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# Genomic Prediction of Sweet Sorghum Agronomic Performance under Drought and Irrigated Environments in Haiti

Jean Rigaud Charles<sup>1\*</sup>, Darline Marie Dorval<sup>1</sup>, Geoffrey Morris<sup>2</sup>, Gael Pressoir<sup>1</sup>

<sup>1</sup> Chibas, Quisqueya University, Haiti, <sup>2</sup> Soil & Crop Sciences | Colorado State University

\*Corresponding author : [jeanrigaud.charles@uniq.edu](mailto:jeanrigaud.charles@uniq.edu)

## Background

In Haiti, sorghum is currently the third most important cereal after maize and rice (Temple et al., 2017; Leclerc et al., 2014), and is an important source of carbohydrates, proteins, lipids, minerals and vitamins (Léder, 2004).

Haiti is one of the most vulnerable country to climate change (David et al. 2021). In 2015, 200 000 farmers are affected by drought (relief web 2017). Across the country, the rainfall is not well distributed and there are different types of soil (pH, salinity, hardpan, fertility, texture). Sugar cane aphid pressure is not the same everywhere. In 2016, 3.6 million Haitians were food insecure (WFP, 2016). Sorghum can be considered as a drought-tolerant crop (Rosenow et al., 1983; Borrel et al., 2014; Varoquauz et al., 2019). Drought is among the major limiting factors to sweet sorghum production around the world, including in Haiti, (Boyer, 1982; Tuberosa et al., 2003).

In sorghum, genomic selection has been successfully applied to predict progeny performance for important agronomic traits, including grain yield, biomass, plant height and drought-adaptation (Hunt et al., 2018; Oliveira et al., 2018; Velazco et al., 2019a, 2019b; Watanabe et al., 2017), and its use for drought tolerance could help accelerate the development of new cultivars.

However, the implementation of GS in sorghum breeding programs could be significantly constrained by genotype x environment (GxE) interactions in some countries (Hunt et al., 2018). To facilitate food security in Haiti, new varieties adapted to erratic-rainfall, particularly in the marginal semi-arid regions are needed.

In the current study, the goal was to evaluate the predictive ability of genomic prediction models across contrasting environments in Haiti using two statistical methods (Bayes B, and BRR).

## Materials and Methods

→ The population consisted of 250 breeding lines derived from three sub-populations developed at Chibas.

→ SNPs were generated for Chibas population and the world sorghum diversity panel at Kansas State University. A total of 160,066 raw SNPs were detected & 28,785 were retained after imputation (MAF and NA).

→ The experiment was carried out at route9 in November 2017 following a split plot design with 4 blocks. 3 water regimes (Irrigated, water stress 1 & water stress 2)

→ Two different planting dates for water stress 1 and water stress 2

→ Genotypes were evaluated for : Grain yield, leaf traits, stem traits, total soluble solids, and height.

→ 2 statistical methods used (Bayes B & BRR)

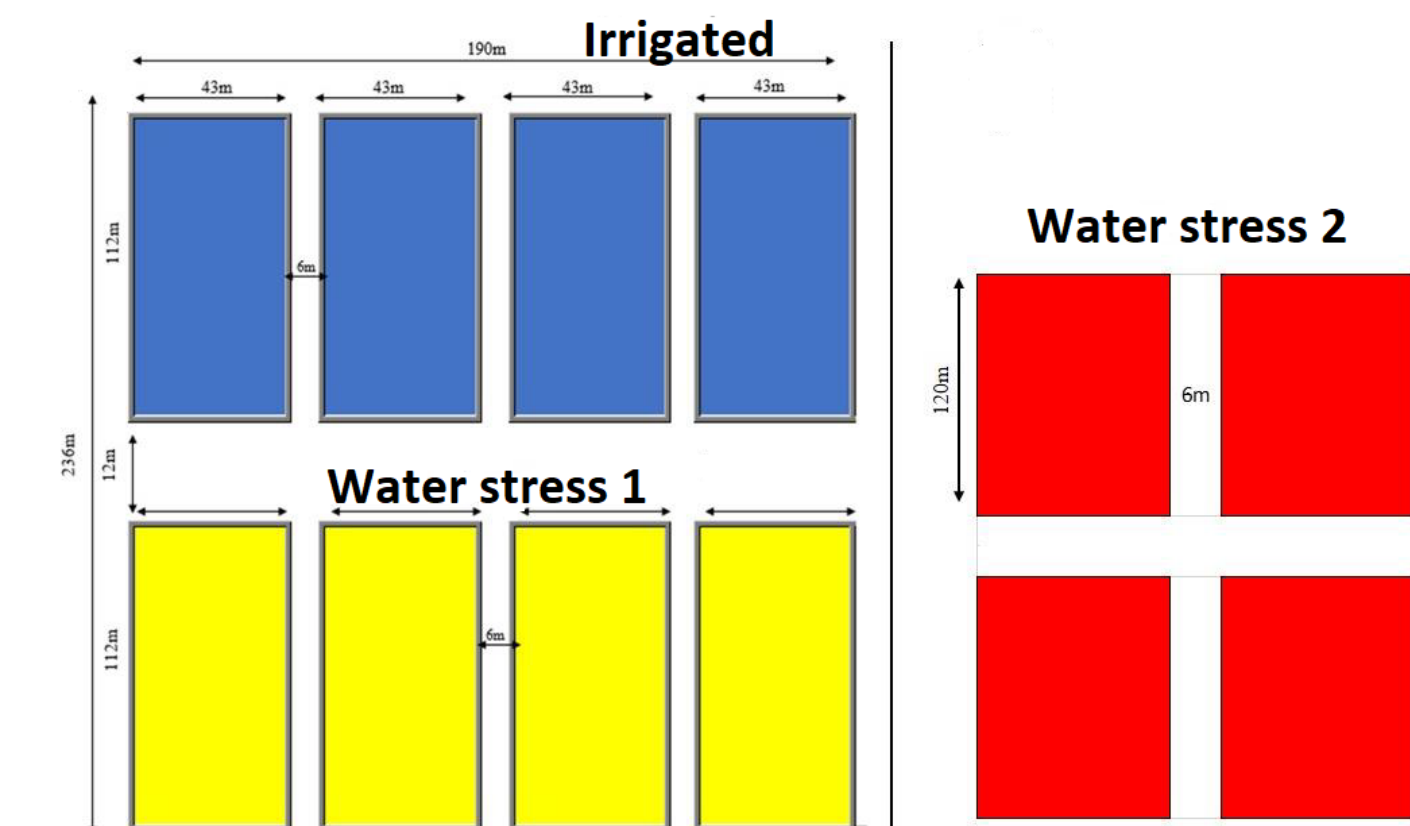


Figure 1 : Split plot design with two factors (water regime & genotypes)

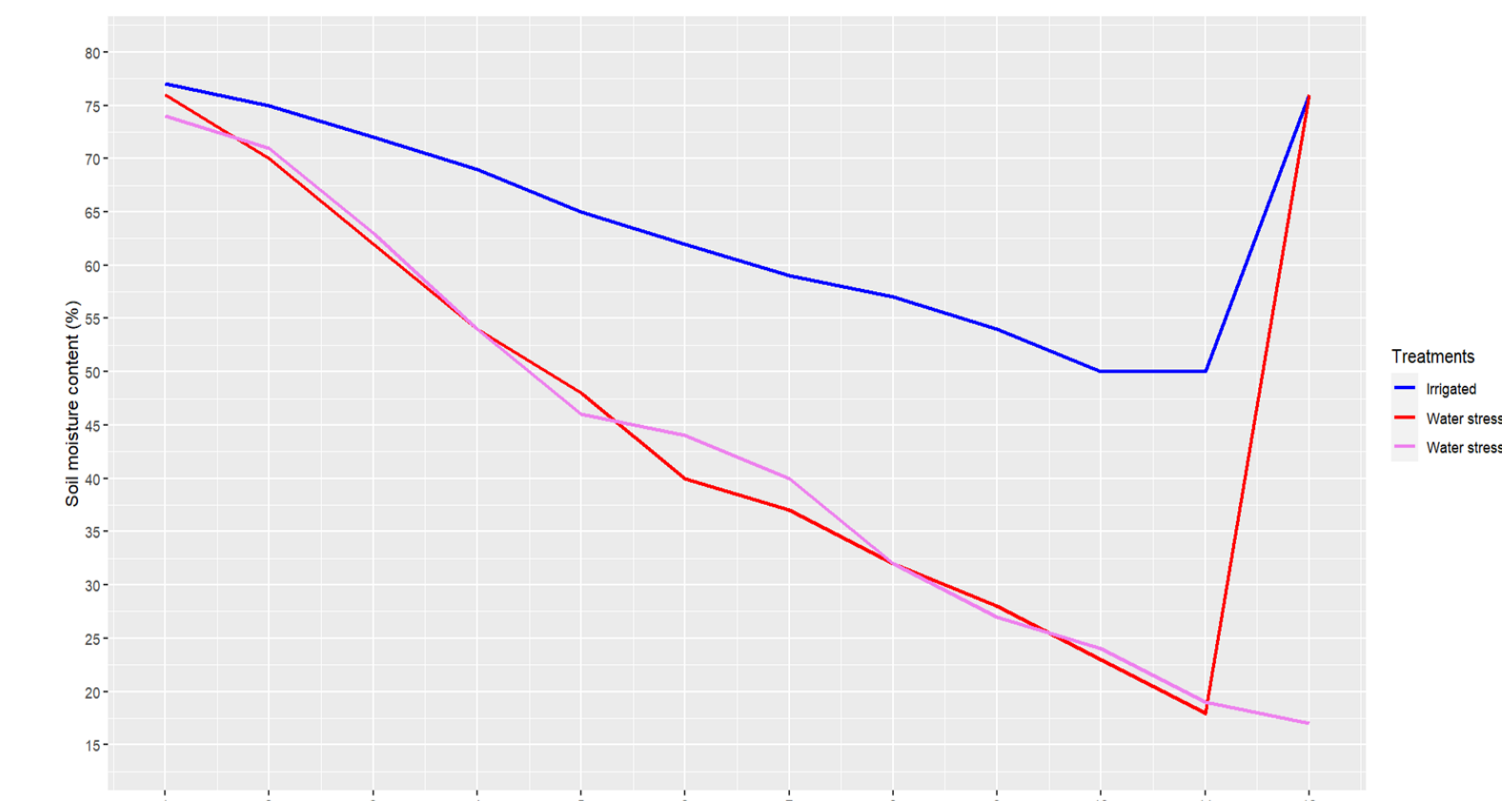


Figure 2 : The blue, orange and red lines respectively represent soil moisture evolution of the irrigation, water stress 1 and water stress 2 conditions.



Picture 1 : " Spectrum FieldScout TDR 150 soil moisture meter"

## Results

- Genomic heritability estimates varied substantially across water regime.
- Overall, the values varied from 0.47 to 0.82 for the irrigated level, 0.44 to 0.77 for the water stress 1 level and 0.33 to 0.79 for the water stress 2 level.
- Overall, all traits presented mid-to-high predictive performances (Figure 4). The highest values for combined predictions were obtained for total soluble solids (average of 0.76), total green leaf (average of 0.72), leaf weight (0.72), and stem weight (0.70), while plant height (0.57), grain yield (0.57), and maturity date (0.54) had the lowest values.
- Bayes B & BRR show similar results for all traits.

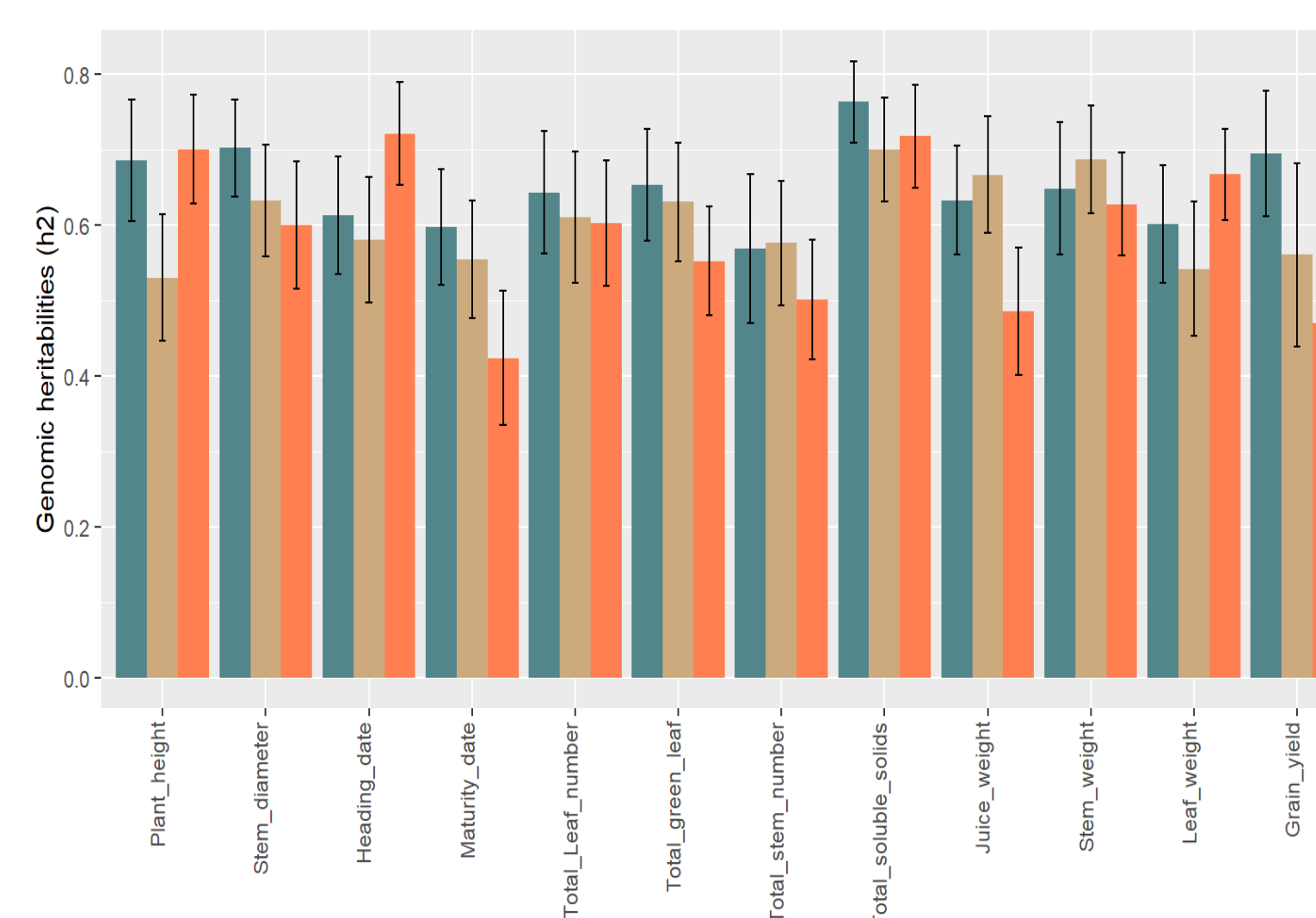


Figure 3. Genomic heritability ( $h^2$ ) computed using SNP markers for 12 sweet sorghum traits across irrigated, water stress 1 and water stress 2 levels.

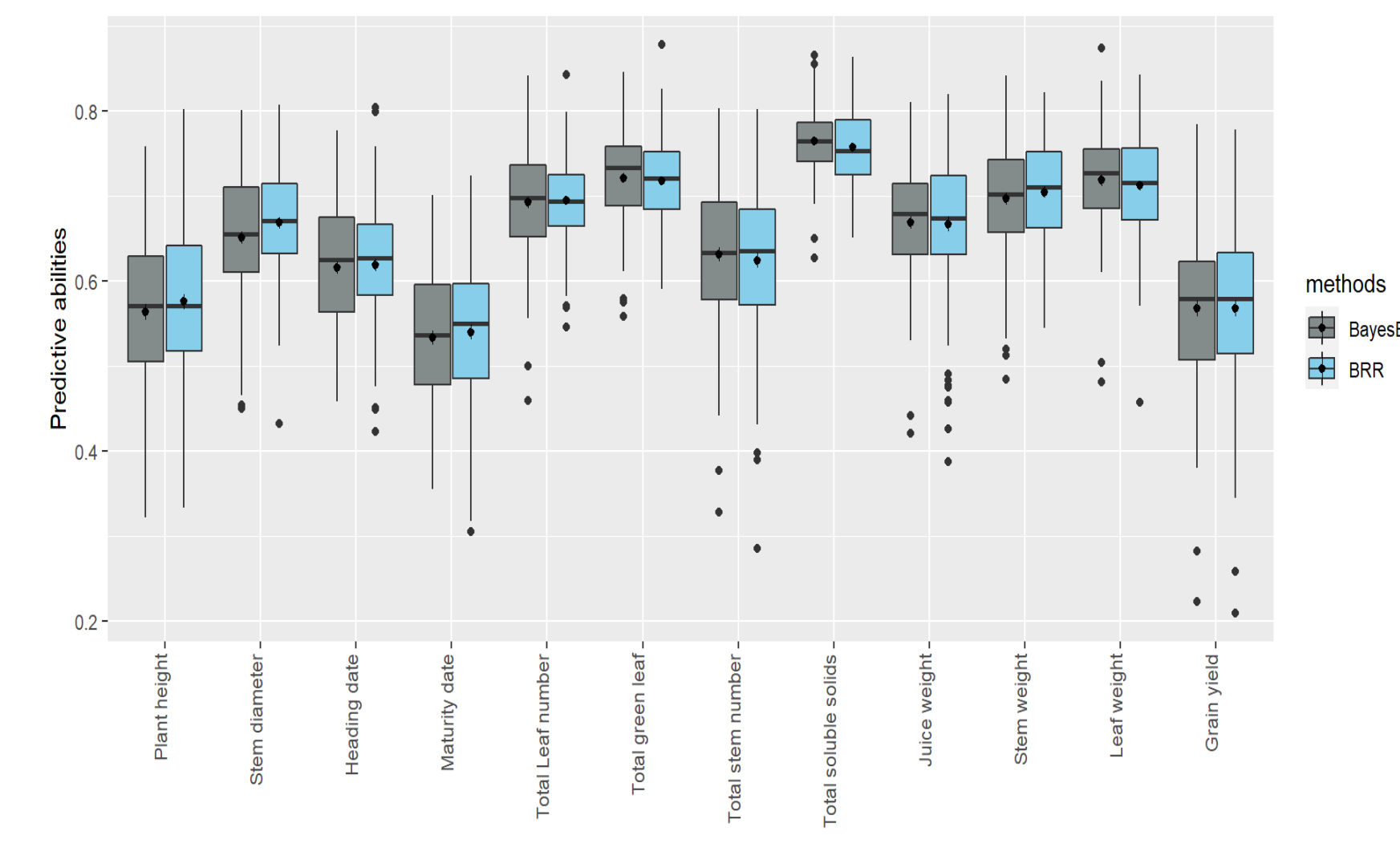


Figure 4. Evaluation of two statistical methods (BRR and Bayes B) for predicting 12 sweet sorghum traits.

→ Overall, stratified prediction yielded higher predictive performances than cross-prediction.

→ The scenario 1 (irrigated level) performs better for total soluble solids (0.71), grain yield (0.55), and stem diameter (0.62).

→ Generally, most scenarios that involved water stress 2 had lower predictive accuracies for almost all traits (scenarios 6, 7, 8, and 9)

→ total soluble solids, leaf number, and total green leaf showed high predictive capacity across all scenarios.

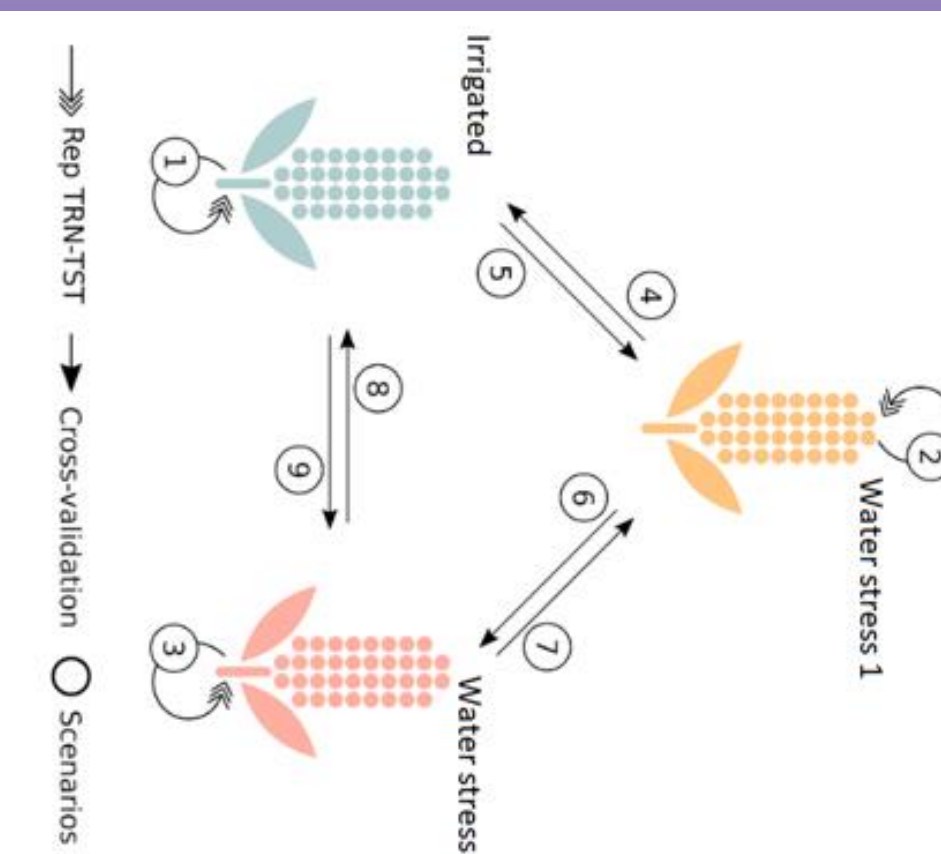


Figure 5. Alternative prediction scenarios defined as either a) stratified (scenarios 1,2 and 3) or cross-predictions (scenarios 4-9) designed to test predictive performances.

	Stratified prediction			Cross prediction					
Plant Height	0.56	0.45	0.60	0.48	0.48	0.14	0.16	0.22	0.26
Stem Diameter	0.62	0.52	0.48	0.60	0.50	0.35	0.36	0.46	0.39
Heading	0.57	0.53	0.64	0.56	0.54	0.32	0.29	0.31	0.30
Maturity	0.58	0.53	0.30	0.57	0.53	0.18	0.23	0.23	0.18
Leaf Number	0.57	0.54	0.55	0.53	0.49	0.55	0.50	0.58	0.56
Green Leaf	0.58	0.58	0.53	0.54	0.51	0.54	0.53	0.58	0.55
Stem Number	0.38	0.41	0.49	0.32	0.35	0.37	0.33	0.35	0.44
Total Soluble Solids	0.71	0.64	0.67	0.65	0.58	0.59	0.59	0.68	0.64
Juice Weight	0.58	0.59	0.41	0.53	0.54	0.30	0.38	0.35	0.30
Stem Weight	0.60	0.59	0.57	0.56	0.54	0.36	0.34	0.43	0.45
Leaf Weight	0.56	0.53	0.63	0.54	0.49	0.47	0.37	0.50	0.57
Grain Yield	0.55	0.43	0.37	0.32	0.34	0.08	0.08	0.13	0.13

Figure 6. Predictive abilities with stratified and cross prediction

## Conclusion

The range of prediction accuracy for grain yield within the environment is 0.37 to 0.55. In contrast, the accuracy of predictions across the environment varies between 0.08 and 0.34, which is occasionally too low to produce genetic gain. We will particularly address this issue in a subsequent study by creating a multi-location prediction model that more accurately forecasts an uncharacterized environment.

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