Genetic Resources Program

Enabling the Effective Use of Maize and Wheat Genetic Resources in support of CIMMYT's mission

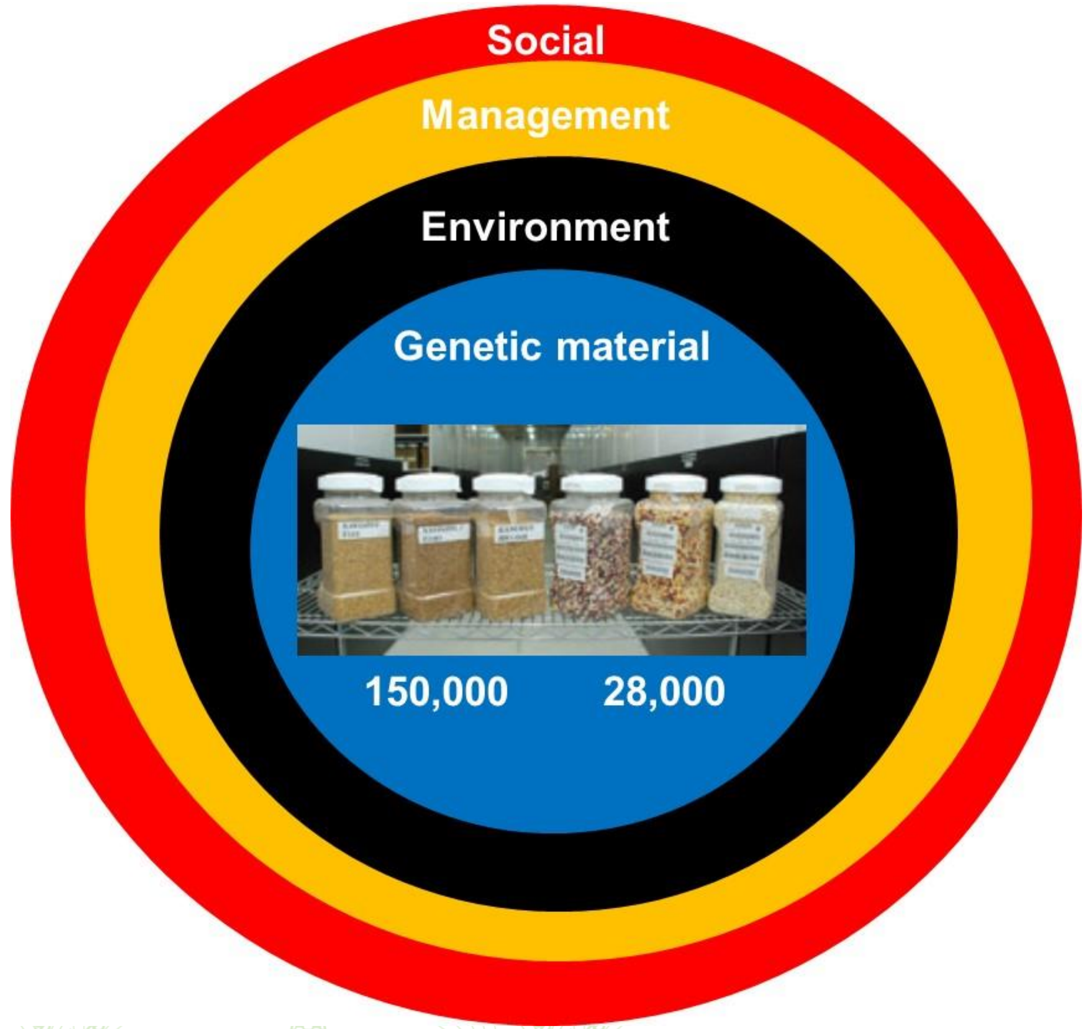
Maize and Wheat Science for Improved Livelihoods

CIMMYT

Outline

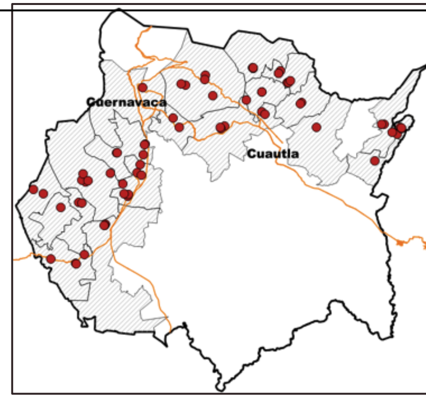
1. The Bank – Conserving more than genetic diversity
2. Understanding diversity
3. Big Data – Managing data FAIR-ly
4. Innovative Science – Using the data!
5. Pre-Breeding – Getting from the bank to farmers
6. Creating Diversity – Genetic engineering
7. Capacity Development – Unleashing innovation

Germplasm bank conserves wheat & maize diversity

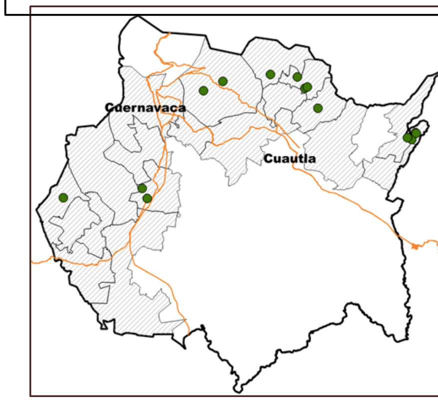


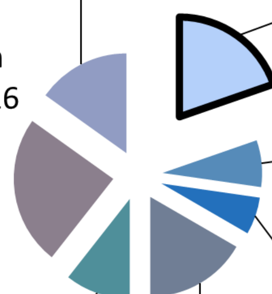
Comparing *in situ* and *ex situ* maize diversity conservation: A case study in Morelos, Mexico

93 collections in1967



14 collections in 2017





In 2017, 13 of 66 families conserve their collections

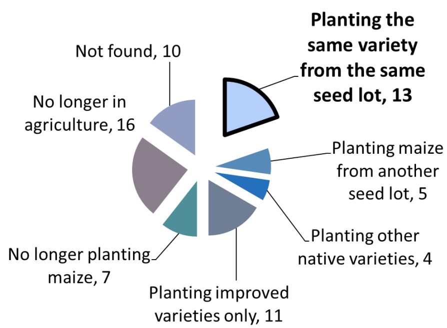
Denisse McLean

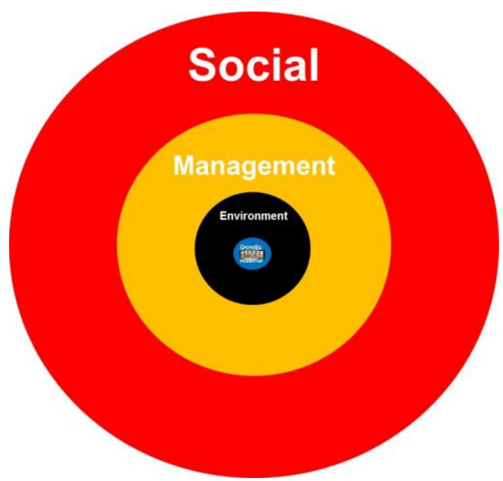
Preliminary Results

Genomewide *ex-situ* and *in-situ* samples are remarkably similar

	***Ex-situ* (1967)**	***In-situ* (2017)**
SNPs at 1% MAF	36916	35879
Heterozygosity	7.4%	7.7%
Average MAF	6.8%	6.8%

Reasons maize diversity was maintained or lost





85% of the collections *in-situ* were lost

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Seeds of Discovery

"searching for needles in a haystack of genetic diversity"

Before SeeD

After SeeD

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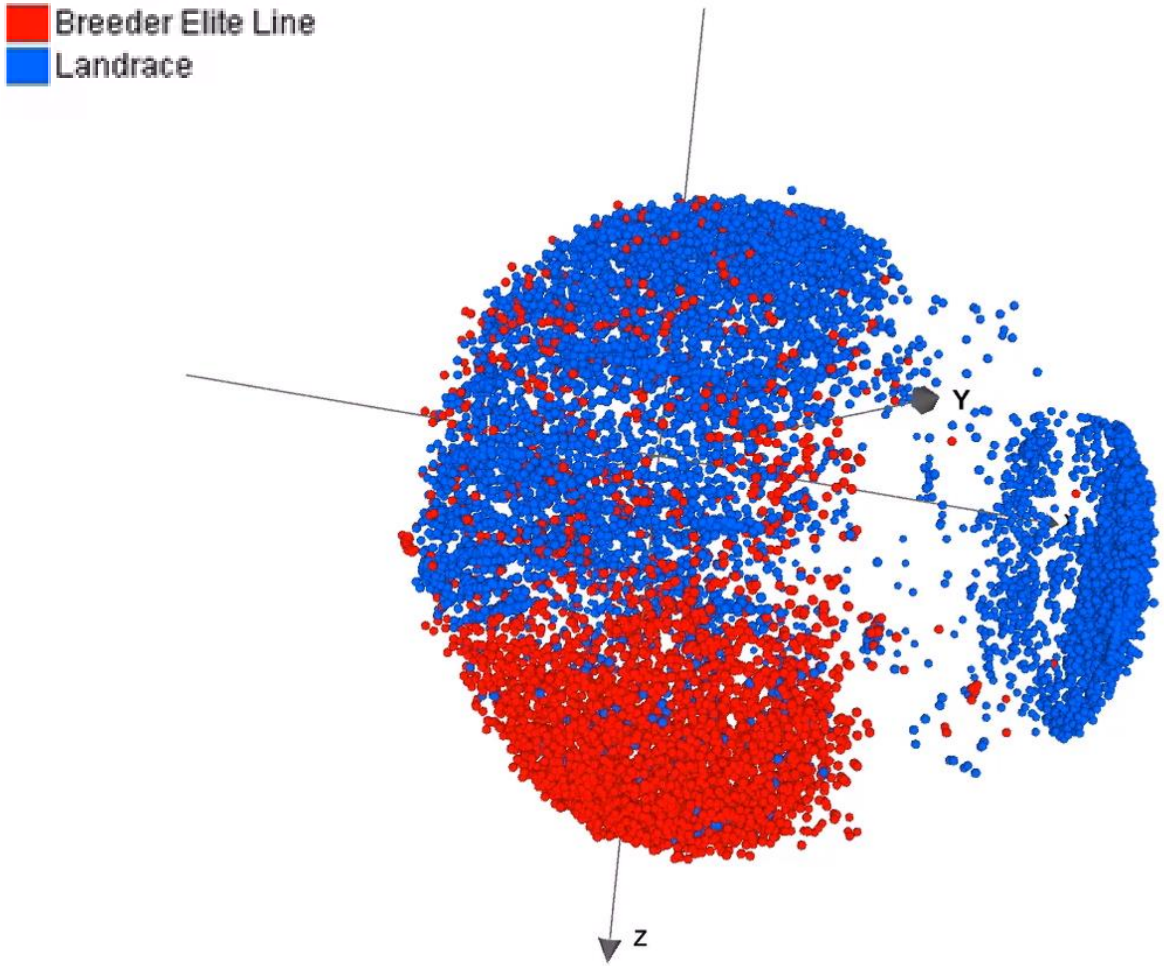
Global diversity study for wheat

- Evaluate genetic diversity among wheat germplasm groups
  - wild relatives, landraces and elite breeding lines
- Elicit insights about diversity that has been underexplored by breeding programs.



Tetraploid

20,000 accessions,

8 domesticated species:

T. durum,
T. aethiopicum Jakubz,
T. turgidum,
T. carthlicum,
T. dicoccum,
T. turanicum,
T. polonicum,
T. karamyschevii

AB genomes,

75 countries

26,527 SilicoDArT

100,000 SNP's

Breeding programs have greatly reduced diversity

- A few elite lines explore a wide range of the landrace diversity
- Many landraces remain completely unexplored
- **Potential reservoirs of novel alleles for breeding.**

Sansaloni *et. al*. (in preparation)

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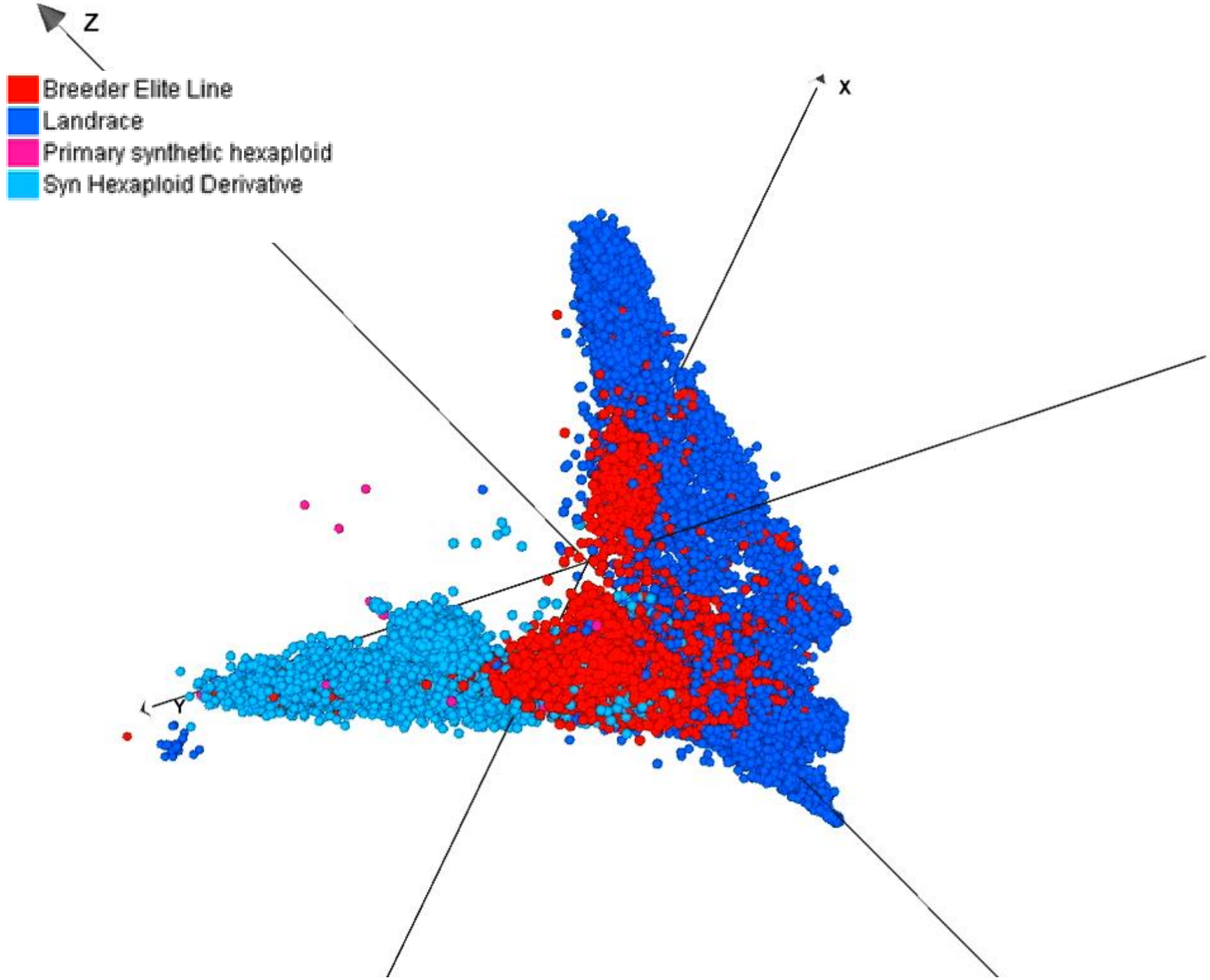

Hexaploid

60,000 accessions,

8 domesticated species:

T. aestivum subs. aestivum,
T. aestivum subs. spelta,
T. aestivum subs. campactum,
T. aestivum subs. sphaerococcum,
T. aestivum subs. macha,
Tritucum hybrid,
x Aegilotriticum
x Triticosecale

ABD genomes,

105 countries

26,500 SilicoDArT

85,500 SNP's

Breeding programs have greatly reduced diversity

- A few elite lines explore a wide range of the landrace diversity
- Many landraces remain completely unexplored
- **Potential reservoirs of novel alleles for breeding.**

Sansaloni *et. al*. (in preparation)

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Global diversity study for wheat

- All data and tools generated will be open access
  - Germinate, Dataverse and Ensemble Plant
  - **A unique and great resource for the global research community**.

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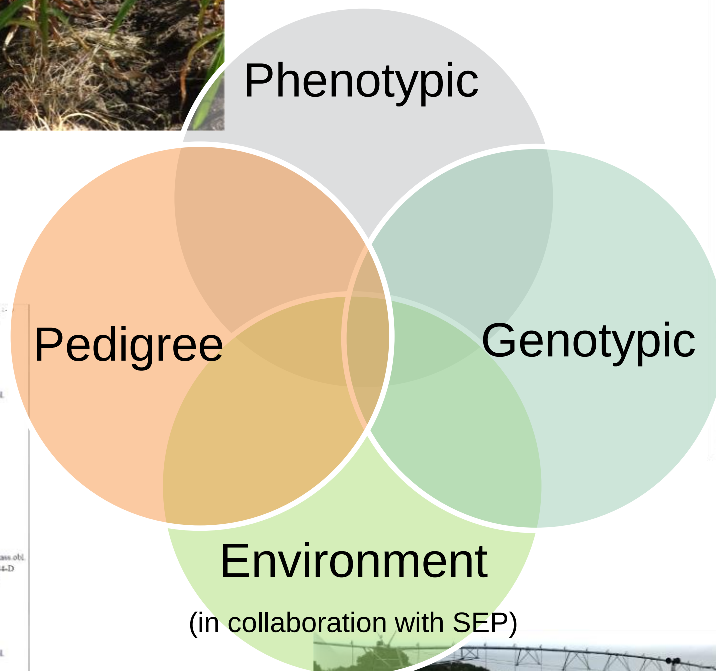
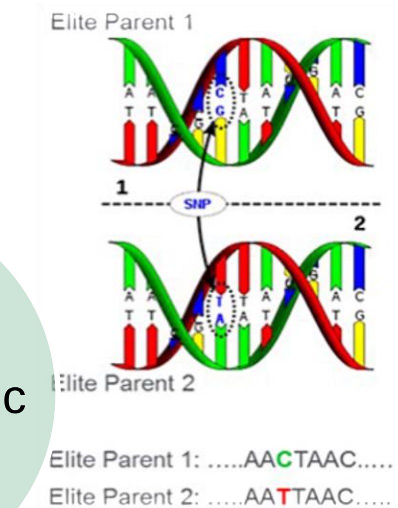
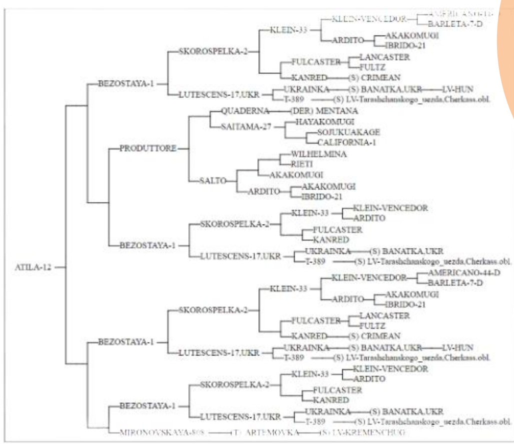
Data Management

for effective use of data







www.cimmyt.org/resources... Data resources; Research Data Repository

Metrics | 60,627 Downloads

Contact | Share

CIMMYT institutional network of scientific datasets and software repositories.

Search this dataverse... | Find | Advanced Search

Repository

CIMMYT Research Data (CIMMYT)

Oct 22, 2014
Free, open access repository of research studies developed by CIMMYT scientists.

CIMMYT Seeds of Discovery (CIMMYT)

Dec 19, 2014
File download is currently disabled for this Dataverse due to system maintenance. Plea
dataset fully.

CIMMYT Research Software (CIMMYT)

Jun 3, 2015
Free, open access repository of research software produced and developed by CIMMY

Repository

Cereal Systems Initiative for South Asia (CSISA) Research Data (CIMMYT, IFPRI & IRRI)

Feb 2, 2017
Free, open access repository of research data produced as part of the Cereal Systems Initiative for South Asia (CSISA) project.

Repository

International Wheat Yield Partnership Research Data (CIMMYT on behalf of IWYP)

Mar 13, 2017
Free, open access repository of research data produced as part of the International Wheat Yield Partnership (IWYP).

Repository

Sustainable and Resilient Farming Systems Intensification in the Eastern Gangetic Plains (SRFSI) Research Data (SRFSI)

Jun 5, 2018
Free, open access repository of research data produced as part of the Sustainable and Resilient Farming Systems Intensification in the Eastern Gangetic Plains (SRFSI) project.

https://data.cimmyt.org/dataverse/root?q=&types=dataverses&sort=dateSort&order=asc&page=1

From Theory to Application (BIG DATA)

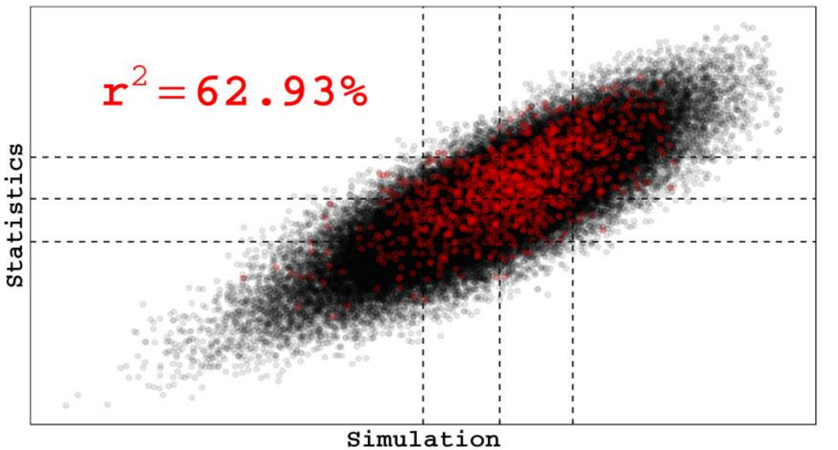
In silico Breeding

Hybrids/Crosses involve the evaluation of a **huge** number of **perspective** pairs

- Too **expensive** or **impossible** to test
- ***In silico*** breeding
- Some good **statistics** enable us to **predict** genotypes
- We can **simulate** hybrids and crosses **without** restrictions
- Opportunities to understand **heterosis** and increase genetic **gains**

Wheat Data (Bhoja Basnet)

- **376** lines
- **>2,500** SNPs
- phenotypes from **2 years x 20 sites**
- **1078** hybrids
- **70,500** possible crosses



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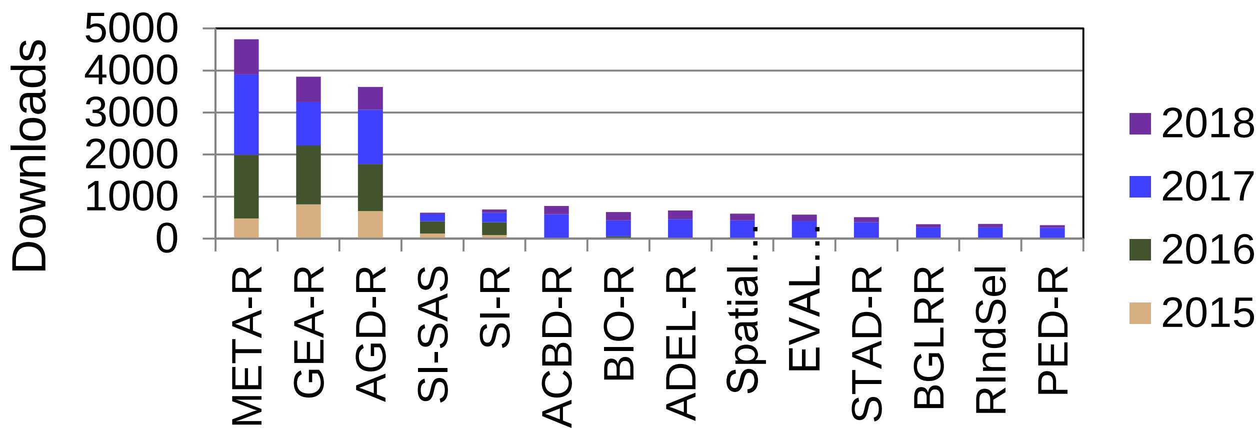
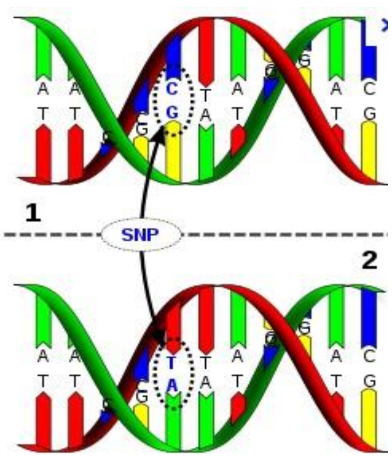
Statistical software tools



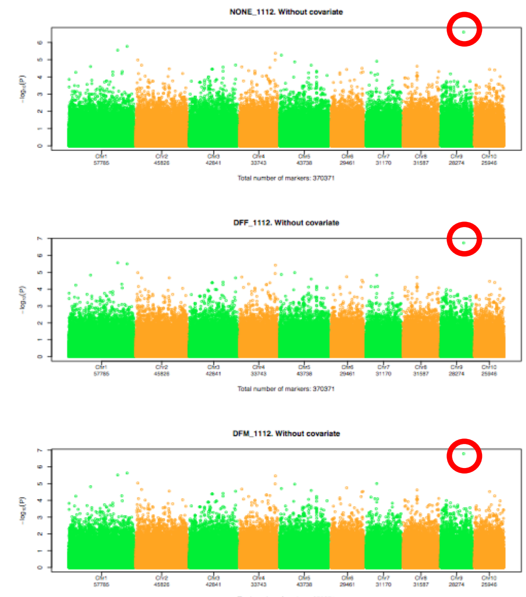
META-R	Multi Environment Trail Analysis.	**BIO-R**	Molecular biodiversity. Cores set.
GEA-R	Stability analysis and genotype x environment interaction analysis.	**SpatialMETA-R**	Spatial Multi-Environment Trial Analysis.
AGD-R	Analysis of Genetic Designs.	**EVAL LxT**	To explore results of line by tester analysis. Identification of best genotypes.
SI-R	Codes for Computing Selection Indices in R.	**STAD-R**	Descriptive statistics of experimental designs.
SI-SAS	A SAS Code to Calculate Several Selection Indexes.	**BGLRR**	Bayesian Generalized Linear Regression for prediction in genome selection.
ACBD-R	Generate and analyze augmented designs.	**RIndSel**	Calculate phenotypic and molecular selection indexes.
ADEL-R	Generate and analyze standard experimental designs.	**PED-R**	Calculate parentage coefficient and pedigree analysis.

Finding genetic variation of breeding value

Genome-wide association studies "GWAS"



~3500 accessions



Molecular markers associated with phenotype of interest

Phenotypic data are expensive to generate!

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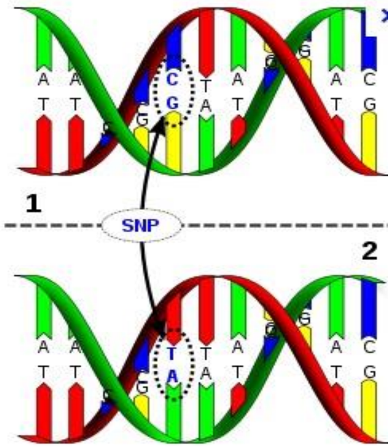
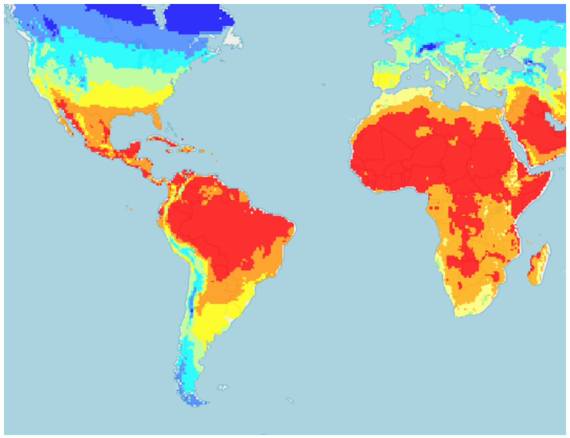
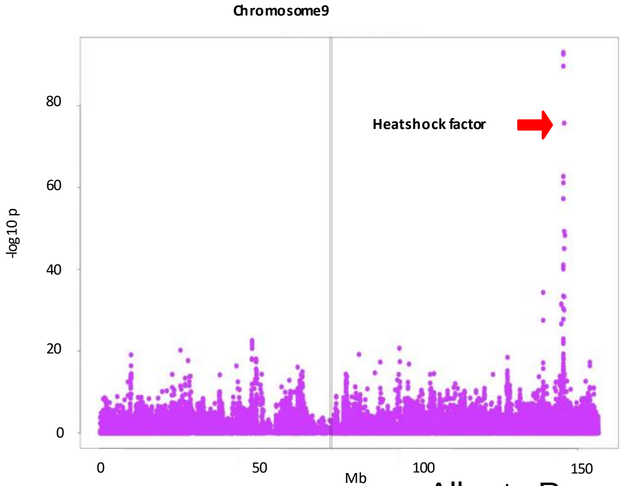
Finding genetic variation of breeding value

Environmental Genome-wide Association Studies "EnvGWAS"







Alberto Romero

GIS-derived collection site data; ~17500 maize accessions

Molecular markers associated with adaptive variation of breeding relevance

GIS data is "virtually" free!

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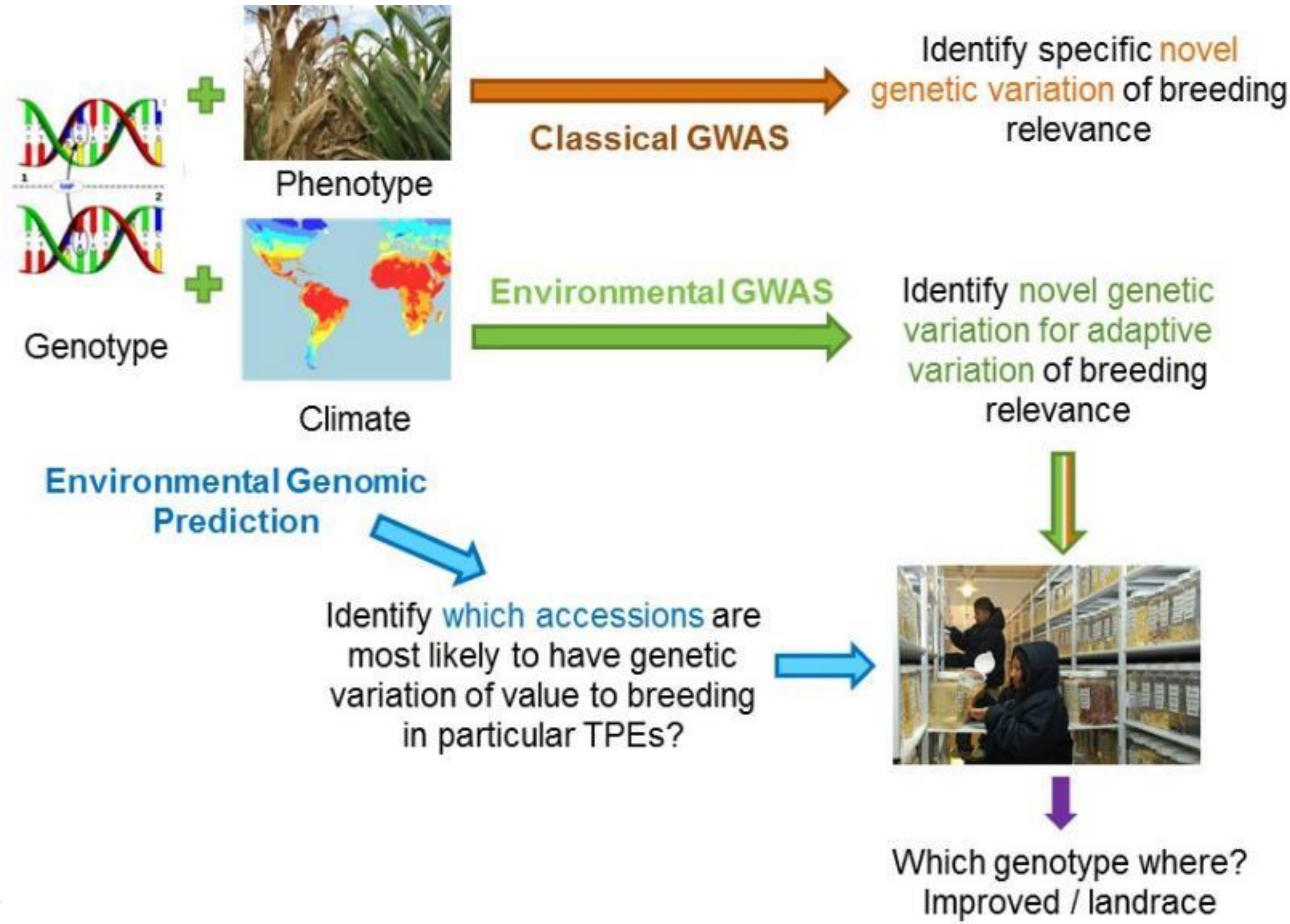
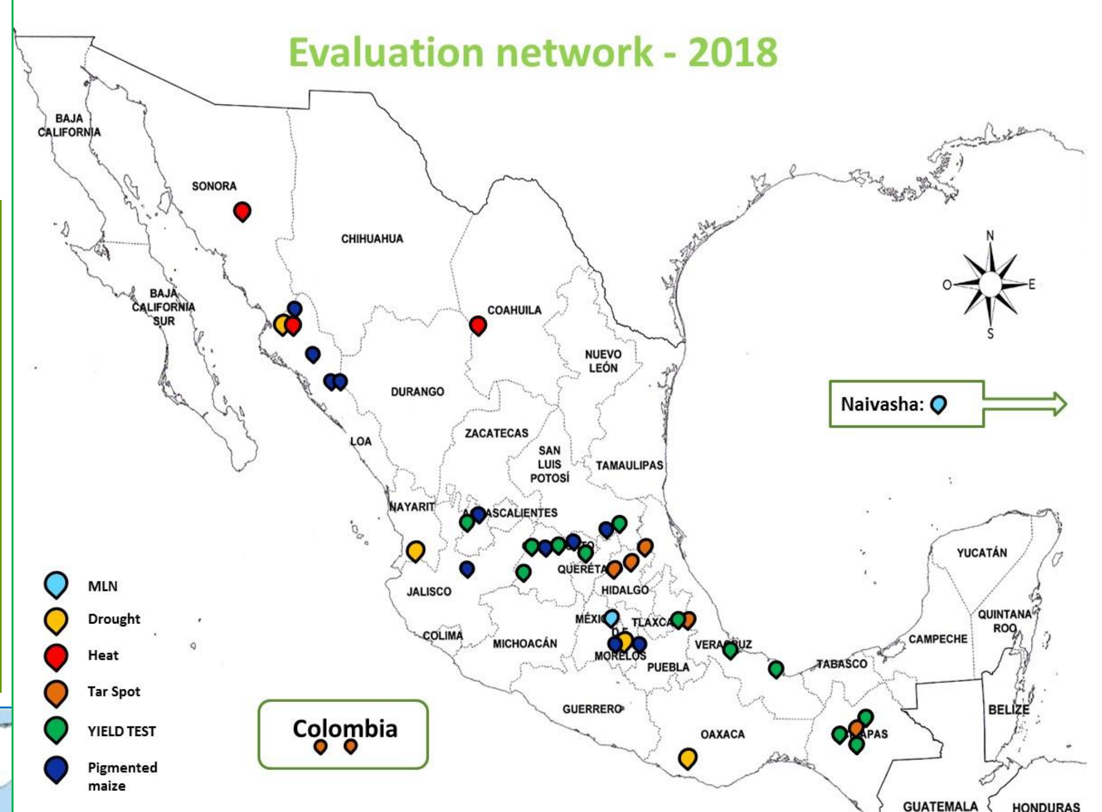
Using “Big Data” from SeeD, the Germplasm Bank and GIS to mine breeding value from accessions

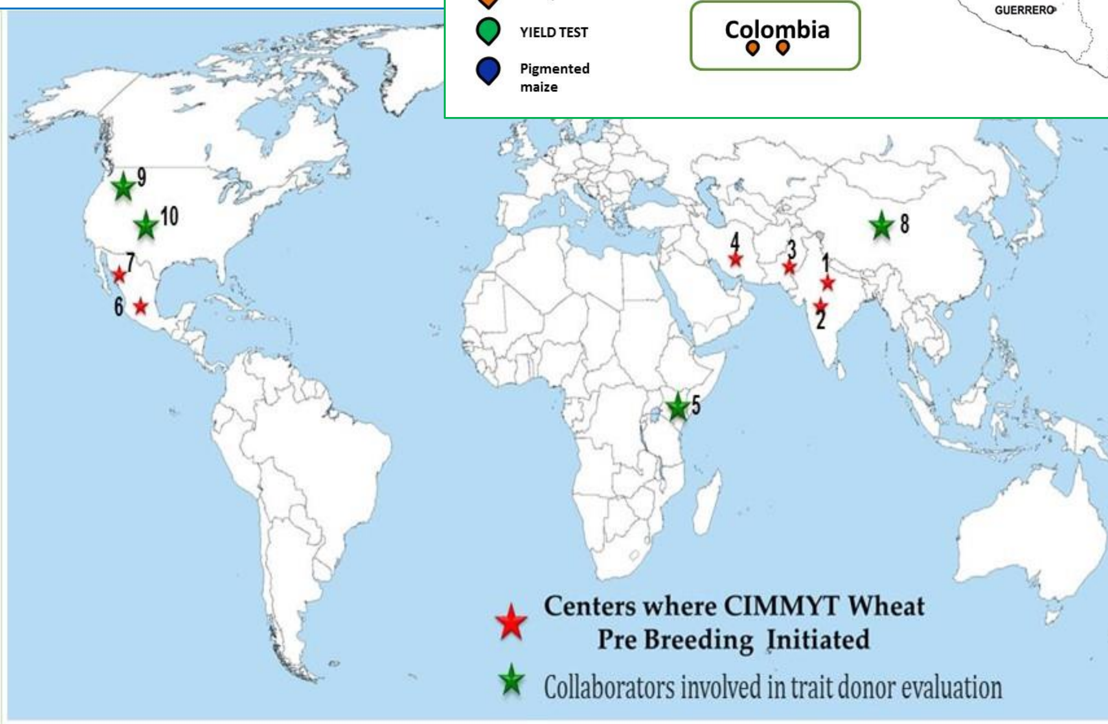


Pre-breeding networks



maize

1. a) CIMMYT-BISA, Ludhiana
   b) PAU, Ludhiana
   c) CSK HPKV, Palampur
2. Nat Inst of Abiotic Stress Management, Pune, India
3. Nuclear Inst of Agric, Tandojam, Sindh, Pakistan
4. Dryland Agric Res Inst, Maragheh, Iran
5. KALRO, Njoro, Kenya
6. INIFAP, Celaya, México
7. INIFAP, Ciudad, Obregon, Mexico
8. Wheat Res Inst, Acad Agric Sci, Ganzou, China
9. Washington State Univ
10. South Dakota State Univ



wheat

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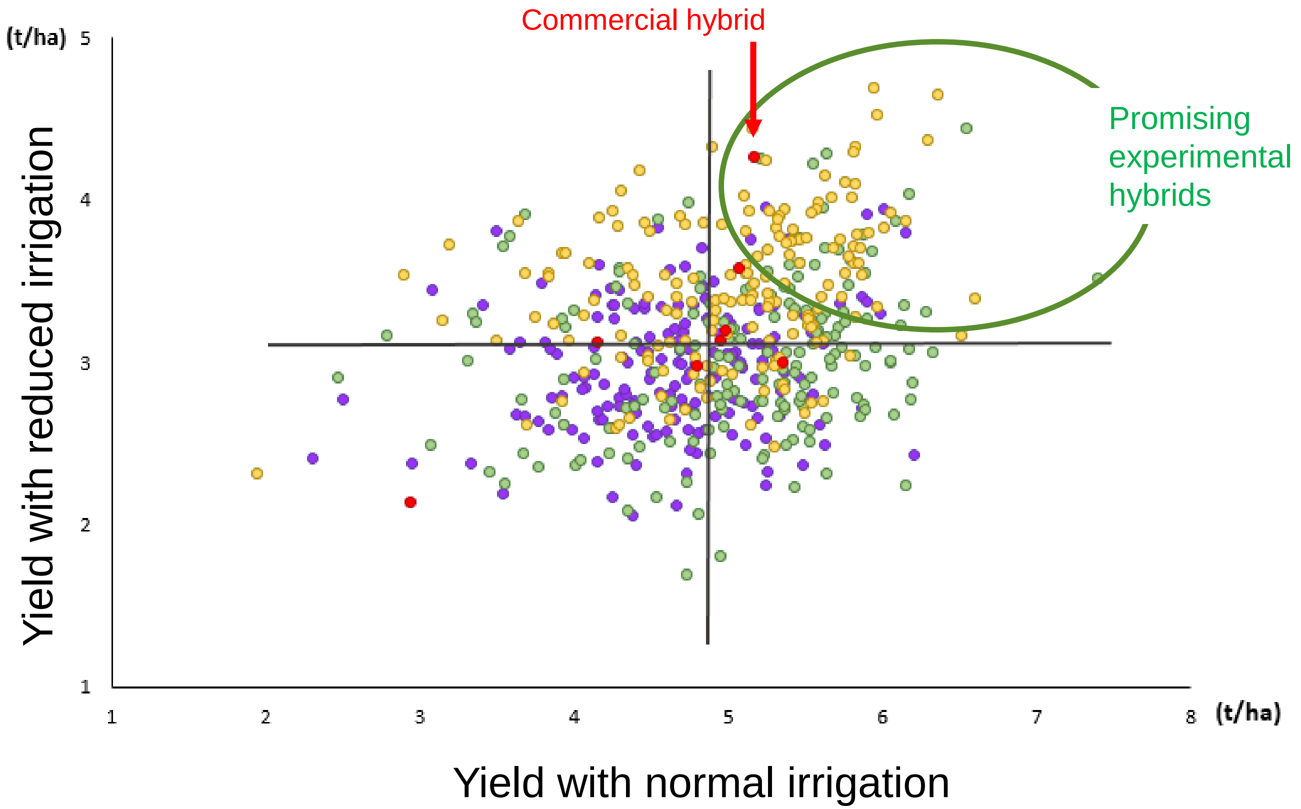
Maize pre-breeding:
Testcross hybrids of drought-tolerant lines

- ✓ Drought
- ✓ Tar spot complex
- ✓ Maize lethal necrosis
- ✓ Blue, anthocyanins*
- ❖ Heat
- ○ Fusarium ear rot



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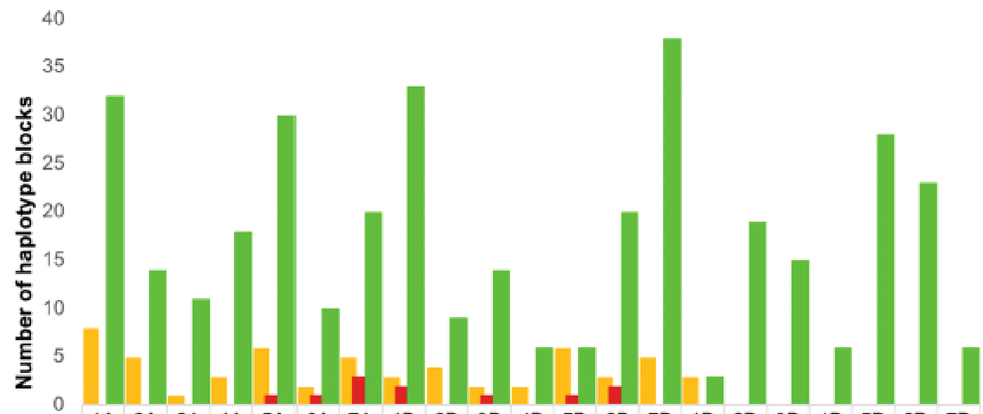
Wheat pre-breeding:
Multi-environment, multi-trait phenotyping; genomic and bioinformatics analyses

- ✓ A. Sharma, P. Srivastava, V.S. Sohu, N.S. Bains: PAU, India
- ✓ S.K. Singh, S. Kumar, G.P. Singh, V.K. Singh: ICAR, India
- ✓ N. Gupta, H.S. Sidhu, U. Kumar: BISA, India
- ✓ A.K. Basandrai, D. Basandrai, H.K. Chaudhary: Palampur, India
- ✓ Sanjay Singh, NRCPB, India
- ✓ D. Pal, ICAR, Shimla, India
- ✓ J.P. Jaiswal, GBPUA, Pantnagar, India
- ✓ M.A.E. Arif: NIAB, Faislabad, Pakistan
- ✓ K.A. Laghari, NIA, Sindh, Pakistan

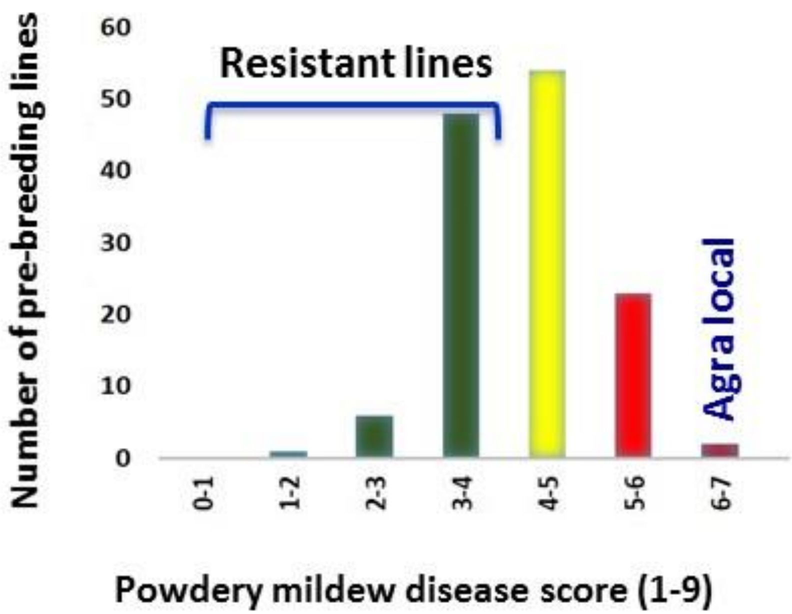
S. Singh et al., 2018, Nat Sci Rep

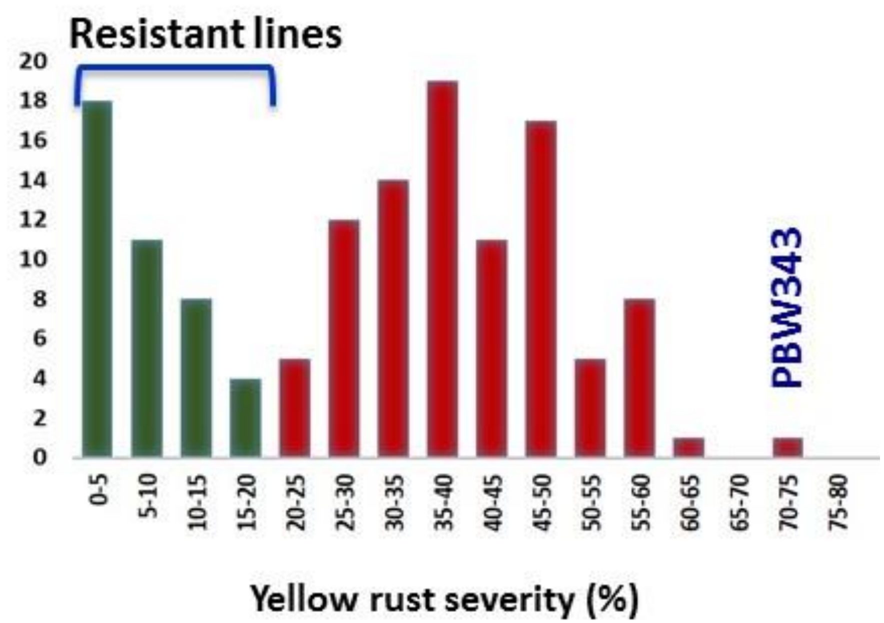


	1A	2A	3A	4A	5A	6A	7A	1B	2B	3B	4B	5B	6B	7B	1D	2D	3D	4D	5D	6D	7D	
Exotic Specific block	8	5	1	3	6	2	5	3	4	2	2	6	3	5	3	0	0	0	0	0	0	= 58
Functional blocks	0	0	0	0	1	1	3	2	0	1	0	1	2	0	0	0	0	0	0	0	0	= 11
Total Haplotypes	32	14	11	18	30	10	20	33	9	14	6	6	20	38	3	19	15	6	28	23	6	= 361

- Partners evaluated 984 F5:6 pre-breeding lines (PBLs) from [(exotic x elite1) x elite2] for many traits
- DNA of the PBLs was 16.1-25.1% exotic
- DNA of exotic origin was associated with improved drought, yellow rust, powdery mildew, and zinc

Wheat pre-breeding:
lines as trait donors for disease resistances





S. Singh et al., 2018, Nat Sci Rep

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Wheat pre-breeding:
lines as trait donors for heat or drought

Grain yield under heat

GID	Exotic parent type	2015-16	2016-17
		------ kg ha^{-1} ------	
7641495	**Synthetic**	2261	2346
7644075	**Synthetic**	2325*	2418**
7645422	**Synthetic**	2338*	2488**
7645970	**Synthetic**	2214	2407*
7689940	**Landrace**	2415*	2362
BAJ #1	**Check**	2144	2216
VOROBEY	**Check**	1769	1985
SOKOLL	**Check**	NA	2023
LSD(0.05)		526	386

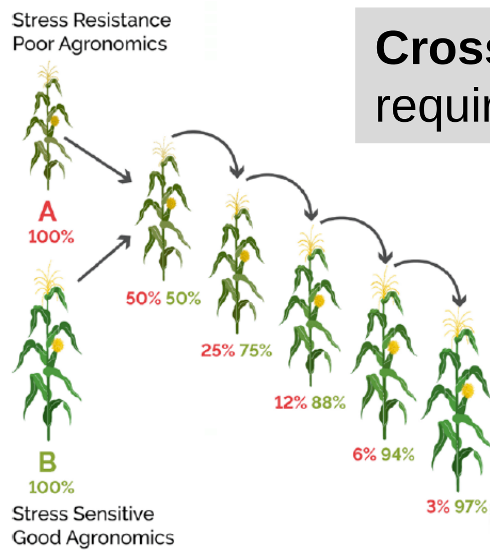
Grain yield under drought

GID	Exotic parent type	2015-16	2016-17
		------- kg ha^{-1} -------	
7643084	**Synthetic**	3587	4510*
7642492	**Synthetic**	3480	4574*
7688508	**Landrace**	3360	4787*
7687479	**Synthetic**	3167	5198**
7642491	**Synthetic**	2766	5151**
VOROBEY	**Check**	3346	4613
BAJ #1	**Check**	3111	4858
SOKOLL	**Check**	NA	3968
LSD(0.05)		868	457

Advantages of gene editing for improving crops, compared to crossbreeding

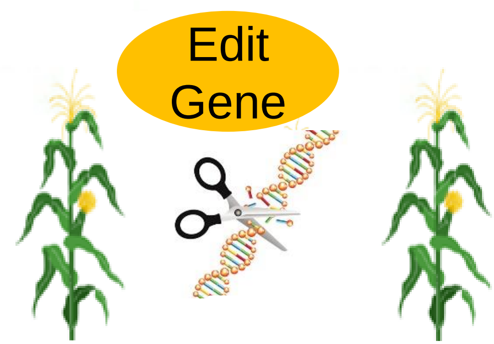
Disease resistant,
poor agronomics,
‘donor’ line

Disease susceptible,
elite line



Crossbreeding and backcrossing requires 5-7 cycles

Disease resistant,
97% elite line



Disease susceptible elite line

Disease resistant elite line

Gene Editing is fast and eliminates linkage drag

Gene Editing requires 1-2 cycles

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Example uses of CRISPR gene editing (from literature; not at CIMMYT)

- CRISPR research for possible use in humans
  - Huntington's disease
  - Leukaemia
  - Editing CCR5 in T cells of persons infected with HIV
- CRISPR is being used in plants
  - Virus, fungus, bacterial disease resistance – rice, cassava, wheat…
  - Salinity, drought – rice, maize…
  - Grain yield – rice, wheat, potato…
  - Biofortification – rapeseed, rice, barley, potato…

General approach

- Identify a mutation in nature (disease resistance!) → Let's make this mutation in other lines!
- Discover a gene required by a pathogen → Let's mutate (inactivate) that gene to give resistance to the pathogen!

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Progress Toward Gene Editing @CIMMYT

1. Initial objective - <u>maize</u>
    - Fine-map and clone *MLN* resistance allele, and recreate it by editing in elite CIMMYT lines currently susceptible to lethal necrosis
2. Initial objectives - <u>wheat</u>
    - Edit *Lr67* gene in Reedling, an elite line, to introduce non-host rust resistance
    - Edit *MLO* genes in Reedling to generate resistance to powdery mildew in elite CIMMYT lines
3. Partnering with Corteva Agriscience

CIMMYT Position Statement on Genome Editing

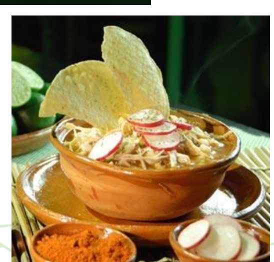
- A useful tool to meet the challenges of agriculture
- However, Genome Editing is not a “magic bullet”
- Consider sovereignty and safety first *(Excellence Through Stewardship)*
- Only when policies and protocols are in place
- Complementary roles of public and private sectors

More information:
https://www.cimmyt.org/wp-content/uploads/2016/04/CIMMYT-Position-Statement-on-Novel-Genome-Editing-Technologies-17Dec2017.pdf

Collaborative Projects

Elote occidental

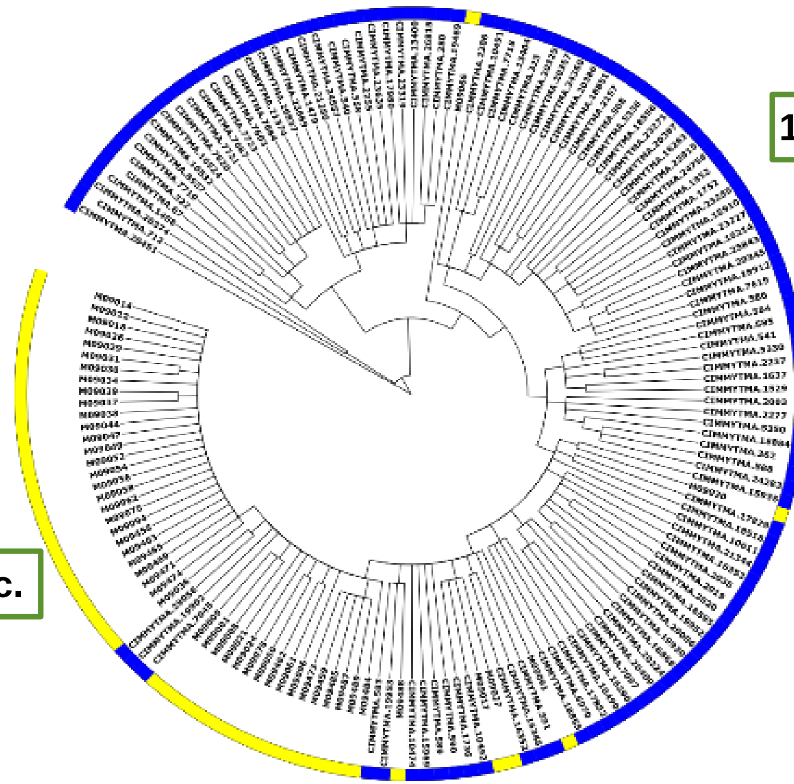
Ears with 8-10 kernel rows; large grains; floury, purple grains



CIMMYT (1960s)

CUCBA Genebank
University of Guadalajara (2003)

112 Acc.



50 Acc.

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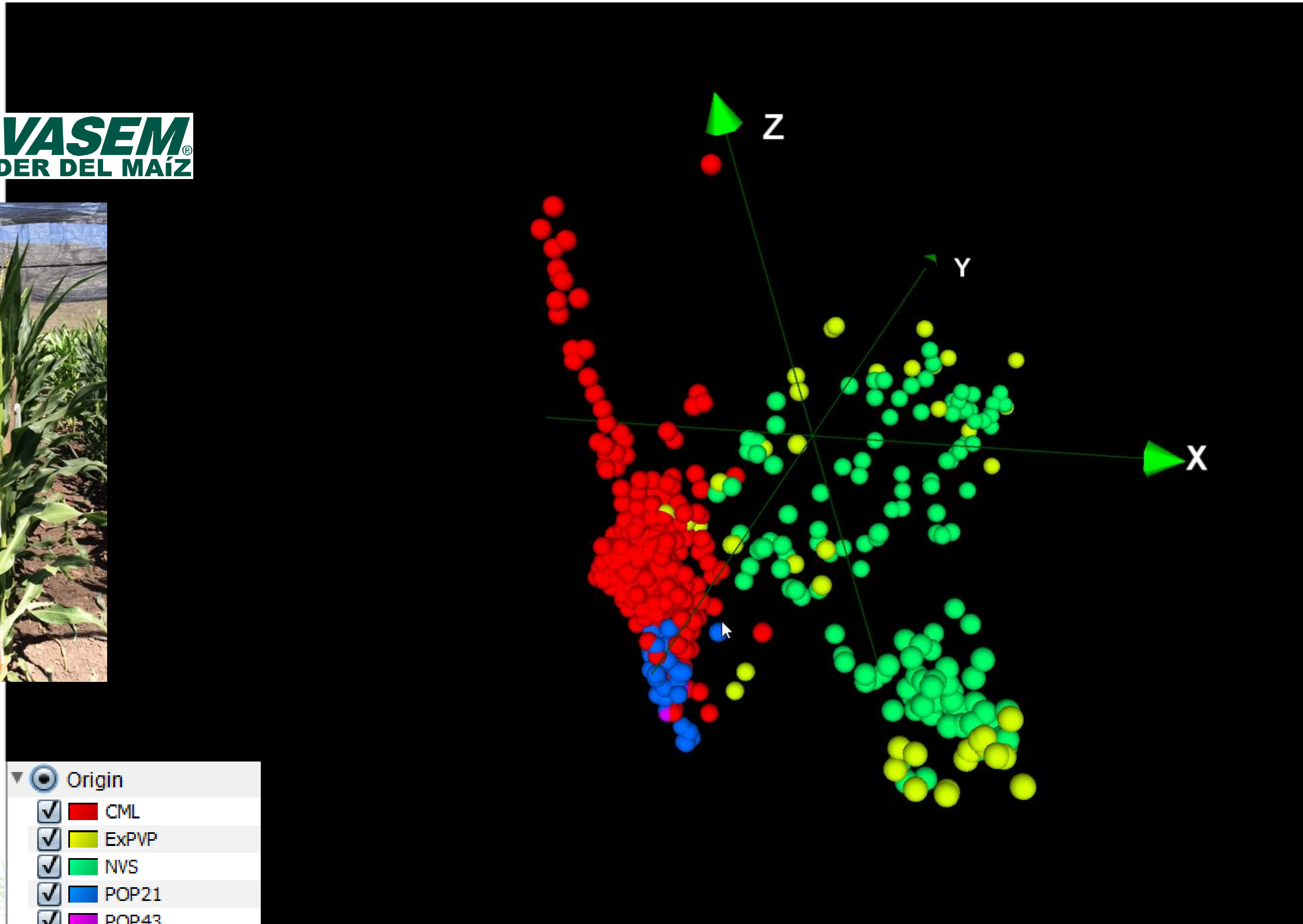
Collaborative Projects

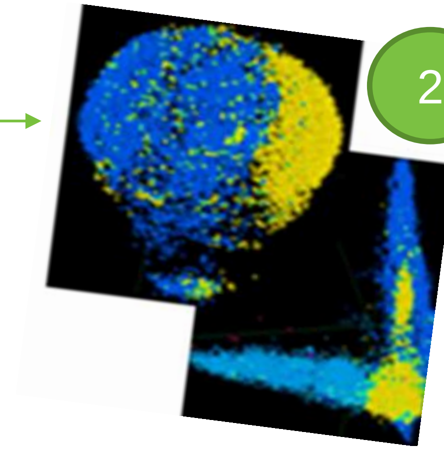
NOVASEM®
EL PODER DEL MAÍZ



CIMMYT's Genetic Resources Program

1

2



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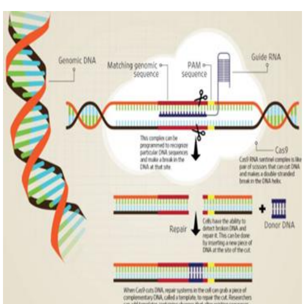

7

Enabling the Effective Use of Maize and Wheat Genetic Resources in support of CIMMYT's mission

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We thank all our partners and funders

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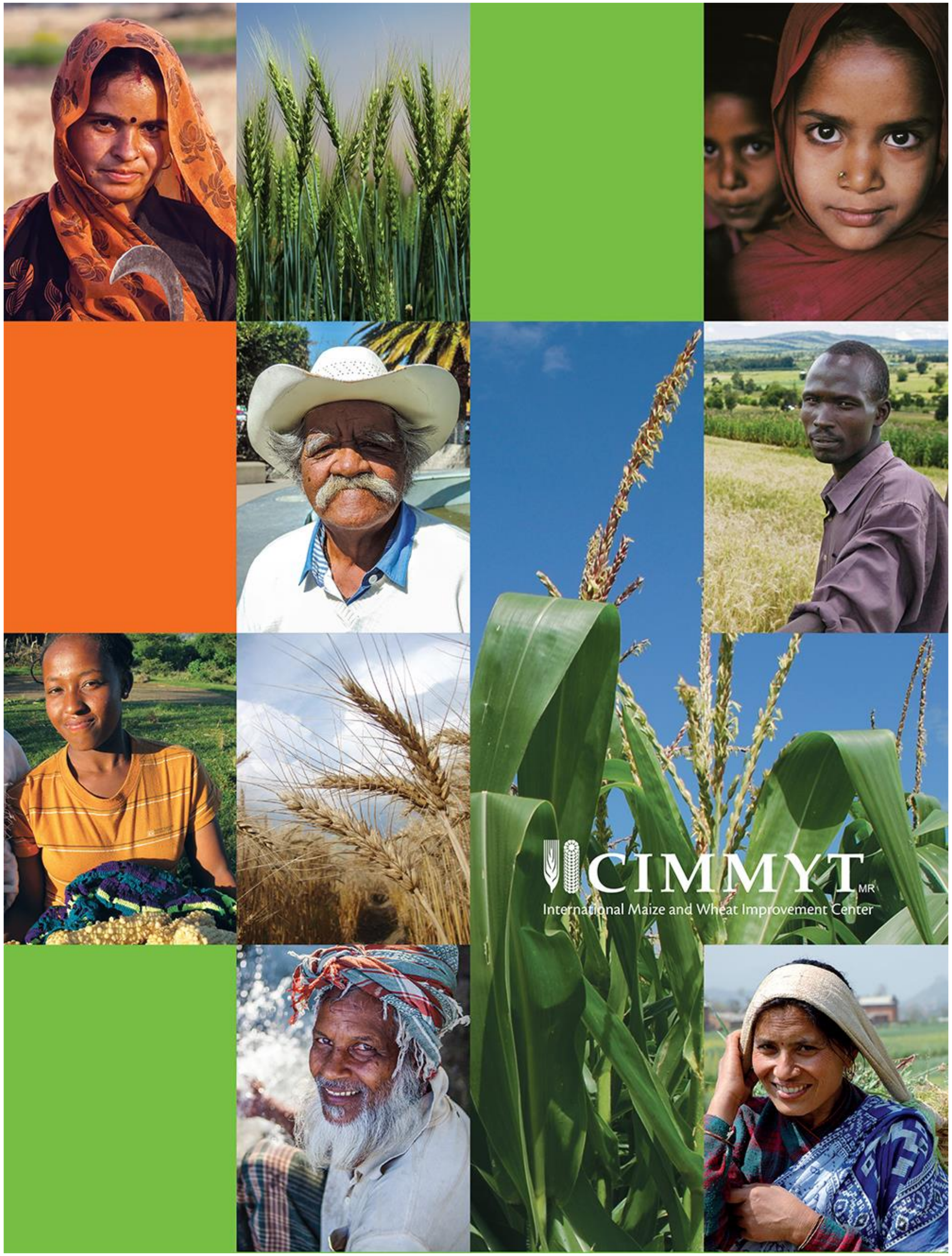

Thank you for your interest!