

Genomes to Fields 2014 Workshop

$G \times E$ ANALYSIS

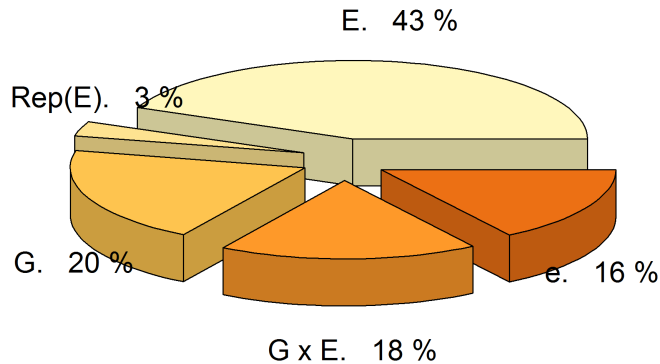
Diego Jarquin

Chicago, IL

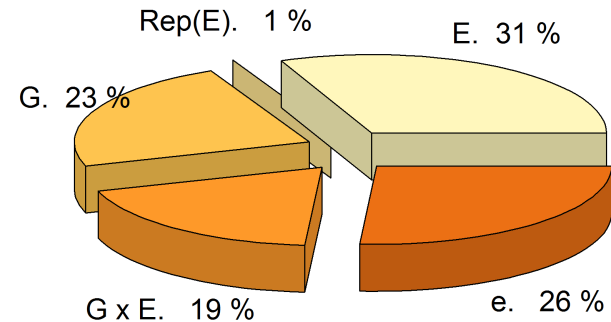
December 10

Variance components for common inbreds and hybrids

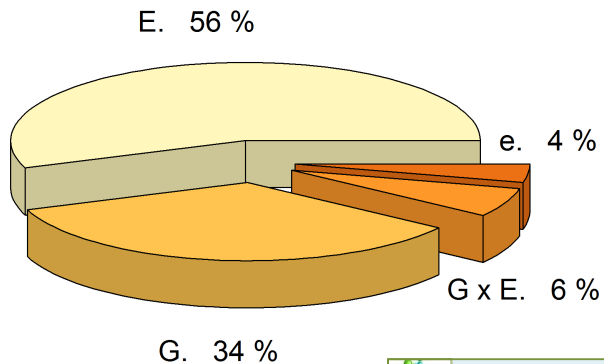
Inbred – Pollen DAP



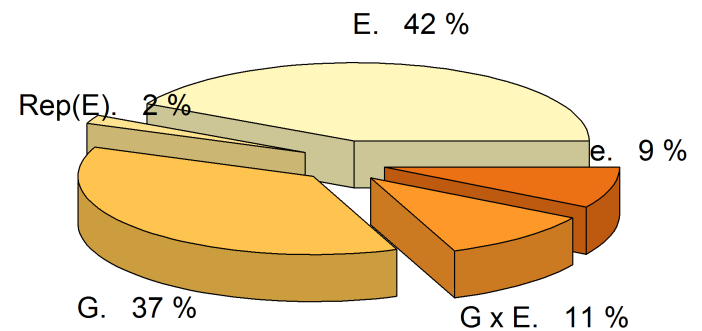
Inbred – Plant height



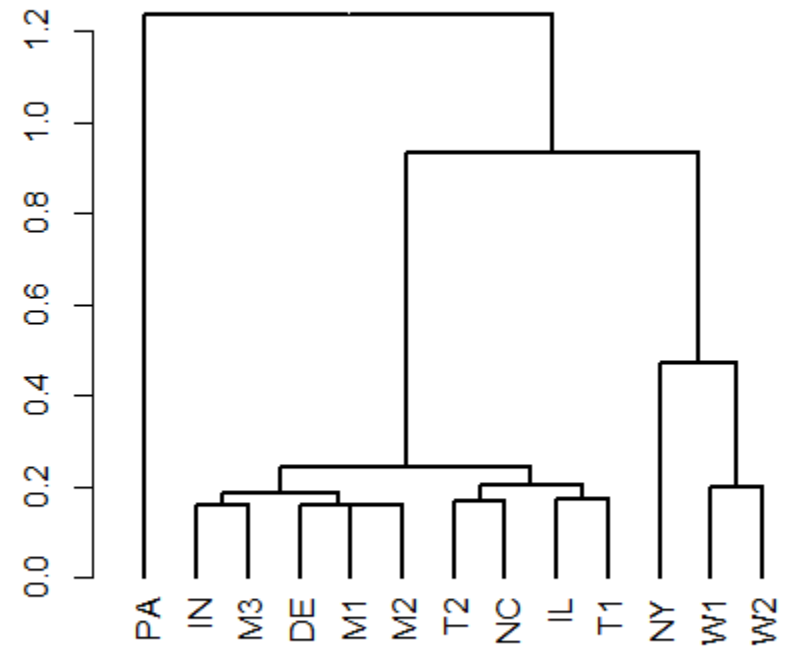
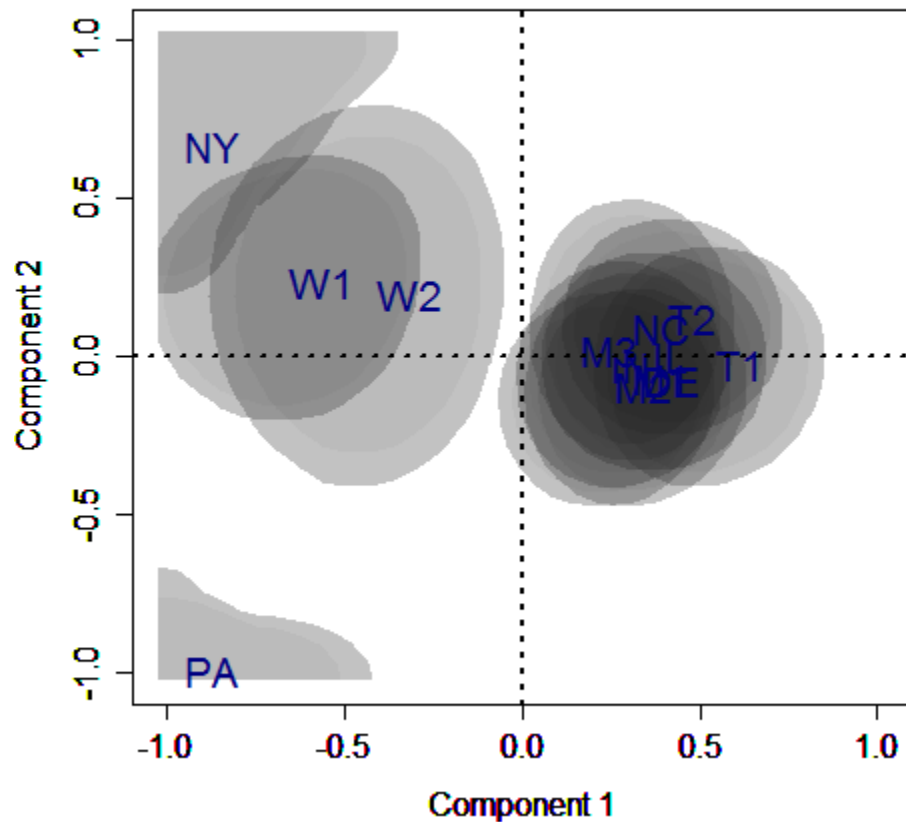
Hybrid – Pollen DAP



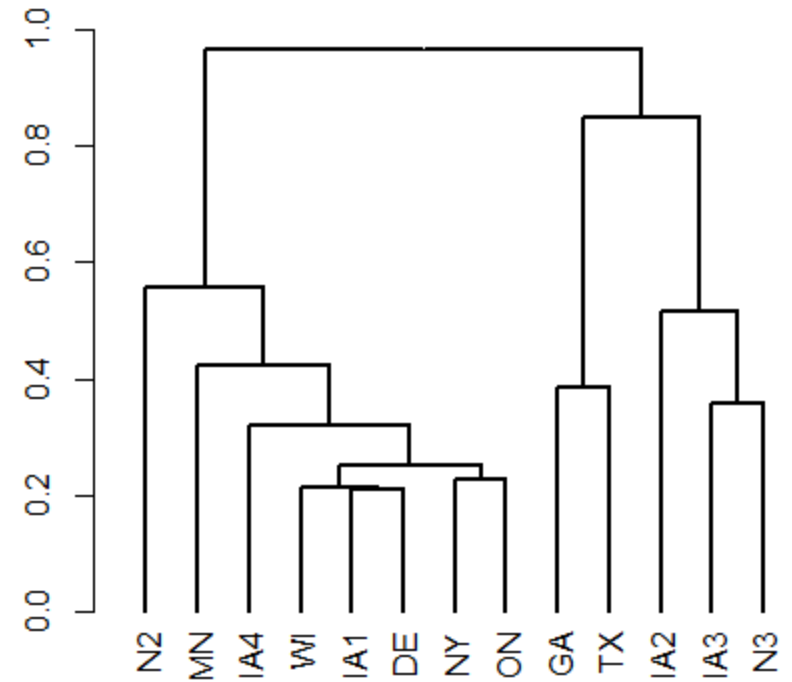
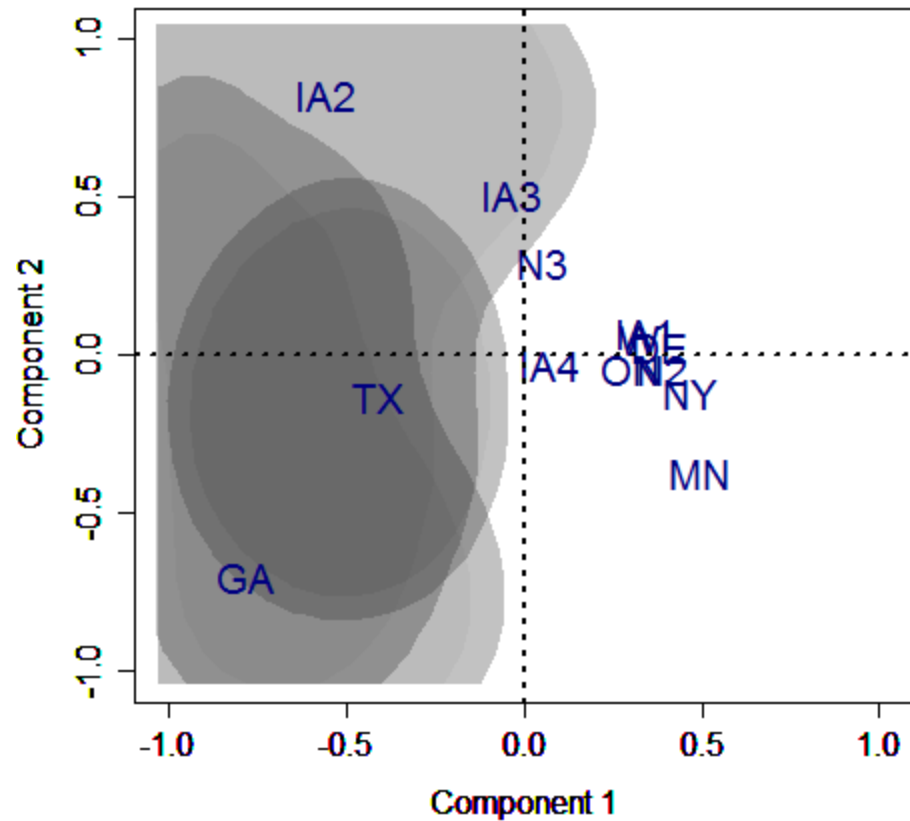
Hybrid – Plant height



Bayesian AMMI Analysis for Inbreds – Plant Height

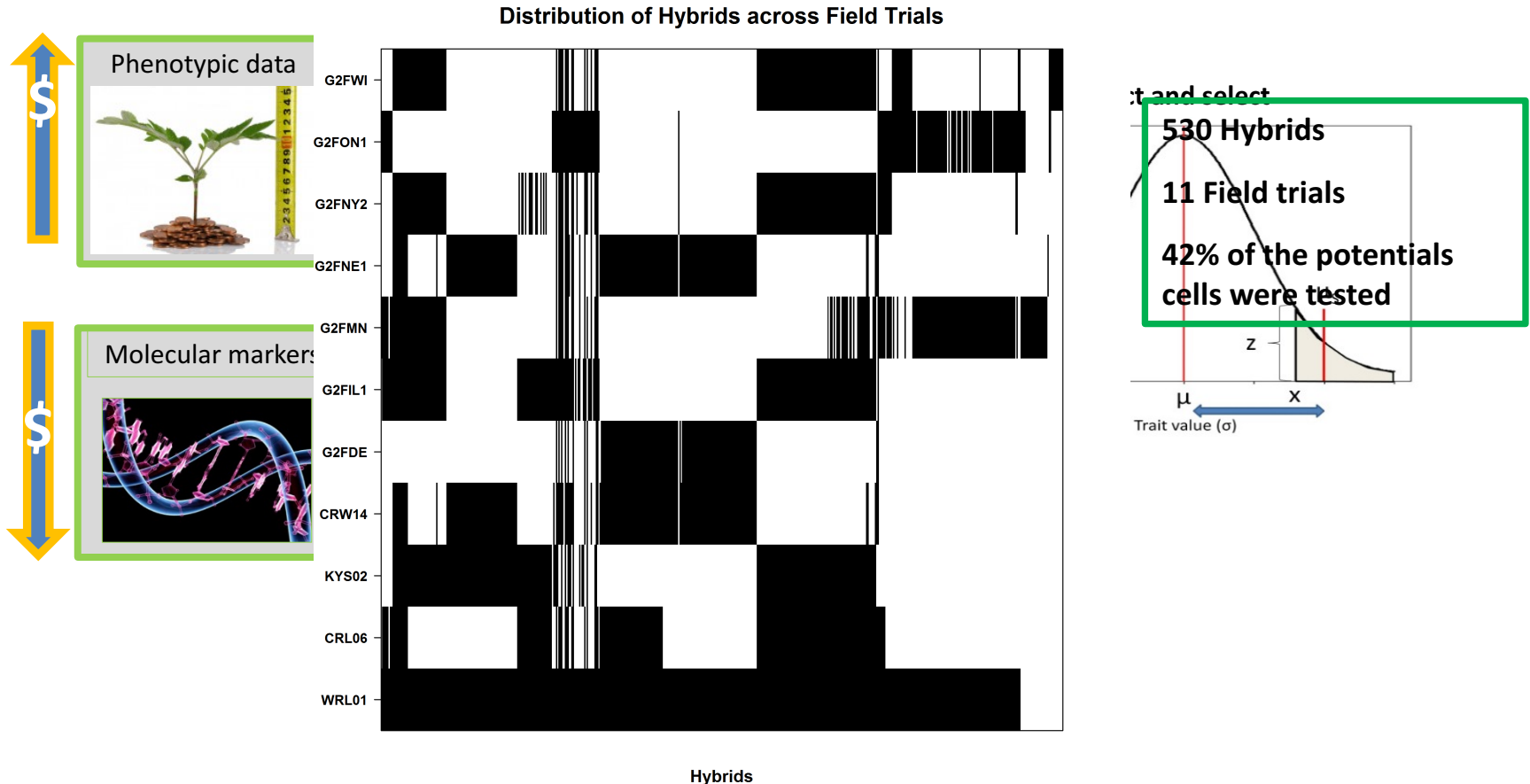


Bayesian AMMI Analysis for Hybrids - Plant height



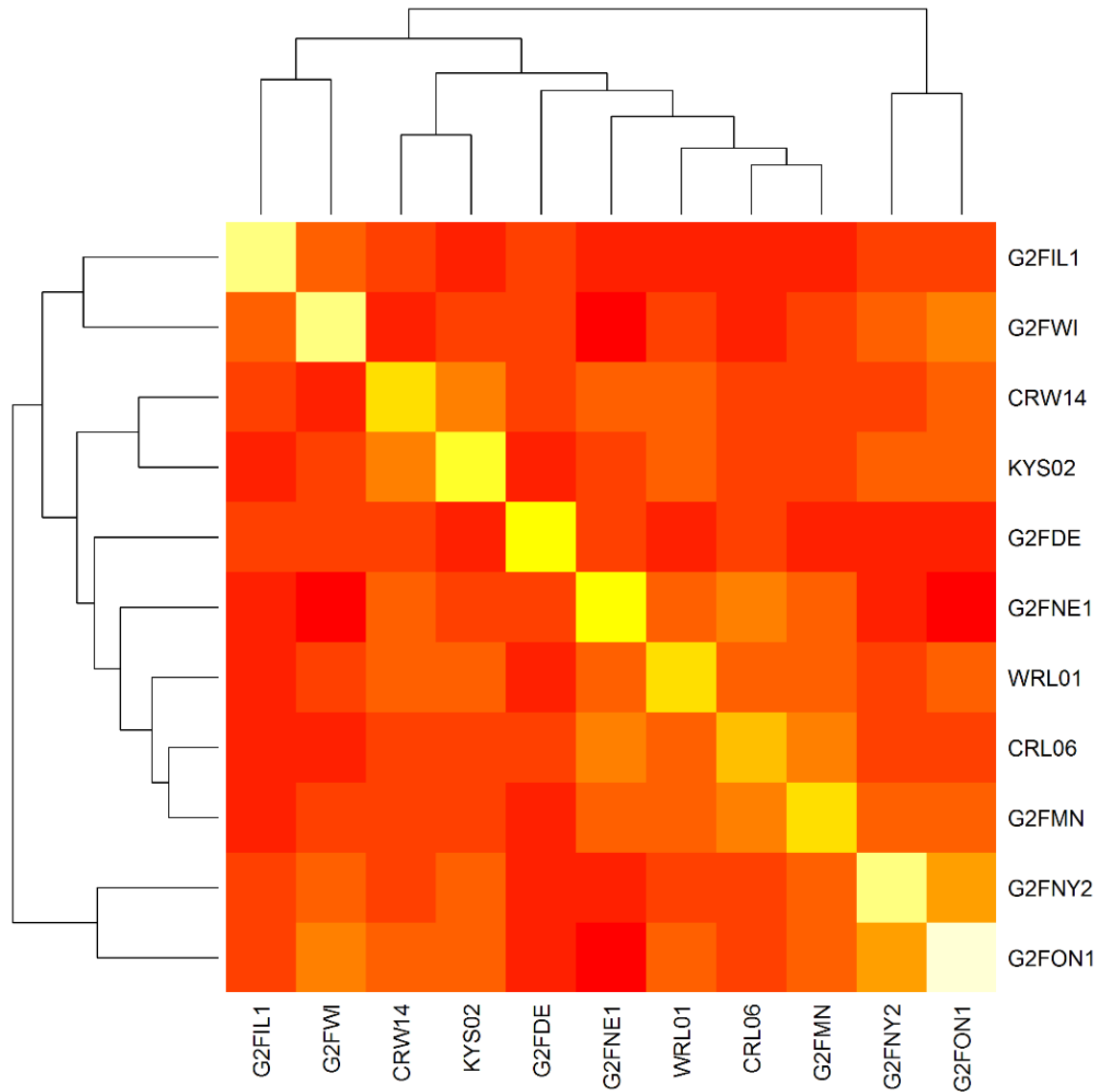
Genomic Prediction

- ✧ Predict performance of hybrids using their whole-genome marker profiles.
- ✧ Potential to save time and money
- ✧ How? Using genotypes and phenotypes to train a model to predict how each genotype is expected to perform in each environment.



Genomic Prediction

Similarities among environments based on environmental covariates



Cross-validation schemes

**Leave-one-out CV
within trials - Baseline**

	E1	E2	E3	E4	E5
Line 1	Y_{11}	Y_{12}	NA	Y_{14}	Y_{15}
Line 2	Y_{21}	Y_{22}	Y_{23}	Y_{24}	Y_{25}
Line 3	Y_{31}	Y_{32}	Y_{33}	Y_{34}	Y_{35}
Line 4	Y_{41}	Y_{42}	Y_{43}	Y_{44}	Y_{45}
Line 5	Y_{51}	Y_{52}	Y_{53}	Y_{54}	Y_{55}

**CV0 - Predicting new
trials**

	E1	E2	E3	E4	E5
Line 1	Y_{11}	Y_{12}	NA	Y_{14}	Y_{15}
Line 2	Y_{21}	Y_{22}	NA	Y_{24}	Y_{25}
Line 3	Y_{31}	Y_{32}	NA	Y_{34}	Y_{35}
Line 4	Y_{41}	Y_{42}	NA	Y_{44}	Y_{45}
Line 5	Y_{51}	Y_{52}	NA	Y_{54}	Y_{55}

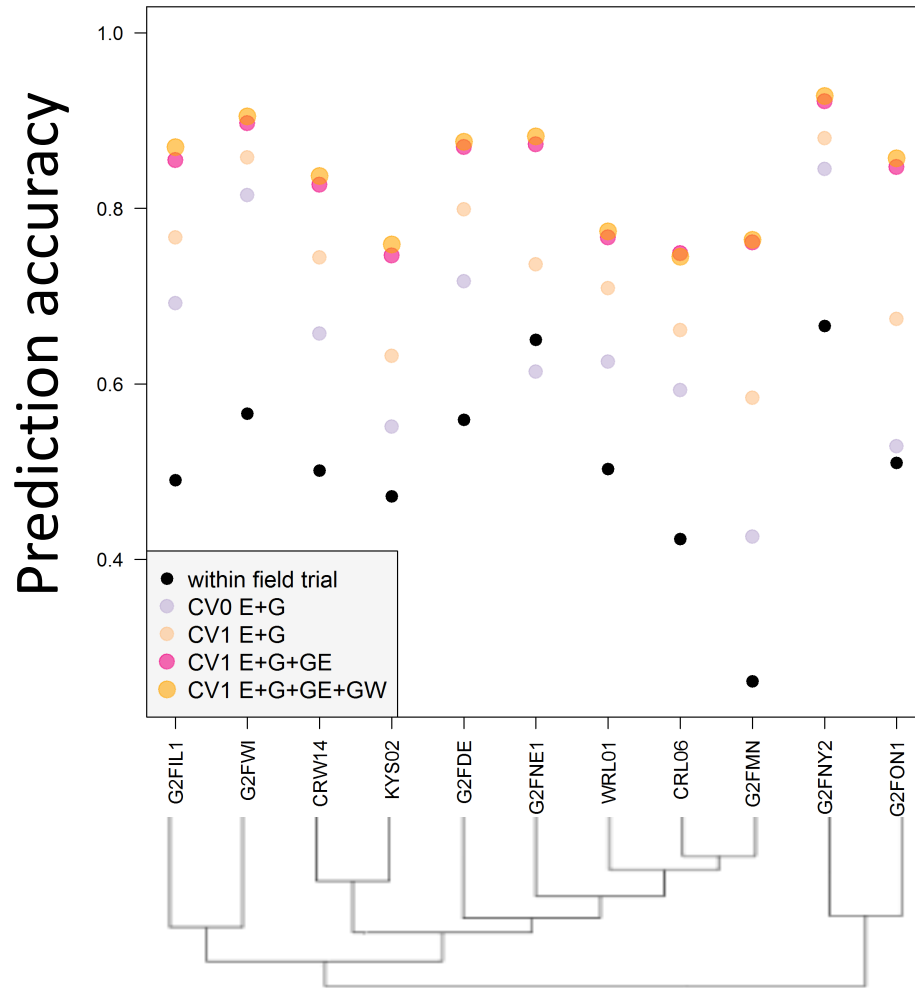
**CV1 - Predicting new
hybrids**

	E1	E2	E3	E4	E5
Line 1	Y_{11}	Y_{12}	Y_{13}	Y_{14}	Y_{15}
Line 2	Y_{21}	Y_{22}	Y_{23}	Y_{24}	Y_{25}
Line 3	NA	NA	NA	NA	NA
Line 4	Y_{41}	Y_{42}	Y_{43}	Y_{44}	Y_{45}
Line 5	Y_{51}	Y_{52}	Y_{53}	Y_{54}	Y_{55}



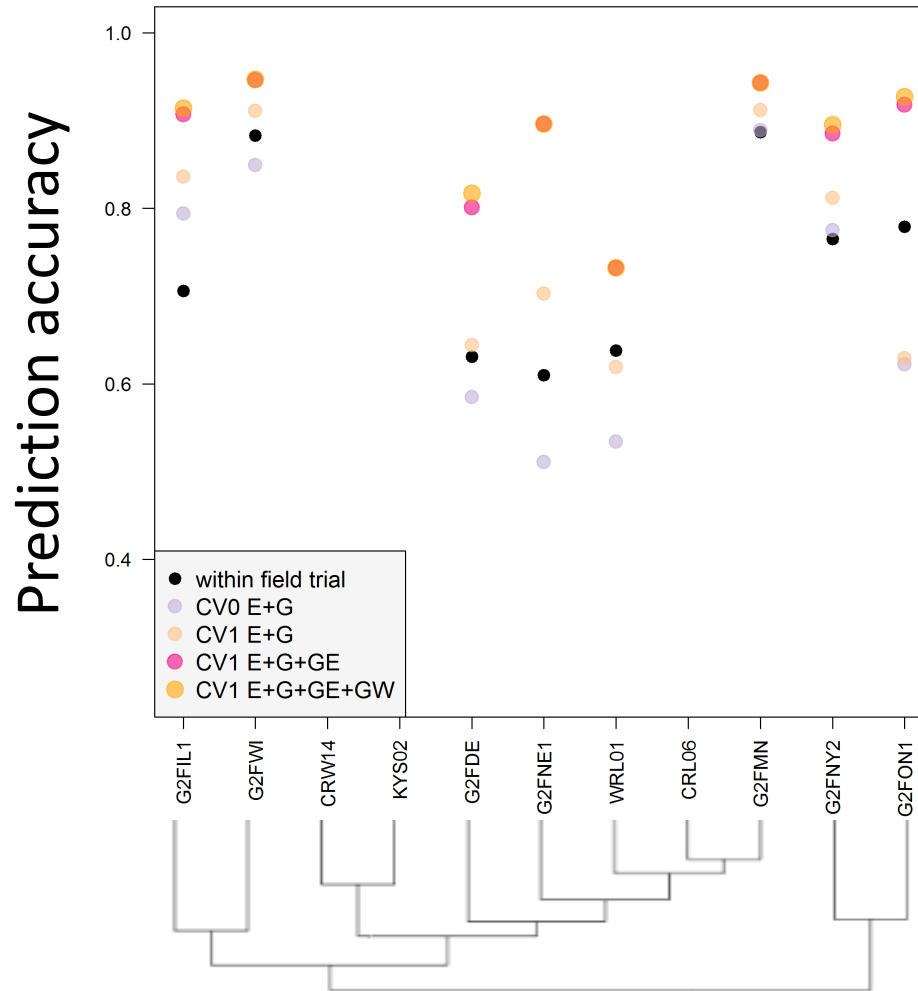
Genomic prediction

Plant height

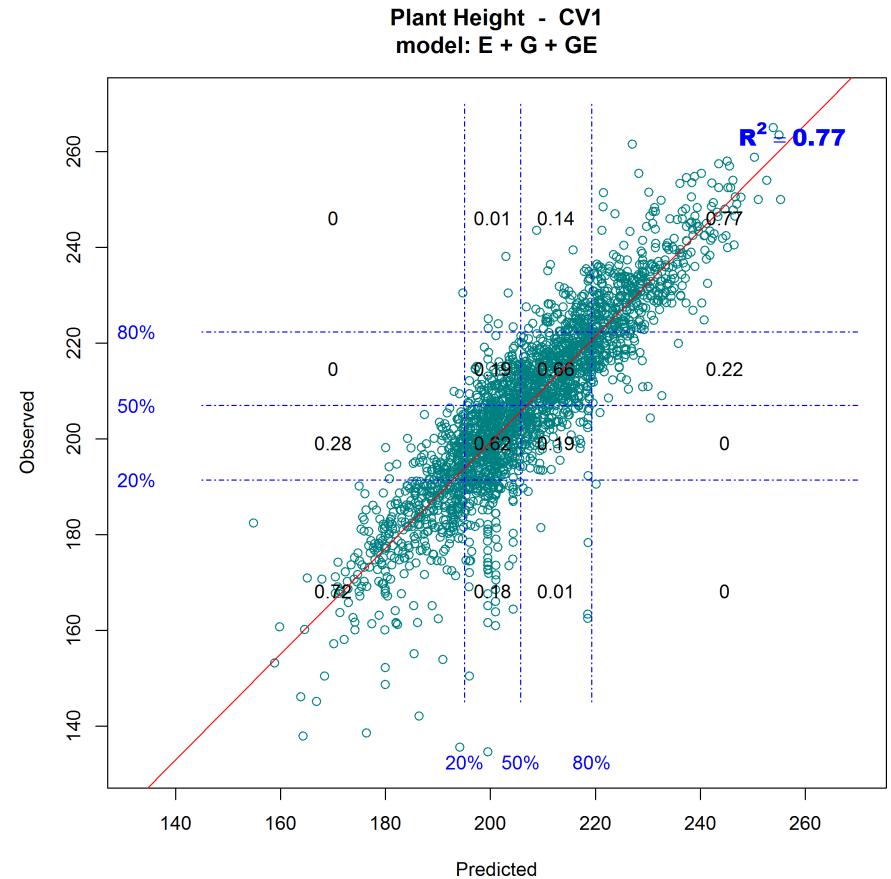
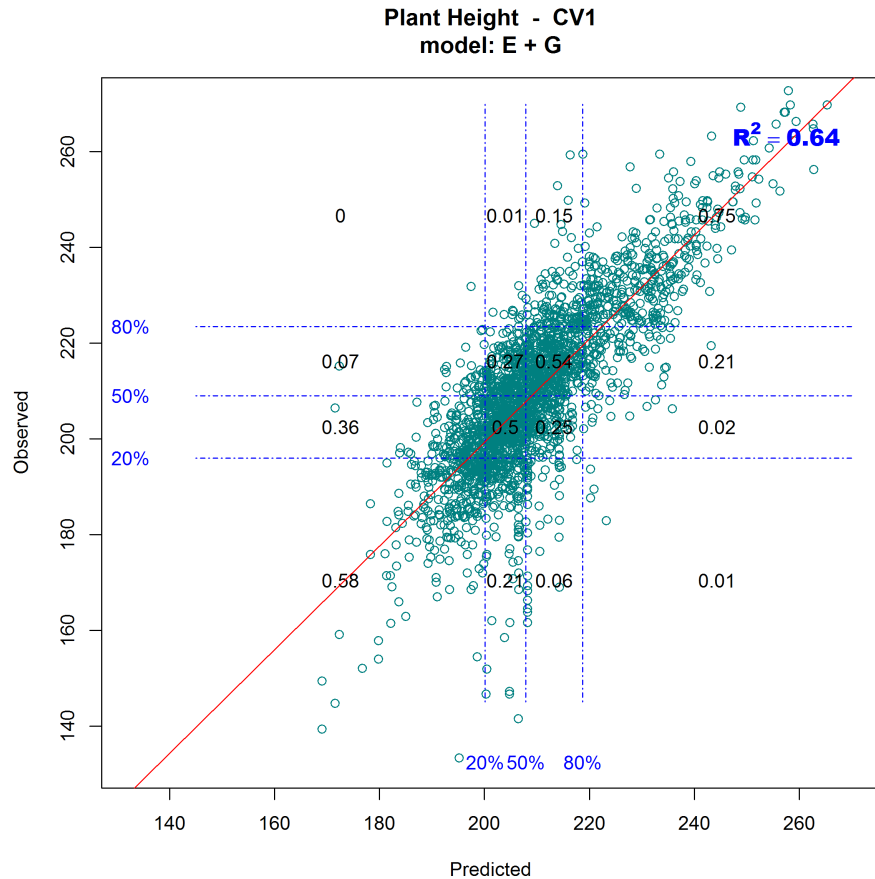


Genomic prediction

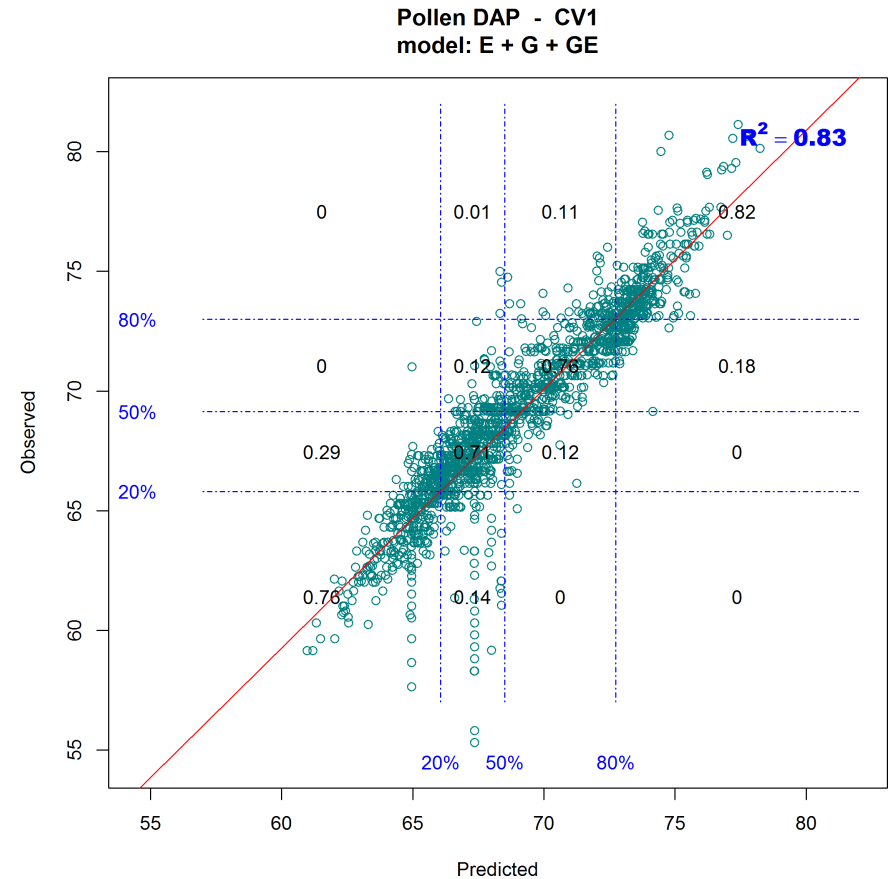
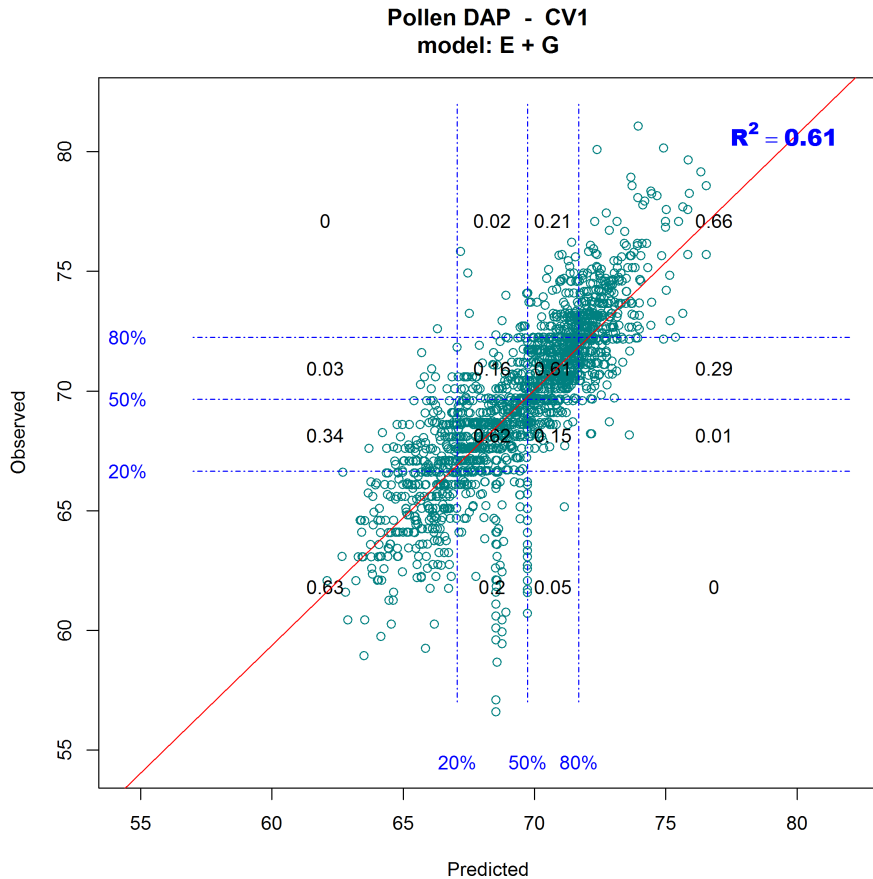
Pollen DAP



Observed vs predicted – Plant Height



Observed vs predicted – Pollen DAP



Final Remarks

- ✧ With large phenotypic and genotypic sets, good predictions for new environments (CV0) can be expected (E+G model).
- ✧ By including information on the performance of other hybrids tested in these environments (CV1), accuracy was improved up to 38% using E+G model.
- ✧ Best results were obtained **considering the interaction components (GE or GW)**, increasing prediction accuracy up to 75% compared to CV0.
- ✧ These results highlight the importance of capturing GxE effects for predicting phenotype from genotype.

