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IS SEX DETERMINATION IN MERINOS HERITABLE?

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SUMMARY

This paper investigates the ability of different linear mixed models to estimate the heritability of sex determination in a sub-set of the Australian Merino population. The dataset used was from Centre Plus Merinos in central-west New South Wales with 25 plus years of full pedigree collection and over 20,000 lambing events where the sex of the progeny were recorded. This study used sex of a lamb as a trait, (i.e. zero phenotype for female and one phenotype for male). We observed a significant, yet normal, amount of phenotypic variation in the sex ratio of progeny for dams, sires, maternal grand sires and maternal grand dams. However, no model was able to estimate significant genetic variation in sex determination and failed to return a heritability above 0.01. Consequently, it can be concluded within this dataset that it would not be possible to select to alter sex determination in Merinos.

INTRODUCTION

Sex determination in mammals occurs at egg fertilisation with females and males typically having XX and XY chromosomes, respectively. Whether a newly conceived embryo is a male or female is determined by the sperm as dams can only ever pass an X chromosome onto their progeny. Kosswig (1964) thought that sex determination was a polygenic trait in some species of fish. Furthermore, Flanders (1965) purported that winged insects exhibited genetic variation in female behaviour to fertilise or not fertilise eggs which influenced sex ratio. There are no estimates of sex ratio estimation in livestock species. However, in humans, Gellatly (2009) showed a heritability of sex ratio of 0.05 and purported that males tend to produce a sex ratio like that produced by their parents, whereas females do not.

Sex determination is a potentially economically important trait to commercial producers where females are worth significantly more than castrated males. Anecdotally we hear sheep and cattle breeders observe that a cow or ewe only ever has one sex (e.g. “that ewe only ever breeds ram lambs”). This paper investigates whether phenotypic variation exists within a deeply pedigreed and well recorded Merino flock that is highly influential on the breed. If phenotypic variation does exist, we propose to run different types of linear mixed models to investigate whether any genetic variation can be quantified.

METHODS

Animals. Animals from the Centre Plus Merinos flock (601250 flock code), born since 1990, were included in the analysis. All animals without sire and/or dam pedigree were removed as well as any dead at birth (DAB) animals (all DABs were recorded as males). Contemporary grouping was defined as year of birth. No other contemporary grouping was significant enough to fit. In the

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case of running a sire, maternal grand sire or dam model, a minimum number of progeny were required to be included in the model (Table 1).

Measurements. Phenotype was defined as the sex of each progeny born. Zero for females and 1 for males. Hence an average of 0.5 was expected (Table 1).

Table 1. Descriptive statistics of each model where direct animal, dam animal, dam dam, service sire, maternal grand sire and maternal grand dam models were run

Analysis model type (min. no. progeny)	n	n Sire	n Dams	n MGS*	n MGD^	Mean	Phen. SD	Min.	Max.
Animal	23228	368	6835	-	-	0.50	0.14	0.00	1.00
Dam – animal (1)	23228	-	6835	-	-	0.50	0.35	0.00	1.00
Dam - dam (7)	6324	-	765	-	-	0.50	0.18	0.00	1.00
Service sire (40)	23120	334	-	-	-	0.50	0.09	0.35	0.67
Mat. grand sire (50)	19260	-	-	186	-	0.50	0.06	0.38	0.65
Mat. grand dam (10)	7676	-	-	-	535	0.50	0.14	0.10	1.00

*MGS – Maternal grand sires; ^MGD - Maternal grand dams

Statistical analysis. Phenotypic variance for each model was assessed prior to any model run to see if the trait was worth investigating (Table 1, Figures 1-4). We also checked to see if average sex ratio sat inside a normal distribution of expectation if sex ratio was random. This is displayed in Figures 1-4 where we can observe distribution sits within a normal bell-curve which suggested enough variation existed to pursue a genetic parameter estimation.

Once phenotypic variance was quantified, we investigated 6 models. These were: 1) animal model where the phenotype of each animal was used; 2) animal model of females where each progeny was a phenotype and multiple progeny were repeated records; 3) dam model similar to a sire model where dam is the random effect estimated; 4) service sire model where the sire of offspring is the estimated random effect; 5) maternal grand sire model similar to sire model; and 6) maternal grand dam model similar to sire model. Contemporary group (defined as year of birth) and conception method (artificial insemination or natural mating) were fitted as fixed effects while age of dam was fitted as a covariate.

Genetic parameters and predicted means were estimated using an animal model in WOMBAT (Meyer 2007). A numerator relationship matrix based on a four-generation pedigree was used.

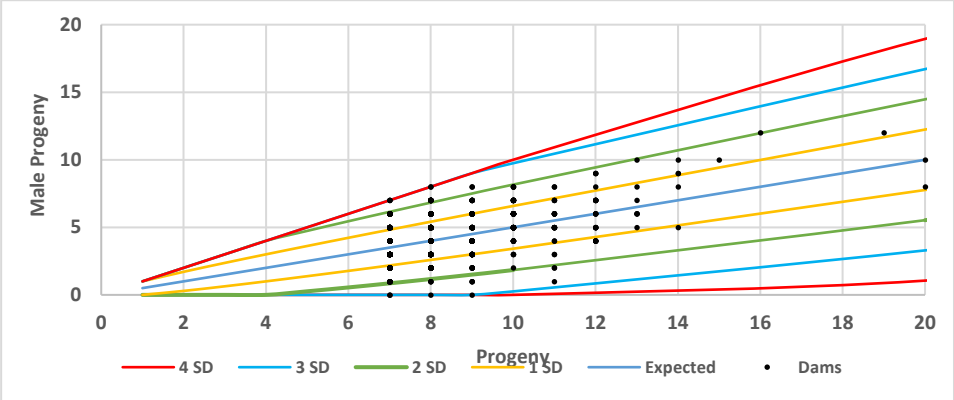

Figure 1. Number of male progeny vs number of progeny for dams and where each dam sits within an expected normal distribution with a minimum of 7 progeny (n=765)

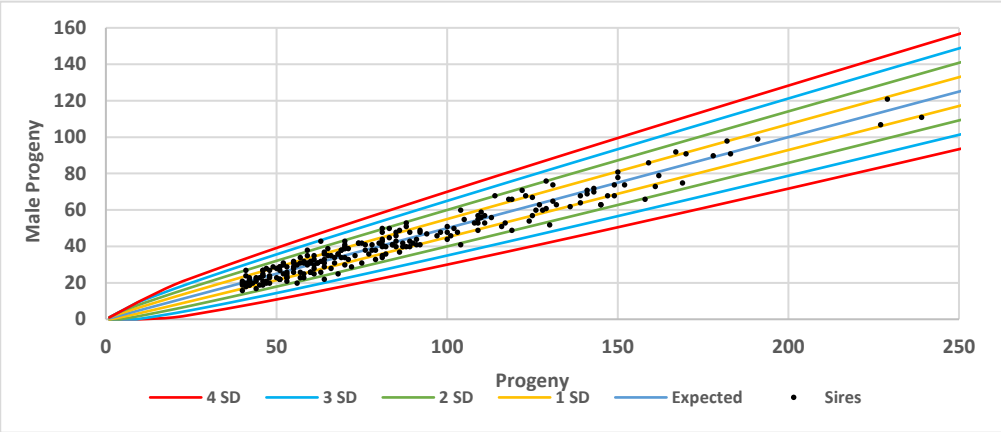

Figure 2. Number of male progeny vs number of progeny for sires and where each service sire sits within an expected normal distribution with a minimum of 40 progeny (n=343)

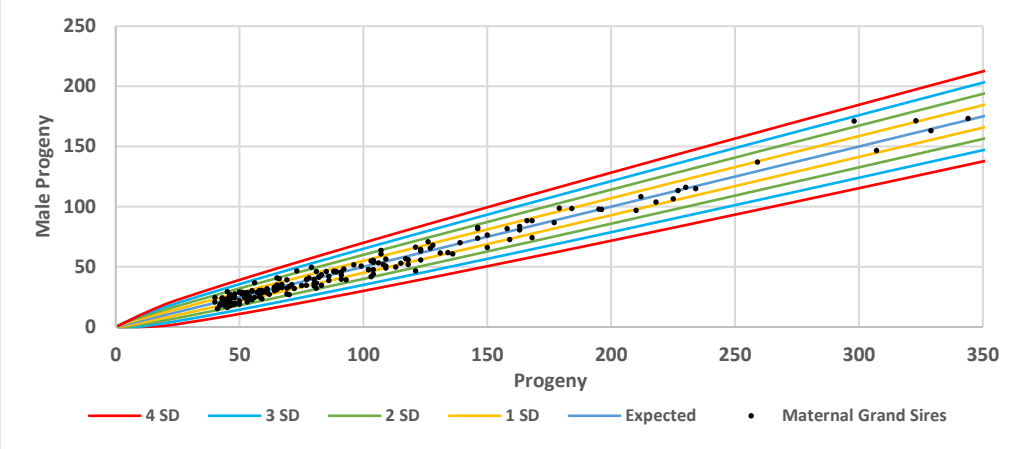

Figure 3. Number of male progeny vs number of progeny for maternal grand sires with daughters that have a minimum of 40 progeny (n=186)

RESULTS AND DISCUSSION

All models converged with negligible genetic variance estimated ($h^2 \leq 0.01$). In model 2, where sex of progeny was used as a phenotype with repeated records, a small but insignificant amount of repeatability (0.02) was estimated. Despite no significant genetic variance being captured by the models, it can be observed in Figures 1-4 that phenotypic variance does exist for dams and sires which suggests that sex ratio is determined by factors outside genetics. If sex determination was random Figures 1-4 demonstrate that the sex ratios sit mostly within the 95% expected rate of a normal distribution with no outliers (i.e. > 4SD above or below the expected).

As there is a reasonable amount of phenotypic variance for all models (Table 1), other genetic sources of variation may be explored. If there were sufficient numbers of genotypes to perform a GWAS for females, a GWAS analysis could be performed. Another avenue of investigation into

potential genetic variance of sex ratio determination could be to use a threshold model (Bulmer and Bull 1982).

With sire and dam sex ratio showing phenotypic variation (Figures 1-4) and potentially little genetic interactions playing a role, other environmental effects may play a role in sex determination. Diet has been shown to influence sex ratio in sheep (Green *et al.* 2008, Gulliver *et al.* 2013). These studies looked at whole flock means rather than individuals. Whether there is a genetic interaction between feed sources and sex ratio variation has not been explained, making it potentially a future cross-discipline study.

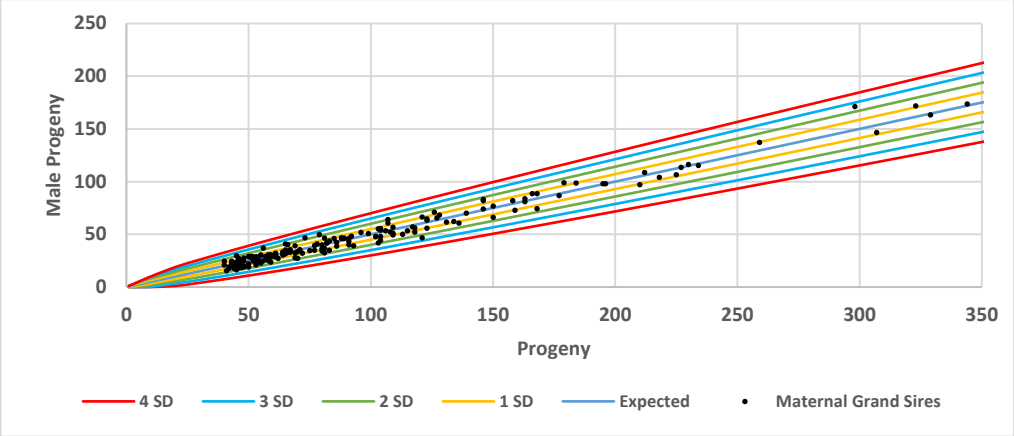

Figure 4. Number of male progeny vs number of progeny for maternal grand dams with daughters that have a minimum of 10 progeny (n=535)

CONCLUSIONS

Phenotypic variation in the Centre Plus Merinos population exists for sex ratio. However, the study was unable to capture any genetic variance from the linear mixed models that were used to assess genetic variation.

ACKNOWLEDGEMENTS

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