Advances in Genomics-assisted Breeding in the CIMMYT Global Wheat Program

Susanne Dreisigacker
Centralized breeding approach

Shuttle breeding and evaluation of fixed lines in preliminary multi-location yield trials in Mexico

Germplasm distribution

Annual seed shipments of approx. 200,000 wheat lines to approx. 450 breeding programs
Genetic gains for grain yield in 27th-34th ESWYT (grown during 2006-2007 to 2014-2015 crop seasons) in irrigated environments

Annual gain: **1.63%** (Attila= PBW343) and **0.72%** (Local Checks)

\[ GYA = 60.84 + 1.63 \times \text{ESWYT} \times P < 0.0001; \text{rsq} = 0.38 \]

\[ GYLC = 79.2 + 0.72 \times \text{ESWYT} \times P < 0.001; \text{rsq} = 0.3 \]
Spring bread wheat releases by regions and origin, 1994-2014
# 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 (nutritional quality)

## Key diseases in specific environments
Durable resistance to diseases and pests
- Septoria tritici blotch
- Spot Blotch
- Tan Spot
- Fusarium – head scab and myco-toxins
- Karnal bunt
- Root rots and nematodes
- Wheat blast- new threat in SA

Packaging multiple traits together is essential under climate change scenario to benefit wheat farmers
Multidiscipline - Wheat Breeding

Genetic Resources
- Germplasm banks
- Trait collections
- Synthetics
- Translocation lines
-Wide Crosses

Genomics Resources
- Physical maps
- Gene and Genome Sequences
- DNA marker platforms
- Gene expression platforms
- Transformation protocols

Methodologies
- Selection schemes
- Modelling and Prediction

Agronomy

Phenotyping
- Field phenotyping
- Phenotyping in controlled conditions
- Multi environmental trials
- High throughput screenings

Improved wheat varieties
Genomics-assisted breeding strategies

Trait

YES

Large-effect genes/haplotypes known

NO

Gene discovery and validation phase

NO

Marker-assisted backcrossing or forward breeding

YES

Populations amenable to genomic selection

Genomic Selection
Traits under selection

**Durable adult-plant and race-specific resistance to rusts:**
- MAS to combine of moderately effective slow rusting genes (some have pleiotropic effects on multiple diseases) with race specific genes
- MAB to introduce new genes

**Resistance to insects:**
- MAB to introduce new genes

**Resistance to fusarium head blight, septoria tritici blotch**
- Polygenic, similar in APR to wheat rusts, closely linked markers for few genes

**Zn enhancement**
- Quantitative, but various QTL observed

**End-use quality**
- Qualitative
- Complete assessment of quality traits is very expensive

**Grain yield under optimum, drought & heat**
- Highly quantitative
### Combining UG99 resistance genes

**Disease rating for stem rust with and without MAS**

31\textsuperscript{st} Semi-Arid Wheat Yield Screening Nursery

<table>
<thead>
<tr>
<th>Selection environment</th>
<th>No</th>
<th>R</th>
<th>R-MR</th>
<th>MR</th>
<th>MR-MS</th>
<th>MS</th>
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<td>No</td>
<td>159</td>
<td>25</td>
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<td>46</td>
<td>10</td>
<td>5</td>
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<td></td>
<td>%</td>
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<td>41.5</td>
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<td>All</td>
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<td>305</td>
<td>92</td>
<td>111</td>
<td>44</td>
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<td>23</td>
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<td></td>
<td>%</td>
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<td>30.2</td>
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Distribution of marker-selected lines in recent nurseries

# MABC in bread wheat - sources and genes

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<thead>
<tr>
<th>Source</th>
<th>Gene</th>
<th>Type</th>
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<tr>
<td>RL6077/AOC-YR</td>
<td>Lr67/Yr46/Sr55/Pm46</td>
<td>Pleiotropic APR</td>
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<td>SUJATA</td>
<td>Lr67/Yr46/Sr55/Pm46, YrSuj-7BL</td>
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<tr>
<td>H-S A/2*MUNAL #1</td>
<td>Sr2 + Fhb1</td>
<td>FHB</td>
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<td>SWSR22T.B.</td>
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<tr>
<td>KACHU/3/WHEAR//2<em>PRL/2</em>PASTOR SHORT SR26 TRANS./4/3*CHIBIA//...</td>
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<td>SR32</td>
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<td>SR47</td>
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<td>SR50</td>
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<tr>
<td>SWSR22T.B.</td>
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<td>Stem rust resistance genes</td>
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<tr>
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<td>CHUAN NONG 19</td>
<td>Yr39</td>
<td>Stripe rust resistance genes</td>
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<tr>
<td>LALBMONO1*4/PVN</td>
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<td>CZHO</td>
<td>ALMT1</td>
<td>Aluminium tolerance</td>
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<td>SERI/T.DIC. PI94623/AE.SQ. (1027)</td>
<td>QZn_4BS, QZn-3AL, QZn-2Bc</td>
<td>Grain Zinc content</td>
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<td>Kenya Swara, PBW343</td>
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<tr>
<td>SERI/T.DIC. PI94623/AE.SQ. (1027)</td>
<td>Gba, QRp.slu-5AL,QRp.slu-5BL</td>
<td>Insect resistance</td>
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<td>PI592729</td>
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<td>PI572542</td>
<td>H25</td>
<td>Hessian fly resistance</td>
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</table>
Examples of marker in validation pipeline

1) Grain Zn Content

3AL (Kenya Swara, 10-15%)

2Bc (PBW343, 10-15%)

4BS (T.DIC (PI94623)/AE.SQUARROSA(1027), 19%)

- Developed KASP markers for each QTL using the survey sequence
- Backcrossed each source into a number of elite lines
- A first set of 106 MAS selected lines (3ALQTL or 3AL + 2BcQTL) for validation
- F1Top populations evaluated for the 4BSQTL
Examples of marker in validation pipeline

2) Fusarium head blight QTL on 2DLc and 3D

Shanghai-3/Catbird  Soru#1/Naxos  Ocoroni/Mayoor

from Frontana (DON)

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<thead>
<tr>
<th>ID</th>
<th>SNP</th>
<th>Chr</th>
<th>TYPE</th>
<th>Resistant</th>
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</tbody>
</table>

✓ International nurseries evaluated for the presence of the genes.
✓ Ready to be combined with the Fhb1-Sr2 recombinant lines.
Genomic selection for grain yield

- Intermate Parents
- Selection candidates
- Preliminary Testing
- Multi-environment testing
- Dissemination

Genomic prediction model
GS predicted vs. actual grain yield
(1st year yield trial data 2014-15, n=9096)
Improve upon visual selection using high-throughput phenotyping and relationship information

- 1092 lines, five environments, pedigree and genomic relationship information.

- Grain yield and weekly measurements of canopy temperature, Green and red normalized difference vegetation index (GNDVI and RNDVI).
Multi-trait models substantially improve selection accuracy

Rutkoski et al. (2016)
Genomic vs. indirect phenotypic selection

- 56,964 lines evaluated in Obregon, of those 1,547 were evaluated in 5 locations in South Asia

- Pedigree and phenotypic information available for all lines, genotypic information available for 29,484 lines.

- Used a multi-environment prediction model with both pedigree and markers- allows borrowing information from relatives and environments:

  - Compared phenotypic prediction vs model-based prediction
Genomic selection > indirect phenotypic selection

Perez et al. (2017)
Genomic prediction for more than yield
E.g. industrial quality traits

Battenfield et al. (2016)
Summary

✓ Genomics-assisted breeding strategies play its role in the CIMMYT Global Wheat Program

✓ Tracing large effect QTL is common practice

✓ Genomic selection is currently employed to predict the future grain yield and quality performance of putative candidate cultivars within Mexico and for key target environments
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WMB team
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Philomin Juliana

KSU:
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Sarah Battenfield

TraitGenetics:
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Joerg Plieske

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