

Implementation of single-step genomic BREEDPLAN evaluations in Australian beef cattle

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Background



- Genomic selection benefits
- DNA SNP microarrays (cheap, accurate)
- Changing dairy - limited use in beef
- Include in existing evaluations
- Drive increased rates genetic progress

BREEDPLAN genetic evaluations



- system developed at AGBU (last 30yrs)
- multi-trait animal linear models (+ threshold)
- evolving use DNA-marker based info
 - prediction equations + independent calibration
 - multi-trait and blending (multi-source) into EBVs
- simplify using SS-GBLUP

[Legarra *et al.* 2014]

➤ **R&D include SS-GBLUP into BREEDPLAN evaluations**

Implementation of SS-GBLUP



July 2016 Brahman GROUP BREEDPLAN															
200	400	600	800	1000	1200	1400	1600	1800	2000	2200	2400	2600	2800	3000	3200
Wt	Wt	Wt	Wt	Wt	Wt	Wt	Wt	Wt	Wt	Wt	Wt	Wt	Wt	Wt	Wt
95%	95%	95%	95%	95%	95%	95%	95%	95%	95%	95%	95%	95%	95%	95%	95%
+2.9	+21	+18	+23	+26	-2	+0.4	+7.1	+14	+3.3	0.2	-0.6	+0.7	-0.06	-0.21	
89%	96%	97%	97%	95%	92%	96%	91%	86%	87%	66%	72%	63%	66%	66%	
+3.7	+28	+37	+55	+61	-1	-0.3	-9.6	+38	-0.6	+0.1	-0.4	+0.6	-0.01	-0.21	
90%	96%	97%	97%	96%	92%	96%	92%	89%	70%	68%	75%	64%	70%	70%	
+0.9	+16	+16	+22	+17	-1	+0.8	-5.4	+12	+3.7	0.0	-0.7	+0.9	-0.12	+0.29	
90%	97%	97%	96%	96%	93%	97%	92%	89%	73%	72%	81%	65%	84%	75%	
+1.8	+16	+21	+32	+33	-8	+0.3	-9.9	+21	+2.4	-0.3	+0.2	+0.6	-0.21	+0.34	
91%	97%	97%	96%	97%	93%	97%	92%	90%	75%	73%	82%	67%	83%	77%	

- 1) Develop genomic pipeline
- 2) Procedures to build G
- 3) Modify mixed model equations
- 4) New accuracy and solver algorithms
- 5) Testing in breeds
- 6) Implement in regular runs

1) Robust genomic pipeline



a) databases to receive raw genotypes

- different SNP platforms, labs, ident
- numerous breeds

b) matching across databases

- labs, countries, breeds

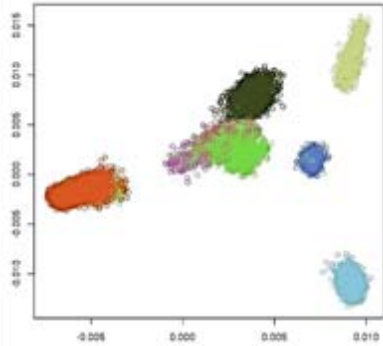
c) genotype quality control checks

- resolve duplicates
- call rates & GC scores
- # missing SNP & MAF
- gender check

[Connors *et al.* 2017]

➤ **Ongoing, routine processing of industry genotypes**

2) Building G matrix



a) genomic breed % check

[Boerner 2017]

b) parentage check (OH approach)

[Hayes *et al.* 2011]

➤ discrepancies G vs A_{22}

c) re-build pedigree

d) impute to common SNP density

[Ferdosi *et al.* 2014]

e) build G

[VanRaden 2008]

➤ **Automated building G each breed**

3) Modified mixed model equations

- **Replace A^{-1} with H^{-1}**

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} - A^{22} \end{bmatrix}$$

[Aguilar *et al.* 2010]

- **Weighting G**

- empirical approach to determine λ

$$G = \lambda G_m + (1 - \lambda) A_{22}$$

[Zhang *et al.* 2017]

- **Explicit fitting genetic groups**

- can't fit dummy ancestors in A^{-1}

- **All fixed, random effects remain unchanged**

4) New accuracy and solver algorithms

- **New accuracy approximation**

[Li *et al.* 2017]

- based effective number of progeny (EPN) approx.
- computes EPN genomic contributions
- add existing EPN phenotypic data
- compared with PEV

- **New solver**

- explicit genetic groups
- improved PCG solver – dense H^{-1} matrix
 - multi-threading (MKL and OpenMP)
 - new solver 450M equations < 24hrs

5) Testing in breed



- **Angus**

- **29,441** animals in G
- 2,215,744 not in G
- 24 traits (d,m)
- 16 genetic groups



- **Brahman**

- **10,905** animals in G
- 420,523 not in G
- 23 traits (d,m)
- 17 genetic groups

5) Testing in breed – Results



- increased accuracies
- increased EBV spread
- variable changes
 - existing accuracies, h^2
 - relatedness to reference poplⁿ
- similar but not identical to blending
- comparable run times

Future work



- Additional breeds
 - sufficient numbers to build G
 - build size reference populations
- New models/methods
 - hybrid models
 - recursive algorithms
 - updating G^{-1}
 - including crossbreds
 - improved diagnostics
- SS - threshold models (CE, temp)

Building genomic reference populations

- more beef breeds
- hard to measure \$\$ traits
- relevant genetics



reproduction



carcase
&
meat quality

BUT

- who pays **P**henotypes ?
- who pays for **G**enotypes ?
- who benefits most?

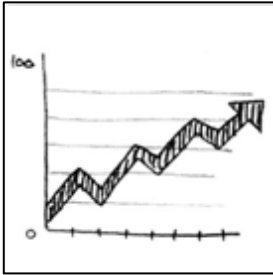
feed intake
&
efficiency



disease



Conclusions



- implemented routine BREEDPLAN evaluations
- genomic pipelines to build G
- run SS-GBLUP effectively
- need build size reference populations

➤ **Driving faster rates genetic progress for the breeding objective**

Acknowledgements

