

Closing the gap

Genomic prediction in genetically diverse populations

C. Warburton^A and B. Hayes^A

^A Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, QLD, Australia

CONTEXT

The Northern Australian beef industry consists of large mixed breed populations - accurate genomic predictions difficult⁽¹⁾

OBJECTIVES

Improve accuracy of genomic predictions for onset of puberty in admixed populations of tropically adapted heifers

METHODS

Phenotypes

AP –Age at first corpus luteum (days) ultrasound measurement⁽²⁾
CLScore –Score trait (0-5 score) ~600day ultrasound – proxy for AP⁽³⁾

Data

Beef CRC⁽²⁾

- Brahman and Tropical Composite
- AP measurements
- n=1828

Queensland Smart Futures research herd (SMF)⁽³⁾

- Brahman, Droughtmaster, Santa Gertrudis
- CLScore measurements
- n=3695

Statistical analyses

$AP/CLScore = 1_n\mu + age + herd_yr_season + animal + e$

Genotypes

6K (Bovine LD Array)

800K (Bovine HD array) - imputed

Further imputed to 23 million SNP (WGS) for pre-selection

Pre-selection of WGS SNP

Conditional or joint (COJO) analysis in GCTA⁽⁴⁾

- COJO 100 – 100 most significant WGS SNP
- COJO 250 – 250 most significant WGS SNP
- COJO CHR – most significant SNP within chromosome

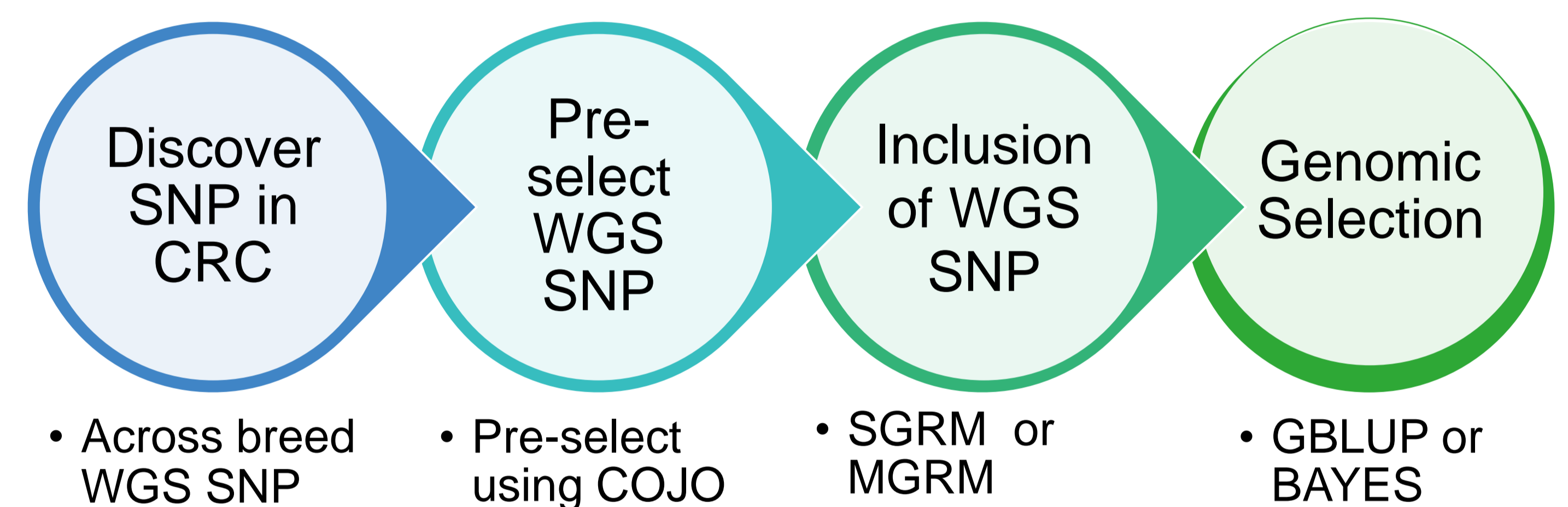
Genomic Selection

GBLUP analyses – GCTA⁽⁵⁾

- Single GRM (SGRM)
 - Marker panel SNP plus WGS SNP in single GRM
- Multiple GRM (MGRM)
 - Marker panel SNP and WGS SNP in separate GRM

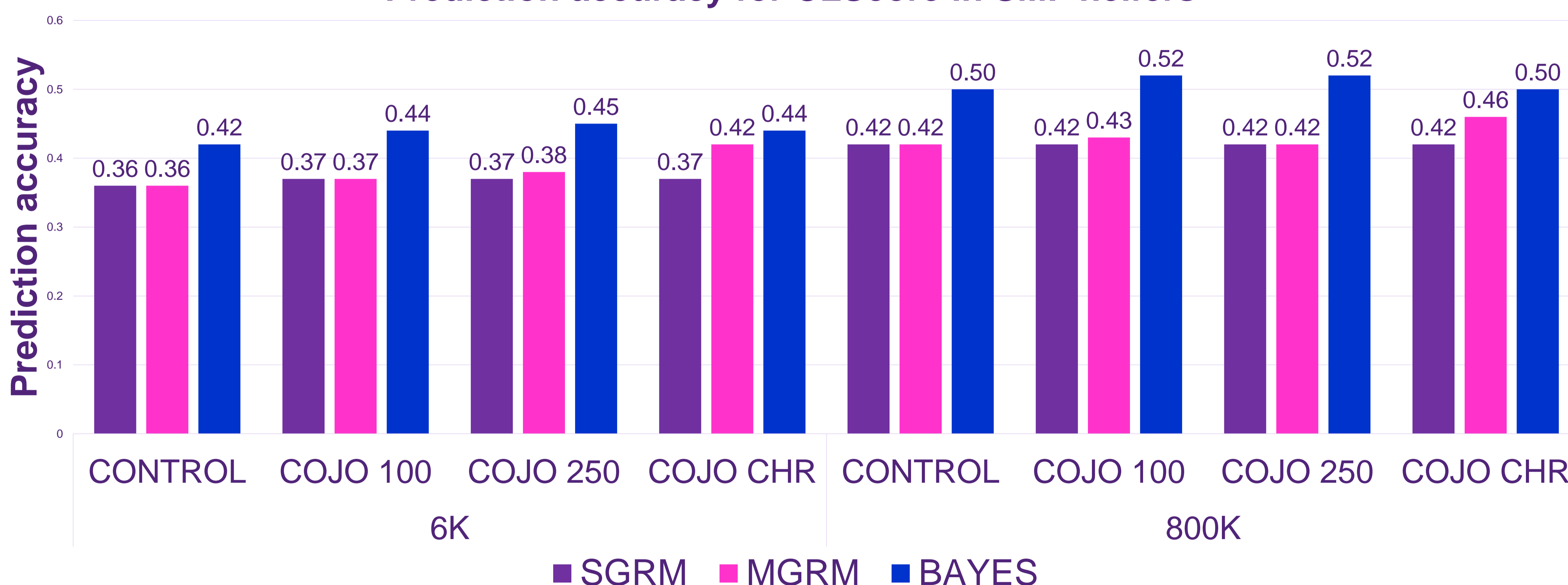
Bayesian analyses – BAYESR⁽⁶⁾

- Single GRM only



RESULTS

Prediction accuracy for CLScore in SMF heifers



Bayesian analyses = highest prediction accuracy

MGRM GBLUP analyses can improve prediction accuracy

6K panel + WGS + MGRM = 800K control accuracy

CONCLUSION

Strategic selection of WGS SNP and use of novel methods can improve prediction accuracy in admixed populations

REFERENCES

1. Warburton, C. L. *et al.* Use of whole-genome sequence data and novel genomic selection strategies to improve selection for age at puberty in tropically-adapted beef heifers. *Genet. Sel. Evol.* **52**, 28 (2020).
2. Johnston, D. *et al.* Genetics of heifer puberty in two tropical beef genotypes in northern Australia and associations with heifer- and steer-production traits. *Anim. Prod. Sci.* **49**, 399–412 (2009).
3. Engle, B. N. *et al.* Multivariate genomic predictions for age at puberty in tropically adapted beef heifers. *J. Anim. Sci.* **97**, 90–100 (2019).
4. Yang, J. *et al.* Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. *Nat. Genet.* **44**, 369–375 (2012).
5. Yang, J., Lee, S. H., Goddard, M. E. & Visscher, P. M. GCTA: A Tool for Genome-wide Complex Trait Analysis. *Am. J. Hum. Genet.* **88**, 76–82 (2011).
6. Moser, G. *et al.* Simultaneous Discovery, Estimation and Prediction Analysis of Complex Traits Using a Bayesian Mixture Model. *PLoS Genet.* **11**, e1004969 (2015).

✉ c.warburton@uq.edu.au

🏠 qaafi.uq.edu.au

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