Genomic prediction and characterization of grain yield and yield stability in sorghum

Salomon J¹, Charles JR¹, Cheremond Y., Johnson K², Dorismond A¹, Tovignan T¹, Morris G², Pressoir G³

Introduction: Haiti has a wide range of variability in terms of nature of soils and microclimates. This pedoclimatic variability changes the relative ranking of sorghum genotype performances when they are growing from one environment to another, which makes selection for broadly adapted genotypes difficult. Thus, choosing efficient and stable lines, identifying the physiological mechanisms and/or the genetic architecture associated with stability and yield are crucial for breeding programs. The characterization of genotype stability is costly since it requires data from multiple environments. To this end, genomic selection is hypothesized to be an effective selection tool to achieve higher genetic gain, shorten selection cycle and reduce phenotyping cycle.

The objective of this work is to i) determine the relationship between brix, stay green and yield stability, ii) investigate the potential of genomic selection models (GS) for yield in new environment based on different prediction indexes.

Materials and methods:

11 Environments
Traits:
- Brix
- Stay green
- Grain yield

Stability index
- Wricke’s ecovalence (1965)
- Eberhart & Russel (1966)
- Shukla’s variance (1972)
- Superiority index (1988)
- Kang’s index (1995)

13344 SNPs
(GBS data)

250 genotypes
(recurrent selection)

GS Models
- G-BLUP
- Bayesians (BRR/BA/BB/BC)

Accuracy of models varied by environment, models and prediction index. Bayesian models and average yield were more accurate to make selection according to these preliminary results (Fig.4).

The genotype stability and performance were mainly explained by the stay green and brix-stay green interaction. ERR slopes is not accurate to predict yield stability (results not shown).

Conclusion: The results in this study suggest that some of the prediction indexes may not be under genetic control and/or these indexes did not capture adequately the GEI patterns. Our goal is to select the best model to predict genotype performance for a new environment.

Results and discussions: Genotypes, environments, and genotype-environment interactions (GEI) were highly significant for grain yield (Fig.1-A); environments and GEI shared the largest proportion of the variance. The GEI variance distribution shows that the ERR slopes explain only a small part (Fig.1-B).

Predictive ability of different models for yield across environment was tested using three prediction indexes: kang’s index, average yield and stay-green. (Additional models, traits, and prediction indexes will be tested).


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