeding program and index the impact of genomic selection (GS), assuming all animals had genomic information available at birth, was assessed. The cost of GS was not accounted for in this study. Genomic information was modeled following the method of Dekkers (2007) which simulates a genomic breeding value as a correlated trait with a heritability of 0.999 and a correlation *r* to the measured trait, where *r* is the accuracy of the genomic breeding value for each trait. The accuracy of the genomic test varied for each trait (Swan *et al.* 2015).

Genotyping strategies

Truncation selection was used in all breeding programs (i.e. the highest ranked rams were randomly mated with the highest ranked ewes). Number of candidates genotyped in each breeding program ranged from zero (control) to 100% (maximum benefit). No ewe or ram selection candidates were genotyped in Scenarios 1-2 and Scenarios 3-5, respectively.

Early-stage selection juvenile rams (Scenario 1)

Juvenile rams were eligible to be genotyped prior to any phenotypic measurements or BLUP breeding values. Juvenile rams were sorted from highest ranked to lowest ranked based on parent average breeding values. No ewe selection candidates were genotyped in this scenario.

Late-stage selection mature rams (Scenario 2)

Ram selection candidates were eligible to be genotyped at genetic evaluation that included a measurement of PWT and a BLUP calculation had been made. These rams were then sorted from highest lowest based on index breeding values. No ewe selection candidates were genotyped in this scenario.

Late-stage selection mature ewes for natural mating (Scenario 3)

Ewe selection candidates prior to their first year of mating were eligible to be genotyped after the initial measurement of PWT and a BLUP calculation had been made. These ewes were then sorted similar to Scenario 2. In the natural mating scenario 500 ewes were selected with the probability of one progeny born per mating.

Late-stage selection mature ewes for MOET matings (Scenario 4)

Ewe selection candidates prior to their first year of mating were eligible to be genotyped after the initial measurement of PWT and a BLUP calculation had been made. These ewes were then sorted similar to Scenario 2. In the MOET mating scenario 125 ewes were selected with the probability of zero to eight progeny born per mating with an average of 4 similar to Granleese *et al.'s* (2016) method.

Early-stage selection juvenile ewes for JIVET matings (Scenario 5)

Juvenile ewes were eligible to be genotyped prior to any phenotypic measurements or BLUP breeding values similar to Scenario 1. Because the generation interval for dams in JIVET sheep breeding programs are as little as 6 months, Scenario 5 required 2 rounds of mating a year. In the JIVET mating scenario 64 ewes were selected annually (or 32 each mating round) with the probability of zero to sixteen progeny born per mating, with an average of 8, similar to Granleese *et al.'s* (2016) method.

RESULTS AND DISCUSSION

When there was no genotyping in any strategy MOET breeding programs yielded the highest genetic gain (Figure 1a). However as genotyping increased in selection candidates, JIVET breeding programs yielded the highest genetic gain (Figure 1a). This corresponds to Granleese *et al.'s* (2016) results. However, genotyping male selection candidates resulted in the most cost-effective way to increase genetic gain in a breeding program when compared to the cost of female reproductive technologies.

The maximum increase due to genomic selection in rams lifted genetic gain by 40% (Figure 1b). Genomic testing of the top 20% of ram selection candidates achieved 80% of the maximum benefit using late-stage genomic selection, while 47% required testing in early-stage genomic testing

(Figure 1c). This demonstrates the importance of using initial measurements and screening on breeding values that use selection indexes that have late-in-life or hard to measure traits. Genetic gain lifted by a maximum of 15-65% for genomic testing in ewe selection candidates (Figure 1b). To achieve 80% of the maximum benefit of genomic selection, 65%, 35% and 45% of ewe selection candidates required genomic testing each year for natural, MOET and JIVET breeding programs, respectively (Figure 1c).

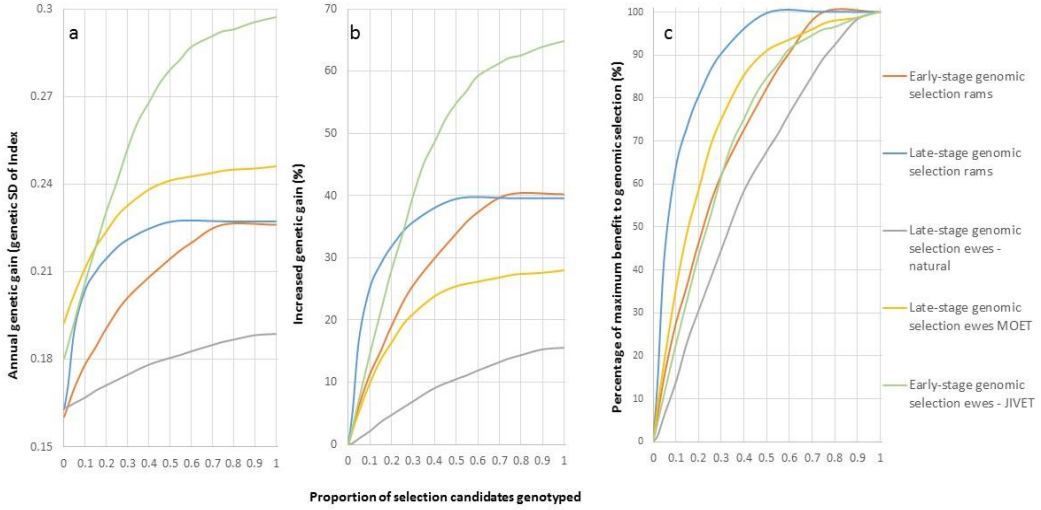

Figure 1: All x-axis are presented in proportion of selection candidates genotyped. a) Genetic gain in genetic standard deviations of the breeding objective; b) Increased genetic gain from genotyping proportions of selection candidates (note that zero % is zero genotyping); c) Percentage of maximum benefit of genotyping selection candidates (note that 100% genotyping is 100% of the benefit)

With the additional cost of producing lambs using female reproductive technologies (Granleese *et al.* 2017), genomic selection of ram selection provides the most favourable cost-benefit. Van der Werf *et al.* (2014) raised the idea of genotyping proportions of male selection candidates to receive the majority of the potential benefit. Our study demonstrates similar outcomes and reinforces that recording initial information prior to genotyping is crucial to achieving the "20-80" rule in ram selection candidates. Furthermore, important rules can be learned for using genomic selection in female selection candidates. It seems uneconomical to genotype all female selection candidates in natural mating or artificial insemination programs, particularly while genotyping costs are still relatively high. It would also be rare to find any sheep flocks in Australia that have their entire nucleus drop born to reproductive technologies as in our scenarios 4 and 5. However, many sheep studs in Australia have a proportion of their lambs born via reproductive technologies. This study and previous studies demonstrate the strong synergies between the two. Therefore, from this study we can use lessons to apply practically. For example if a breeder wanted to perform 10 MOETs or JIVETS on ewes, to get 80% of the maximum genomic selection benefit they should genotype 35 or 45 selection candidates, respectively.

CONCLUSIONS

Genotyping strategies in sheep breeding programs are necessary to reduce cost. This study provides evidence that late-stage genomic selection is far more efficient than early-stage genotyping methods particularly when there is late-in-life or hard-to-measure traits in the breeding objective.

We demonstrate that strong synergies exist between genomic selection and female reproductive technologies and show that genotyping efficiencies exist too with females when using reproductive technologies.

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