Breeding Stress Resilient Maize

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Outline

• Introduction

• Product concept

• Breeding for stress resilient maize

• New tools and technologies to accelerate product development:
  – Use of DH technology
  – Application of molecular markers (MARS/GS)
Maize is vital for food security in Sub-Saharan Africa

- Over 300 million people depend on maize in SSA
- Example: consumption in Kenya 103 kg/yr/person
- Maize yield in SSA is low
- Major constraints:
  - Drought
  - Low soil nitrogen
  - Diseases
  - Lack of access to quality seed

Source: FAOSTAT (2017) for 2012-14 yield data
Plant breeding is a cyclic process:

1. Assemble your germplasm
2. Characterize the genetic variation in your germplasm
3. Select appropriate parents for breeding
4. Generate progeny
5. Evaluate progeny
6. Select superior progeny
7. Repeat evaluation and selection
8. Release

The result is incremental gain.
Accelerating genetic gains in plant breeding

\[ G(y) = h^2 i \sigma / I \]

- \( G(y) \) = Response to selection for trait \( y \)
- \( h^2 \) = Heritability
- \( i \) = Selection intensity
- \( \sigma \) = Variance
- \( I \) = Generation interval = length of breeding cycle

Fundamentals

- Experimental designs and control of the plot-to-plot variability
- GxE -- correlation among experimental trials (farmer’s field)
- High throughput phenotyping
- Genetic diversity
CIMMYT-GMP Breeding Approaches

**Accelerate forward breeding** – recycling elite lines from different breeding streams

- DT elite line x DT elite line
- DT elite line x Insect resistant elite line
- DT elite line x NUE elite line
- DT elite line x MLN tolerant line
- DT elite line x Off-PVP line

**Integrated application of technologies to enhance genetic gains and breeding efficiency**

- DH technology
- MARS and GS in breeding pipelines
- Trial networking system
- Decision support tools (META-R, AGD-R, GEA-R)

**Product profiles for targeted agro-ecologies**

- Descriptors for lines and single cross
- Male and female yield, Flowering synchronization
Product concept

- White hybrids (SC, 3-way, Double-cross, OPV)
- Yield improvement compared to the best commercial checks:
  - Managed drought 45 kg/ha/year
  - Low N 45 kg/ha/year
  - Optimal 110 kg/ha/year
  - Per se female yield 45 kg/ha/year
  - MLN 250 kg/ha/year
- General Product Requirements
  - Maturity: early, intermediate and late
  - Disease resistance: GLS, NLB, MSV and **MLN**
  - Agronomic traits: root lodging, maturity, husk cover
  - Grain Texture: flint to flinty-dent
  - Color
Defining drought tolerance

In case of maize (as per CIMMYT), “drought tolerance” is the ability of a genotype to show a substantive and statistically significant yield advantage over the widely grown commercial checks (tested in several drought stress locations), and often under severe drought conditions, including flowering and grain filling period.
Effect of moisture stress at different growth stage in maize

<table>
<thead>
<tr>
<th>Growth stage</th>
<th>Susceptibility of yield to drought</th>
<th>Probability of stress</th>
<th>Probability of breeding success</th>
</tr>
</thead>
<tbody>
<tr>
<td>Germination, establishment</td>
<td>High</td>
<td>Usually high</td>
<td>Low</td>
</tr>
<tr>
<td>Pre-flowering</td>
<td>Low</td>
<td>Depending on the environment</td>
<td>Medium</td>
</tr>
<tr>
<td>Flowering</td>
<td>High</td>
<td>Depending on the environment</td>
<td>High</td>
</tr>
<tr>
<td>Post-flowering</td>
<td>Medium</td>
<td>Usually high</td>
<td>Medium</td>
</tr>
</tbody>
</table>

The aim of managed drought is not to simulate a farmers field, but create a screen that has high probability of occurrence in farmers’ fields and clearly reveals genotypic differences under stress.

Apply so much stress that yield is reduced by at least 50% (better 65-75 %) of the unstressed screening at that site

=> Genotype-by-stress interactions become visible
CIMMYT’s success in breeding stress-resilient maize germplasm has four decades of continuous efforts.

<table>
<thead>
<tr>
<th>Population</th>
<th>Description</th>
<th>Genetic material</th>
</tr>
</thead>
<tbody>
<tr>
<td>DTP-Y and DTP-W</td>
<td>60% lowland tropical, 20% subtropical, 20% temperate</td>
<td>Derived from 25 putative drought tolerance sources (Tuxpeño Sequia, Latente, Michoacan21, Suwan 1, CIMMYT Pops. 22, 32, 62, 64, and 66); 11% landraces; rest from elite drought tolerant sources, Corn Belt hybrids, germplasm from Thailand and S. Africa</td>
</tr>
<tr>
<td>La Posta Sequia (LPS)</td>
<td>Lowland tropical, late-maturing, white dent.</td>
<td>Derived from CIMMYT Population 43 C, SR.</td>
</tr>
</tbody>
</table>

Drought and low N stress tolerant germplasm development via recurrent selection was initiated at CIMMYT in 1975.
Objective of managed flowering drought stress

Experiments are conducted during a rain-free period and irrigation regime is designed so that delay silking and ear abortion

- Leaves are severely rolled at flowering
- Anthesis-silking interval: 3 to 8 days
- Ears per plant: 0.3 to 0.7
- Yields: 1 - 3 t/ha (15-25 % well watered)
Objective of managed post-flowering drought stress

Experiments are conducted during a rain-free period and irrigation regime is designed so that ....

- **Anthesis-silking interval** is less than 3 days
- Leaf **senescence** is accelerated
- **Yields**: < 50% of yield under well-watered conditions at that site
Useful traits under managed drought stress

- Grain yield => increase
- Ears per plant => increase
- Anthesis-silking interval (ASI) => decrease
- Leaf senescence => decrease
- Leaf rolling => decrease
- Tassel size => decrease

Other secondary traits: Leaf and stem elongation rate, canopy temperature, leaf photo-oxidation, leaf chlorophyll concentration, seedling survival under drought, osmotic adjustment, leaf erectness.
Selection for reduced leaf rolling under drought

Score = 1

Score = 3

Score = 5
Selection for reduced tassel size

Score = 1

Score = 5
Selection for reduced leaf senescence

Score = 1

Score = 3

Score = 5
Drought tolerant and susceptible hybrids under managed drought at Kiboko in 2017

Commercial check
WE5138 (Released)
WE6101 (NPT2 in Kenya and Uganda)

- Date of planting: 4th June 2017
- Date of 1st irrigation: 5th June 2017
- Date of last Irrigation: 24 July 2017
Drought tolerant and susceptible hybrids under managed drought at Kiboko in 2017
Genetic variability for grain yield under optimum and drought condition
Selection works in OPVs and hybrids

Unselected

Four cycles of selection for tolerance at flowering

Contemporary commercial hybrid check

Stress tolerant hybrid
CIMMYT –derived Hybrids vs. Commercial Hybrids in ESA - Head-to-Head Comparison

- Best 10-15 hybrids from different maturity groups (extra-early, early, intermediate, late) vs. corresponding checks from each of DTMA, WEMA and IMAS nodes in ESA
- 7073 comparisons across different maturity groups.
- Results of combined analyses across Optimum-moisture & N-application; Managed-drought; & Low-N Environments.
- Identified best products cutting across environments vis-à-vis popular commercial hybrids
Driving genetic gain under drought

Grain yield (t ha\(^{-1}\))

- 32 kg/ha/year
- 45 kg/ha/year
- 60 kg/ha/year
Doubled haploidy is central to modern maize genetics and breeding

- **Acceleration** of homozygous (parental) line development
- **Simplified** logistics – significant savings in land, labour and other resources
- Reduces within-family variance (= **improved phenotyping accuracy**)
- Eliminates genetic drift during advancement
- Genetic dissection of traits using **immortal mapping populations** (RILs vs DH)
- Opportunity to effectively couple **molecular markers-based selection** for important traits.
Maize Doubled Haploid (DH) Facility at KALRO-Kiboko, Kenya

Offering DH development service as centralized platform to NARS and SME seed company partners → economy of scale!

The facility is producing annually >60,000 DH lines from diverse source populations

CIMMYT DH Facility in Agua Fria/Maztitlan produces ~15,000 DH lines each year.
Genetic variability for drought tolerance among the DH lines

- Date of planting: 4th June 2017
- Date of 1st irrigation: 5th June 2017
- Date of last Irrigation: 24 July 2017
Performance of top 10 yielding lines (DH and pedigree) evaluated across at six locations in East Africa in 2014.

- # inbred lines = 124 (34 are CML and 90 are elite lines)
- Inbred lines were categorized into five era of release
- Year of developed – 1996 to 2013 developed through pedigree and DH technology
  - Pre-1996 = 12 lines
  - 1996-2000 = 6 lines
  - 2001-2005 = 27 lines
  - 2006-2010 = 34 lines
  - 2011-2013 = 45 lines
- Evaluated in 6 sites in Kenya and Uganda

<table>
<thead>
<tr>
<th>Entry</th>
<th>Year of release</th>
<th>Yield (t/h) Across</th>
</tr>
</thead>
<tbody>
<tr>
<td>CKDHL0165</td>
<td>5</td>
<td>4.9</td>
</tr>
<tr>
<td>CKDHL0186</td>
<td>5</td>
<td>4.5</td>
</tr>
<tr>
<td>CML543</td>
<td>4</td>
<td>4.4</td>
</tr>
<tr>
<td>CKDHL0590</td>
<td>5</td>
<td>4.4</td>
</tr>
<tr>
<td>CKDHL0282</td>
<td>5</td>
<td>4.4</td>
</tr>
<tr>
<td>CML395</td>
<td>2</td>
<td>4.2</td>
</tr>
<tr>
<td>CKDHL0364</td>
<td>5</td>
<td>4.2</td>
</tr>
<tr>
<td>CKDHL0323</td>
<td>5</td>
<td>4.2</td>
</tr>
<tr>
<td>CKDHL0295</td>
<td>5</td>
<td>4.0</td>
</tr>
<tr>
<td>CKL08002</td>
<td>4</td>
<td>4.0</td>
</tr>
<tr>
<td>Mean</td>
<td></td>
<td>3.0</td>
</tr>
<tr>
<td>LSD(0.05)</td>
<td></td>
<td>1.3</td>
</tr>
<tr>
<td>Repeatability</td>
<td></td>
<td>0.65</td>
</tr>
</tbody>
</table>

*Regasa et al. (2016): Euphytica*
DH Lines now increasingly part of improved maize hybrids developed by CIMMYT in Africa

More than 50 CIMMYT hybrids released between 2013-16 through WEMA Project by CIMMYT in Kenya, Tanzania, Uganda, South Africa and Mozambique are based on DH lines.
What about marker assisted selection

- Conventional Plant Breeding
  - Untested
  - Stage 1
  - Stage 2
  - Stage 2
  - Stage 3

- Molecular Plant Breeding
  - Untested
  - Stage 1
  - Stage 2
  - Stage 2
GS/MARS at CIMMYT-Africa maize breeding

- **Objective:** To improve drought tolerance using GS and MARS

- 34 bi-parental populations (total = 6252 F$_{2:3}$, each with ca. 184 progenies)
- Each pop phenotyped in 2-4 managed water-stressed, 3-4 well-watered environments, and genotyped with 190-286 SNPs

- Genetic gain studies completed for 18 populations
  - 10 populations using MARS
    - Selection at $C_0$ based on phenotype and marker data, followed by one recombination and two selfing
  - 8 populations using GS
    - Selection at $C_0$ based on phenotype only, followed by two cycles of marker only recombination
Genetic Gains in Grain Yield Through Genomic Selection in Eight Bi-parental Maize Populations under Drought Stress

Yoseph Beyene, Kassa Semagn, Stephen Mugo, Amsal Tarekegne, Raman Babu, Barbara Meisel, Pierre Sehabiague, Dan Makt, Mateo Vargas, Michael Olsen

Feature Review
Genomic Selection in Plant Breeding: Methods, Models, and Perspectives

José Crossa,*, Paulino Pérez-Rodríguez, Jaime Cuevas, Osval Montesinos-López, Diego Jarquín, Gustavo de los Campos, Juan Burgueño, Juan M. Camacho-González, Sergio Pérez-Elizalde, Yoseph Beyene, Susanne Dreisigacker, Ravi Singh, Xuecai Zhang, Manje Gowda, Manish Roorkwal, Jessica Rutkoski, and Rajeev K. Varshney

Improving Maize Grain Yield under Drought Stress and Non-stress Environments in Sub-Saharan Africa using Marker-Assisted Recurrent Selection


Performance and grain yield stability of maize populations developed using marker-assisted recurrent selection and pedigree selection procedures

Yoseph Beyene, Kassa Semagn, Stephen Mugo, Boddupalli M. Prasanna, Amsal Tarekegne, John Gakunga, Pierre Sehabiague, Barbara Meisel, Sylvester O. Oikeh, Michael Olsen, Jose Crossa
Conduct genetic gain studies (cross C₀, C₁, C₁S₁, C₁S₂, F₅:₆ and founder parents) with a single-cross tester and evaluate the testcrosses and commercial checks in multi-location water-stress and well-watered environments.
MARS and GWS Recombination nurseries

Leaf sampling

Pollination

Critical steps:
1. Planning and coordination
2. Data turnaround time from leaf sampling to genotyping
3. Data analysis and selection
4. Synchrony and pollination
Gain in grain yield using genomewide SNPs under drought environments in SSA

Genetic gain from conventional breeding in Africa
18 kg ha\(^{-1}\) yr\(^{-1}\) (Edmeades, 2013)
32 kg ha\(^{-1}\) yr\(^{-1}\) (Masuka et al., 2017)
Genetic gain from GS is 2-4 times higher than the gains from conventional breeding reported in sub-Saharan Africa.

Overall gain in GY: 70.5 kg ha\(^{-1}\) year\(^{-1}\)
Performance of hybrids developed from GS-C3-DH lines, founder parents and commercial checks under drought

- Phenotyped under managed drought locations
- Gain over the commercial checks = 47.3 to 98.2%
- Gain over the parents = 17.2 to 57.3%
Drought tolerant lines and hybrids developed through MARS/GS

Susceptible line  DT line

DT line  Susceptible line

DT Hybrid  Susceptible hybrid

DT Hybrid  Susceptible hybrid
Scheme of Phenotypic and Genomic Selection in Maize breeding

### Phenotypic selection

<table>
<thead>
<tr>
<th>Year</th>
<th>Season</th>
<th>Events</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>A x B</td>
</tr>
<tr>
<td>1</td>
<td>B</td>
<td>F1 - Inducer</td>
</tr>
<tr>
<td>2</td>
<td>A</td>
<td>Haploids</td>
</tr>
<tr>
<td>2</td>
<td>B</td>
<td>DH per se – seed increase</td>
</tr>
<tr>
<td>3</td>
<td>A</td>
<td>DH for TCs – stage I</td>
</tr>
<tr>
<td>3</td>
<td>B</td>
<td>First stage multi-location evaluation of TCs</td>
</tr>
<tr>
<td>4</td>
<td>A</td>
<td>Line C x Line D</td>
</tr>
<tr>
<td>4</td>
<td>B</td>
<td>F1 - Inducer</td>
</tr>
<tr>
<td>5</td>
<td>A</td>
<td>Haploids</td>
</tr>
<tr>
<td>5</td>
<td>B</td>
<td>DH per se – seed increase</td>
</tr>
<tr>
<td>6</td>
<td>A</td>
<td>DH for TCs – stage I</td>
</tr>
<tr>
<td>6</td>
<td>B</td>
<td>First stage multi-location evaluation of TCs</td>
</tr>
</tbody>
</table>

### Phenotypic + Genomic selection

<table>
<thead>
<tr>
<th>Year</th>
<th>Season</th>
<th>Events</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>A x B</td>
</tr>
<tr>
<td>1</td>
<td>B</td>
<td>F1 - Inducer</td>
</tr>
<tr>
<td>2</td>
<td>A</td>
<td>Haploids</td>
</tr>
<tr>
<td>2</td>
<td>B</td>
<td>DH per se – seed increase + Genotyping</td>
</tr>
<tr>
<td>3</td>
<td>A</td>
<td>50% DH for TCs – stage I</td>
</tr>
<tr>
<td>3</td>
<td>B</td>
<td>50% in cold room</td>
</tr>
<tr>
<td>4</td>
<td>A</td>
<td>Line C x Line D</td>
</tr>
<tr>
<td>4</td>
<td>B</td>
<td>F1 - Inducer</td>
</tr>
<tr>
<td>5</td>
<td>A</td>
<td>Haploids</td>
</tr>
<tr>
<td>5</td>
<td>B</td>
<td>DH per se – seed increase + Genotyping</td>
</tr>
<tr>
<td>6</td>
<td>A</td>
<td>DH for TCs – Stage II</td>
</tr>
<tr>
<td>6</td>
<td>B</td>
<td>Second stage multi-location evaluation of TCs</td>
</tr>
</tbody>
</table>
Correlation between observed and predicted on 853 lines

\[ R^2 = 0.7249 \]

\[ R^2 = 0.7582 \]
The outlier ID1 and ID2 were not covered by the training set and not a part of stage I.

A total of 254 lines were selected to go to stage II. 181 lines were selected based on GEBV.
### Summary of lines that are phenotyped, genotyped and # lines selected for Stage II trials

<table>
<thead>
<tr>
<th>No</th>
<th>Trial</th>
<th>Phenotyped (Training set)</th>
<th>Genotyped (Predicting set)</th>
<th>Selected for Stage II at 20% SI</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Training set</td>
<td>Predicting set</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>WET17A-EVALITWC-02</td>
<td>87</td>
<td>166</td>
<td>17</td>
</tr>
<tr>
<td>2</td>
<td>WET17A-EVALITWC-05</td>
<td>91</td>
<td>172</td>
<td>18</td>
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<tr>
<td>3</td>
<td>WET17A-EVALITWC-06</td>
<td>108</td>
<td>217</td>
<td>22</td>
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<tr>
<td>4</td>
<td>WET17A-EVALITWC-07</td>
<td>68</td>
<td>130</td>
<td>14</td>
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<tr>
<td>5</td>
<td>WET17A-EVALITWC-09</td>
<td>88</td>
<td>166</td>
<td>18</td>
</tr>
<tr>
<td>6</td>
<td>WET17A-EVALITWC-10</td>
<td>53</td>
<td>103</td>
<td>11</td>
</tr>
<tr>
<td>7</td>
<td>WET17A-EVALITWC-14</td>
<td>63</td>
<td>118</td>
<td>13</td>
</tr>
<tr>
<td></td>
<td>Total</td>
<td>558</td>
<td>1072</td>
<td>112</td>
</tr>
</tbody>
</table>

Each line crossed with three SC testers from opposite heterotic group for evaluation in 2018 maize season.
Maize Lethal Necrosis (MLN) is a viral disease caused by combined infection of maize with Maize Chlorotic Mottle Virus (MCMV) and any of the Potyviruses infecting cereals, especially Sugarcane Mosaic Virus (SCMV).

The disease was first reported in Africa, particularly in Kenya in Sept 2011, and since then reported in Uganda, Tanzania, Rwanda, D.R. Congo, and Ethiopia.
• **Individual infection with each virus can also cause disease**
• Typically, infection with one virus results in milder symptoms than MLN but reaction depends on germplasm and viral strain.
Responses of some commercial maize hybrids against MLN
Responses of some elite CMLs against MLN

CML442  CML443  CML448  CML444
Identification of MLN -Tolerant Lines

Susceptible  Resistant
KS23-6-B

Susceptible  Resistant
CKDHL120918
Yield comparison under optimum across locations and artificial MLN inoculation in Naivasha between MLN tolerant hybrids and commercial checks

Yield (t/ha) under MLN AI

Commercial checks

Best bet MLN tolerant hybrids

Yield (t/ha) under optimum
Performance of MLN-tolerant & Comm. Check Under AI MLN; Without MLN; & Optimum Condition

CKHMLN1500084

Naivasha under AI MLN  Naivasha without MLN  Kiboko-Optimum

DK8031
Distribution of 704 lines for MLN tolerance

![Distribution of 704 lines for MLN tolerance](image)
New MLN tolerant DH lines, 2017

CKDHL164090

CKDHL163627

KS23-6
Results of Yield loss study due to MLN

Performance of selected hybrids under artificial MLN inoculation

- Commercial hybrids
- 1st generation MLN tolerant hybrids
- 2nd generation MLN tolerant hybrids

Performance of selected hybrids without MLN inoculation

- Commercial hybrids
- 1st generation MLN tolerant hybrids
- 2nd generation MLN tolerant hybrids

<table>
<thead>
<tr>
<th></th>
<th>GY (t/ha)</th>
<th>EPP</th>
<th>MLN3 (1-5)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Heritability</td>
<td>0.8</td>
<td>0.5</td>
<td>0.93</td>
</tr>
<tr>
<td>n Replicates</td>
<td>3.0</td>
<td>3.0</td>
<td>3.00</td>
</tr>
<tr>
<td>n Locations</td>
<td>2.0</td>
<td>2.0</td>
<td>2.00</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>GY (t/ha)</th>
<th>EA (1-5)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Heritability</td>
<td>0.69</td>
<td>0.59</td>
</tr>
<tr>
<td>n Replicates</td>
<td>3</td>
<td>3</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Hybrid Type</th>
<th>Yield (t/ha) without MLN</th>
<th>Yield (t/ha) under MLN</th>
<th>Yield loss due to MLN (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Commercial hybrids</td>
<td>3.0</td>
<td>0.7</td>
<td>77.7</td>
</tr>
<tr>
<td>1st generation MLN tolerant hybrids</td>
<td>4.4</td>
<td>3.4</td>
<td>22.9</td>
</tr>
<tr>
<td>2nd generation MLN tolerant hybrids</td>
<td>4.7</td>
<td>4.6</td>
<td>3.1</td>
</tr>
</tbody>
</table>
GCA effect of the top 8 inbred lines for MLN severity scores and grain yield

<table>
<thead>
<tr>
<th>No</th>
<th>Pedigree</th>
<th>GY (t/ha)</th>
<th>MLN-early</th>
<th>MLN-late</th>
</tr>
</thead>
<tbody>
<tr>
<td>13</td>
<td>CKDHL120918</td>
<td>1.21***</td>
<td>-0.47**</td>
<td>-0.54**</td>
</tr>
<tr>
<td>27</td>
<td>CML550</td>
<td>0.64*</td>
<td>-0.11*</td>
<td>-0.1</td>
</tr>
<tr>
<td>12</td>
<td>CKLTI0227</td>
<td>0.61*</td>
<td>-0.13</td>
<td>-0.18*</td>
</tr>
<tr>
<td>24</td>
<td>CML494</td>
<td>0.5</td>
<td>-0.15*</td>
<td>-0.22</td>
</tr>
<tr>
<td>18</td>
<td>CKLMARSI0022</td>
<td>0.41</td>
<td>-0.03</td>
<td>-0.01</td>
</tr>
<tr>
<td>8</td>
<td>CKDHL0500</td>
<td>0.35</td>
<td>-0.14*</td>
<td>-0.21*</td>
</tr>
<tr>
<td>15</td>
<td>CKLTI0137</td>
<td>0.29</td>
<td>-0.2*</td>
<td>-0.25*</td>
</tr>
<tr>
<td>23</td>
<td>CKLTI0136</td>
<td>0.21</td>
<td>-0.04</td>
<td>-0.07</td>
</tr>
<tr>
<td>14</td>
<td>CKLTI0138</td>
<td>0.16</td>
<td>-0.19*</td>
<td>-0.19*</td>
</tr>
</tbody>
</table>

Beyene et al 2017; Euphytica
Development MLN resistant / tolerant hybrids

- MLN resistant hybrid

MLN tolerant hybrids are also good for yield under optimum condition and early maturing.

MLN tolerant hybrid at Kiboko Demo, Sep 2017

- Commercial checks, susceptible to MLN
Fall Armyworms in Africa

- Migratory pest, native to Americas - the tropical regions of the Americas from the United States to Argentina and the Caribbean region
- Polyphagous; almost 80 recorded host plants in 26 families.
- Prefers grass species, including maize, millet, sorghum, rice, wheat, and sugarcane

Countries where FAW reported (June 2017)
Frequency distribution of 96 lines for resistance to FAW at Kakamega under natural infestation

<table>
<thead>
<tr>
<th>FAW leaf damage score</th>
<th>Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 - 1.9</td>
<td>0</td>
</tr>
<tr>
<td>2 - 2.9</td>
<td>0</td>
</tr>
<tr>
<td>3 - 3.9</td>
<td>1</td>
</tr>
<tr>
<td>4 - 4.9</td>
<td>8</td>
</tr>
<tr>
<td>5 - 5.9</td>
<td>21</td>
</tr>
<tr>
<td>6 - 6.9</td>
<td>23</td>
</tr>
<tr>
<td>7 - 7.9</td>
<td>39</td>
</tr>
<tr>
<td>8 - 8.9</td>
<td>4</td>
</tr>
<tr>
<td>More</td>
<td></td>
</tr>
</tbody>
</table>

Explanation/definition of damage | Rating scale
--- | ---
Minimal visible leaf damage; *(Low)* | 0-4
Marginal leaf damage *(Medium)* | 5-7
Extensive leaf damage *(High)* | 8-9
Screening of maize lines for resistance to FAW at Kiboko under natural infestation

- Susceptible
- Resistant-developed from highland maize
- Susceptible
- Resistant-developed from MBR population
Screening of experimental hybrids for FAW under natural infestation at Kiboko

CKDHH170037

**Resistant hybrid** showed no damage on the ears at both replication.

**Susceptible hybrid** showed ear damage, shriveled and ear rot.
Thank you for your interest!