GENETIC DIVERSITY OF THE GUATEMALAN CLIMBING BEAN COLLECTION

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2017 Feed the Future Legume Innovation Lab Grain Legume Research Conference
Ouagadougou, Burkina Faso
August 15th, 2017
Introduction

• The most important pulse crop for human consumption around the world.
• Source of protein and iron.
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Guatemala has the highest rate of chronic malnutrition in Latin America.
Milpa system and climbing bean collections

- Intercropping array
- Maize, climbing bean and squash.
- *In situ* collection of climbing beans, n=600 (50 years).
- Survey collection, n=500 (MSU and ICTA, 2015).
- Genetic diversity and development of varieties.
**Races**

- Middle America
  - Mesoamerica
  - Durango
  - Jalisco

- Andean
  - Perú
  - Nueva Granada
  - Chile

*Singh et al. (1991)*
Genetic diversity of Middle American gene pool

• Beebe et al. (2000), using RAPDs, proposed race Guatemala, mostly Guatemalan climbing beans.

• Blair et al. (2009), using microsatellites, supported race Guatemala (61 accessions). Also, proposed Durango-Jalisco complex.
Objectives

• Analyze the genetic diversity of Guatemalan climbing bean collections using single-nucleotide polymorphism (SNP) markers.

• Correlate the genotypic data with phenotypic traits of economic/agronomic importance, using a genome-wide association study.
Materials and Methods

• Population selection
  – 369 Guatemalan accessions (old collection).
  – Mesoamerican Diversity Panel (MDP):
    • 100 accessions of race Mesoamerica.
    • 100 accessions of race Durango-Jalisco.
  – 12 wild accessions from Guatemala (USDA-GRIN)
Materials and Methods

- Tissue collection
- DNA extraction
- Genotype by sequencing
  - Msel and Taqα1 restriction enzymes.
- SNP calling (136,382 SNPs)
  - Samtools, BWA mapping, GATK.
  - Filtering for 0.05 MAF (102,343 SNPs)
- Population structure and genetic diversity analysis
  - PCA, ML tree (SNPhylo), STRUCTURE, Fst, He, PIC values.
- Genome wide association study (GWAS)
  - GAPIT, 4 models.
STRUCTURE analysis
Guatemalan collections and Mesoamerican races
Phylogenetic tree
Guatemalan collections and Mesoamerican races

Durango/Jalisco
Mesoamerica
Guatemala (new)
Guatemala (old)
Wilds

Guatemala (New)
Guatemala (Old)
Durango/Jalisco
Mesoamerica
Wilds

0.2 LD
Principal Components Analysis

Guatemalan collections and Mesoamerican races

- Durango/Jalisco
- Mesoamerica
- New collection
- Old collection
- Wilds

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## Diversity Statistics

<table>
<thead>
<tr>
<th>Sup-population</th>
<th>$H_o$</th>
<th>$H_e$</th>
<th>PIC</th>
<th>%Monomorphic</th>
<th>$F_{st}$ value</th>
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</thead>
<tbody>
<tr>
<td>Durango/Jalisco</td>
<td>0.4597</td>
<td>0.3437</td>
<td>0.2680</td>
<td>8.17</td>
<td>0.2904</td>
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<td>Mesoamerica</td>
<td>0.4569</td>
<td>0.3366</td>
<td>0.2625</td>
<td>8.08</td>
<td>0.3054</td>
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<tr>
<td>Guatemala (old)</td>
<td>0.4755</td>
<td>0.3623</td>
<td>0.2842</td>
<td>3.30</td>
<td>0.1474</td>
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<tr>
<td>Guatemala (new)</td>
<td>0.4892</td>
<td>0.3897</td>
<td>0.3052</td>
<td>0.50</td>
<td>0.1192</td>
</tr>
</tbody>
</table>
Phylogenetic tree of Guatemalan beans

- Guatemala old collection
- Guatemala new collection
- Guatemala wilds
PCA based on regions, new collection
PCA based on elevation, new collection
Association mapping

Elevation

- Flowering process

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Conclusions

• Guatemalan climbing beans did not group with any of the previously defined races of common bean.

• Race Guatemala represents a new source of genetic diversity.

• Genomic regions were associated with several traits of economic importance.

• Genomic regions were associated with local adaptation in the Guatemalan climbing beans.
Acknowledgements

• Dr. Phillip McClean
• Dr. Juan Osorno
• Dr. Samira Mafi
• Rian Lee
• Julio Villatoro
• Carlos Maldonado
• Angela Miranda
• Dr. Jill Hamilton
• Dr. Ali Soltani