Seeds of Discovery Project: using maize genetic resources for breeding tolerance to biotic and abiotic stresses

Marcela Carvalho Andrade

Genetic Resource Program, CIMMYT

II International Symposium of Genetics and Plant Breeding (SIAGMP-UENF)

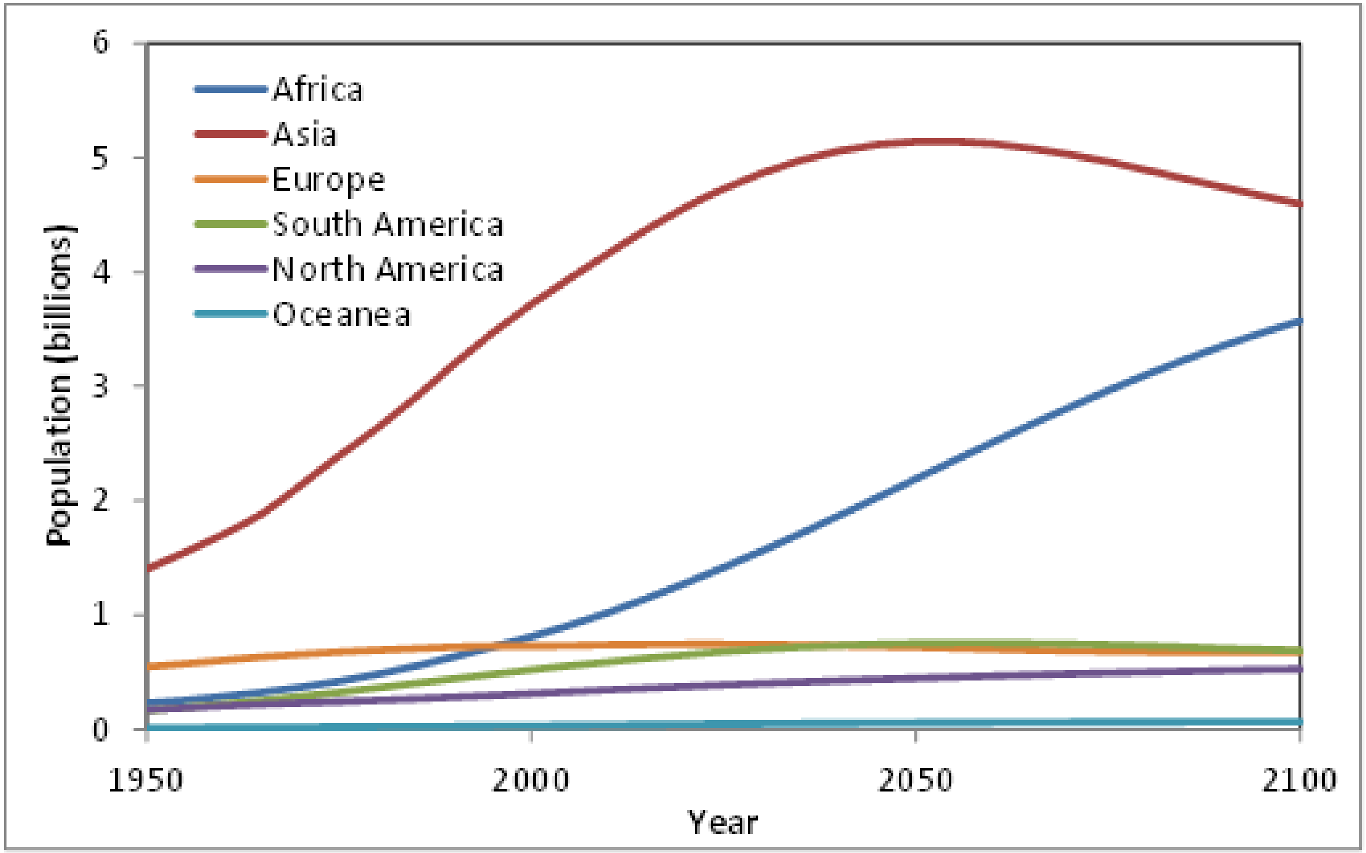
March 21-22, 2018

CIMMYT

Challenges

TO: Shutterstock

Projected Population Increase to Year 2100



The Energy Collective, 2013

Demand for food will **increase by 50-60%** during the 21st century

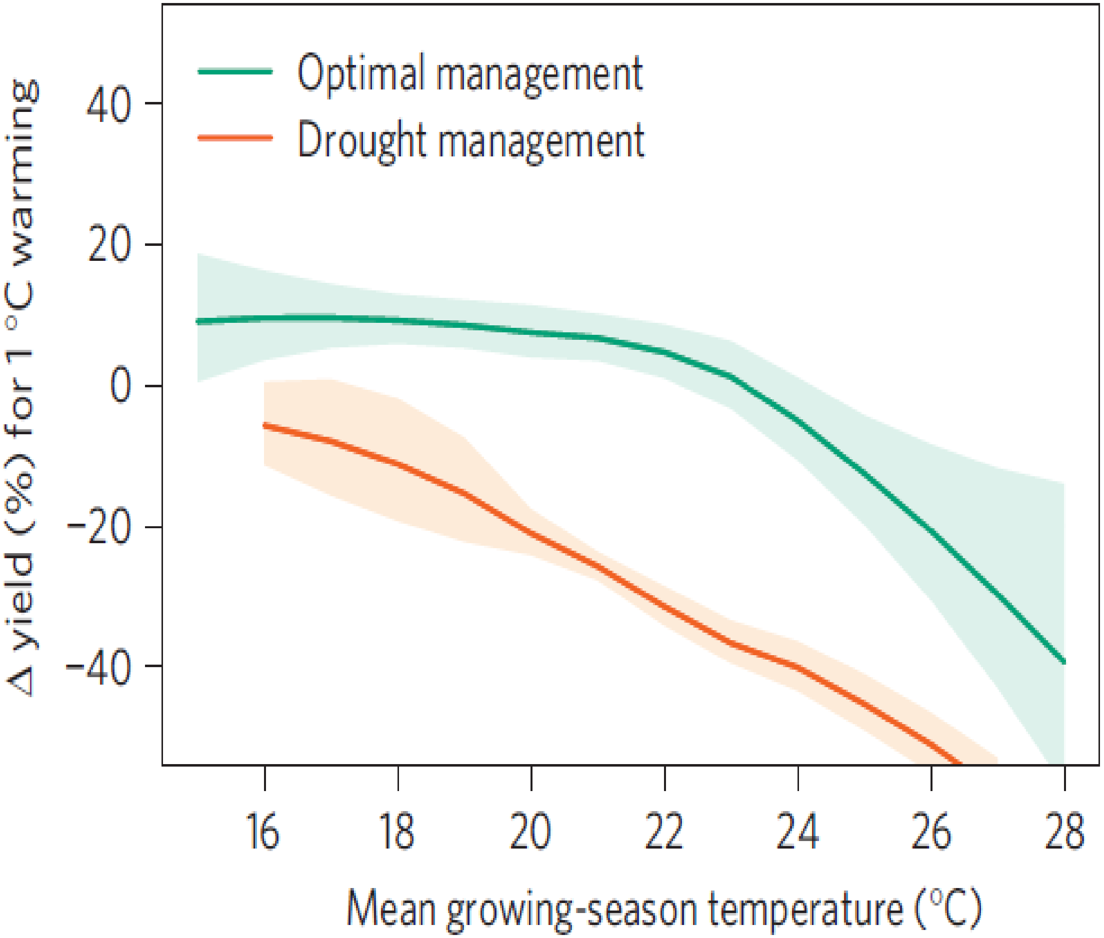
Climate Changes

- Genetic gains in the developing world are **around 1% each year**
- Climate change **lowers** crop yields by about **5% per degree of warming.** It eradicates 2-3 out of 10 years of breeding.
- Environmental changes associated with the new diseases.

Drought susceptible maize variety devastated by drought in Zimbabwe.
Photo: Peter Lowe/CIMMYT

Climate Changes

Heat & drought effects on maize in Africa



- **Historical data:**

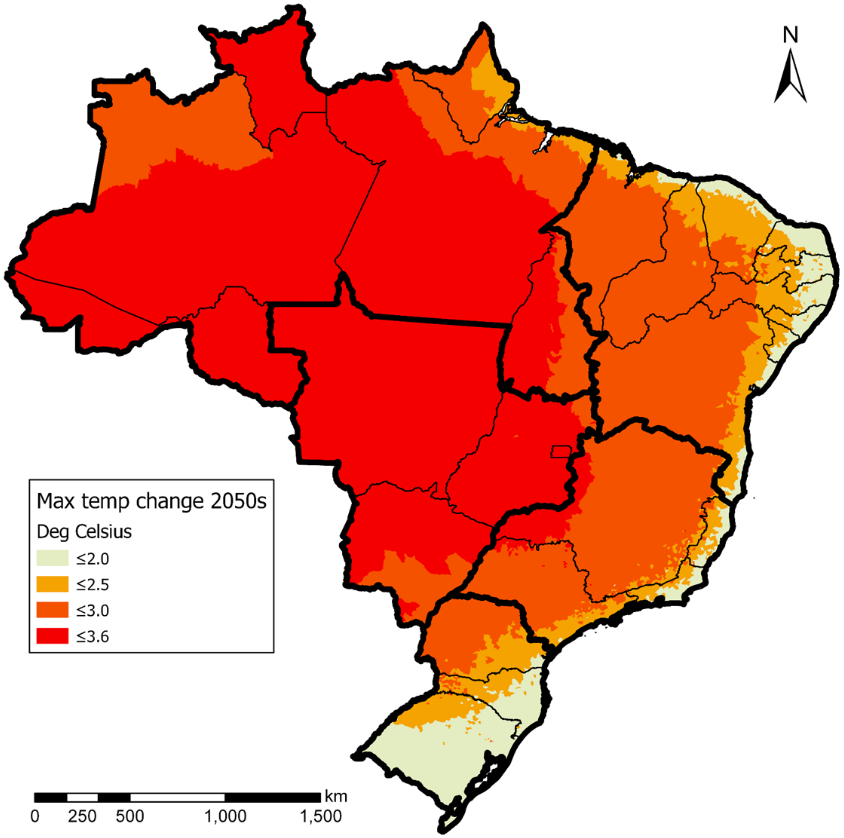
  >20,000 yield trials

- **Each degree day above 30°C lowers yield**
  - 1% under optimal
  - 1.7% under drought

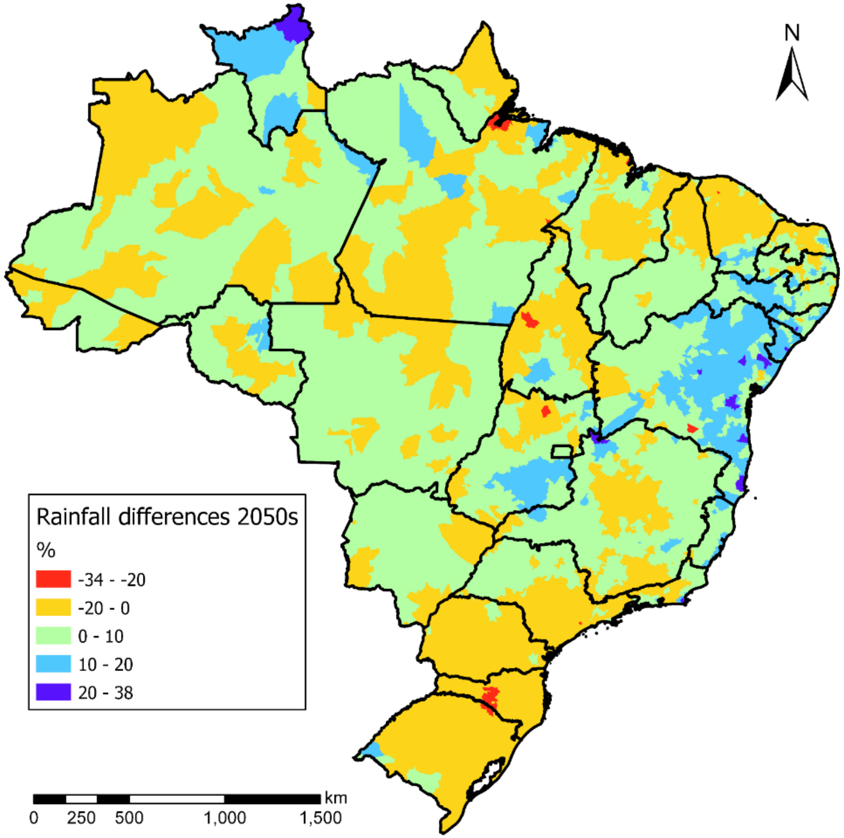
Lobell et al. Nature Climate Change 2011

Climate Changes in Brasil – 2050s

Temperature



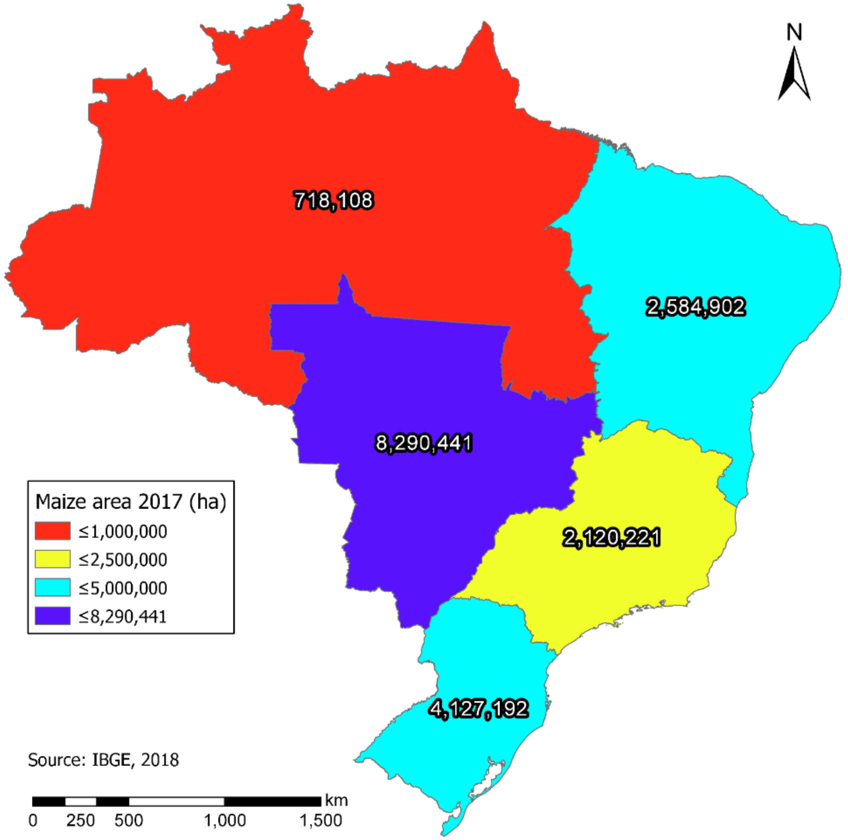
Rainfall



Based on comparison Worlclim 1.4 (1950-2000) with RCP 8.5 ensemble of 32 GCM (CCAFS) outputs 2050s

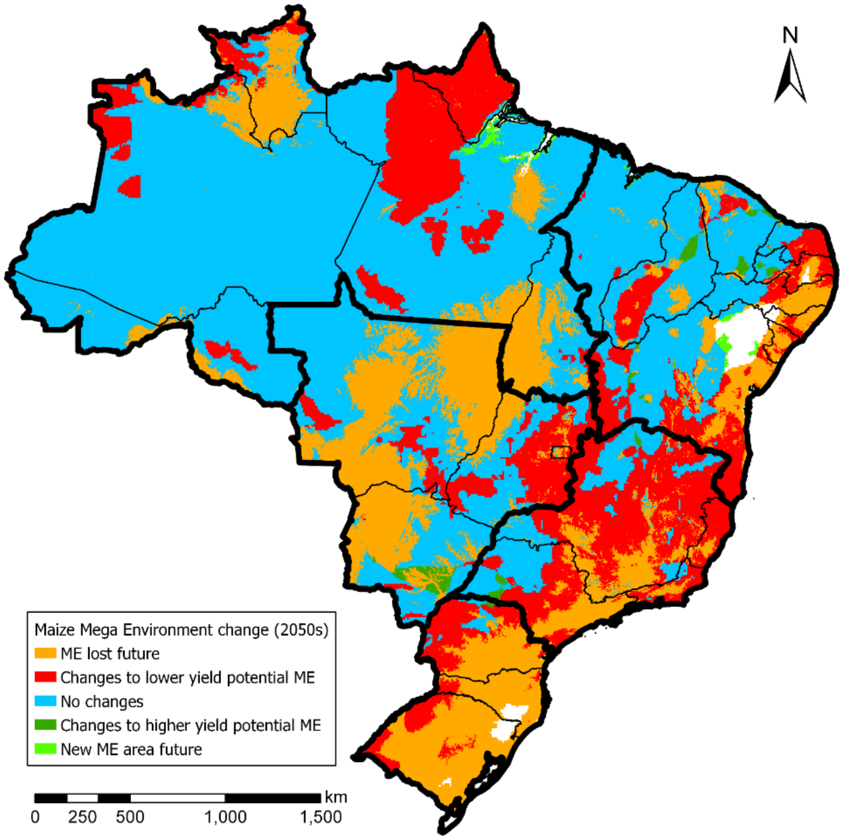
Climate changes in Brasil – 2050s

Maize Area (ha) in 2017 by Regions



Source: IBGE, 2018

Maize Environment Change for 2050s



Sonder et al. 2015 (unpublished)
Based on comparison Worlclim 1.4 (1950-2000) with RCP 8.5 ensemble of 32 GCM (CCAFS) outputs 2050s

CIMMYT

Developing World

- 45% of the global area sown to major staples is found in low- and lower-middle income countries, along with 84% of the world’s poor
- However, these countries receive just 5% of private sector breeding investment
- Address issues that can affects crop production and threaten food security.
- Adding efforts to track these issues and improve livelihood

CGIAR-CIMMYT


Photo: CIMMYT


Photo: CIMMYT


Photo: Peter Lowe/CIMMYT

CIMMYT AROUND THE WORLD

🟩 Projects in over 40 countries

Countries with offices:

Afghanistan
Bangladesh
China
Colombia
Ethiopia
Guatemala
India
Iran
Kazakhstan
Kenya
Mexico
Nepal
Pakistan
Turkey
Zimbabwe

Seeds of Discovery
GRP - CIMMYT

TO: Shutterstock

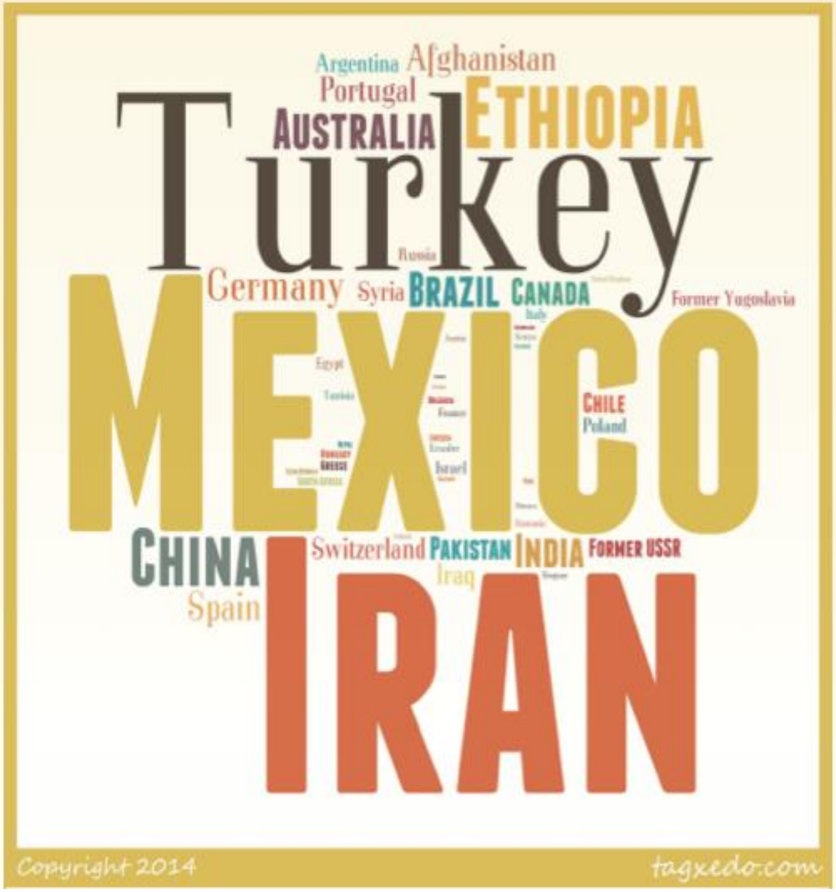
Seeds of Discovery or “SeeD”

(MasAgro Biodiversidad)

- Maize & Wheat
- Part of Genetic Resource Program
- Principally financed by the Mexican government (2011)
- Four Components:

1. **Phenotypic & molecular characterization of genetic resources in the Bank.**
2. Informatics genetic analysis tools.
3. **Breeding and new germplasm release.**
4. Capacity building and training.

CIMMYT Wheat Germplasm Bank holds accessions from



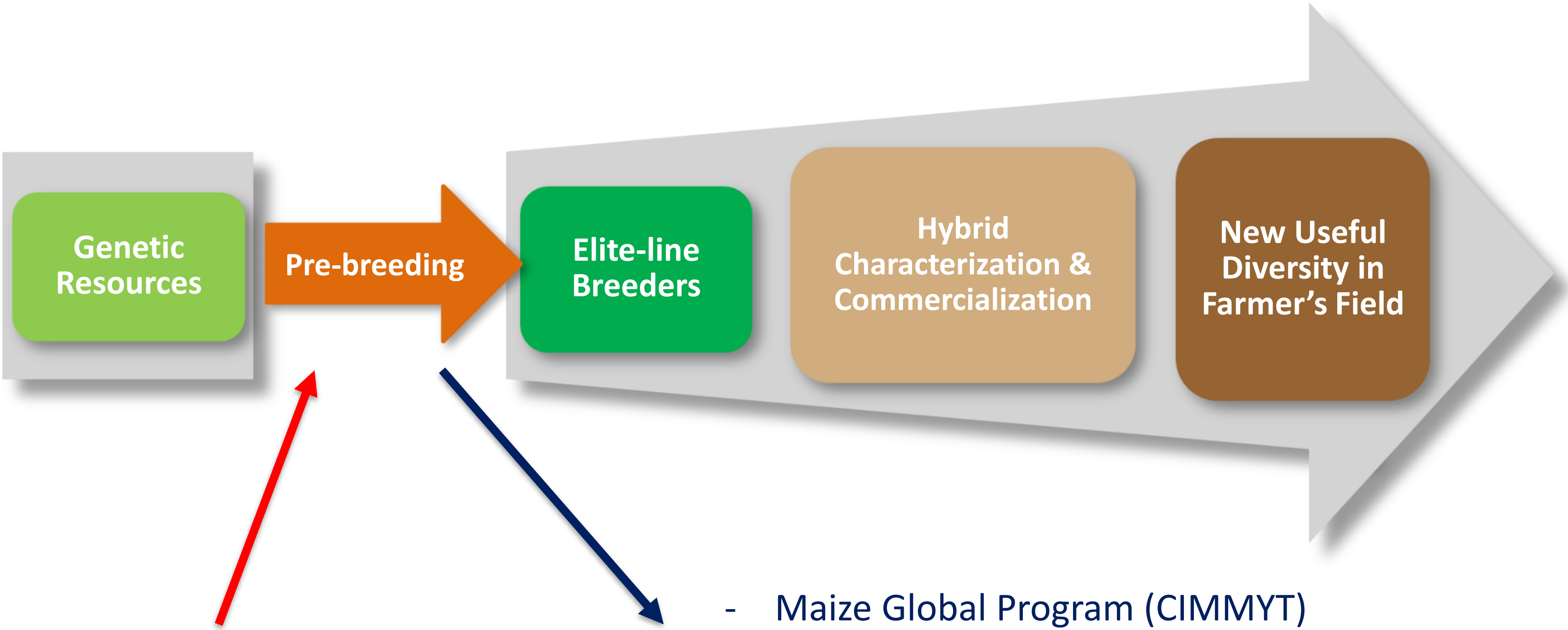
$\sim 150,000\ accessions$

CIMMYT Maize Germplasm Bank holds accessions from

$\sim 27,000\ accessions$

CIMMYT MR

Concept: to bridge the gap between germplasm banks & breeders.



Genetic Resources

Pre-breeding

Elite-line Breeders

Hybrid Characterization & Commercialization

New Useful Diversity in Farmer's Field

SeeD
Genetic Resource Program

- Maize Global Program (CIMMYT)
- Wheat Global Program (CIMMYT)
- Seed companies
- Farmers
- Any interested institution

Why are breeders unwilling to work with landraces?

- Linkage drag
- Disruption of conserved linkage blocks.
  - ~100 year of selecting & collecting the most favorable alleles.
- Low yield.
- Accession material is difficult to work.
  - Extreme genetic diversity (some would say too much!).
  - Photo-period sensitivity, adaptation issues (altitude), ears too high & plants too tall, weak stalks & roots.
- Lack of information on the materials in the banks.
- Time-consuming and expensive

Linkage drag

When do we return to the germplasm banks?

- When we have little or no diversity for a target trait
  - e.g. MLN resistance, possibly heat tolerance

- When we have diversity but feel we do not have all the alleles necessary to cope with a foreseeable problem such as climate change.
  - e.g. Drought tolerance, fusarium ear rot, and heat tolerance

- When there is a market demand for a parameter we can’t meet with improved germplasm.
  - e.g. QPM, pro-vitamin A, high-anthocyanin, low-phytate maize

SeeD Maize Breeding Projects

Resistence/tolerance to:

- Drought at flowering time (>600, MasAgro)
- High temperatura during flowering & grain fill (>200, MasAgro/CGIAR)
- Tar Spot Complex (>800, MasAgro/CGIAR)
- Maize Lethal Necrosis virus complex (>1000, CGIAR)

Quality/New Markets - Maize with pigmented grain:

- Blue Maize with high anthocyanin levels (>200, MasAgro/Kellogg's)
- Red Maize (>200, MasAgro/Kellogg's)

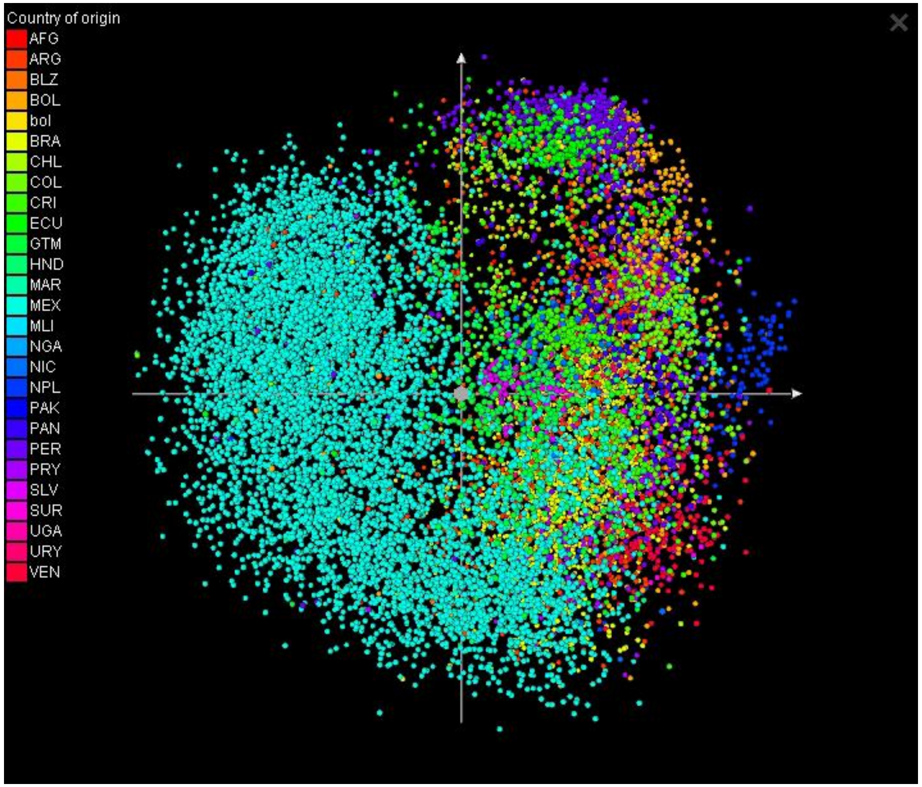
(In parenthesis the number of landraces or populations evaluated & the donor organization)

Accessions/Landrace Selection

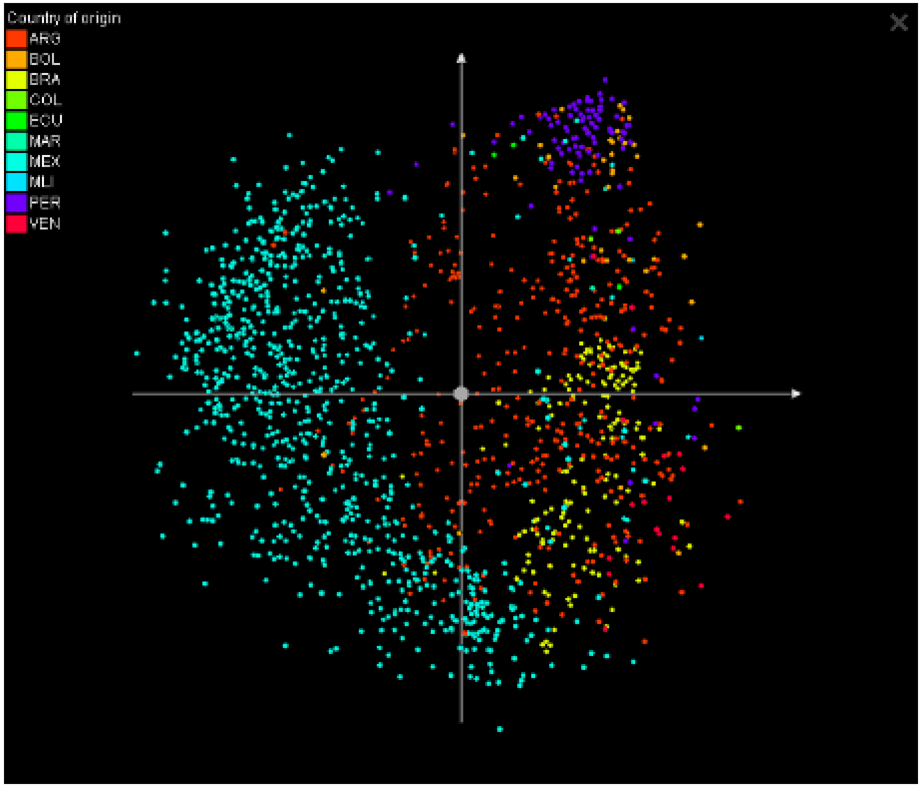
Consider all the information that is available:

- *Passport information*: origin; collection site; collection date; race; color…
- *Environment*: altitude; latitude; temperature; areas with low or unreliable rainfall; disease pressure…
- *Genetic information*: select a representative sample of the genetic diversity.

Accessions/Landrace Selection

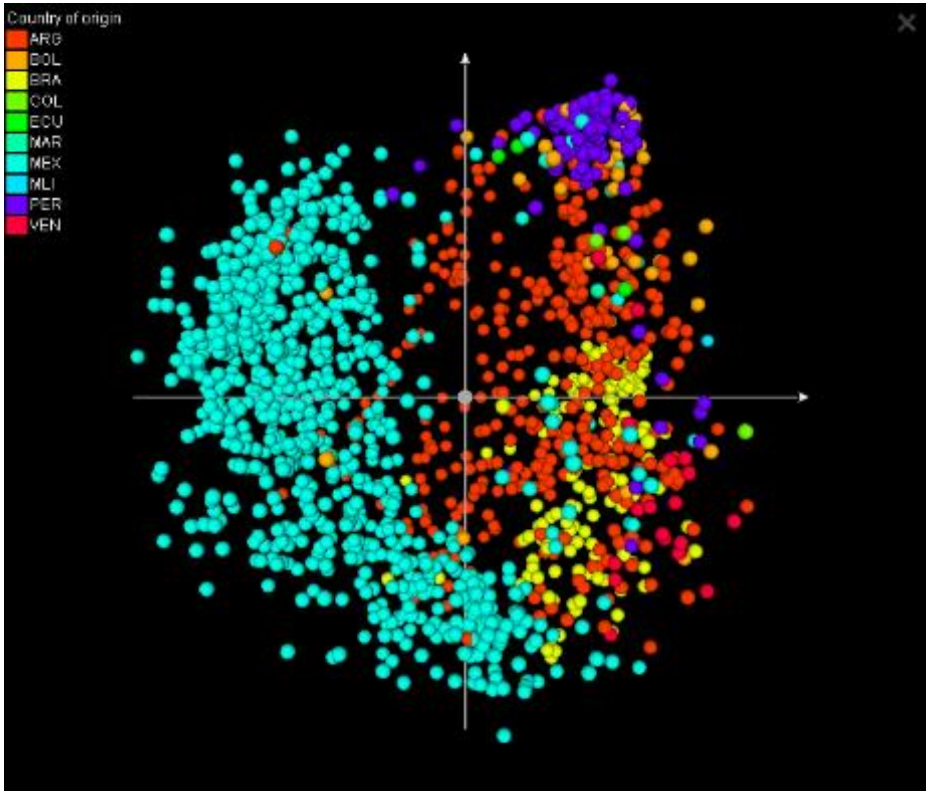


15,384 landraces

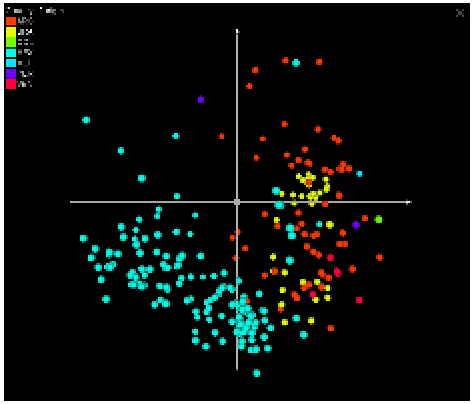


1,549 landraces from drought prone environments

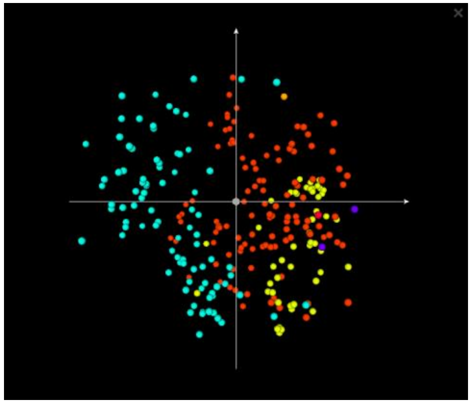
MDS euclidian genetic distances



1,549 landraces from drought prone environments

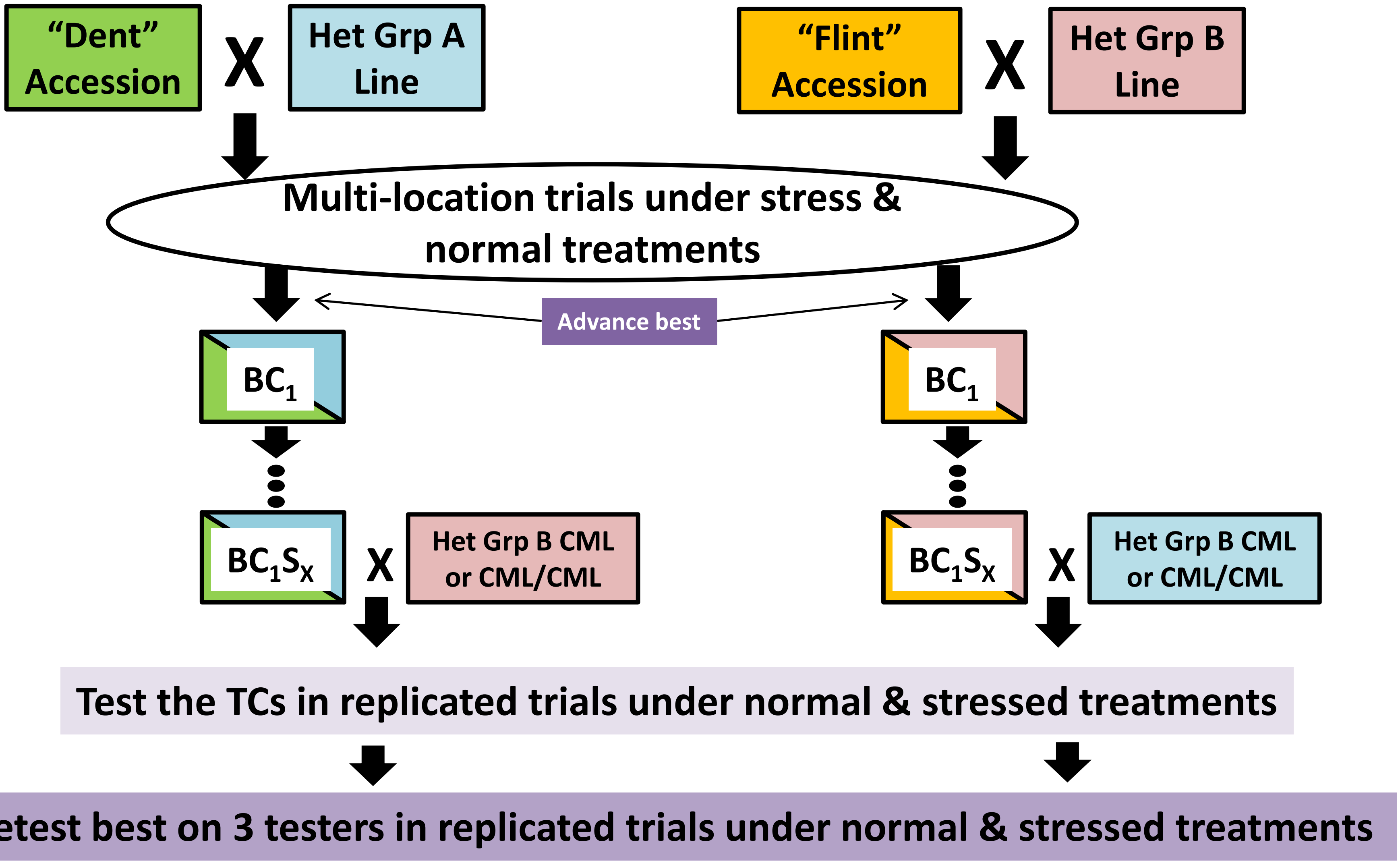


250 Tropical



250 Sub-tropical

SeeD Breeding Method



“Dent” Accession X Het Grp A Line

“Flint” Accession X Het Grp B Line

Multi-location trials under stress & normal treatments

Advance best

BC_1

BC_1

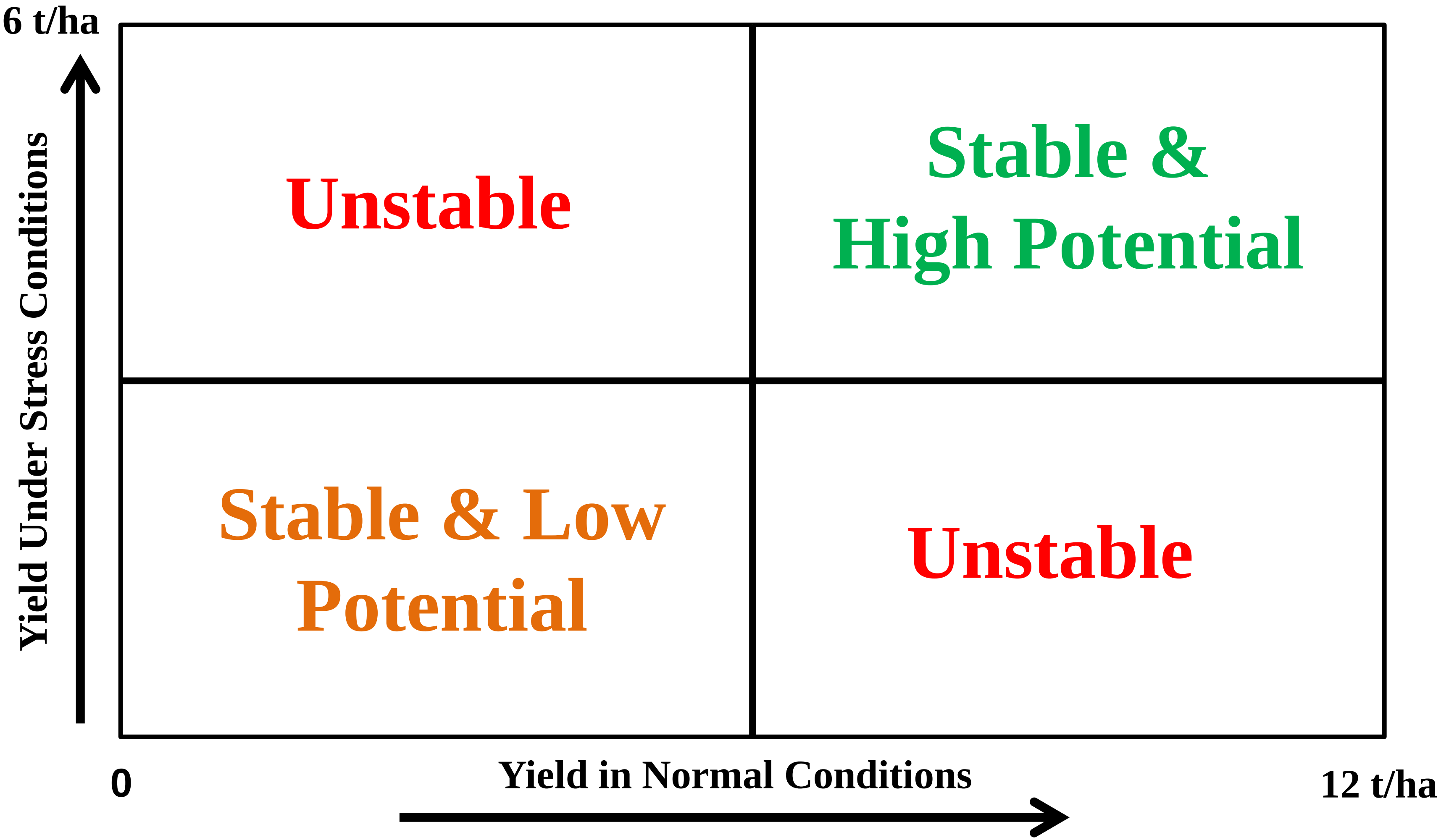
BC_1S_X X Het Grp B CML or CML/CML

BC_1S_X X Het Grp B CML or CML/CML

Test the TCs in replicated trials under normal & stressed treatments

Retest best on 3 testers in replicated trials under normal & stressed treatments

Selection Strategy



6 t/ha

Yield Under Stress Conditions

Unstable

Stable &
High Potential

Stable & Low
Potential

Unstable

0

Yield in Normal Conditions

12 t/ha

Objectives of Germplasm Release Lines

1. Must contain novel alleles for target trait.
   - Should be better than elite germplasm for target trait.
   - Or, be able to demonstrate additive effect of novel alleles.

2. Yield potential - **if none, breeders won’t use**.

3. Decent agronomics – has to be a reasonable line.
   - Ear & plant height, stalk & root lodging, key disease resistances.

⇩

May not be possible to fill all agronomic criteria.
Try to achieve as many as possible

Genomic Association Study

- Check if we are bringing novel alleles or if we are simply selecting for the elite recurrent parent.

- Study what areas of the genome (or haplotypes) remain conserved and what areas of the genome from the accessions are passed to filial lines (within and across landraces).

- Idea: “reverse GS” – what haplotypes from elite parents are essential to their elite status?

Should we be looking at the regions associated with standability, ear/plant height, etc. coming from the elite parents and select for those regions while letting other regions segregate at random?

Maize Lethal Necrosis (MLN)

MLN = MCMV + any maize-infecting potyvirus

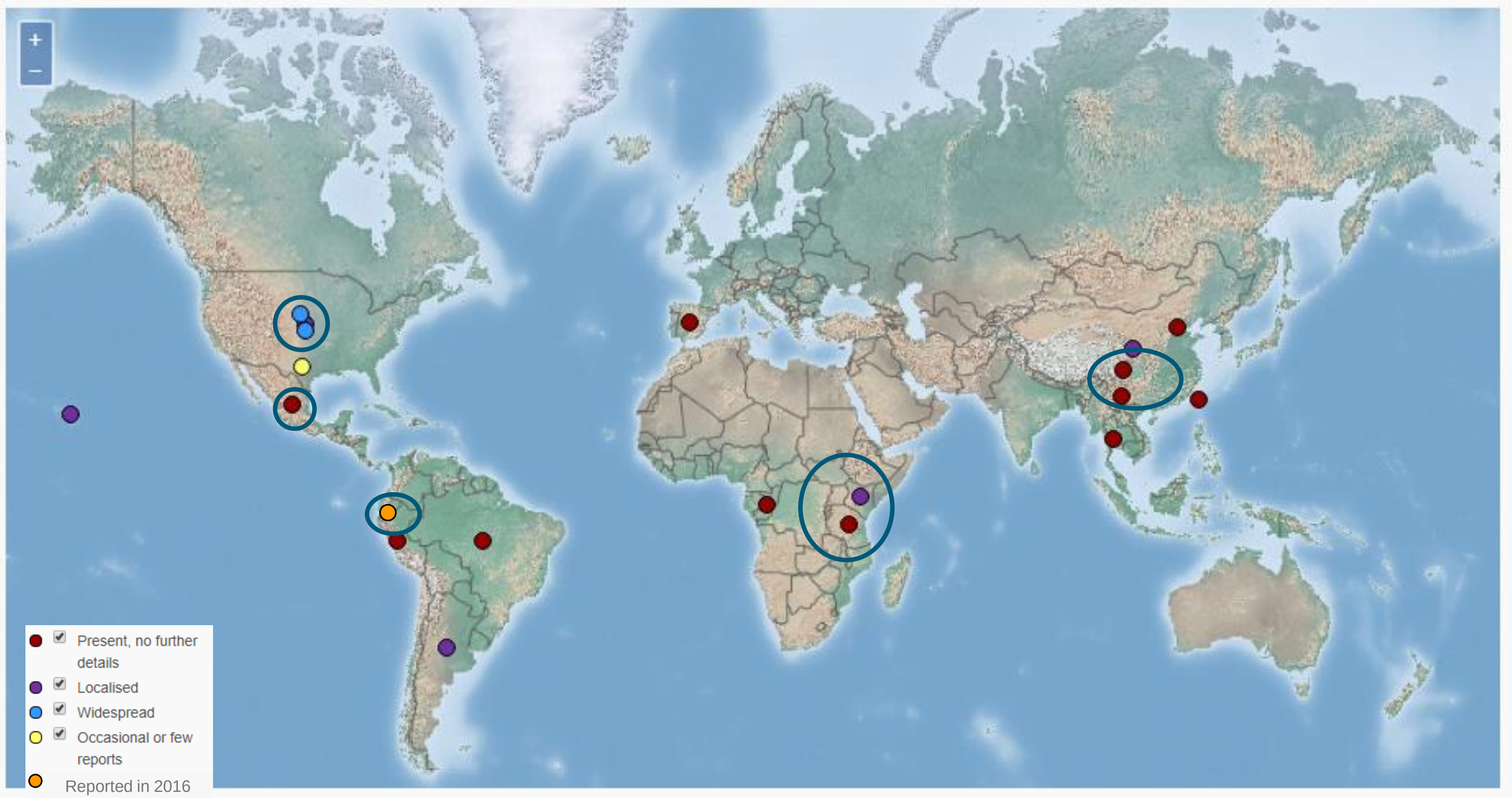
Sugarcane Mosaic Virus (SCMV)

Wheat streak mosaic virus (WSMV)

Maize dwarf mosaic virus (MDMV)

Maize Cholorotic Motlle Virus (MCMV) is considered the major factor in MLN disease development

MCMV Distribution Around the World



Adapted from CABI/EPPO, 2014.
Quito-Avila et al, 2016.

CIMMYT MR

Tackling the MLN Crisis

Initiative to identify new sources of MLN resistance in maize landrace accessions.

Naivasha, February 2018.

Tackling the MLN Crisis

Initiative to identify new sources of MLN resistance in maize landrace accessions.

- 4000 accessions: pre-selected as potential sources of MLN tolerance based on areas known to have high virus pressure, especially MCMV.
- Genetic information was used to ensure broad genetic diversity and to reduce the number of accessions to 1000.
- 1000 accessions were evaluated for MCMV and SCMV.
- 20 of these accessions were selected for promising tolerance to MCMV, SCMV or both.
    - These accessions were crossed to CIMMYT lines aiming to transfer this tolerance into elite lines.

MCMV Tolerant Lines

Initial Cross	F3 lines	F4 lines
CUBA9/CML550	37	110
PUER2/CML550	27	80
HAIT44/CML494	26*	-
SCRO1/CML537	5	15
RDOM169/CML537	3	12
ECUA327/CML537	2	6
OAXA106/CML549	2	6
Total	**102**	**229**

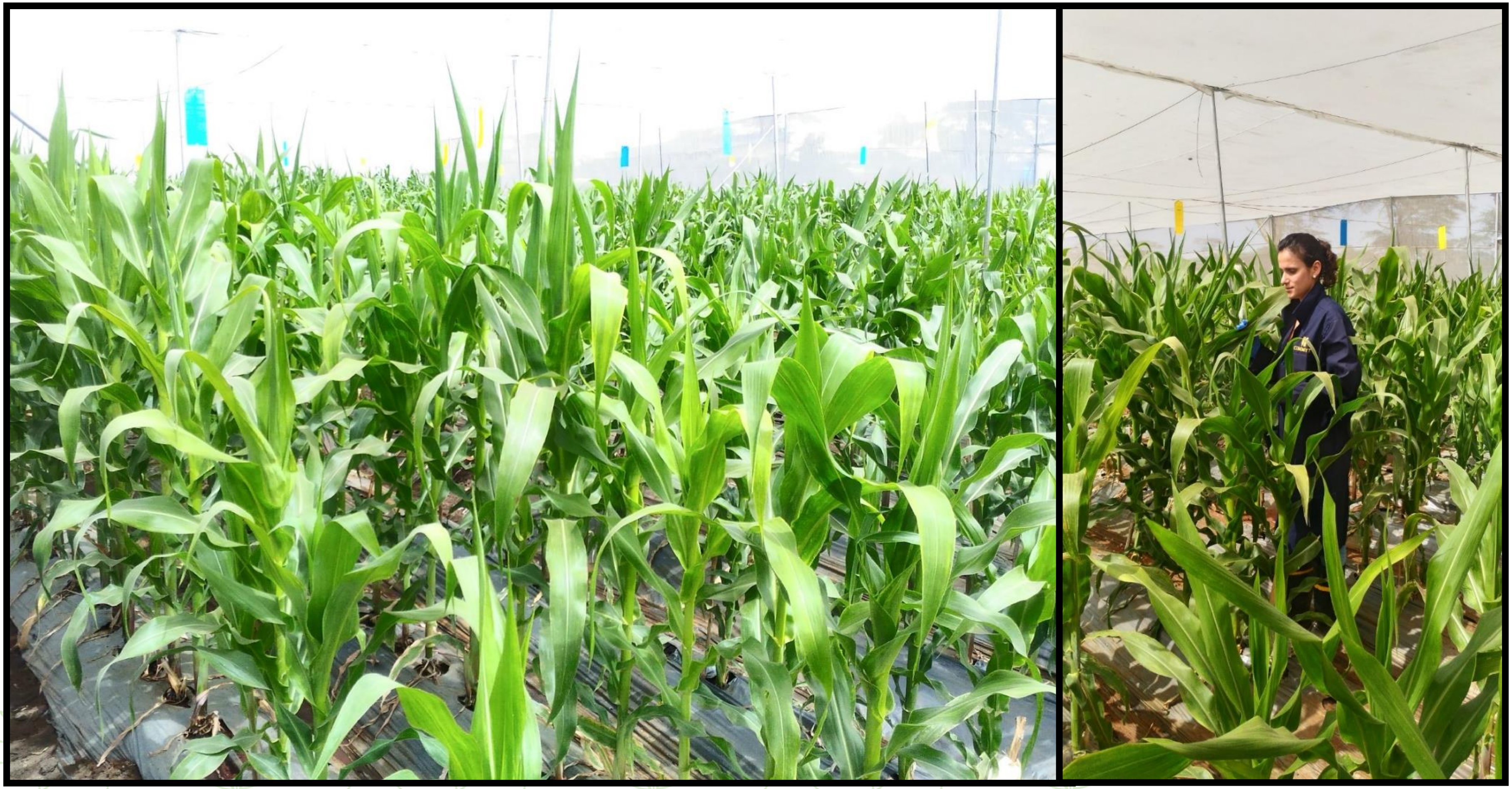
* F3 lines was sent to Naivasha. This lines will be advanced on 18A nursery

- 102 F3 lines were selected as tolerant to MCMV.
- 229 F4 lines derived from the tolerant F3 lines & 26 F3 lines derived from HAIT44, were selected to be evaluated in Naivasha.

MCMV Evaluation in Naivasha – Kenya

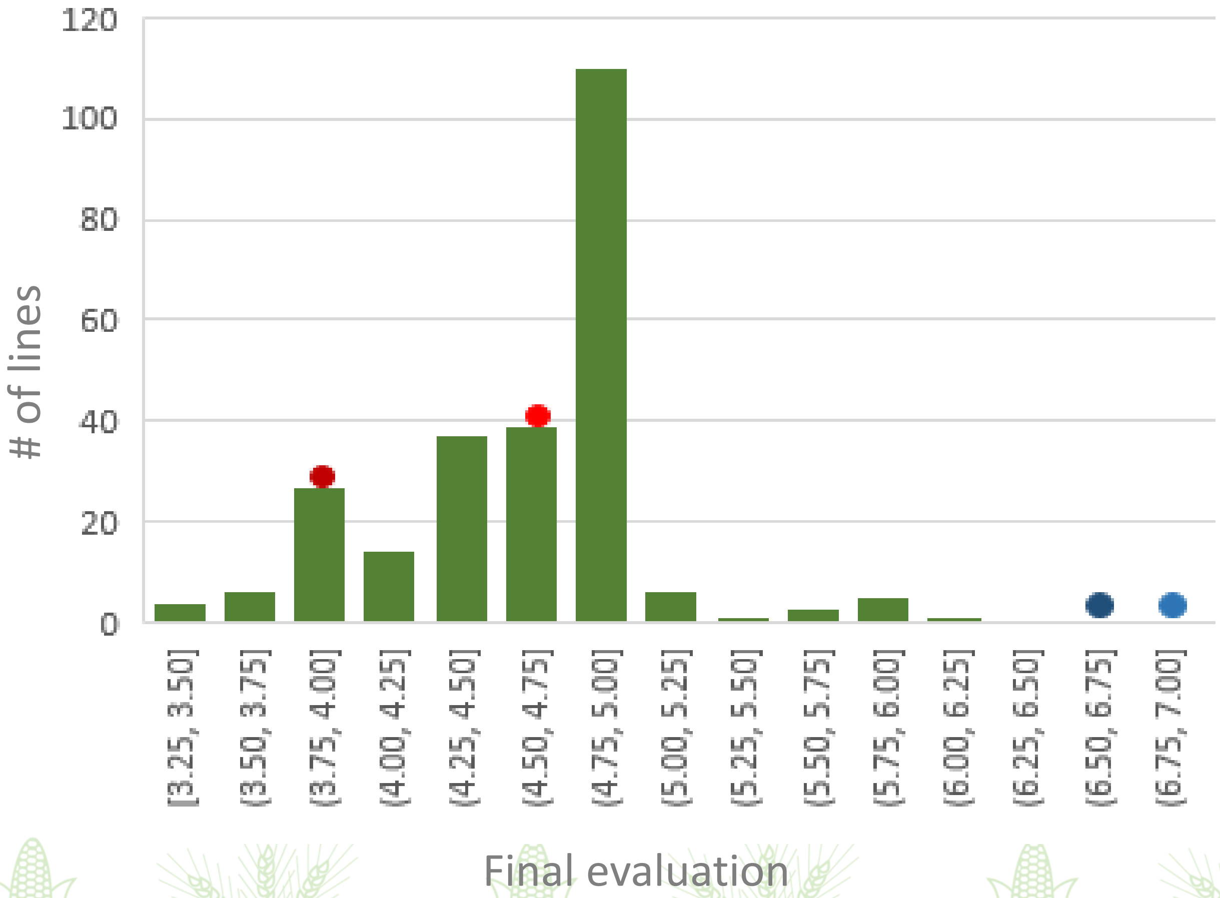
MCMV Evaluation in Naivasha – Kenya

- 253 lines were evaluated to MCMV in Naivasha, in Jan & Feb 2018.
- These lines are being advanced at the 2018A nursery in Puerto Vallarta.



MCMV Results in Naivasha – Kenya

# lines	% F4 lines ≤ CML494	% F4 lines ≤ CML550	% F4 lines ≥ CML228	% F4 lines ≥ CML442
253	4.74% (12)	42.29% (107)	0% (0)	0% (0)



(CML537/RDOM169)

(CML549/OAXA106)

(CML550/PUER2)

(CML550/CUBA9)

(CML494/HAIT44)

- ● CML494 = 3.91
- ● CML550 = 4.66
- ● CML228 = 6.47
- ● CML442 = 6.75

MCMV Results – F4 Lines Evaluation

CML550

(CML537/RDOM169)-B-3-1-2

CML228

- F5 lines derived from F4 lines tolerant to MCMV will be evaluated to MLN tolerance (MCMV+SCMV) and yield in Naivasha, Kenya, this year.

Genomic Association Study

- Identify genomic regions associated to MCMV tolerance and determine if sources are novel.

- Genomic association study is been performed at F3 generation

- Results!? Working on it…

Getting strong phenotypic & genotypic signal in maize pre-breeding populations is extremely difficult. In fact, even in elite programs, not much has worked with segregating populations (F3 or BC1 derived lines).

Goals for 2018 and further…

- First lines to be released for:

    - Drought tolerance (4 years of yield evaluations)

    - Tar Spot disease tolerance (2 years yield evaluations + “per se” disease evaluations)

    - MLN tolerance (“per se” evaluation only)

- Continue using genetic resources for breeding tolerance to biotic stresses, abiotic stresses and pigmented kernels

Address issues that can affects maize production and threaten food security.

Adding efforts to track these issues and improve livelihood.

SAGARPA
SECRETARÍA DE AGRICULTURA, GANADERÍA, DESARROLLO RURAL, PESCA Y ALIMENTACIÓN

MasAgro
Modernización Sustentable de la Agricultura Tradicional

BILL & MELINDA GATES foundation

DUPONT
PIONEER

CGIAR

NOVASEM

Forage Genetics International

inifap
Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias

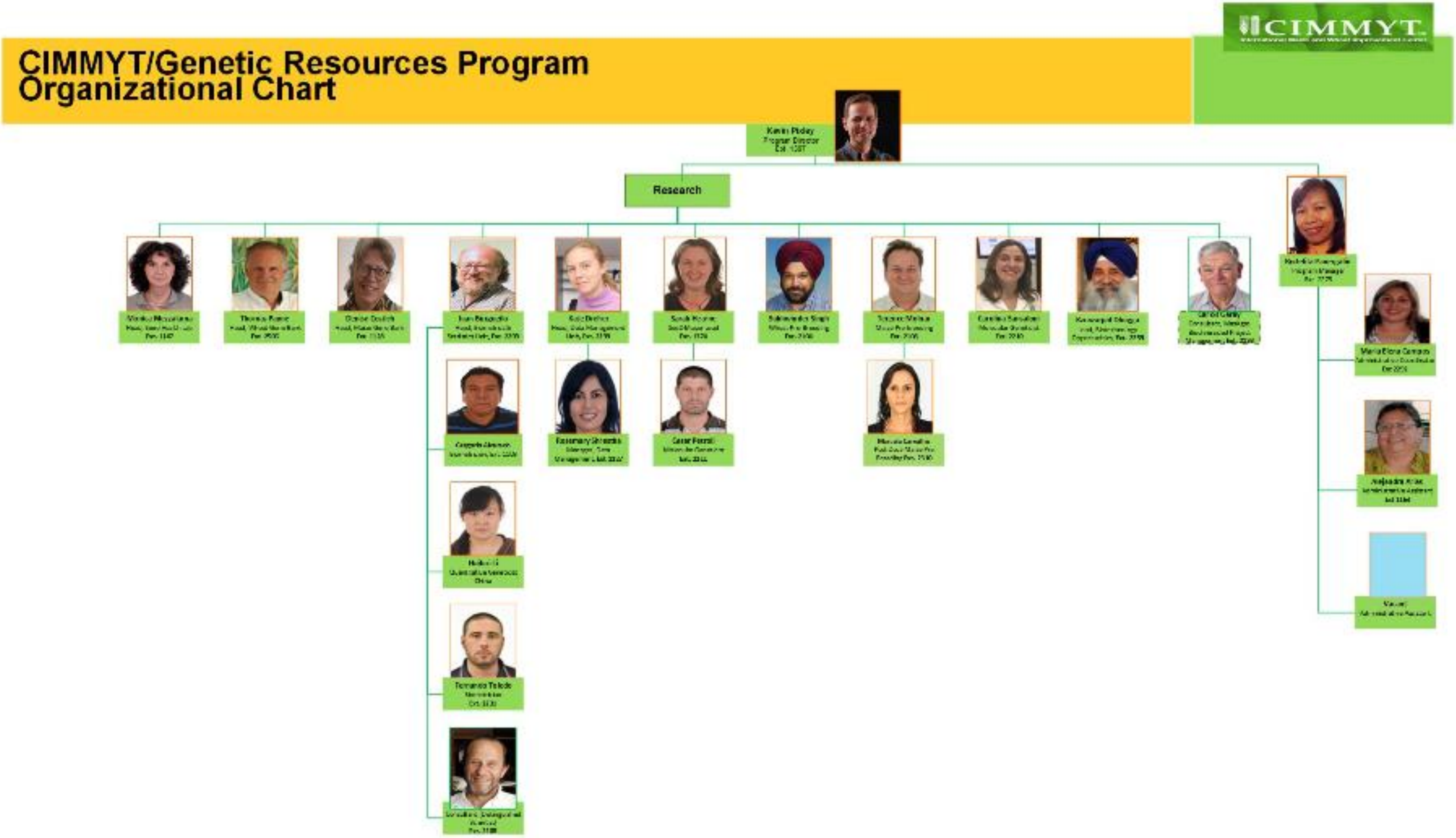
Semillas CERES

Kellogg's

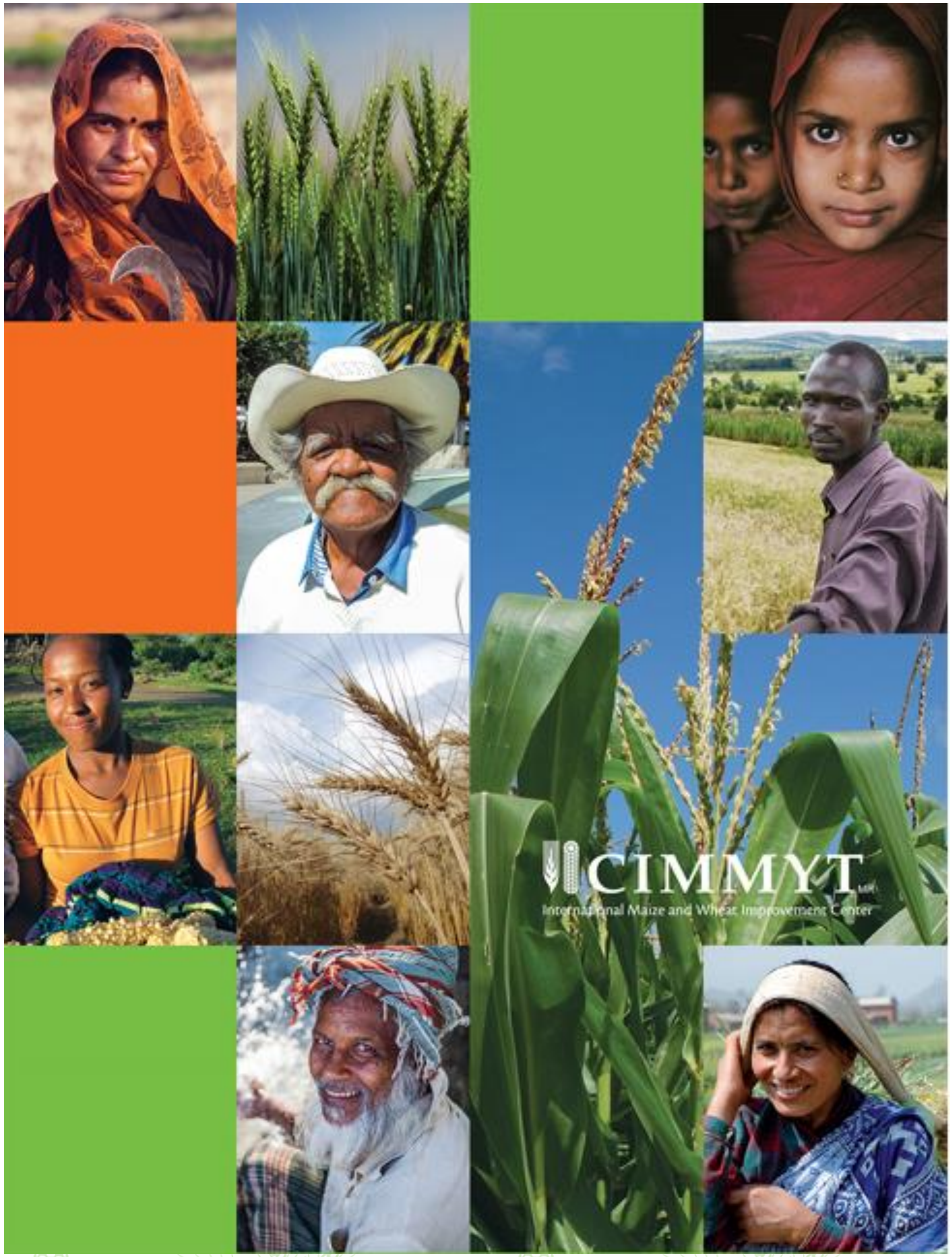
Proase

GLOBAL Seed Genetics

Terrasemilla



Enrique Rodríguez Chanona; Daniel Chepetla Calderón; José Javier Rodríguez;
Juan Margarito Espinoza; Gustavo Santiago Tellez; Felipe Pura Espinoza; Gustavo Martínez



Obrigada!

m.carvalho@cgiar.org

- In 2015 through 2016, the F1s were advanced to F3 generation.

Accession	CIMMYT	Origin	Evaluated
BRVI2	CML549	British Virgin Islands	x
CUBA32	CML494	Cuba	
CUBA9	CML550	Cuba	x
ECUA327	CML537	Ecuador	x
HAIT44	CML494	Haiti	x
OAXA106	CML549	Mexico	x
PERU558	CML537	Peru	x
PUER15	CML494	Puerto Rico	
PUER2	CML550	Puerto Rico	x
RDOM169	CML537	Dominican Republic	x
RDOM309	CML494	Dominican Republic	
SCRO1	CML537	Virgin Islands	x
SVIN8	CML494	St Vincent Island	
VENE1014	CML494	Venezuela	
VERA179	CML537	Mexico	x
VERA203	CML537	Mexico	x
VERA413	CML549	Mexico	
VERA470	CML537	Mexico	
VERA73	CML494	Mexico	
VERA756	CML549	Mexico	

- 11 F3 families were evaluated.
- 715 F3 lines were screened for MCMV during 2016 and 2017 .

MCMV Symptoms in Greenhouse

MCMV Results – F3 Lines Evaluation