

# The strategy and potential utilization of temperate germplasm for tropical germplasm improvement—a case study of maize (*Zea Mays* L.)

Weiwei Wen<sup>1</sup>, Tingting Guo<sup>2</sup>, Victor. H. Chavez Tovar<sup>1</sup>, Jianbing Yan<sup>1, 2</sup>, Suketoshi Taba<sup>1</sup>

1. International Maize and Wheat Improvement Center (CIMMYT), Apartado Postal 6-640, 06600 Mexico, DF, Mexico

2. National Maize Improvement Center of China, China Agricultural University, Beijing 100193, China

## Introduction

In order to exploit heterosis in breeding for high yielding hybrids, maize germplasm must be organized into genetically divergent heterotic groups. In this study, we assembled 148 inbred lines as well as 321 Tuxpeño (landrace accessions), from GEM (US Germplasm Enhancement of Maize Project) and the CIMMYT maize genebank, and characterized them using 1,266 SNPs. We investigated SNP diversity among them and discussed the possible use of GEM lines for enhancement of heterosis in tropical maize lines in combination with genomic selection and association analysis.

## Materials

**GEM lines:** Temperate adapted lines of US Germplasm Enhancement of Maize project, n=54

**CML:** Tropically adapted CIMMYT Maize Lines, n=94

**F1:** CML(A heterotic group) x GEM(SS), CML(B heterotic group) x GEM(NSS), n=654

**Tuxpeño race accessions:** Mexican landrace, a core subset of 321 accessions (2 plants of each accession were genotyped)

Table 1. Summary of 148 lines used in this study.

	Heterotic group	No	Designation
CML	A	48	Dent
	B	38	Flint
	A/B	8	Dent/Flint
GEM	SS	35	Stiff stalk
	NSS	19	Non-stiff stalk
Total		148	

## Methods

**Genotyping:** 1,266 SNPs with good quality, distributed on all 10 chromosomes

**Phenotyping:** anthesis (AT), silking (ST), plant height (PH), ear height (EH), field weight (FW), weight per plant (WPP), and weight per ear (WPE), at breeding nursery in two locations, 2008.

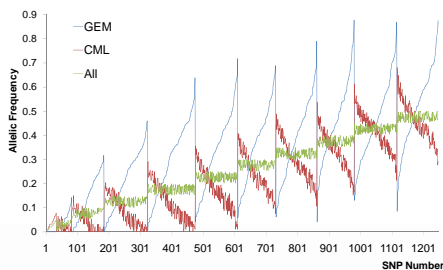
**Genetic structure and kinship analysis**

**Association analysis**

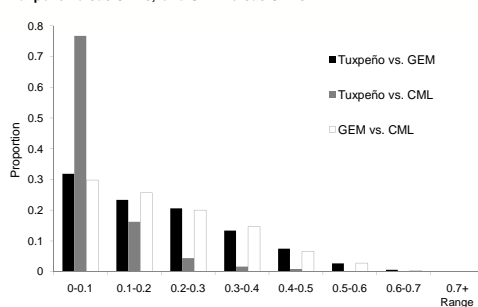
**Genomic prediction based on BLUP**

## Results

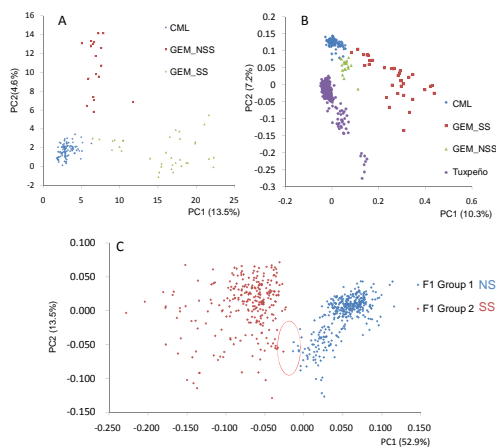
Allelic frequency difference between GEM and CML lines



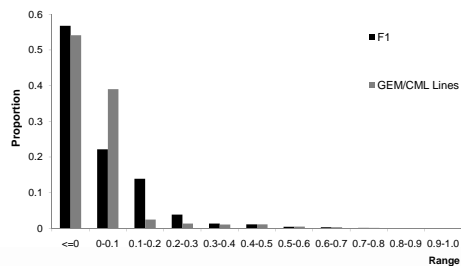
Distribution of allelic frequency differences: Tuxpeño versus GEM lines, Tuxpeño versus CMLs, and GEM versus CMLs



Principal component analysis (PCA) of 148 GEM/CML lines (A), Tuxpeño/GEM/CML lines (B), and 654 lines from F1 of GEM x CML (C)

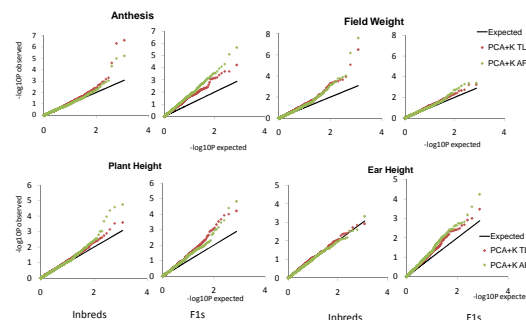


Distribution of kinship relations between any two lines in both 148 GEM/CML lines and 654 F1s of GEM x CML.

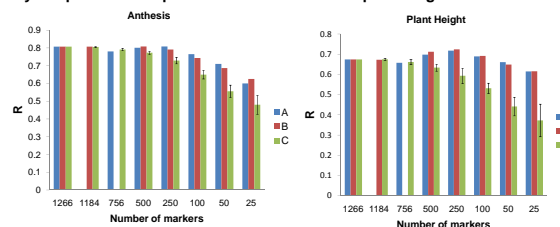


Association analysis of 7 agronomical traits based on both 148 GEM/CML lines and 654 F1s of GEM x CML.

Type I error could be controlled using PCA+K model when association analysis was performed on lines. However, when performing association analysis on F1 for some traits, type I error could not be well controlled.



Hybrid performance prediction for anthesis and plant height



A: group of markers chosen from association analysis on F1 population

B: group of markers chosen from association analysis on inbred lines

C: group of markers chosen randomly from the whole genome

The prediction accuracy benefited from adoption of markers associated with QTLs for both traits. However, it does not necessarily increase with the raise of associated marker density. High correlations between actual and predicted phenotypic values of F1 indicated the possibility to choose high performing parental combinations of phenotypic traits using SNP markers.

## Discussions

- Unique alleles harbored within GEM and CML lines imply potential of mutual improvement.
- Clear and divergent heterotic patterns shown in GEM lines can be used for breeding more genetic ally divergent lines for heterosis in tropical maize germplasm. We propose enhancement of the tropical maize germplasm (CML) by incorporating temperate germplasm (GEM) through genomic selection.
- Prediction of hybrid performance using less, but associated markers with traits may be more effective than using entire set of genome-covering markers. Using markers selected by association analysis improved predictive efficiency and can reduce cost of genotyping.

## Acknowledgement

We would like to thank GEM project and CIMMYT maize genebank for the materials used in this study.