# Genetic evaluation for male fertility **Can information from females increase reliability?**

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### **INTRODUCTION**

In dairy cattle the successful selection for milk production traits has led to a decline in female fertility due to the unfavourable genetic correlation between fertility and production. As a result, genetic improvement programs in dairy cattle have also focused on female fertility but ignored male fertility because the artificial insemination (AI) industry was able to properly screen and standardize the quality of semen before it is widely distributed. Most published studies did not find significant genetic differences between males used for AI which could be due to prior screening of bulls. With the recent shift in the dairy industry towards the intensive use of young genomically selected bulls before adequate screening, quantifying the extent genetic variation in bull fertility has become an emerging area of research.

### QUESTIONS

- Is there a useful genetic correlation between male & female fertility to improve the reliability of genetic evaluations?
- **Did the introduction of genomic selection (GS) increase** genetic variation of male fertility?
- Is the low additive genetic variance in male fertility due to significant dominance variance?
- What is the relationship between male fertility and other economic traits including milk yield?

### **DATA & ANALYSES**

Insemination outcomes were coded as successful (1) or failed (0) of about 2 million mating records collected between 2002 and 2019 were analysed fitting all the known fixed and random effects. The insemination outcomes, called non-return rate (NRR) was assumed to be the trait of the bull (male) or cow (female) that was mated.

The analyses included data on about 5,770 AI bulls with pedigree of which 2,800 (Holsteins) had genotype data. The number of cows was over 500,000, most with repeated matings. Data were analysed using different models including the permanent and genetic effects of the bull and cow that was mated.

- The mean NRR of all matings in this study was 0.50.
- Heritability of NRR in males was lower (0.002-0.008) than females (0.016).
- The genetic correlation between male and female fertility is effectively 0 with a large standard error as the genetic variance of male fertility is small (~0.2% of the total).
- Jointly fitting the genetic and permanent environmental effect as a single component captured more variance (4 times) and the correlation between male and female fertility was even smaller.
- Correlations of bull solutions for male and female fertility (sires of the cows) varied from -0.19 to -0.34 (Table 1).
- Table 1 shows that male fertility has unfavourable correlations with traits associated with functional traits, such as survival, udder health (SCC), etc. The mechanism for this relationship is not understood at this stage and could simply be due to the sample of bulls considered.
- Genetic variance in bulls born after GS is similar to that before GS suggesting the AI industry has adequate quality control in place.

Table 1. Simple correlation of male and female fertility bull solutions with EBVs for some traits evaluated in Australia.

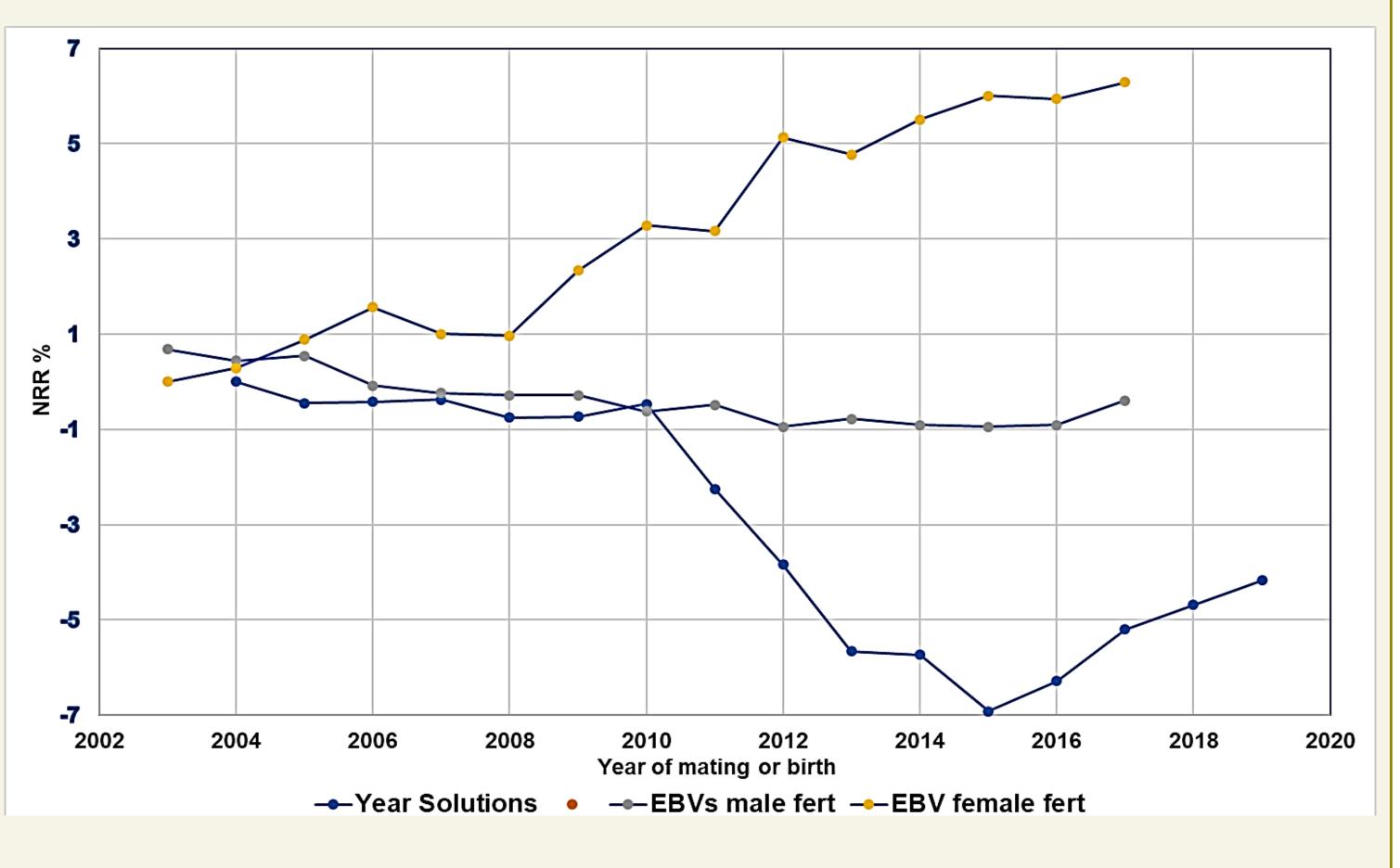
Traits	Male (EBV+PE)	Male genetic only	Female
<b>Protein yield</b>	-0.12	-0.18	0.17
Survival	-0.24	-0.52	0.61
Calving ease	-0.18	-0.38	0.45
SCC	-0.25	-0.51	0.48
Fertility	-0.19	-0.34	0.73
<b>Gestation length</b>	0.13	0.22	-0.26
Mammary system	-0.16	-0.31	0.13
Body depth	0.17	0.36	-0.56



### **RESULTS & DISCUSSION**

them using NRR data of 2800 Holstein bulls.

Fig. 1 The genetic trend for male fertility is declining while female fertility is improving due to selection that was practiced over about a decade. However, the trend in male fertility is very small and the year solutions which shows a bigger trend is the phenotypic trend.



CONCLUSIONS ✓ Male fertility has no or little genetic correlation with either female fertility or milk yield in **Australian Holsteins.** ✓ Male fertility appears to be unfavourably correlated with traits associated with functionality. ACKNOWLEDGEMENTS ✓ Data provided by DataGene ✓ DairyBio funding

• For male fertility the dominance variance was about a third of the genetic variance capture when SNP data was used to separate

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