Comparison of Genomic Selection Models for Wheat Breeding

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Genomic or Genomewide Selection (GS)

• MAS without identifying markers associated with a trait
• Considers all markers without significance test
• Prediction of genomic estimated breeding values (GEBVs)
• Captures major and small effect QTL
• Unbiased marker effect estimates
• No multiple testing
Genomic Selection Procedures

Training population

Phenotypes

+ Marker Genotypes

Train Model

Marker Genotypes

Selection candidates

\[ GEBV = \sum_{i=1}^{p} X_i \hat{g}_i \]

\[ y = \mu + x g + \varepsilon \]

Estimate marker effects
Cross-validation

Selection
Genomic Selection

• Widely used in livestock breeding programs
  - Long generation interval
  - Milk production on bulls, meat quality

• Improved genetic gain

• Growing interest in crop breeding programs

• Insufficient information for practical application

• Empirical studies are necessary to validate GS in wheat breeding
Hypothesis:

• GS has the potential to predict GEBVs with accuracy sufficient to allow selection without repeated phenotyping.

Objectives:

1) To evaluate single and multiple trait GS models for wheat breeding.

2) To examine prediction accuracy when modelling G × E interaction.
Single and Multiple Trait Prediction

- 231 Spring bread wheat lines
- Genotyped using the wheat 90K iSelect assay
- 18K polymorphic SNPs used for analysis
- Traits
  - Days to heading
  - Days to maturity
  - Plant height
  - Grain yield
  - Test weight
  - 1000-kernel weight
  - Grain protein
  - Falling number
  - SDS sedimentation
Statistical Methods

1) Single Trait Models
- Ridge regression BLUP
- Genomic BLUP
- Bayesian Lasso
- Bayesian ridge regression
- BayesA
- BayesB
- BayesC
- RKHS
- RKHS-KA

2) Multiple Trait Models
- MT-BayesA
- MT-BayesA matrix
- MT-BayesA scale

• Models were fitted in R
  BGLR package (Perez and de los Campos, 2014)
  rrBLUP package (Endelman, 2011)
  C programs (Jiang et al., 2015)
Fivefold Cross-Validation

• Divide the population into five groups
• Use four to train the model and one to validate
• Accuracy in each fold is the correlation between GEBVs and phenotypes of individuals in the validation
• Repeated until each group is used as validation
• Averages of the fivefold reported
Modelling $G \times E$ Interaction

- 81 spring bread wheat lines
- Three approaches using G-BLUP (Lopez-Cruz et al., 2015)
  1) $M \times E$ interaction model ($M \times E$)
  2) Across-environment (AcrossEnv)
  3) Single-environment (SingleEnv)
- 80% TP : 20% validation
- Prediction was made for grain yield
- Two cross-validation schemes
# Cross-Validation Schemes

## CV1: Prediction for newly developed lines

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<th>E2</th>
<th>E3</th>
<th>E4</th>
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<td>Y52</td>
<td>Y53</td>
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## CV2: Prediction for incomplete field trials

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*Jarquín et al. 2014*
Results
Single Trait Prediction Accuracy

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<tr>
<th>Trait</th>
<th>RR-BLUP</th>
<th>G-BLUP</th>
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<th>BB</th>
<th>BC</th>
<th>BL</th>
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Multiple Trait Prediction Accuracy

![Bar chart showing the prediction accuracy of different traits using various methods. The traits include HD, HT, MAT, YLD, TWT, TKW, PRO, FN, and SDS. The methods compared are ST-BayesA, MT-BayesA, MT-BayesA Matrix, and MT-BayesA Scalar. The accuracy is measured as the correlation coefficient (r(GEBV:Phenotype)).]
Modelling GxE Interaction (Yield)

CV1

CV2

KER: Kernen
SWC: Swift Current
Conclusion

• No difference among single trait prediction models.
• Multiple trait prediction accuracy was similar or lower than single trait prediction accuracy.
• No relationship between trait heritability and accuracy.
• No benefit of modelling $G \times E$ interaction.
• Accuracies obtained in this study are encouraging.
• In wheat, GS can be implemented using G-BLUP.
Acknowledgements

- Dr. Curtis Pozniak
- Advisory Committee
  - Dr. Aaron Beattie
  - Dr. Fiona Buchanan
  - Dr. Pierre Hucl
  - Dr. Yuguang Bai
- Durum field crew
- Durum molecular lab crew
- Wheat quality lab crew
- Durum professional staff
Thank You!