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

David J. Johnston*, MH Ferdosi, NK Connors, V. Boerner, J Cook, CJ Girard, AA Swan, B Tier

Animal Genetics and Breeding Unit, University of New England, Armidale, AUSTRALIA
• 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

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, idents
   - numerous breeds

b) **matching across databases**
   - labs, countries, breeds

c) **genotype quality control checks** [Connors et al. 2017]
   - resolve duplicates
   - call rates & GC scores
   - # missing SNP & MAF
   - gender check

➢ **Ongoing, routine processing of industry genotypes**
2) Building G matrix

a) genomic breed % check

b) parentage check (OH approach)
   - discrepancies $G$ vs $A_{22}$

c) re-build pedigree

d) impute to common SNP density

e) build G

➤ Automated building $G$ each breed

[Boerner 2017]
[Hayes et al. 2011]
[Ferdosi et al. 2014]
[VanRaden 2008]
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 $\lambda$
  \[ G = \lambda G_m + (1 - \lambda)A_{22} \]  
  [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**
  - 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

[Li et al. 2017]
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

BUT

- who pays Phenotypes ?
- who pays for Genotypes ?
- who benefits most?
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