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COST-BENEFIT OF A GENOMIC REFERENCE POPULATION FOR GOATS IN AUSTRALIA

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SUMMARY

There is currently no genomic-based information available to Australian goat meat breeders to make selection decisions. This is due to a lack of performance-recorded goats with genomic information and a lack of genetic evaluation infrastructure. The Measured Goats project is the beginning of a genomic reference population that will help provide the data infrastructure to rectify both challenges. This study reports a cost-benefit analysis of investment of genomic reference populations for goat meat where commercial breeders breeding their own bucks could genomic test their "clean-skin" male selection candidates. The study demonstrates that the Measured Goats project is an excellent start to building a genomic reference population to underpin commercial genomic selection. All testing scenarios return a profit on investment to the industry in years 11-13. The genomic prediction accuracy and hence the response to selection is dependent on effective population size and the number of tested animals in the genomic reference population.

INTRODUCTION

Currently, little is known about the phenotypic and genetic performance of Rangeland goats (captured feral goats) and their crossbred progeny. The Australian Rangeland goat population, however, underpins the Australian goat meat industry which is an export industry valued at $288 million per annum (MLA 2024). Rangeland does will continue to be the basis of the goat meat industry owing to their numbers relative to the limited number of pure or crossbred does.

There is considerable potential for genetic improvement in Rangeland goat herds, although the benefits from research in genetics and genomics are yet to be realised (Kijas 2012; Aldridge and Pitchford 2018). Kijas (2012) reported that the Rangeland goat population was one of the most genetically diverse domesticated species in the world. Aldridge and Pitchford (2018) suggest that performance recording and understanding the genetic parameters of Rangeland goats would help increase breeding goat enterprise's profitability by better understanding the genetic capability of Rangeland goat genetics and hence enable better informed selection decisions.

The Measured Goats project (Granleese *et al.* 2023) is building a genomic reference population to complement the current KIDPLAN database. When a genomic reference population is established, there are possibilities to both enhance "single-step" analysis as well as make genomic predictions for individuals who have no known pedigree and/or performance recording (defined as "clean-skins" in this paper). Genomic prediction of clean-skin individuals could be of particular value to goat breeders who run extensive and rangeland production systems where precise breeding programs are impossible.

Genomic prediction accuracy is determined by factors such as effective population size (Ne), reference population size, and the relationship between reference and target populations. Smaller Ne increases linkage disequilibrium (LD), improving marker-trait associations. Larger genomic

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reference populations enhance accuracy by capturing more genetic variance and reducing sampling error. A close genetic relationship between reference and target populations also boosts accuracy due to shared genetic architecture.

This paper will investigate the impact of the size of genomic reference population targeted for the Australian goat meat industry and the modelled cost-benefit and will focus on prediction for two populations the Rangeland and combined meat breeds (Boer and Kalahari) populations.

MATERIALS AND METHODS

Genomic selection accuracy. Genomic selection accuracy was calculated using Goddard *et al.* (2011) methods with notation from Dekkers (2007) where the correlation between true and predicted breeding values was estimated. This method reflects how well genomic predictions capture genetic variation. Accuracy was estimated using: $r_g = \sqrt{\frac{Nh^2}{Nh^2+Me}}$, where *N* is the size of the reference population, h^2 is the heritability of the trait, and *Me* is the effective number of independent chromosome segments. *Me* is calculated by: $Me = \frac{2NeLk}{ln(NeL)}$ where L is the average chromosome size, *k* is the number of chromosomes goats have (30), ln is the natural logarithm and the effective population size (Ne) for meat breeds for Boer and Kalahari combined was estimated using pedigree data obtained from Boer Goats Breeder Association of Australia. Given we have no pedigree information and little genomic information on Rangelands animals, it was assumed that this population had little inbreeding and two effective population sizes of 2,500 and 1,000 animals were tested following estimates for other global wild goat populations. The equation to calculate Ne for meat breeds was: $N_e = \frac{1}{2\Delta F}$ where ΔF is the rate of inbreeding per generation (Falconer & Mackay 1996). The proportion of genetic variance captured by markers is defined by $q^2 = \frac{M}{Me+M}$ where *M* is the number of markers on the genomic test (70,000). The variance ratio of residual and effective QTL variance was calculated as: $\lambda = \frac{Me}{q^2h^2}$. The accuracy of genomic prediction as a predictor of effects captured by markers was calculated by $r\hat{Q} = \sqrt{\frac{T}{T+\lambda}}$ where T is the number of training individuals in the reference population. The accuracy of genomic prediction as a predictor of the true breeding value was calculated as: $r_{GBV} = \sqrt{q^2 r\hat{Q}}$.

Response to selection. Using the accuracies of genomic prediction calculated above, genomic accuracies for each trait (Table 1) adapting the “Kid Survival Plus” (KSV+) index developed by Aldridge and Pitchford (2018) were used in deterministic simulations using truncated selection. Heritabilities of traits within the KSV+ index ranged from 0.1 to 0.5. The genetic standard deviation of the KSV+ index is $11.53. Response to selection was calculated assuming all traits in the KSV+ index were measured in the reference population and only genotyping of male selection candidates were used in selection in clean skin herds. The only variable that changed within scenarios was accuracy of genomic prediction over time (Table 1) for each breeding scenario. This simulates the model where extensive breeders do no phenotyping on their property and genotype only eligible male candidates.

Cost-benefit to industry. The cost-benefit to the industry was calculated as genetic gain multiplied by total breeding does mated annually to genetically improved bucks using the geneflow method (Hill 1974), applying a cumulative discount of expression of 0.07. The starting operating cost of $700,000 to run the reference population in year one was deducted as a cost. Each year the cost increased on the previous year by 3%. The number of commercial does mated to genetically improved bucks began in year 6 starting with 50,000 commercial does mated, then increased by

50,000 annually until capped at 750,000 does in year 20. The cost-benefit was calculated cumulatively.

Testing scenarios. Three scenarios were assessed with straight meat breeds and Rangelands goats with two different Ne sizes of 1000 and 2500.

RESULTS AND DISCUSSION

Benefits to the industry from genetic gain were not realised until year six of the program due to the establishment phase of the genomic reference population where 1,000 or 2,500 individual animals for each breed are recorded in the genomic nucleus each year. We can observe that meat breeds get the highest genomic prediction accuracy (Table 1) due to the lower effective population size which is associated with fewer independent chromosome segments. Goddard *et al.* (2011) emphasizes that M_e depends on the balance between genetic diversity and the recombination potential of the genome. A smaller N_e or shorter genome size reduces M_e, leading to stronger linkage disequilibrium and fewer independent chromosome segments.

Table 1. Genomic prediction accuracies (r_g) for traits with three heritabilities (h^2), the possible genetic gain using KSV+ selection index for cleanskin herds testing male selection candidates only with 2500 and 5000 individuals recorded in the genomic reference population for each breed

Scenario	ΔF	Ne	2500 ref individuals rec				5000 ref individuals rec			
			$r_g\_h^2$ =0.1	$r_g\_h^2$ =0.3	$r_g\_h^2$ =0.5	dG/yr KSV+	$r_g\_h^2$ =0.1	$r_g\_h^2$ =0.3	$r_g\_h^2$ =0.5	dG/yr KSV+
Meat	0.0061	75	0.40	0.60	0.69	$3.68	0.52	0.72	0.80	$4.58
R'land 1,000	0.0020	1000	0.13	0.23	0.29	$1.69	0.19	0.31	0.39	$2.15
R'land 2,500	0.0002	2500	0.07	0.14	0.18	$1.27	0.10	0.19	0.24	$1.47

As the effective population size is much smaller in meat breeds, it allows up to a \$4.58 gain per year increase in clean-skin herds when simply genotyping male selection candidates. We observed a larger response to selection as more animals were recorded in the reference population (Table 1). Rangelands Ne 1000 and Ne 2500 had a more modest annual response of up to \$2.15 and \$1.47, respectively. There are a number of assumptions underpinning Rangeland goat prediction, which may be inaccurate. Firstly, it is assumed Rangeland goat genetics have the same genetic parameters as meat breeds, where in reality, the current KSV+ genetic parameters are only based on meat breeds. The actual difference in breeds and/or combined genetic analysis will not be estimated until the end of the Measured Goats project. The study also assumes that the Ne of the Rangeland goats is somewhere between 1,000 and 2,500 as the Rangeland goat population has no known pedigree information and a small representation of animals genomic tested. Once the project has more Rangeland genomic data on a broader range of the Rangeland goat population, the project will be able to get a better understanding of Ne by calculating the expected decay of LD with distance between markers, which reflects historical recombination and genetic drift.

All breeding scenarios demonstrate that benefits of selection are generated from year 6, and that the industry cost-benefit hits break-even at years 11-13 (Figure 1) Further, the simulation assumes that either meat breeds or Rangeland breeds are run separately. In reality, Rangeland does are usually mated to meat breed bucks where some level of "breeding-up" from Rangeland does to a higher meat content animal is bred over time in the pursuit of higher carcase weights. If this were to happen genomic prediction accuracy for first cross animals would be lower than Rangeland animals given the Ne of first cross animals is higher than Rangelands. But as meat breed content increases over generations, the Ne would then sharply decrease and genomic prediction accuracy and hence response to selection would increase for these clean skin animals.

The modelling in this paper suggests that a better understanding of genetic architecture of the Rangeland goat population will help design and allocate funding towards goat meat genomic resource herds. This modelling demonstrates that the investment in a genomic resource herd is beneficial when assessed from an industry perspective. It also demonstrates that despite low genomic prediction accuracy for Rangeland goat populations, it is still an economically worthwhile exercise to do. Further, it demonstrates that the Measured Goats project is building the initial foundations required to help build a database that allows goat breeders to use genomic selection.

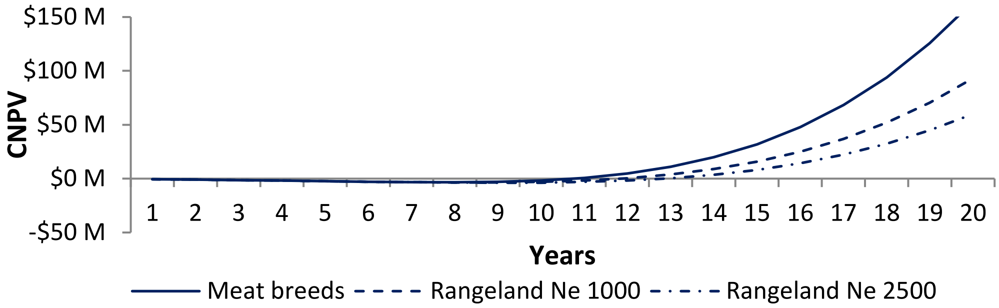

Figure 1. Cumulative net present value (CNPV) for investment of reference population and extra profitability earned by the goat industry under three investment scenarios

CONCLUSION

The Measured Goats in the Rangelands project is forming a valuable resource population for commercial breeders to genomic test “clean skin” animals. It will be important to focus on performance recording Rangeland animals to help build the number of animals given their hypothesised large effective population size. A better understanding of the effective population of Rangelands goats is required to help with reference population design as well as cost-benefit analysis.

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