

Genomic Selection for Tropical Maize Improvement

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Introduction

The availability of molecular markers has made possible the use of genomic selection in plant breeding. In order to understand how to implement genomic selection (GS) for tropical maize improvement, several proof-of-concept experiments had been applied in CIMMYT maize program. Results from these proof-of-concept experiments will encourage us to utilize genomic selection as an effective strategy to accelerate tropical maize improvement.

Materials and Methods

- ✓ Twenty three partial connected bi-parental tropical maize populations were used to test genomic selection prediction accuracy for selecting best untested inbreds as parents, which were comprised around 200 F2 individuals each, genotyped with around 200 SNPs and phenotyped in several drought and optimal environmental conditions.
- ✓ RKHS (Reproducing Kernel Hilbert Spaces) method was used to estimate predicted genotypic value.
- ✓ The accuracy of genomic selection (r) was expressed as the correlation between observed phenotypic values and predicted genotypic values.
- Rapid cycle genomic selection for population improvement within multi-parental population was tested with 1000 S1 lines from each heterosis group formed by 15-18 parents after two diallel cross generations and one self-pollination generation.
- 1000 S1 lines from each heterosis group were genotyped with GBS (Genotyping by Sequencing) platform from Cornell University, and their testcrosses were phenotyped under 4 optimal environmental conditions.
- RKHS and GBLUP (Genomic Best Linear Unbiased Prediction) methods were used to estimate predicted genotypic value, and tenfold cross validation was applied to evaluate the accuracy of genomic selection.

Discussion

- ✓ Using multiple related bi-parental populations and high density genotyping platform can improve the prediction accuracy. Twenty three bi-parental populations genotyped with GBS are being used to test how GBS and genetic information from related populations can improve the prediction accuracy.
- Rapid cycle genomic selection could dramatically accelerate the genetic gain through its shorter subsequent breeding cycles without further phenotyping. Two selection cycles per year using all molecular markers is being implemented in Mexico to estimate the genetic gain per unit time and cost.

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Results

- ✓ Increasing population size of training set and number of markers had a positive impact on prediction accuracy.
- ✓ When 90 F2 individuals and all SNPs were used to predict the rest, prediction accuracy for grain yield under optimal condition was up to 0.58. But it dropped to around 0.40, when 30 individuals were sampled.
- ✓ Predictive accuracy for all the traits under drought condition was worse than that under optimal condition, which confirmed the importance of improving field evaluation under stress conditions.
- In rapid cycle genomic selection experiment, prediction accuracy was up to 0.547 and 0.418 for grain yield and anthesis date, respectively.
- RKHS and GBLUP methods showed similar overall prediction accuracy for both traits.

Table 1. Mean values of the accuracy of genomic selection across 23 bi-parental populations

| Trait/Env. | Population size of training set | Number of SNPs | | |
|------------|---------------------------------|----------------|-------|-------|
| | | 50 | 100 | All |
| GY_Optimal | 30 | 0.279 | 0.354 | 0.400 |
| | 50 | 0.337 | 0.423 | 0.481 |
| | 70 | 0.384 | 0.472 | 0.532 |
| | 90 | 0.425 | 0.518 | 0.580 |
| GY_Drought | 30 | 0.131 | 0.163 | 0.229 |
| | 50 | 0.149 | 0.202 | 0.293 |
| | 70 | 0.206 | 0.268 | 0.355 |
| | 90 | 0.221 | 0.285 | 0.378 |

Table 2. Prediction accuracy of rapid cycle genomic selection

| Model | Heterosis Group | Traits | Accuracy |
|-------|-----------------|--------|----------|
| RKHS | A | AD | 0.258 |
| | | GY | 0.209 |
| | B | AD | 0.418 |
| | | GY | 0.547 |
| GBLUP | A | AD | 0.257 |
| | | GY | 0.182 |
| | B | AD | 0.404 |
| | | GY | 0.543 |