





Closing the gap: Genomic predictions in genetically diverse populations

The north Australian beef industry is unique because it consists of many beef breeds and composites that originate from two genetically different sub-species.

Beef cattle breeds in Australia can broadly be broken up into two sub-species *Bos indicus* and *Bos taurus*¹. It is believed that these two sub-species diverged from a common ancestor between approximately 332,000² and 2.0 million³ years ago. It is estimated that between $2\%^4$ and $10\%^5$ of the Australian Brahman genome is *Bos taurus* in origin.

Sub-species admixture in Australian beef **Beef cattle evolution** Bos taurus Bos indicus -330.000 vears* B. taurus x B. indicus crossbreeding is Bos tauru *Achilli *et al.* (2008) used to improve Admixed composite breeds the production and efficiency of Many B. taurus x B. indicus composite breeds have been B. indicus breeds developed in north Australia. Some whilst are stabilised composites that are maintaining now recognised as a pure breed Admixed composite tropical breeds adaptation. Challenge for genomic selection Due to time since divergence these sub-species are Bos indicus likely to have different mutations affecting economic traits. We need to accurately account for these genomic differences between sub-species to improve accuracy of genomic evaluations

Queensland Alliance for Agriculture and Food Innovation (QAAFI) qaafi.uq.edu.au

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Contact

Christie Warburton Centre for Animal Science E: c.warburton@uq.edu.au T: +61 7 3346 2714



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The aim of this research is to determine if there are differences in the DNA sequence between *Bos indicus* and *Bos taurus* breeds of cattle in order to develop accurate multibreed genetic evaluations.

Ancestral alleles in admixed populations



Analysis

We are investigating the impact of breed differences in a multi-breed genetic analysis using breed-specific DNA information. We used genotypes and puberty phenotypes from 3695 tropically adapted heifers from three purebred populations, Brahman, Santa Gertrudis and Droughtmaster. Two of these breeds, Santa Gertrudis and Droughtmaster, are stabilised composites of varying *Bos indicus* x *Bos taurus* ancestry and the third breed, Brahman, has *Bos indicus* ancestry⁶.

Results

Our results show that there are very distinct DNA differences between the three breeds in this analysis. By taking these differences into consideration in our genetic evaluations, we were able to improve our ability to estimate genetic effects for puberty in a multi-breed genetic evaluation.

Implications

- Breed-specific genetic variation can be used to account for genetic differences in diverse beef populations.
- Understanding genetic differences in beef populations will be essential for the development of accurate multi-breed genetic evaluations.
- This research is ongoing, with plans to investigate breed-specific genetic differences in larger datasets representing more beef breeds.

Researcher Profile

Christie Warburton

Christie is a second year PhD student with the Queensland Alliance for Agriculture and Food Innovation in the Centre of Animal Science. Her research interest centres on the development of genomic evaluations for the north Australian beef industry. Currently, her work is investigating novel statistical methods to implement multi-breed genomic evaluations in genetically diverse populations. Christie is passionate about the north Australian beef industry and hopes that the outcomes from her research will provide tangible benefits to beef producers.



References

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Queensland Alliance for Agriculture and Food Innovation (QAAFI)

qaafi.uq.edu.au

CRICOS Provider Number 00025B

Contact

Christie Warburton Centre for Animal Science E: c.warburton@uq.edu.au T: +61 7 3346 2714



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