Maize Phenotyping under the Seeds of Discovery Initiative: *The Brute Force Method*

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Seeds of Discovery
Genome Wide Association Study (GWAS) in Maize

- Breeder’s Core Collection from the CIMMYT Maize Germplasm Bank (4471 accessions).
- One plant per accession crossed with a CIMMYT hybrid to make a series of modified topcrosses.
  - The same plant was sampled for DNA extraction/GBS
- Accessions were crossed hybrids of their same environmental adaptation (where possible).
  - Tropical Accessions X Tropical Hybrid
  - Subtropical Accessions X Subtropical Hybrids
  - Highland Accessions X Highland Hybrid
StockID: BA11-SeeD-838
Plot: 838  Entry: 838
IDACC: 10435  BANKACC: 10435  MEXI 58
Race1: CONICO 9  Race2: 
Males (?)
Rows: 1  3 PLANTS
Origin: BA87 -2901- 68
Cross with Highland Single Cross
Trial Sites in Mexico: GWAS

- **Drought; Heat**
  - Obregon, Sonora

- **Heat & Drought**
  - Torreon, Coahila

- **Cercospora**
  - San Pedro Lagunillas, Nayarit

- **Stalk Rot**
  - Celaya, GTO

- **Stalk Rot; Quality**
  - Cortazar, GTO

- **Low Nitrogen, Ear Rot, Quality, Turcicum**
  - Obregon, Sonora

- **Low Nitrogen**
  - Low Nitrogen

- **Tar Spot Complex**
  - Guadalupe-Victoria, Chiapas

- **Drought**
  - Tarimbaro, Michoacan
Phenotypic Trials

- 36 trials planted - 34 harvested (34,606 rows and over 687,000 unique data points)
- 19 Trials for abiotic Stresses (Drought, Heat, Low Nitrogen)
- 11 Trials for diseases (Tar Spot Complex, Grey Leaf Spot, Turcicum Leaf Blight, Fusarium Ear Rot, Fusarium and Acremonium Stalk Rot)
- 3 Trials hand pollinated to produce grain for Quality Component Analysis.
Yield and Agronomic Data Taken: All Locations

- Yield (field weight, grain and cob weight, moisture, number of ears)
- Plant Height and Ear Height
- Male and Female Flowering (50% of row)
- Stalk and Root Lodging
Experimental Design

- Unreplicated augmented row-column design
- For each trial location accessions are selected for adaptation zone and maturity.
- Overlapping sets of topcross entries
- Two widely adapted commercial checks and resistant and susceptible checks where appropriate
### Example of Trial Design

Standard commercial checks (yellow and red) to adjust for spatial variance and link trials from multiple locations and trait specific, resistant (yellow) and susceptible (red) checks, to adjust for spatial variation for specific traits within the trial.
BLUPs - (Best Linear Unbiased predictors) calculated for male accession parent by removing the average effect of the hybrid tester and using check entries to adjust for spatial variation.
Challenges

- Range of maturities (flowering extends for 5 weeks)
- Lodging
- Segregation
- Diversity of environments (both origin of accessions and evaluation sites).
Comparison of average female flowering date with range of female flowering for 191 accession topcrosses (per plant data)
Tar Spot Complex

The symptom caused by *Monographella maydis*

The symptom caused by *Phyllachora maydis*
Tar Spot Complex

Photo: Rosemary Shrestha
Tar Spot Trials

- 2011B Guadalupe-Victoria, Chiapas – 600 Accession/Topcross entries
- 2012B Guadalupe-Victoria, Chiapas – 810 accession/topcross entries (including accessions per se)

- 2 foliar ratings 0-5 scale (Ceballos and Deutsch) two weeks apart.
- Data taken both by row and as average of 6 plants per row
Relationship between Tar Spot rating and Yield (2nd foliar rating: scale 0-5; average of 6 plantas)

- = Accessions;
- Topcrosses;
- Commercial Checks
Relationship between Root Lodging and Tar Spot Rating (2nd foliar rating)

- Red circles = Accessions;
- Gray circles = Topcrosses;
- Blue circles = Commercial Checks
Characterization for Stalk Rot
Fusarium Stalk Rot: Artificial Inoculation
Relationship between Yield and Stalk Rot Scale (percentage of stalks with disease x intensity of disease)

- = Topcrosses;
- = Commercial Checks
# Evaluation of Accessions PerSe for Acremonium Stalk Rot

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<thead>
<tr>
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<tbody>
<tr>
<td></td>
<td>Stalk Rot Scale Average</td>
<td>Stalk Rot Scale Average</td>
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<tr>
<td>Commercial (resistant check)</td>
<td>0.43</td>
<td>0.5</td>
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<tr>
<td>PUEB45</td>
<td>1.16</td>
<td>1.7</td>
</tr>
<tr>
<td>MORE85</td>
<td>1.53</td>
<td>2.3</td>
</tr>
<tr>
<td>GUER125</td>
<td>1.59</td>
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<td>NAYAGP6</td>
<td>2.13</td>
<td>2.5</td>
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<tr>
<td>CHIS128</td>
<td>2.56</td>
<td>2.9</td>
</tr>
<tr>
<td>MICH21</td>
<td>3.21</td>
<td>2.9</td>
</tr>
<tr>
<td>TC X URUG39 (susceptible)</td>
<td>4.5</td>
<td>5.97</td>
</tr>
</tbody>
</table>
Lots of data still to analyze...

Thank You