Assessing the value of whole genome sequence in selecting for age at puberty in tropically adapted beef heifers

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INTRODUCTION

Age at puberty (AP)

- Age at which a heifer begins her reproductive life
- Favourably correlated to lifetime reproductive performance
- Heritability estimates range from 0.11(1) to 0.66(2)
- Intensive and difficult to measure

Genomic selection (GS) for AP

- Genomic selection (GS) is the use of DNA information to identify animals with high merit for AP
- Has been shown to be viable in tropically adapted heifers
- Could potentially improve cow lifetime productivity
- However, the accuracy of selection has been low (2)

OBJECTIVE

Determine if whole genome sequence (WGS) data may be used to improve selection accuracy of age at puberty (AP) across a number of tropically adapted beef breeds

METHODS

Data

- Queensland Smart Futures research herd (SMF) (3)
  - Brahman, Droughtmaster, Santa Gertrudis
  - n=3695 measured for AP
- Beef CRC(4)
  - Brahman n=868 measured for AP
  - Tropical Composite n=960 measured for AP

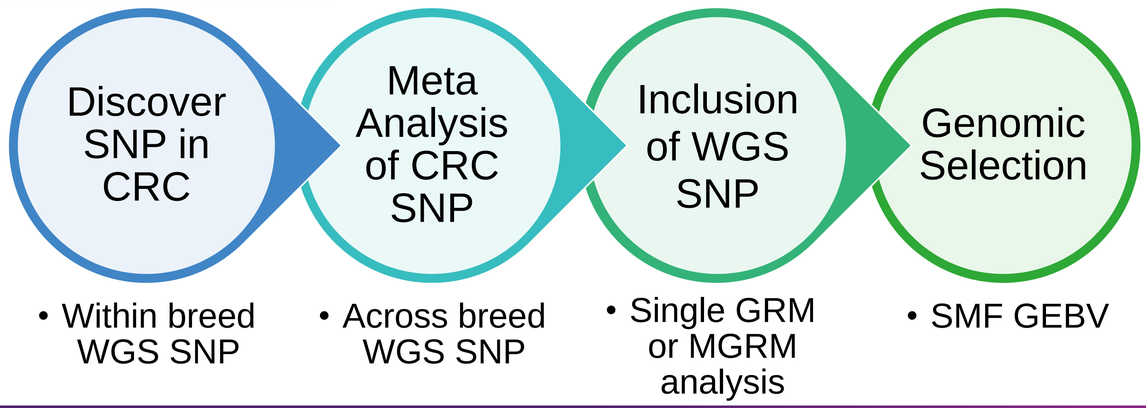
Genotypes

- All heifers imputed to 728,785 SNP (Bovine HD array)
- Further imputed to 23 million SNP (WGS)

Statistical analyses

$$AP = 1_n\mu + age + herd\_yr\_season + animal + e$$

Genomic Selection



RESULTS

Table 1: Number of significant whole genome sequence SNP discovered in Beef CRC heifers by chromosome

Chromosome	Number of SNP
3	4
5	87
14	1460
21	40
TOTAL	1591

- ~92% of significant WGS SNP are on chromosome 14
- Potentially large numbers of redundant WGS SNP due to linkage disequilibrium (LD) with significant SNP

Table 2: Average prediction accuracy for age at puberty in Smart Futures heifers by analysis

Analysis	Prediction Accuracy ± SE
6K	0.36 ± 0.04
6K plus WGS	0.40 ± 0.05
50K	0.41 ± 0.05
50K plus WGS	0.43 ± 0.06
800K	0.42 ± 0.05
800K plus WGS	0.44 ± 0.05

- Prediction accuracy improved with both increasing marker panel density and inclusion of WGS SNP
- Most benefit of WGS inclusion was seen in lower density marker panels

CONCLUSION

- Incorporation of WGS SNP beneficial in improving accuracy of AP prediction, especially in low density marker panels
- More research is required to determine if alternative methods of WGS SNP selection can further improve prediction accuracy for AP

REFERENCES

1. Engle, B.N, Corbet, N.J, Allen, J.M et al. (2019). *Journal of animal science* **97**, 90.
2. Farah, M.M, Swan, A.A, Fortes, M.R.S et al. (2016). *Animal Genetics* **47**, 3-11.
3. Burns, BM, Corbet, NJ, Allen, JM et al. (2016) Final Report University of Queensland, Saint Lucia.
4. Johnston, D, Barwick, SA, Corbet, N, et al. (2009). *Anim. Prod. Sci.* **49**, 399-412.

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