

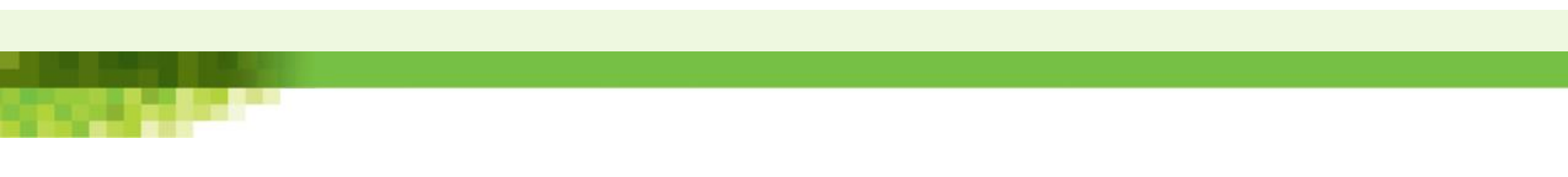
Comparison of Genomic Selection Models for Wheat Breeding

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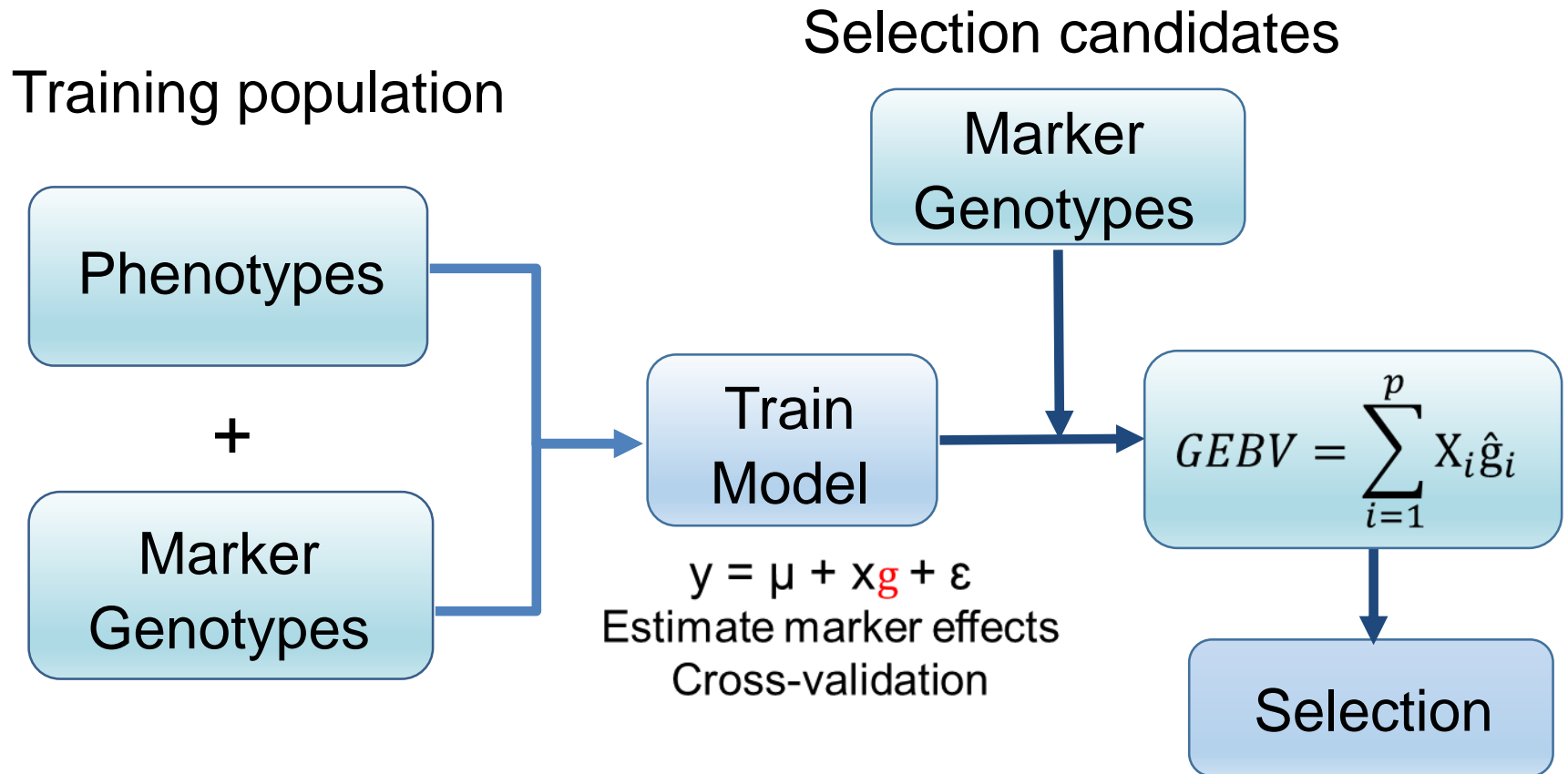
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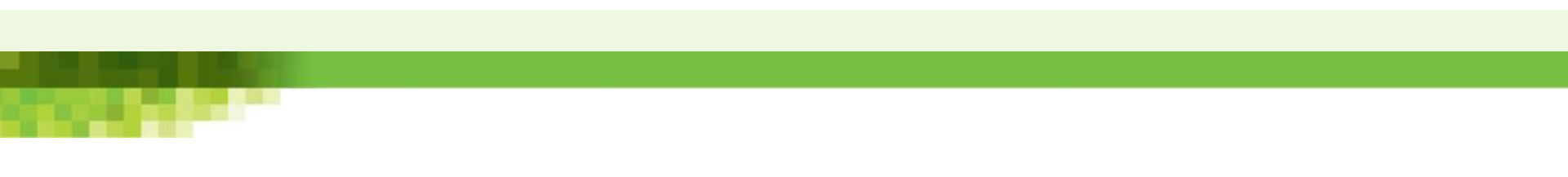
Genomic or Genomewide Selection (GS)

- 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
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Genomic Selection Procedures



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
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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 $G \times E$ 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

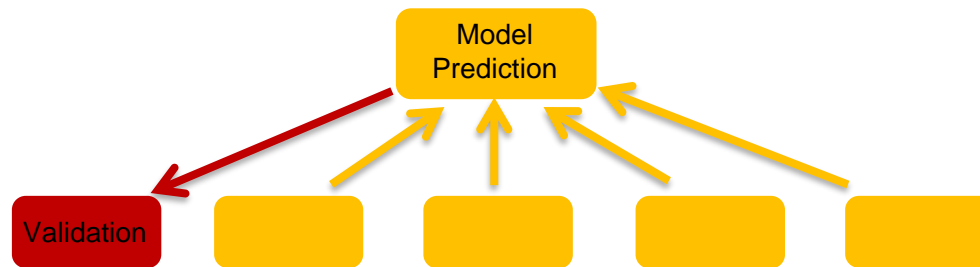
- Ridge regression BLUP
- Genomic BLUP
- Bayesian Lasso
- Bayesian ridge regression
- BayesA
- BayesB
- BayesC
- RKHS
- RKHS-KA

2) Multiple Trait Models

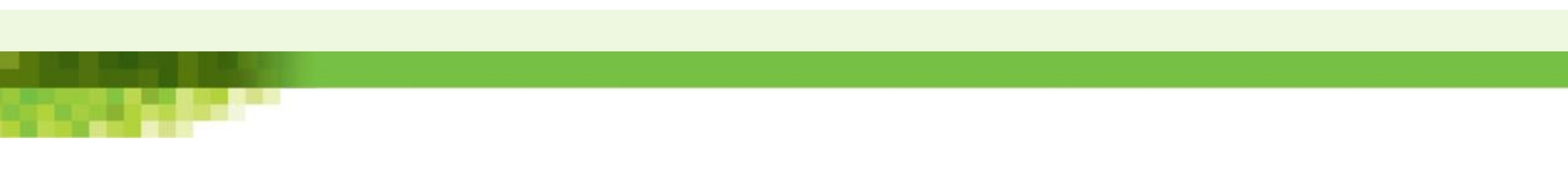
- MT-BayesA
- MT-BayesA matrix
- MT-BayesA scale
- Models were fitted in R
 - BGLR package (Perez and de los Campos, 2014)
 - rrBLUP package (Endelman, 2011)
 - C programs (Jiang et al., 2015)

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
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Cross-Validation Schemes

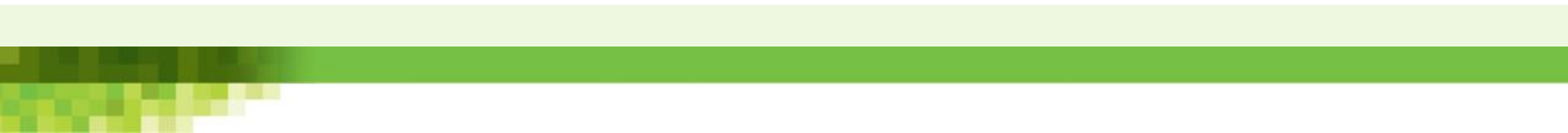
CV1: Prediction for newly developed lines

	E1	E2	E3	E4	E5
Line 1	Y11	Y12	Y13	Y14	Y15
Line 2	Y21	Y22	Y23	Y24	Y25
Line 3	NA	NA	NA	NA	NA
Line 4	Y41	Y42	Y43	Y44	Y45
Line 5	Y51	Y52	Y53	Y54	Y55

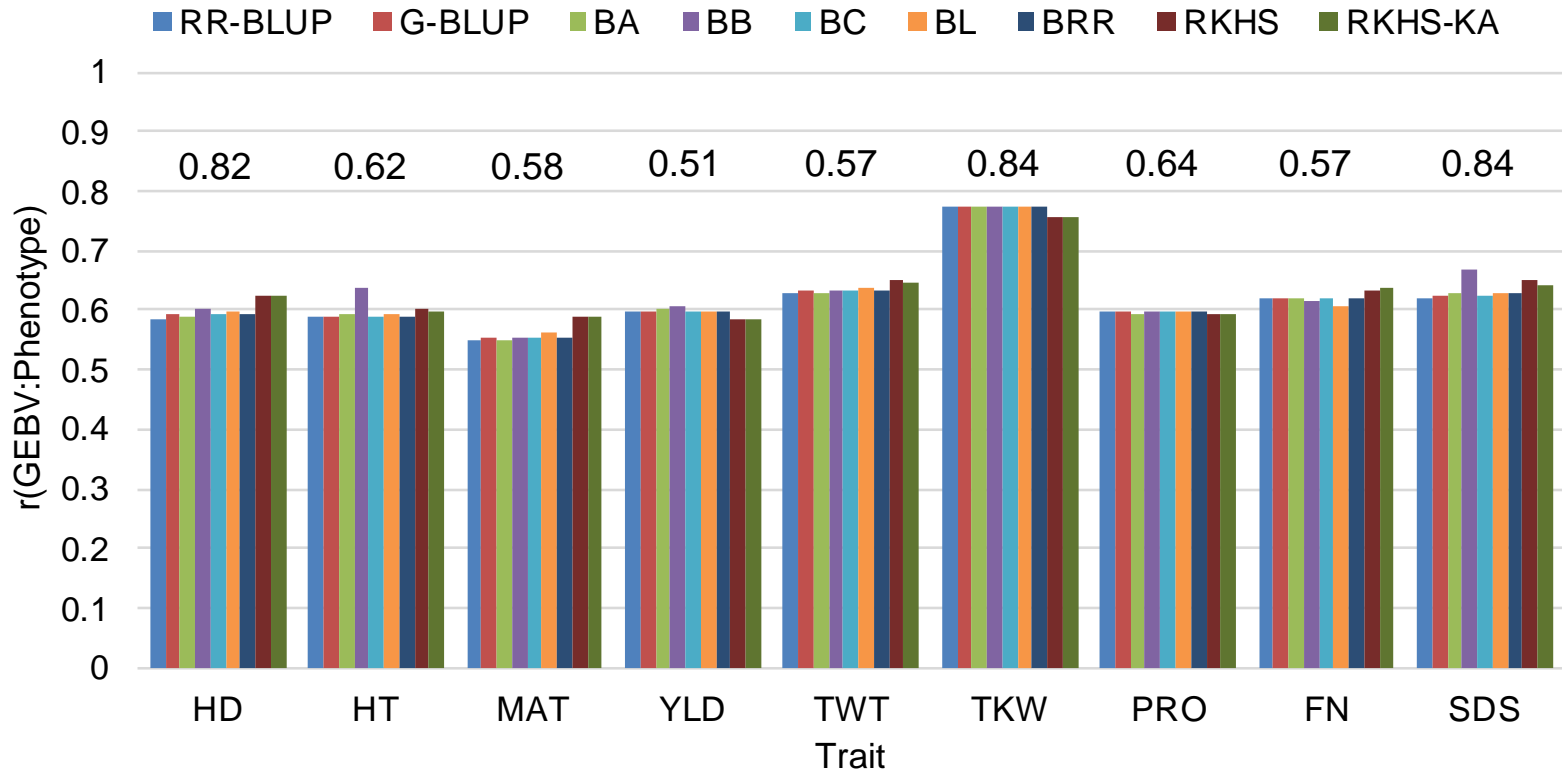
CV2: Prediction for incomplete field trials

	E1	E2	E3	E4	E5
Line 1	Y11	NA	Y13	Y14	Y15
Line 2	Y21	Y22	NA	Y24	Y25
Line 3	Y31	Y32	Y33	Y34	NA
Line 4	Y41	Y42	Y43	NA	Y45
Line 5	NA	Y52	Y53	Y54	Y55

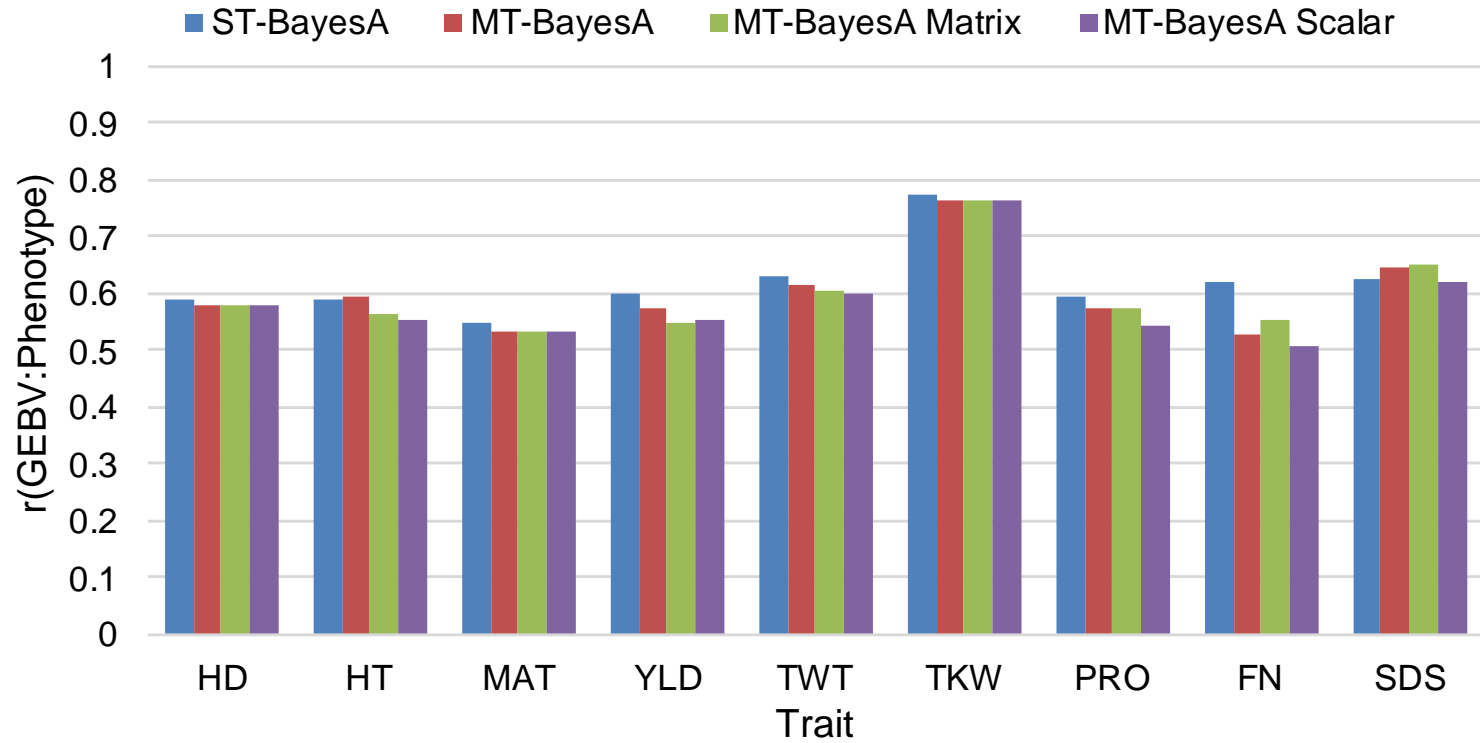
Results



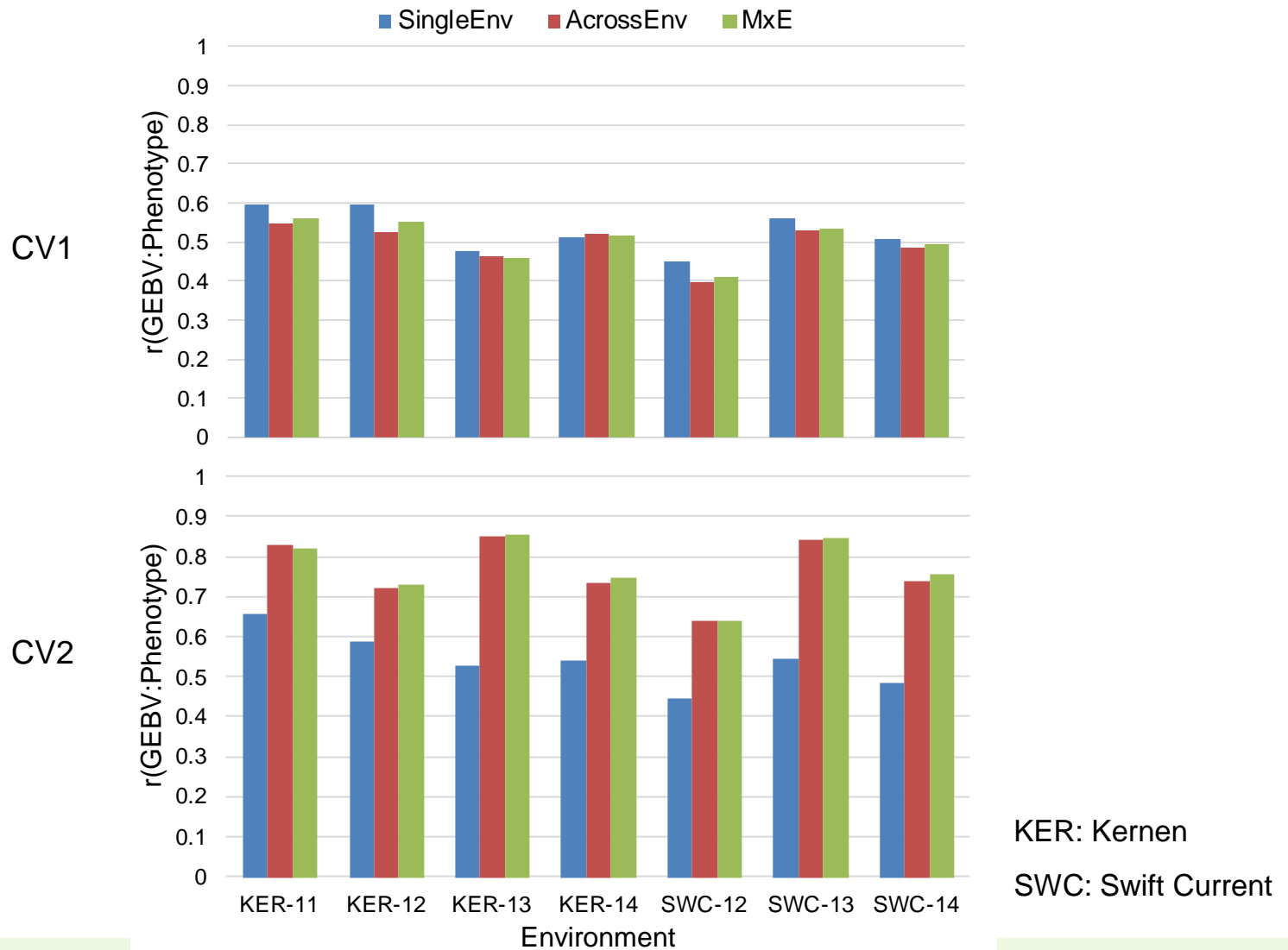
Single Trait Prediction Accuracy



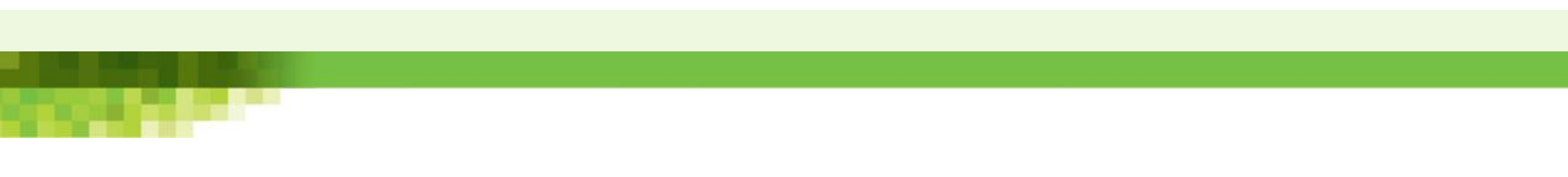
Multiple Trait Prediction Accuracy



Modelling GxE Interaction (Yield)



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.
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Thank You!

