Breeding for rust resistance at CIMMYT

**Spring Bread Wheat Improvement Team**

**Global Wheat Program**
CIMMYT Wheat Improvement Program in Mexico -
Targeted area: 60 m ha

- Irrigated (Mega-environment 1):
  30 m ha
- High rainfall (Mega-environment 2):
  5 m ha
- Semiarid (Mega-environment 4):
  15 m ha
- Irrigated-Warmer (Mega-environment 5):
  10 m ha

About half of the varieties released in South Asia, Sub-Saharan Africa and West Asia & North Africa are direct CGIAR derived; and >30% have at least one parent.
Bread Wheat Breeding Priorities

Core traits

- High and stable yield potential
- Durable resistance to Rusts-Stem (Ug99), Stripe and Leaf
- Water use efficiency/Drought tolerance
- Heat tolerance
- Appropriate end-use quality
- Enhanced Zn and Fe content for nutrition (South Asia)

Key diseases in specific mega-environments

- Durable resistance to diseases and pests
  - Septoria leaf blight (ME2)
  - Spot Blotch (ME5)
  - Tan Spot (ME4)
  - Fusarium – head scab and myco-toxins (ME2/4/5)
  - Karnal bunt (ME1)
  - Root rots and nematodes (ME4)

Packaging multiple traits together is essential under climate change scenario to benefit wheat farmers
1. Maximizing the probability of identifying rare transgressive segregants (outperformers)

- Refinement of breeding scheme to adequately manage the highly quantitative genetic control of several traits including yield

- Optimizing the number of crosses and population sizes
- Single-backcross approach for targeted improvement
- Selected bulk scheme for handling large numbers of plants in segregating populations
- Large numbers of head rows/individual plants derived F6/F7
- Yield testing of large number of advanced lines
Crossing strategy & detail

- Types of crosses per year
  - Simple: 1600
  - Single-backcross: 700
  - Top (3-way): 700

- Selection of parents is paramount
  - Use of phenotypic & genotypic information for various traits
  - Parents with complementary traits
  - At least one of the parents must have high yield
  - Higher yielding parent used as back-cross parent
  - Third parent with high yield as top-cross parent

Comparison of grain yield of entries derived from various types of crosses

Cd. Obregon 2004-05
- Simple/Top cross (n=4088)
- Back Cross 1 (n=728)

Cd. Obregon 2010-11
- Simple cross (n=2988)
- Top cross (n=1394)
- Back-Cross1 (n=2303)
Comparison of different selection schemes

<table>
<thead>
<tr>
<th>Trait</th>
<th>Selection scheme</th>
<th>Pedigree</th>
<th>Modified bulk</th>
<th>Nonselected bulk</th>
<th>Selected bulk</th>
<th>LSD (P=0.05)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grain yield (t ha⁻¹)</td>
<td></td>
<td>6.65(3)a¹</td>
<td>6.79(1)a</td>
<td>6.71(2)a</td>
<td>6.79(1)a</td>
<td>0.16</td>
</tr>
<tr>
<td>Biomass (t ha⁻¹)</td>
<td></td>
<td>14.99(3)a</td>
<td>14.98(4)a</td>
<td>15.20(2)a</td>
<td>15.46(1)a</td>
<td>0.68</td>
</tr>
<tr>
<td>Harvest index (%)</td>
<td></td>
<td>44.60(2)a</td>
<td>45.44(1)a</td>
<td>44.47(3)a</td>
<td>44.10(4)a</td>
<td>2.00</td>
</tr>
<tr>
<td>Kernel wt (mg)</td>
<td></td>
<td>38.10(3)a</td>
<td>39.25(1)a</td>
<td>38.89(2)a</td>
<td>39.25(1)a</td>
<td>2.64</td>
</tr>
<tr>
<td>Spikes m⁻²</td>
<td></td>
<td>317.46(4)a</td>
<td>322.46(3)a</td>
<td>331.16(2)a</td>
<td>334.11(1)a</td>
<td>38.06</td>
</tr>
<tr>
<td>Kernels m⁻²</td>
<td></td>
<td>17583.09(1)a</td>
<td>17365.00(4)a</td>
<td>17402.00(2)a</td>
<td>17400.00(3)a</td>
<td>1353.00</td>
</tr>
<tr>
<td>Kernels/spike</td>
<td></td>
<td>41.17(2)a</td>
<td>41.61(1)a</td>
<td>40.92(3)a</td>
<td>38.48(4)a</td>
<td>3.39</td>
</tr>
<tr>
<td>Test wt (kg hl⁻¹)</td>
<td></td>
<td>80.78(4)a</td>
<td>81.50(1)a</td>
<td>81.43(2)a</td>
<td>81.07(3)a</td>
<td>1.01</td>
</tr>
<tr>
<td>Heading (d)</td>
<td></td>
<td>76.63(2)a</td>
<td>75.88(3)a</td>
<td>75.85(4)a</td>
<td>79.50(1)a</td>
<td>3.69</td>
</tr>
<tr>
<td>Maturity (d)</td>
<td></td>
<td>126.45(2)ab</td>
<td>125.88(3)b</td>
<td>125.05(4)b</td>
<td>128.70(1)a</td>
<td>2.51</td>
</tr>
<tr>
<td>Height (cm)</td>
<td></td>
<td>85.25(4)a</td>
<td>90.00(1)a</td>
<td>88.50(2)a</td>
<td>87.38(3)a</td>
<td>5.75</td>
</tr>
</tbody>
</table>

¹Numbers in parentheses indicate the ranking and different letters denote significant differences at P ≥ 0.05.

Singh et al. 1998
Table 8. Origin of the highest yielding 10, 20 and 30 lines from four selection schemes

<table>
<thead>
<tr>
<th>No. of highest yielding lines</th>
<th>Highest yielding lines derived from</th>
<th>Pedigree</th>
<th>Modified bulk</th>
<th>Nonselected bulk</th>
<th>Selected bulk</th>
<th>( \chi^2 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td></td>
<td>1</td>
<td>4</td>
<td>2</td>
<td>3</td>
<td>1.9(^1)</td>
</tr>
<tr>
<td>20</td>
<td></td>
<td>4</td>
<td>4</td>
<td>5</td>
<td>7</td>
<td>1.2(^1)</td>
</tr>
<tr>
<td>30</td>
<td></td>
<td>5</td>
<td>9</td>
<td>5</td>
<td>11</td>
<td>4.1(^1)</td>
</tr>
</tbody>
</table>

\(^1\) Non-significant \( \chi^2 \) values at \( P = 0.05 \).
Selection Method: Selected Bulk
(Harvest and thresh one spike from each of the selected plants of a population as bulk)

- Permits selection of unlimited number of plants that have good agronomic features and desired level of resistance to diseases
- Increases possibility to identify transgressive segregants due to larger population sizes
- Field operation is easy, fast and economic
- Allows moving of populations between different field sites for shuttle breeding
- Higher proportion of crosses end up producing high yielding advanced lines
### Flow of breeding materials in the Mexico-Kenya shuttle scheme, utilizing two crop seasons per year, for developing high-yielding wheat germplasm combining adult plant resistance to stem rust with other traits

<table>
<thead>
<tr>
<th>Year</th>
<th>Locations</th>
<th>Activities</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Cd. Obregon, El Batan</td>
<td>New crosses made. F&lt;sub&gt;1&lt;/sub&gt; grown, BC&lt;sub&gt;1&lt;/sub&gt; &amp; F&lt;sub&gt;1&lt;/sub&gt;-Top made on selected F&lt;sub&gt;1&lt;/sub&gt;.</td>
</tr>
<tr>
<td>2</td>
<td>Cd. Obregon</td>
<td>BC&lt;sub&gt;1&lt;/sub&gt; &amp; F&lt;sub&gt;1&lt;/sub&gt;-Top (350 plants), F&lt;sub&gt;2&lt;/sub&gt; (1000 plants from simple crosses) grown &amp; selected for agronomic traits and leaf rust resistance. Spikes from selected plants harvested as bulk &amp; plump grain retained.</td>
</tr>
<tr>
<td></td>
<td>Toluca</td>
<td>F&lt;sub&gt;2&lt;/sub&gt; (1000 plants from BC&lt;sub&gt;1&lt;/sub&gt; and F&lt;sub&gt;1&lt;/sub&gt;-Top) and F&lt;sub&gt;3&lt;/sub&gt; (350 plants from F&lt;sub&gt;2&lt;/sub&gt; simple) grown and selected for agronomic traits, resistance to stripe rust, Septoria tritici. Spikes from selected plants harvested as bulk &amp; plump grain retained.</td>
</tr>
<tr>
<td>3</td>
<td>Njoro</td>
<td>F&lt;sub&gt;3&lt;/sub&gt; and F&lt;sub&gt;4&lt;/sub&gt; (800 plants) grown under stem &amp; stripe rust pressures. Plants with high to adequate resistance tagged and harvested as bulk. Plump grains retained.</td>
</tr>
<tr>
<td></td>
<td>Njoro</td>
<td>F&lt;sub&gt;4&lt;/sub&gt; and F&lt;sub&gt;5&lt;/sub&gt; (800 plants) grown, spikes from short plants resistant to stem and stripe rust selected &amp; harvested as bulk. Plump grains retained.</td>
</tr>
<tr>
<td>4</td>
<td>Cd. Obregon</td>
<td>F&lt;sub&gt;5&lt;/sub&gt; and F&lt;sub&gt;6&lt;/sub&gt; (350 plants) grown &amp; selected for agronomic traits and resistance to leaf rust. Plants harvested individually and those with plump grains retained.</td>
</tr>
<tr>
<td></td>
<td>El Batan, Toluca</td>
<td>Advanced lines grown as small plots, selected for agronomic traits and resistance to stripe rust and Septoria tritici at Toluca and leaf rust at El Batan. Best lines harvested in El Batan and those with plump grains promoted to yield trials.</td>
</tr>
<tr>
<td>5</td>
<td>Cd. Obregon, Njoro and Santa Catalina</td>
<td>Advanced lines grown as replicated yield trials at Cd. Obregon and as small plots at all three sites, &amp; phenotyped for leaf rust, stem rust and stripe rust at Cd. Obregon, Njoro and Santa Catalina, respectively. Best lines retained.</td>
</tr>
<tr>
<td></td>
<td>El Batan, Toluca, &amp; Njoro</td>
<td>Seed of International Nurseries Candidates multiplied at El Batan. Lines also grown at all sites and phenotyped for leaf rust, stripe rust, stem rust, Septoria tritici, Fusarium head blight, etc. Quality analysis conducted using Obregon grain.</td>
</tr>
<tr>
<td>6</td>
<td>Cd. Obregon, Mexicali &amp; Njoro</td>
<td>2nd year yield trials conducted in 5 environments at Obregon, seed multiplication for international distribution at Mexicali &amp; phenotyped for stem rust resistance at Njoro.</td>
</tr>
<tr>
<td></td>
<td>El Batan</td>
<td>International Yield Trials and Screening Nurseries prepared and distributed.</td>
</tr>
<tr>
<td>7</td>
<td>International</td>
<td>Countries with wheat seasons between April-December.</td>
</tr>
<tr>
<td>8</td>
<td>International</td>
<td>Countries with wheat seasons between October-June.</td>
</tr>
</tbody>
</table>
Rapid cycling of breeding materials

Mexico (Cd. Obregón-Toluca/El Batan)- Kenya International Shuttle Breeding

A five-year recurrent breeding cycle

- Targeted crosses for shuttle breeding made in 2006 and 1st group of populations planted in Kenya in 2008
- 2000 F3/F4 populations undergo Mexico-Kenya shuttle
- High yielding, resistant lines derived from 1st group of Mexico-Kenya shuttle distributed worldwide each year since 2011
Yield testing of advanced lines
Cd. Obregon, Mexico (2014-15)

1\textsuperscript{st} year yield trials
Irrigated (9100 entries + Checks):
30 entries/trial, 2 reps, alpha-lattice design
- Raised bed-5 irrigations

2\textsuperscript{nd} year yield trials or EYT (1345 entries + Checks):
30 entries/trial, 3 reps, alpha-lattice design
- Flat-5 irrigations (8-9 t/ha)
- Raised bed-5 irrigations (8-9 t/ha)
- Raised bed-2 irrigations (3-4 t/ha)
- Flat- drip irrigation (2-2.5 t/ha)
- Raised bed-Early (30 days) sown- (8-9 t/ha)
- Raised bed-Late (85 days) sown- (3-4 t/ha)
Characterization of entries in 2nd year trial

• Diseases:
  – Leaf rust- seedling and field (El Batan and Cd. Obregon)
  – Yellow rust- seedling and field (Toluca and Ecuador)
  – Stem rust- seedling and field: off- and main-seasons (Kenya)
  – Septoria tritici- Toluca
  – Fusarium- El Batan
  – Karnal Bunt- Cd. Obregon
  – Tan (yellow) spot- seedling, El Batan greenhouse
  – Stagnospora nodorum blotch- seedling, El Batan greenhouse
  – Spot blotch- Aguas Frias

• Various quality traits including grain weight & test weight
• Agronomic traits: height, heading, maturity, lodging
Worldwide distribution of new High Yielding Wheat Germplasm through Trials and Nurseries

<table>
<thead>
<tr>
<th>Trial/Nursery</th>
<th>Abbreviation</th>
<th>Entries (No.)</th>
<th>Target environment</th>
<th>Grain color</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Yield Trials (Replicated):</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Elite Spring Wheat Yield Trial</td>
<td>ESWYT</td>
<td>50</td>
<td>ME1, ME2, ME5</td>
<td>White</td>
</tr>
<tr>
<td>Semi-Arid Wheat Yield Trial</td>
<td>SAWYT</td>
<td>50</td>
<td>ME4</td>
<td>White</td>
</tr>
<tr>
<td>High Rainfall Wheat Yield Trial</td>
<td>HRWYT</td>
<td>50</td>
<td>ME2, ME4</td>
<td>Red</td>
</tr>
<tr>
<td>Heat Tolerance Wheat Yield Trial</td>
<td>HTWYT</td>
<td>50</td>
<td>ME1, ME4, ME5</td>
<td>White</td>
</tr>
<tr>
<td>HarvestPlus Yield Trial</td>
<td>HPYT</td>
<td>50</td>
<td>ME1, ME5</td>
<td>White</td>
</tr>
<tr>
<td><strong>Screening nurseries:</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Int. Bread Wheat Screening Nursery</td>
<td>IBWSN</td>
<td>250-300</td>
<td>ME1, ME2, ME5</td>
<td>White</td>
</tr>
<tr>
<td>Semi-Arid Wheat Screening Nursery</td>
<td>SAWSN</td>
<td>200-250</td>
<td>ME4</td>
<td>White</td>
</tr>
<tr>
<td>High Rainfall Wheat Screening Nursery</td>
<td>HRWSN</td>
<td>100-150</td>
<td>ME2, ME4</td>
<td>Red</td>
</tr>
<tr>
<td>HarvestPlus Advanced Nursery</td>
<td>HPAN</td>
<td>100</td>
<td>ME1, ME5</td>
<td>White</td>
</tr>
<tr>
<td><strong>Disease based nurseries:</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Stem Rust Resistance Screening Nursery</td>
<td>SRRSN</td>
<td>100-150</td>
<td>All MEs</td>
<td>White/Red</td>
</tr>
<tr>
<td>International Septoria Observation Nursery</td>
<td>ISEPTON</td>
<td>100-150</td>
<td>ME2, ME4</td>
<td>White/Red</td>
</tr>
<tr>
<td>Leaf Blight Resistance Screening Nursery</td>
<td>LBRSN</td>
<td>100-150</td>
<td>ME4, ME5</td>
<td>White/Red</td>
</tr>
<tr>
<td>Fusarium Head Blight Screening Nursery</td>
<td>FHBSN</td>
<td>50-100</td>
<td>ME2, ME4</td>
<td>White/Red</td>
</tr>
<tr>
<td>Karnal Bunt Resistance Screening Nursery</td>
<td>KBRSN</td>
<td>50-100</td>
<td>ME1</td>
<td>White/Red</td>
</tr>
</tbody>
</table>

- 120-150 sets of each trials/nurseries distributed annually worldwide
- 40-50% increase in demand during the last decade
Rust menace - continued fight with an old enemy

Yellow (stripe) rust
*Puccinia striiformis*

Brown (leaf) rust
*Puccinia triticina*

Black (stem) rust
*Puccinia graminis*
Race Specific resistance

≈ seedling genes

Monogenic

≈ Race-specific

≈ Major genes
(Intermediate type-Sr22, Sr25,Srtemp)

≈ Hypersensitive
(Boom & Bust) eg: Sr31, Sr24, Srtmp

NBS-LRR-cloned genes

Sr33, Sr35, Sr22, Sr45, Sr50

Use in MAS
Major gene infection type response

0  R  R-MR  MR  MR-MS
Race-specific genes: challenges

- Preparedness for **boom-and-bust cycles**
- Longer resistance remains effective greater the effect of “bust” in farmers’ fields (large area or several varieties/Mega varieties) and on **breeding program** (large proportion of breeding materials)- *(Sr31, Yr27, Srtmp)*
- Continuous search for **new sources of resistance** their assessment and utilization in breeding program
- Identifying molecular markers **tightly linked** to resistance genes for MAS/MAB
Race-specific genes: deployment strategies

- Combinations of effective resistance genes (gene pyramids) lead to resistance longevity due to a negligible probability of simultaneous mutations from avirulence to virulence in the same rust spore.

Episitatic effects - difficult in phenotyping unless diagnostic markers available

- Marker assisted selection for gene combinations coupled with selection for other traits (e.g. grain yield) can lead to the successful development of new varieties.

Pyramids loose stacking when used for crossing in breeding programs

- Gene cassettes: stacking few genes on a single translocation

2 BLADES foundation
Diversity: race-specific genes effective to Ug99 and other important races

• **Genes available for immediate use:** Sr22, Sr26, Sr35, Sr42/SrCad, Sr45, Sr50, SrSha7, SrNing, SrND643, SrHUW234, Sr1A1R, SrWeb/SrGabo56

• **Under development**
  • 10 genes on reduced alien chromosome segments: Sr32, Sr37, Sr39, Sr40, Sr43, Sr44, Sr47, Sr50, Sr51, Sr53
  • “New” genes from wild tetraploids, landraces, *Ae. tauschii*, *T. monococcum* (*SrTm4, SrTm5*)
  • “New” alien genes (*H. villosa, Ae. sharonensis, Ae. searsii, Th. ponticum, Th. intermedium, Ae. caudata*, etc.)
  • Stacking/Pyramiding multiple race specific genes (*Sr22, Sr25, Sr26*)
  • Race specific genes do not confer immunity when deployed singly- enhanced phenotypic effects of intermediate effect genes can be achieved in combination with APR genes- Sr25, Sr SrHUW234
Ug99 stem rust resistance in wheat entries identified for international distribution in 2015 (Based on highest disease severity recorded in four seasons of field testing at Njoro, Kenya and seedling test)

<table>
<thead>
<tr>
<th>Resistance Category</th>
<th>Entries</th>
<th>No.</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Race-specific (28.8%):</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sr13</td>
<td></td>
<td>18</td>
<td>2.7</td>
</tr>
<tr>
<td>Sr25</td>
<td></td>
<td>11</td>
<td>1.7</td>
</tr>
<tr>
<td>Sr26</td>
<td></td>
<td>2</td>
<td>0.3</td>
</tr>
<tr>
<td>Sr42</td>
<td></td>
<td>71</td>
<td>10.8</td>
</tr>
<tr>
<td>Sr1A.1R</td>
<td></td>
<td>2</td>
<td>0.3</td>
</tr>
<tr>
<td>SrBau</td>
<td></td>
<td>26</td>
<td>4.0</td>
</tr>
<tr>
<td>SrHuw234</td>
<td></td>
<td>24</td>
<td>3.7</td>
</tr>
<tr>
<td>SrND643</td>
<td></td>
<td>13</td>
<td>2.0</td>
</tr>
<tr>
<td>SrYanac</td>
<td></td>
<td>13</td>
<td>2.0</td>
</tr>
<tr>
<td>Sr?</td>
<td></td>
<td>9</td>
<td>1.4</td>
</tr>
</tbody>
</table>

- Durable APR gene Sr2 present in >80% lines
- Our goal is to increase the frequency of high yielding lines in NIR and R categories for deployment in East Africa
Adult plant resistance

≈ APR genes
Polygenic
≈ Race-nonspecific
≈ Minor genes
≈ Slow rusting/ Partial
≈ Interactions with environment
(Durable)
Cloned APR genes
ABC- Transporter Lr34
Sugar transporter –Lr67

IT-4  MS-S
Characteristics of slow rusting resistance

- **Minor genes with small to intermediate effects**
- **Gene effects are additive**
- **Resistance does not involve hypersensitivity**

**Genes confer slow disease progress through:**

- Reduced infection frequency
- Lower disease severity, Increased latent period
- Small to large compatible pustules on stems
- Reduced spore production
- Interactions with environment
Breeding minor, slow-rusting genes based adult plant resistance: a better strategy

- Leads to resistance durability
- Higher returns from investments due to long-term effectiveness
- Significantly enhanced knowledge of the genetic basis
- Several characterized genes have pleiotropic genetic control on all three rusts, powdery mildew and some other diseases
- Field based selection in conjunction with other traits
- High-yielding wheats with high levels of resistance to all three rusts now available
- Higher focus can now be given to breed for other important traits
APR gene response

Susceptible
Sr2 transferred to wheat from ‘Yaroslav’ emmer in 1920s by McFadden and linked to pseudo-black chaff (~90 years)

Sr2 still provides moderate levels of resistance in Kenya (~30% reduction in disease severity)

Seedling and APR genes with intermediate effects in combination with Sr2 produce enhanced levels of resistance

Formed the basis of durable resistance historically in some CIMMYT wheat

Essential to reduce/curtail the evolution of Ug99 in East Africa and other high risk areas
Breeding options: APR

Adult plant resistance

- **Sr2, Sr55, Sr56, Sr57, Sr58** and other QTLs: 2BS, 5BL, etc.
- **Sr2 complex**: Sr2 + 3-4 loci: high levels of APR in CIMMYT wheat backgrounds
- Thatcher+Sr57 (or Sr55) also has high level of APR in the absence of Sr2: QTL on 3BS overlapping Sr12, 1AL & 2BS in Thatcher/McNeal population (Rouse et al. 2014)
- Bi-parental recombinant inbred lines mapping populations (Bhavani et al. 2011, Njau et al. 2012)

Other sources:
APR identified in improved wheat lines e.g. Kingbird, Kiritati, Juchi, Pavon, Parula

**Older Kenyan varieties** Kenya Swara, Kenya Nyangumi, Kenya Fahari, K.kudu etc.

Kingbird- APR to Ug99 race group
Mapping of APR to Ug99 and other *Pgt* races

- Bi-parental recombinant inbred lines mapping populations
  
  (Bhavani et al. 2011, Njau et al. 2012)
  
  - 15 populations developed and phenotyped
  - QTL analysis completed for six populations

- Pleiotropic effects of *Lr34/Yr18, Lr46/Y29* & *Lr67/Yr46* on slow rusting to stem rust established; corresponding resistance genes designated as *Sr57, Sr58* and *Sr55*, respectively

- Association mapping identified various genomic regions
  
  (Yu et al. 2011)
Pleiotropic durable slow rusting resistance gene *Lr67/Yr46/Sr55/Pm46* (present in C306, Sujata, Yaqui 50 and some other old tall varieties) mediated resistance in resistant (R) and susceptible (S) mutant sibs.

- Stem rust (Obregon, Mexico)
- Leaf rust (Cobbitty, Australia)
- Leaf & Yellow rusts (Vollebekk, Norway)
- Powdery mildew (Vollebekk, Norway)

- Gene clone: encodes a hexose transporter, a novel resistance mechanism
- Gene sequence based molecular markers available for breeding

Moore et al. 2015. Nature Genetics 47:1494-1498
Selection & phenotyping for Ug99 race group

Segregating populations:
- F3 and F4 selected bulk populations received from Toluca, Mexico grown at Njoro off-season, selected and harvested (Jan-May)
- F4 and F5 selected bulk populations grown again at Njoro main-season, selected, harvested and sent back to Mexico (June-November) for planting at Obregon

Advanced lines:
- >8000 new lines in 1st year yield trials in Obregon phenotyped simultaneously for stem rust at Njoro in the off-season.
- >1400 lines selected based on yield, stem rust and other agronomic traits phenotyped in the main-season at Njoro and for various traits in Mexico
- >1100 lines retained for 2nd year yield trials under 6 environments at Obregon phenotyped for stem rust at Njoro during the off and main-seasons
- Between 300-400 selected lines phenotyped at seedling stage in USDA-ARS greenhouse, CDL, St. Paul, MN.

Highest severity recorded during the four seasons of field evaluation, seedling reactions and marker information (where relevant) used in assigning a reaction category for lines distributed internationally.
Comparison of grain yield performance of 602 bread wheat entries distributed in 2014 (derived from crosses made in 2008) when selected under Mexico shuttle and Mexico-Kenya shuttle breeding schemes.

Data source: Cd. Obregon 2012/13; yield trials under irrigated conditions on flat and bed planting systems.
Ug99 stem rust resistance in wheat entries identified for international distribution in 2015 (Based on highest disease severity recorded in four seasons of field testing at Njoro, Kenya and seedling test)

<table>
<thead>
<tr>
<th>Resistance Category</th>
<th>% Severity</th>
<th>No.</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>High-Adequate APR (44.8%)</strong>:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NIR (Near-Immune resistant)</td>
<td>1</td>
<td>14</td>
<td>2.1</td>
</tr>
<tr>
<td>R (Resistant)</td>
<td>5-10</td>
<td>46</td>
<td>7.0</td>
</tr>
<tr>
<td>R-MR (Res.-Moderately Res.)</td>
<td>15-20</td>
<td>122</td>
<td>18.6</td>
</tr>
<tr>
<td>MR (Moderately resistant)</td>
<td>30</td>
<td>112</td>
<td>17.1</td>
</tr>
</tbody>
</table>

**Adequate APR depending on location of deployment (15.9%)**:

<table>
<thead>
<tr>
<th>Resistance Category</th>
<th>% Severity</th>
<th>No.</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>MR-MS (Mod. Res.-Mod. Sus.)</td>
<td>40</td>
<td>104</td>
<td>15.9</td>
</tr>
</tbody>
</table>

**Inadequate-Susceptible (10.5%)**

<table>
<thead>
<tr>
<th>Resistance Category</th>
<th>% Severity</th>
<th>No.</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>MS (Moderately Susceptible)</td>
<td>50-60</td>
<td>39</td>
<td>5.9</td>
</tr>
<tr>
<td>MS-S (Mod. Sus.-Susceptible)</td>
<td>70-80</td>
<td>22</td>
<td>3.4</td>
</tr>
<tr>
<td>S (Susceptible)</td>
<td>90-100</td>
<td>8</td>
<td>1.2</td>
</tr>
</tbody>
</table>

- Durable APR gene *Sr2* present in >80% lines
- Our goal is to increase the frequency of high yielding lines in NIR and R categories for deployment in East Africa
Wheat varieties released during 2005-2016 showing high to adequate resistance to Ug99 race group
Progress in breeding APR to leaf rust

Leaf rust resistance in wheat entries identified for international distribution in 2015

(Based on greenhouse tests and field data from Cd. Obregon 2013-14 & El Batan 2013 recorded when susceptible checks became necrotic following 100% rust severity)

- A majority of lines (>60%) distributed each year have high levels of APR.
- Lines with APR & race-specific resistance have similar severities in field.
Yellow rust resistance in wheat entries identified for international distribution in 2015

Phenotyping at Toluca (Mexico), Njoro (Kenya) and Ludhiana (India) helping in identifying highly resistant lines in field even though they show continuous variation for seedling reactions.
Achieving near-immune resistance to yellow rust at all growth stages

- Resistance based on 4-5 slow rusting APR genes in different growth stages is usually adequate in areas where yellow rust infection initiates from stem elongation stages onwards (APR genes are already functioning by then).

- With the spread of aggressive races, infection in some areas initiates as early as tillering when APR genes still not fully functional.

- A simpler strategy is to utilize combinations of slow rusting APR genes with small/intermediate effect race-specific resistance genes that have enhanced expression due to additive effects.

- Field based selection can be done simultaneously with other traits that increases genetic gains for multiple traits.