SeeD

A learning model towards effective and equitable use of genetic resources

El Batan – 15th February 2017

CIMMYT

Seeds of Discovery (SeeD)
(MasAgro Biodiversidad)

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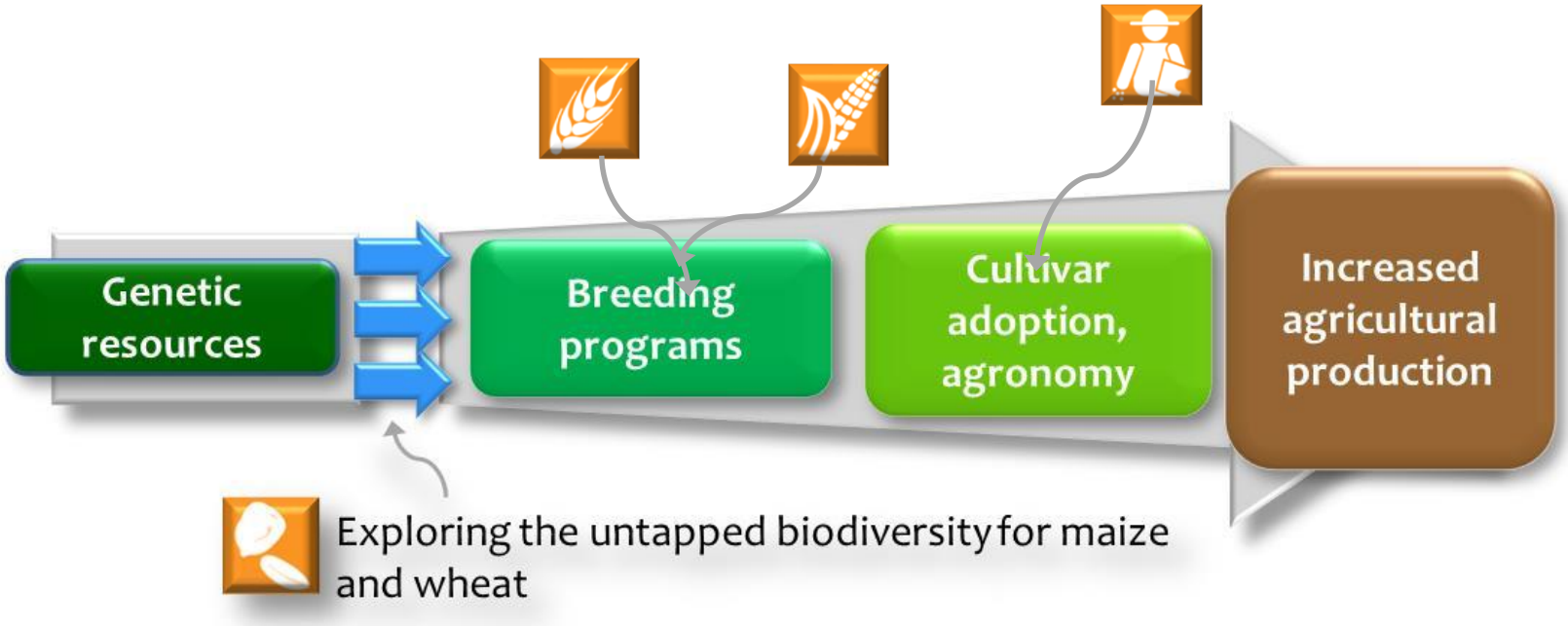
SAGARPA
SECRETARÍA DE AGRICULTURA, GANADERÍA, DESARROLLO RURAL, PESCA Y ALIMENTACIÓN

- Initiated September 2011
- Mostly funded by the Mexican government



Four pillars of work

Genotypic characterization of germplasm banks and public elite germplasm

Phenotyping and Marker-trait associations

Pre-breeding

Capacity Development
Data Management

Genotyping

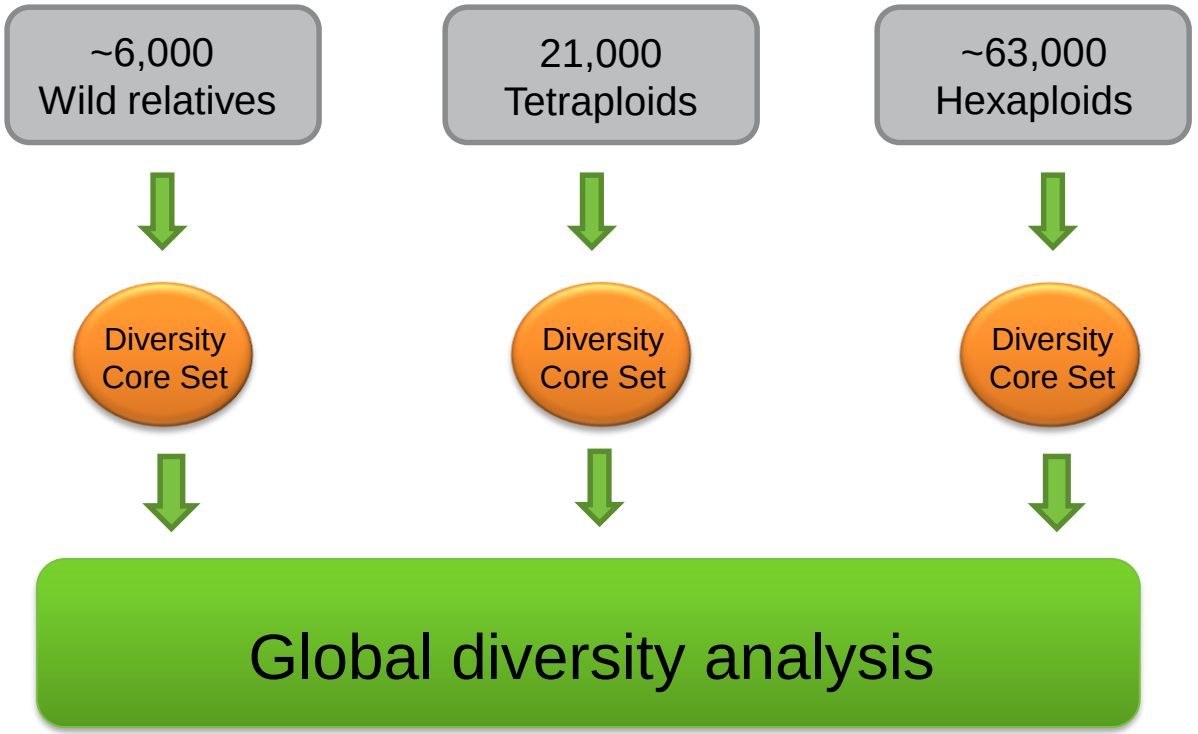
DArTseq for both wheat and maize

GbS for select maize GWAS analysis

KASP for select wheat markers and samples

Genotyping wheat

- Genomic characterization of DArTseqSNP and SilicoDArT markers
- Wheat Diversity Analysis (CIMMYT/ICARDA)



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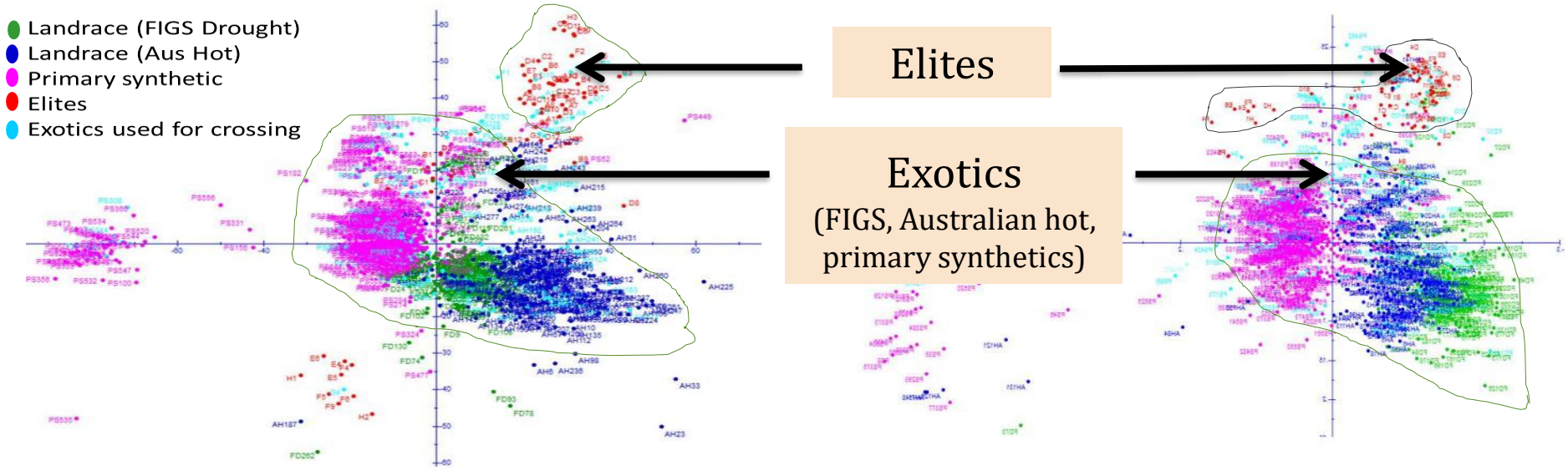
Diversity Profiles of Gene Bank Accessions



General genetic diversity
DArTSeq SNP

Functional diversity
~20 KASP

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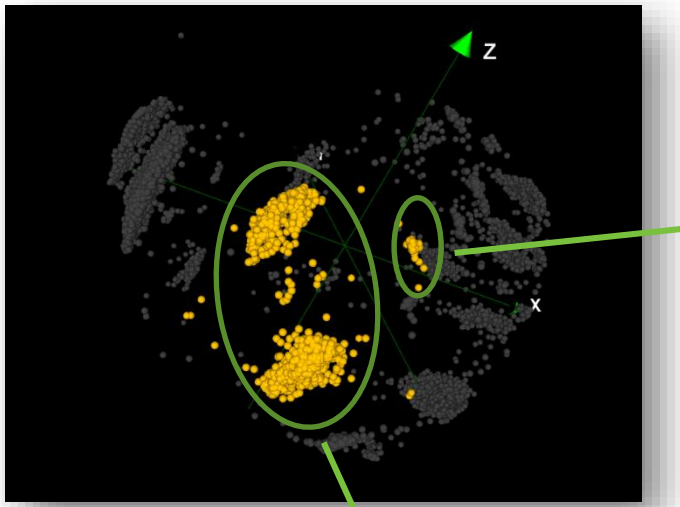
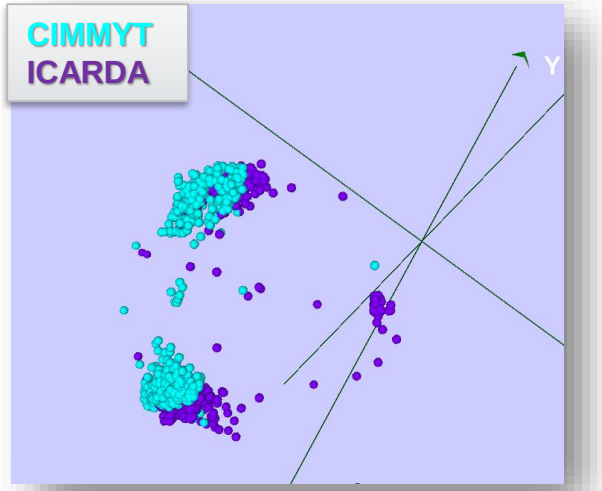
Diversity analysis within important groups using SNP D genome



43 Aegilops ventricosa
DN genome



930 *Aegilops tauchii*
D genome

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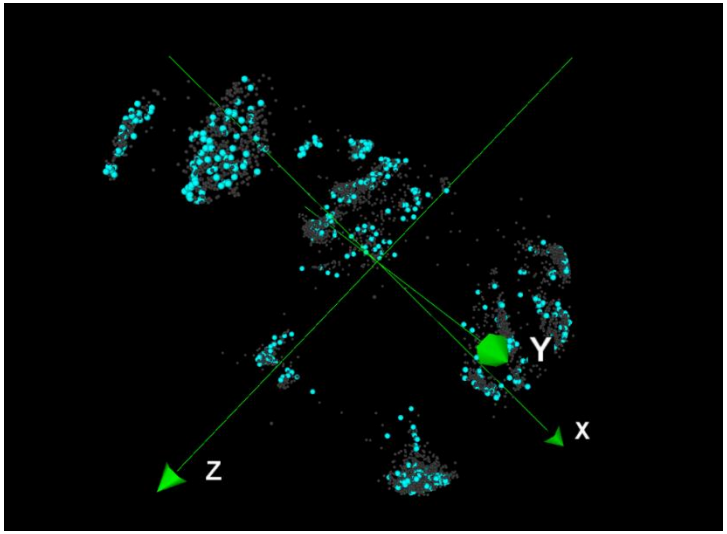
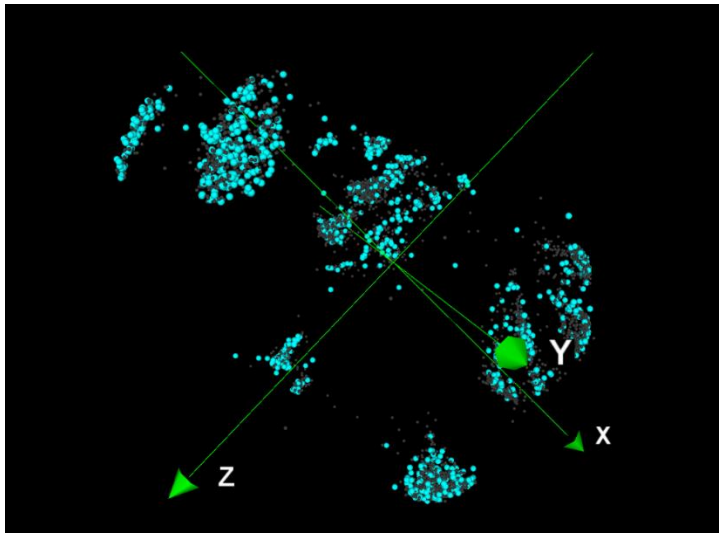
Genetic Core sets of Wild relatives





Full collection: 5000
Core set collection: 500

Full collection: 5000
Core set collection: 1000

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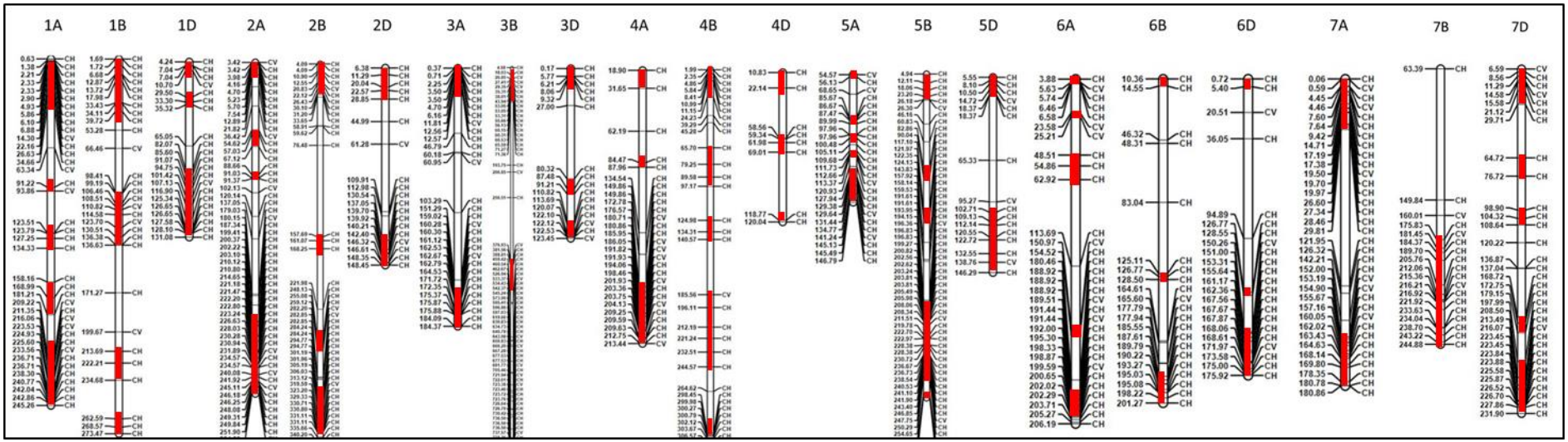
Genomic regions on 21 wheat chromosomes having fixed alleles in Mexican landrace accessions of Chihuahua and Central Valley region.



Genotyping maize

- Genomic characterization of DArTseqSNP and SilicoDArT markers
- Modified protocol- composite samples

25000 Landraces

~2000 Pools, Pops, Varieties, Composites

~400 Wild relatives

570 CML

Diversity analysis
Breeder oriented cores
Selection sweeps

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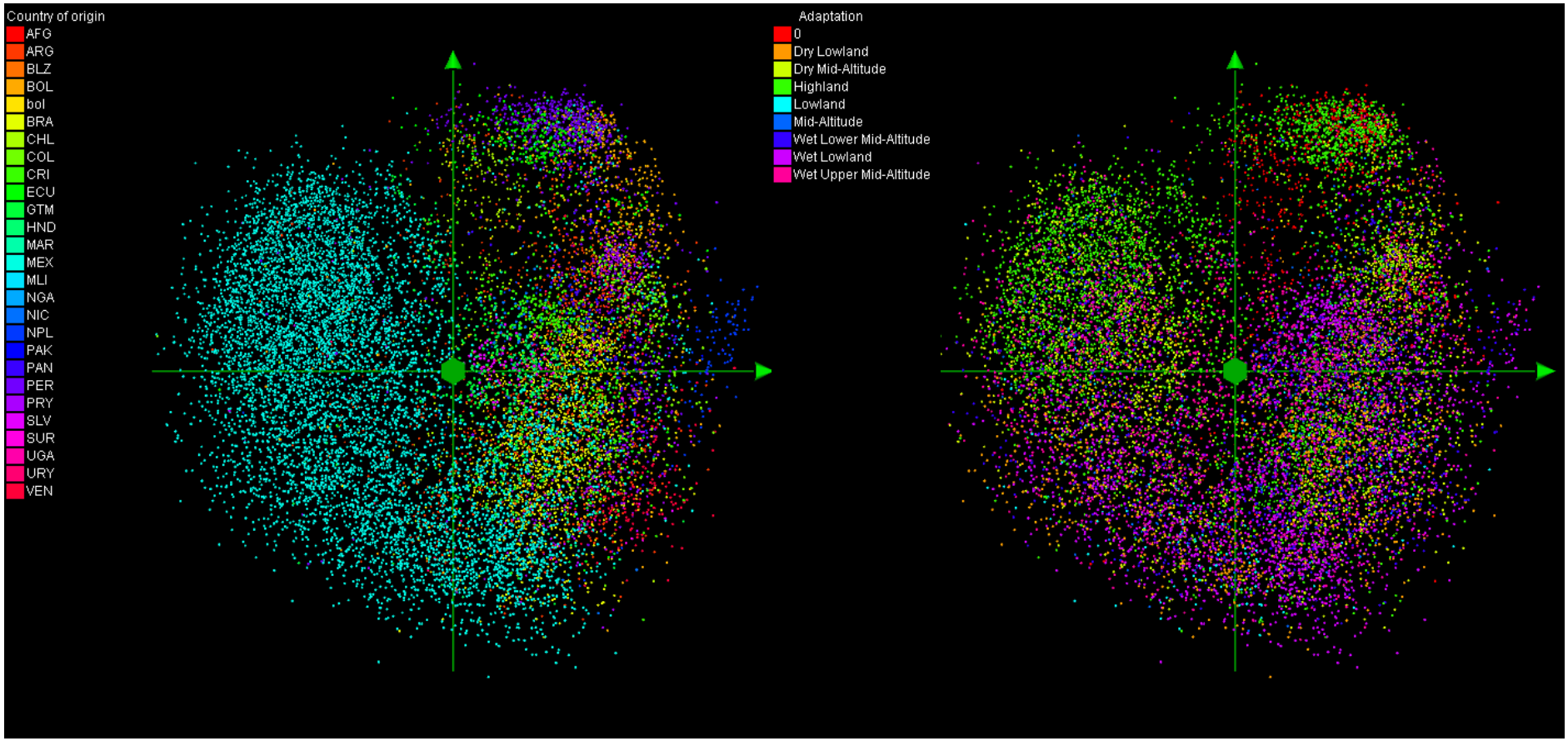
Diversity



15384 Landraces with GIS data

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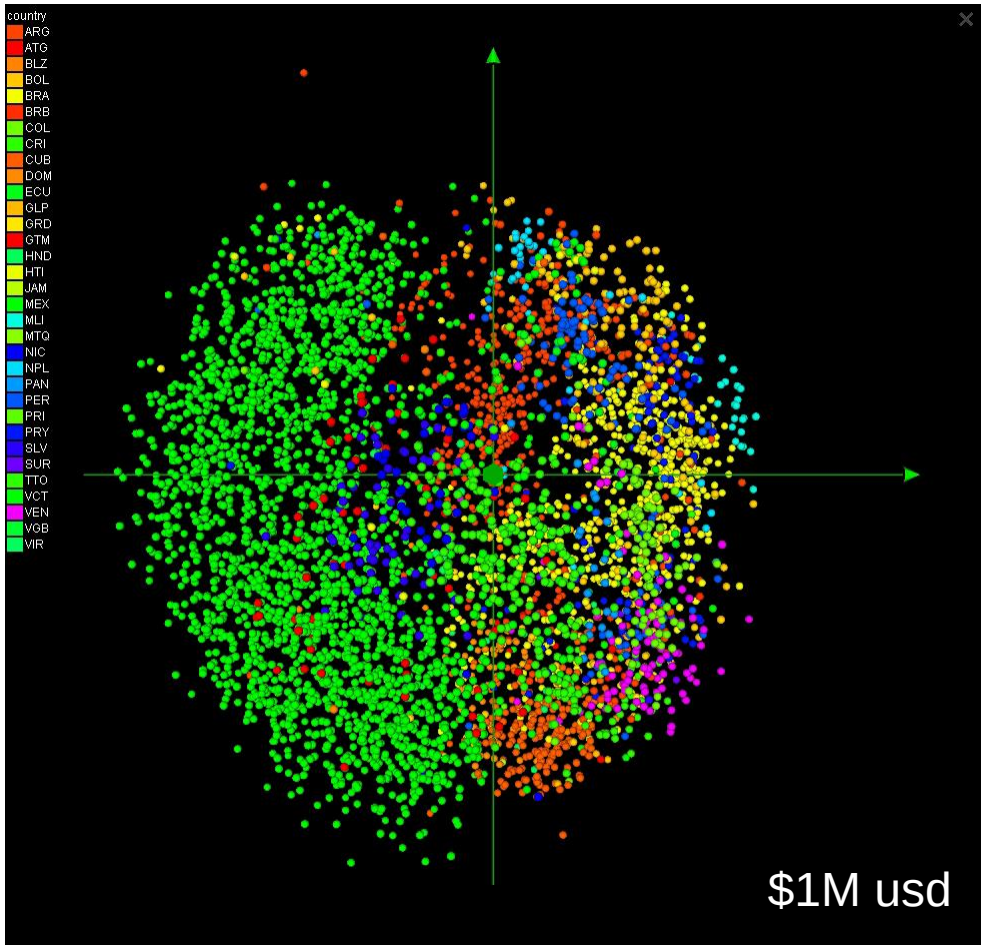
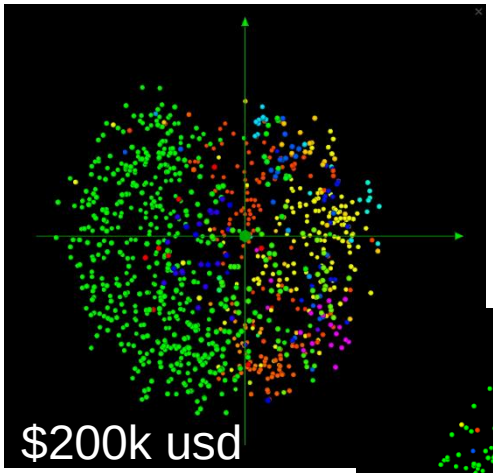
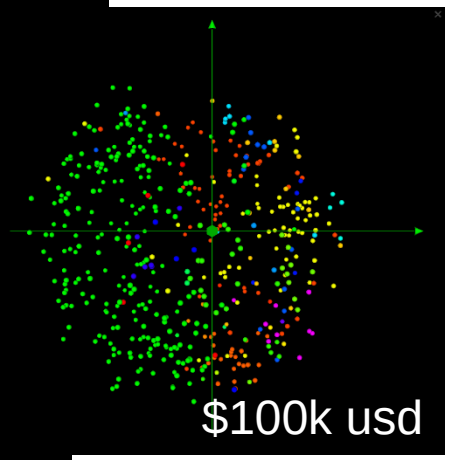
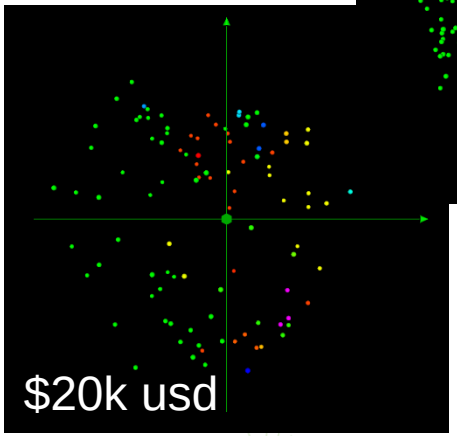
Breeder cores









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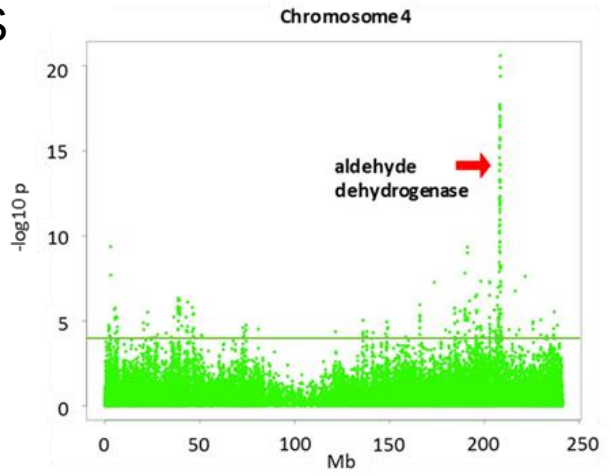
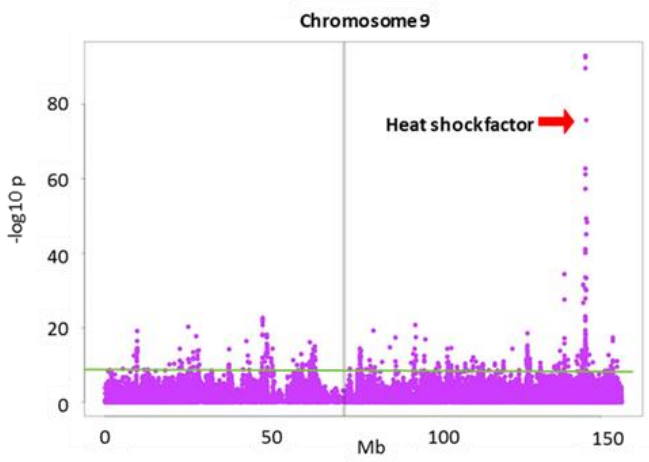
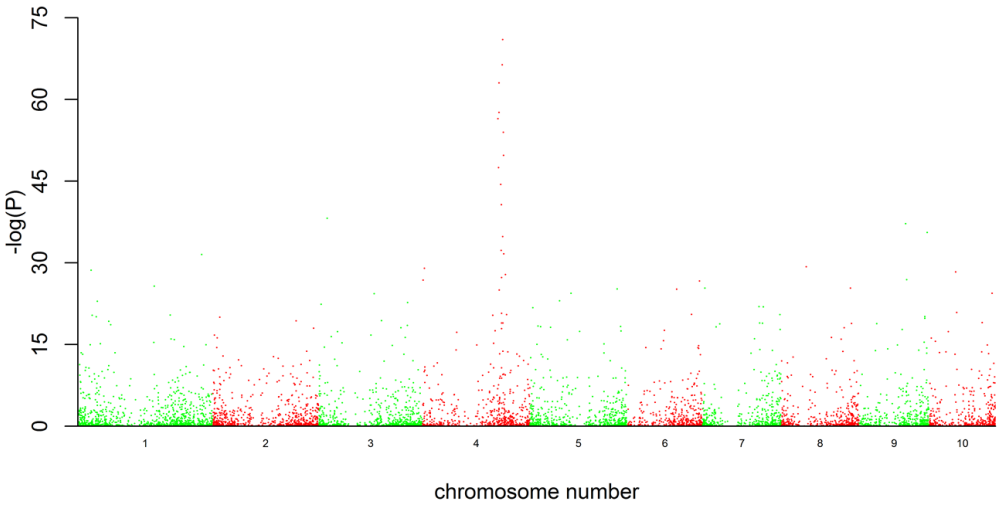
Selection sweep

Environmental GWAS





Pcadapt
XP-CLR



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Focus on field-based phenotyping

Traits	Maize	Wheat
Abiotic stresses	heat	heat
	drought	drought
	low N	low P
Biotic stresses	tar spot, ear rot, stalk rot, *Turcicum*, *Cercospora*, *MLN (MCMV & SCMV)*	tan spot, spot blotch, (*Fusarium*, blast), karnal bunt
Grain quality	hardness, starch, oil, amino acids, phenolics	hardness, color, protein, test weight, yellow berry, Fe, Zn

- **Wheat**: >1.5m data points from 30 trials across 9 locations
- **Maize**: >1.5m data points

Impact of heat on wheat

- ~ 10% yield loss per 1°C increase in temperature
- By 2050, 20-30% yield loss in South Asia alone, affecting over 1 billion people

SeeD: ~70,000 wheat gene bank lines screened under heat stress (2011-2013)

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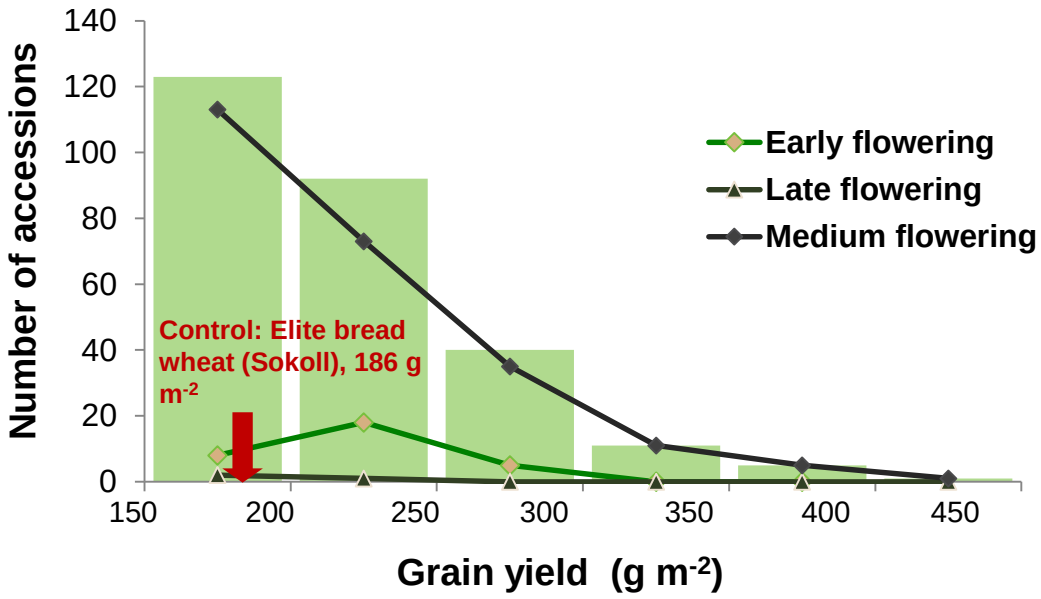
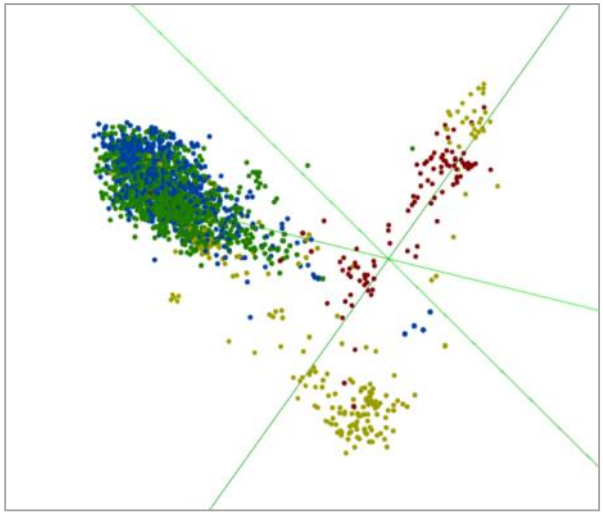
Exploring the Gene Bank for Heat Tolerant Wheat

Mexican landraces with grain yield >150 g m^{-2} under heat stress (Cd. Obregón, México)



PCA



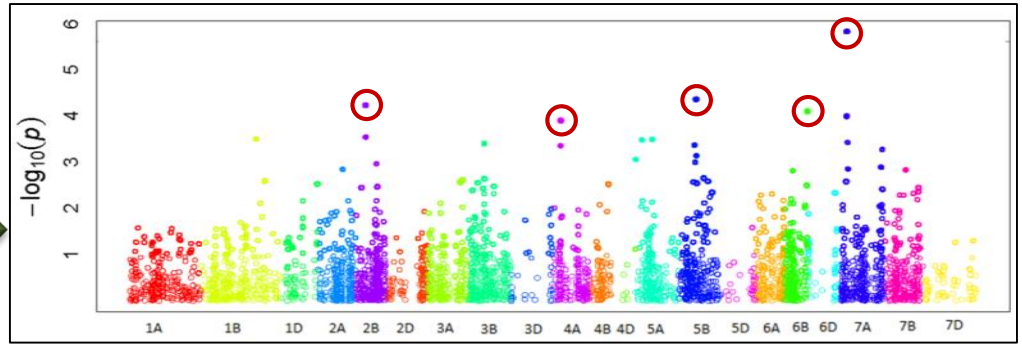
- **Tolerant Mexican landraces (YELLOW)**
- **Tolerant Iranian landraces (RED)**
- **Elite lines (BLUE & GREEN)**

Screening Gene Bank for Yellow Rust – adventitious phenotyping

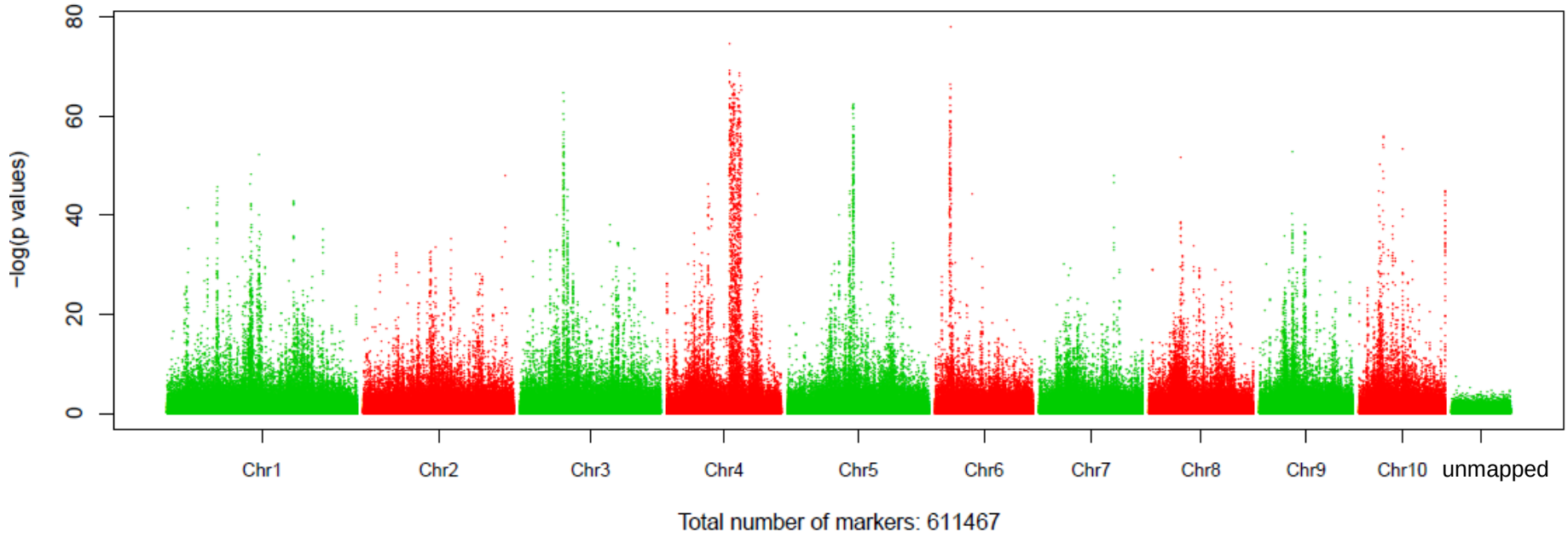
Yellow rust resistant wheat landraces

Accession / Pedigree	YR (%) in Mexico	YR (%) in India
CHIH95.5.18	20	10
CHIH95.5.23	10	10
DGO95.3.8	20	10
OAX93.1.1.1	20	5
Susceptible check	100	100

Association mapping for yellow rust in wheat landrace



Maize: Grain protein content



→ Comprehensive **catalogue of >100 haplotypes** and associated markers which increase grain protein content

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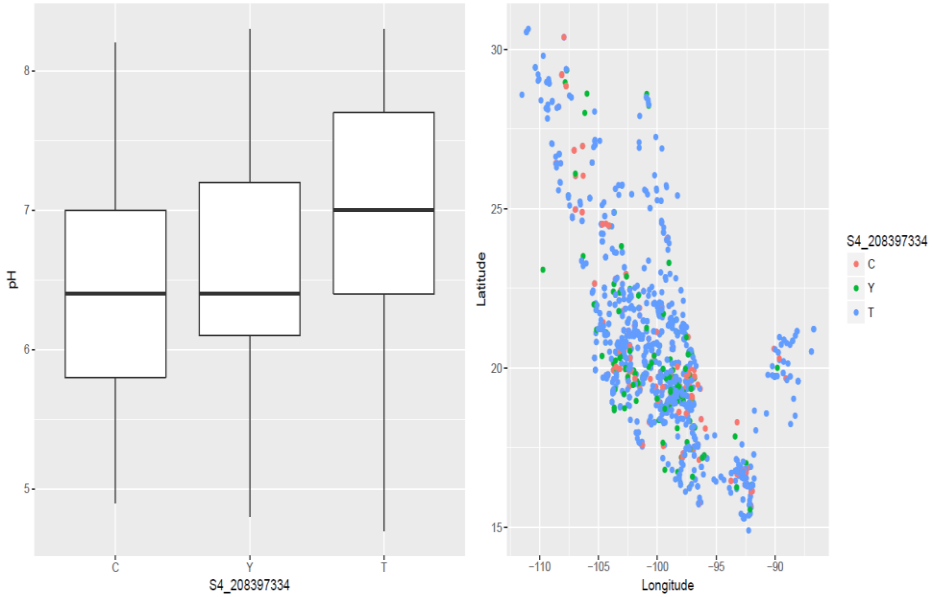
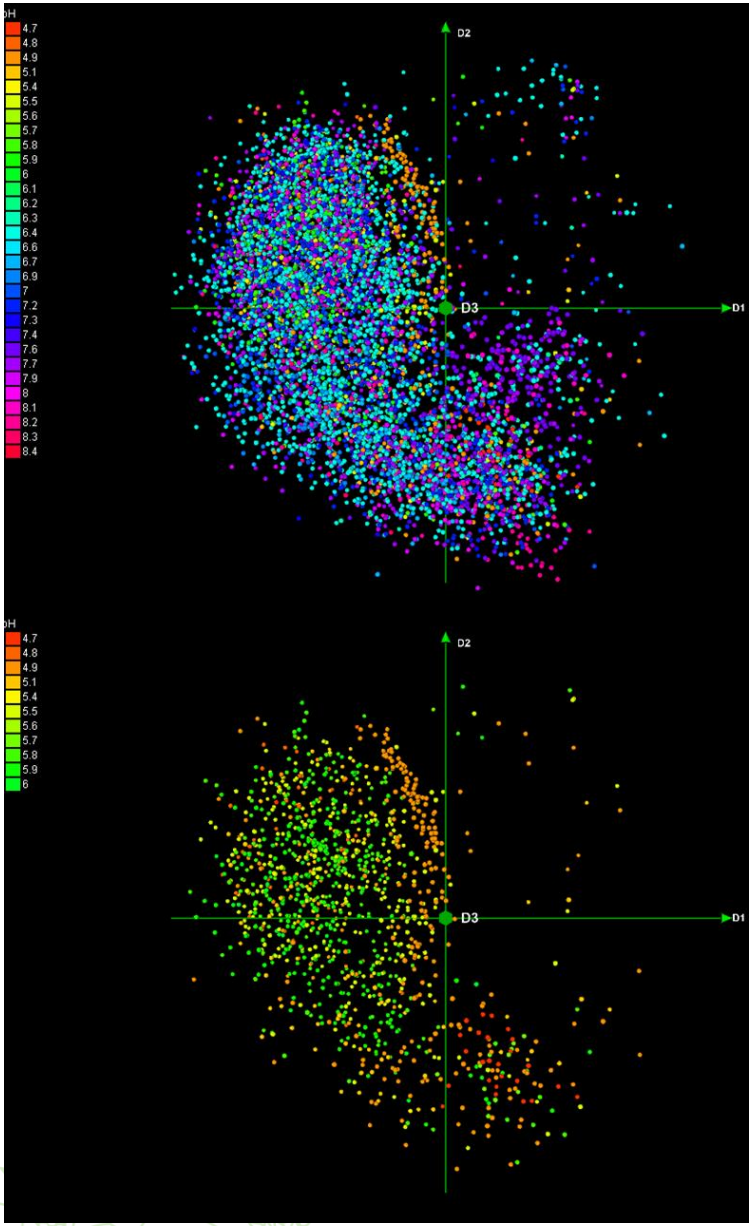
Identified 1367 accessions of value for acid soil tolerance evaluation and 353 accessions carrying favorable allele for acid soil adaptation





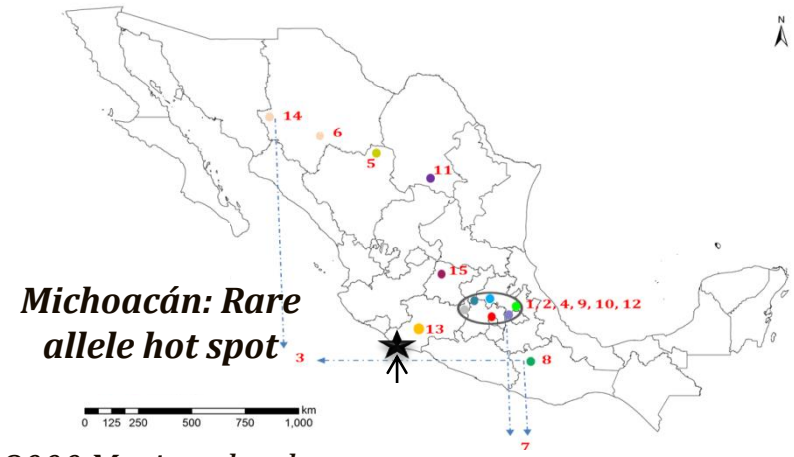
Realizing promise- pre-breeding

- Development of inbred and semi-inbred germplasm which contains high value exotic introgressed alleles in elite backgrounds

- Good agronomic performance is needed in addition to novel genetic variation

Gene Bank to Breeding Pipeline

(A) Diversity analysis



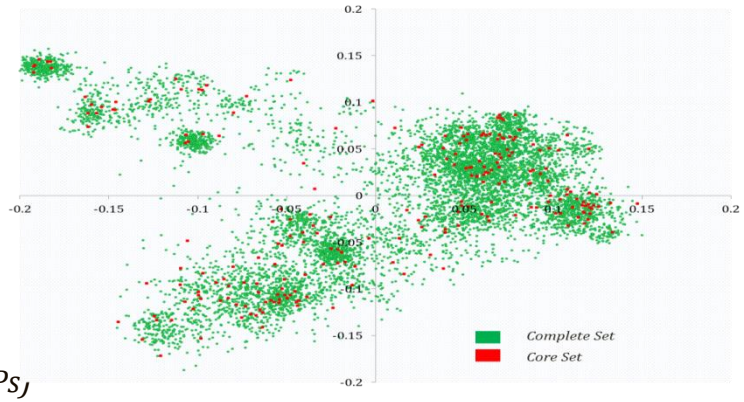
Michoacán: Rare allele hot spot

8000 Mexican landraces

Phenotype *(Heat, Drought, Quality)*

GBS profiling *(20K SNPs)*

(B) Core set development



(C) Core set evaluation

(D) Trait donor identification

Heat, Drought
Diseases, Quality

(E) Pre-breeding

Large-scale efforts to move useful gene bank diversity to breeding pipelines

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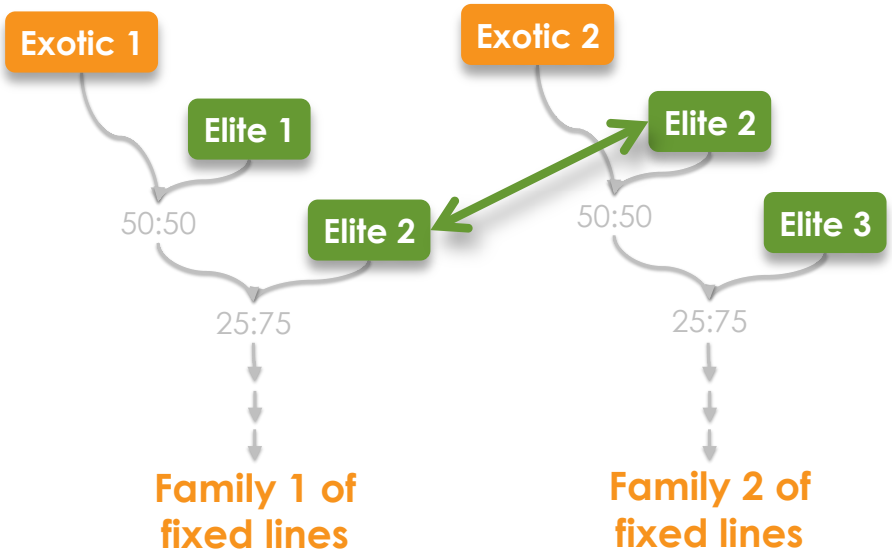
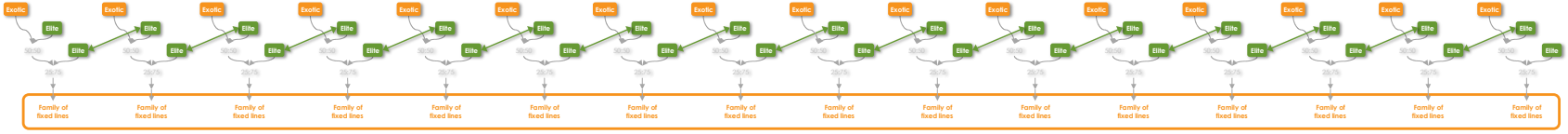
Wheat ‘bridging germplasm’



Linked topcross panel (LTP)

- Evaluate effects of exotic alleles in **elite genetic backgrounds**
- Large number of **small, but expandable populations** (ca. 10,000 lines in total)
- TC chains with partly overlapping parents to facilitate **joint linkage/association mapping**



Prebreeding @ Obregon

Selections made from 600 populations under heat and drought stresses

Prebreeding @ El Batan

Evaluations made from 8000^{+} advanced pre breeding lines at El Bataan and Toluca

Wheat ‘bridging germplasm’

- Over 1000 donors used in pre-breeding, generating >15,000 F6/7/8 fixed lines
- Preliminary selections of 2000 with acceptable agronomy, drought and heat tolerance
- Partners evaluating pre-bred germplasm

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Maize ‘bridging germplasm’

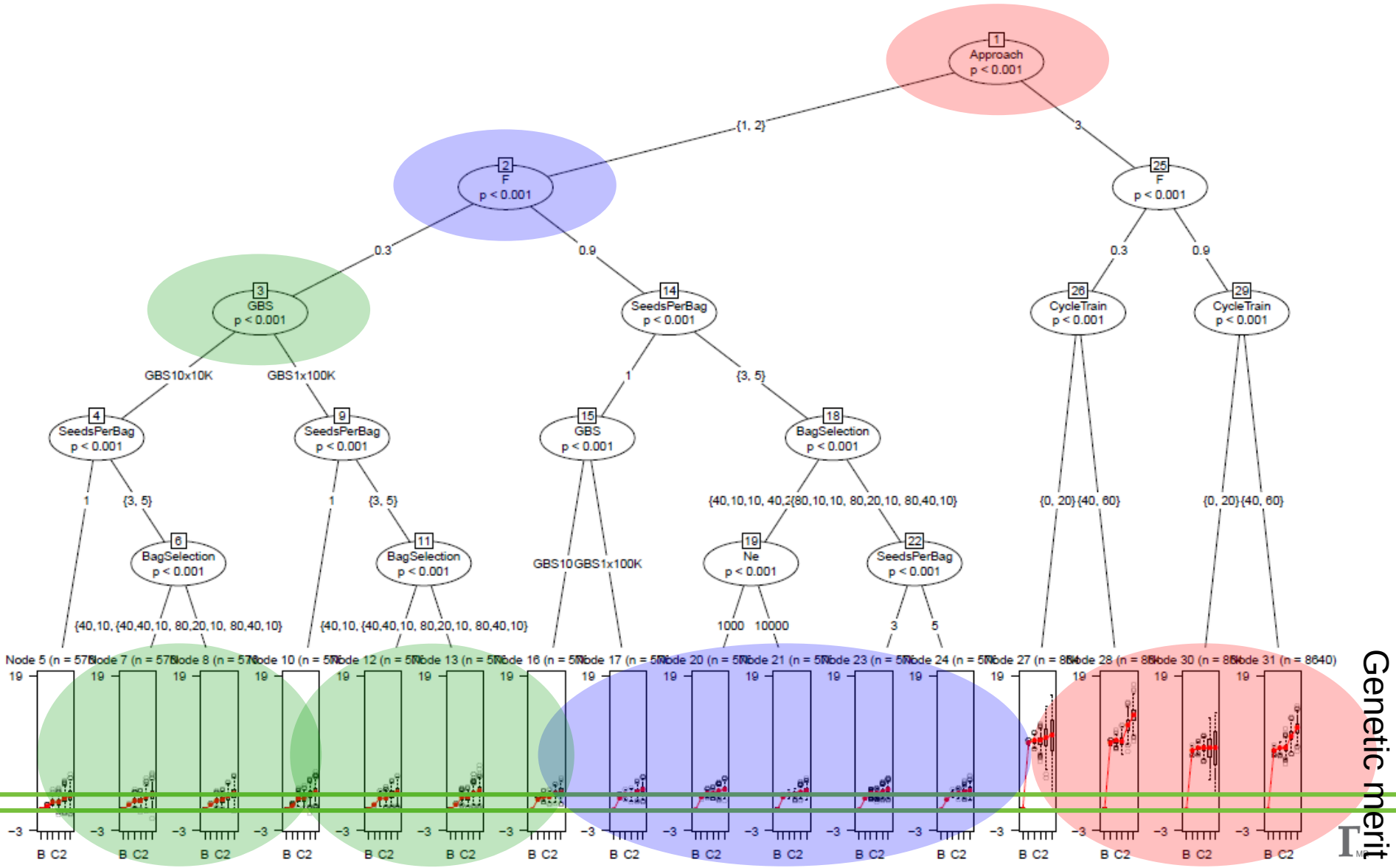
Useful novel alleles & haplotypes

Early generation lines & pools enriched for favorable alleles

…using **multiple strategies** defined by trait complexity and breeder needs (desired input germplasm, demand for new sources)

Breeder demand	Trait complexity		
	Monogenic (1-3)	**Oligogenic (4-10)**	**Polygenic (>10)**
Urgent	DH from landrace & landrace / line crosses, selfing	DH from landrace & landrace / line crosses, selfing	GS with MABC for BC1S1 development
Medium-term	MABC	MARS & prediction index	GS with MABC for BC1S2 development
Long-term	MABC & GS	MARS, prediction index & GS	GS with MABC for BC1S2 development

Assessment of options; simulations



Genetic merit

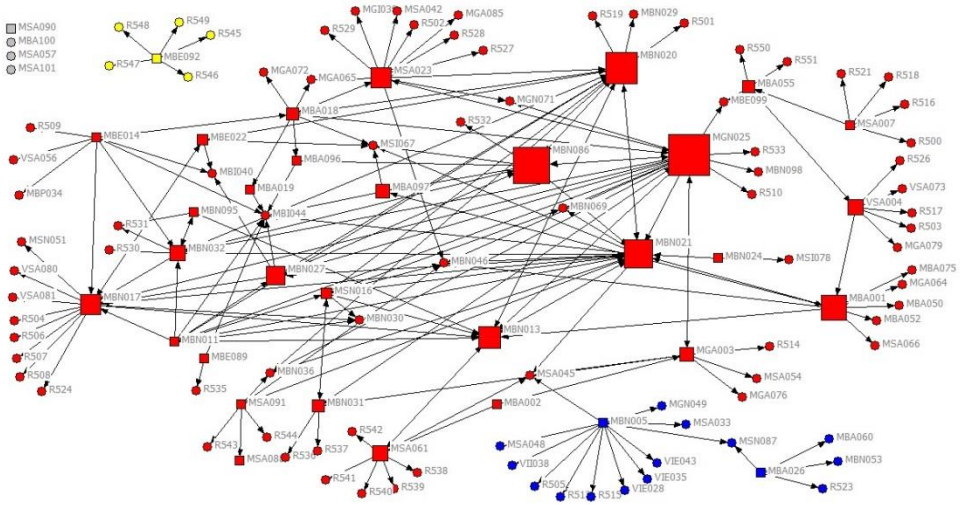
GS options

- Saint Pierre, C., J. Burgueno, J. Crossa, G. Fuentes Davila, P. Figueroa Lopez, E. Solis Moya, J. Ireta Moreno, V.M. Hernandez Muela, V. Zamora Villa, P. Vikram, C. Sansaloni, D. Sehgal, D. Jarquin and S. Singh. 2016. Genomic prediction models for grain yield of spring bread wheat in diverse agro-ecological zones. Nature Scientific Reports
- Gorjanc, G., J. Jenko, S.J. Hearne and J.M. Hickey. 2016. Initiating maize pre-breeding programs using genomic selection to harness polygenic variation from landrace populations. BMC Genomics, 17, DOI:10.1186/s12864-015-2345-z
- Hickey, J.M., S. Dreisigacker, J. Crossa, S. Hearne, R. Babu, B.M. Prasanna, M. Grondona, A. Zambelli, V.S. Windhausen, K. Mathews and G. Gorjanc. 2014. Evaluation of genomic selection training population designs and genotyping strategies in plant breeding programs using simulation. Crop Science, 54(4):1476-1488.
- Faux AM, Gorjanc G, Gaynor RC, Battagin M, Edwards SM, Wilson DL, Hearne SJ, Gonen S, Hickey JM 2016. AlphaSim: Software for Breeding Program Simulation. Plant Genome. doi: 0.3835/plantgenome2016.02.0013.

Capacity Development

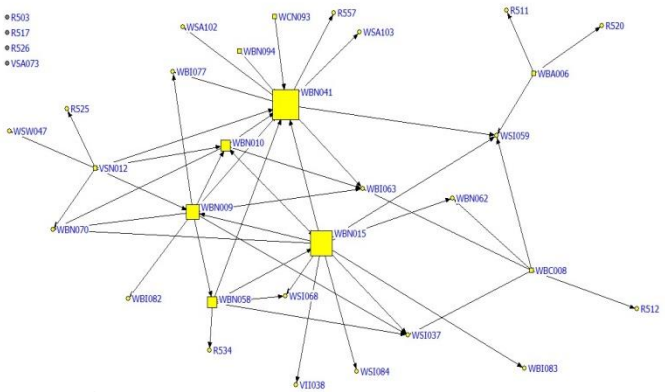
- 238 researchers, professors, and graduate students in courses and workshops 2012-2015.
- 33 PhD, MSc, & BSc students in SeeD to date.
- Scientists are conducting research projects to apply SeeD products in their own programs.

Targeting capacity-strengthening efforts



maize breeders

- Workshops
- Online learning modules
- Visiting scientists and projects
- Postgraduate program



wheat breeders

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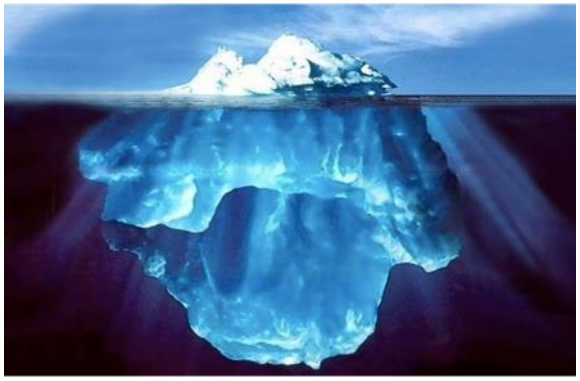
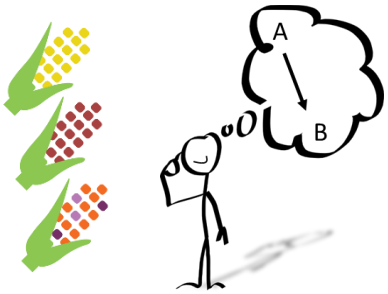
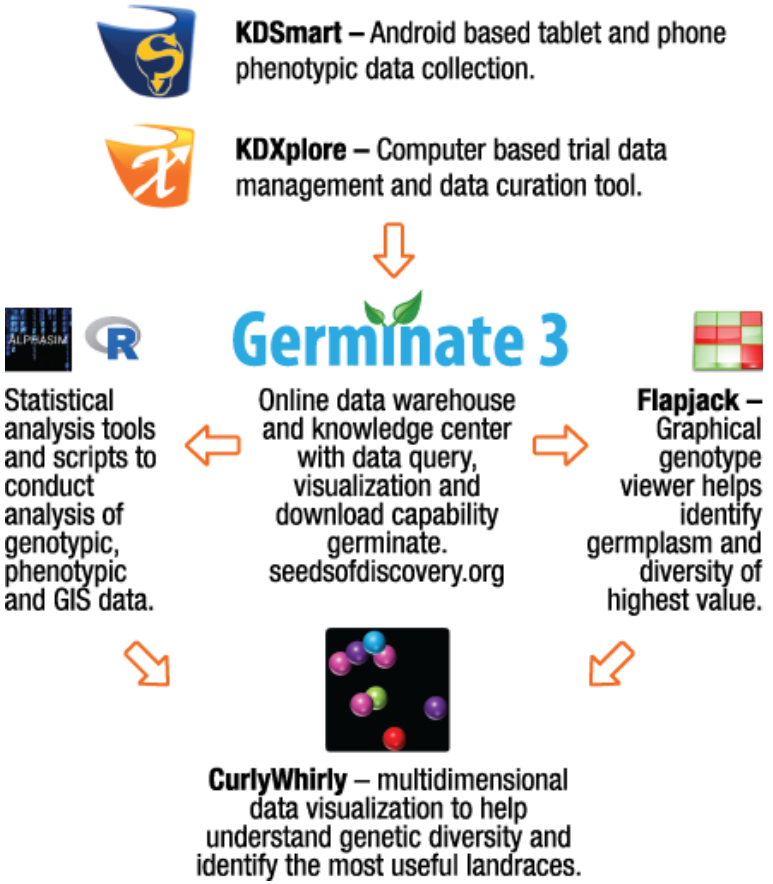
Putting knowledge together- Molecular Atlas





Components

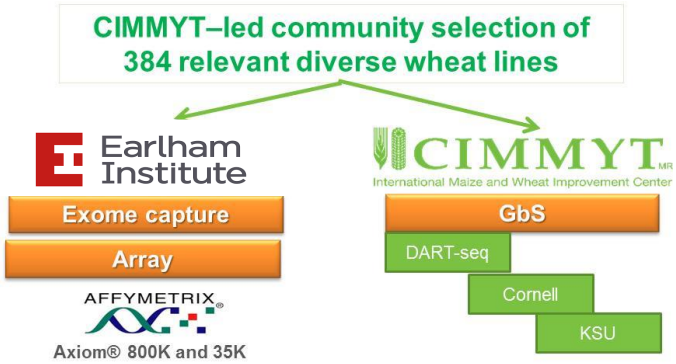
- **Data-** genotypic, phenotypic, GIS, passport.
- **Knowledge-** marker-trait associations, germplasm panels, protocols, “how to”.
- **Tools-** data collection software, online query tools, data visualization tools and software, statistical analysis methods, training links.



UK-SeeD Data Analysis Infrastructure

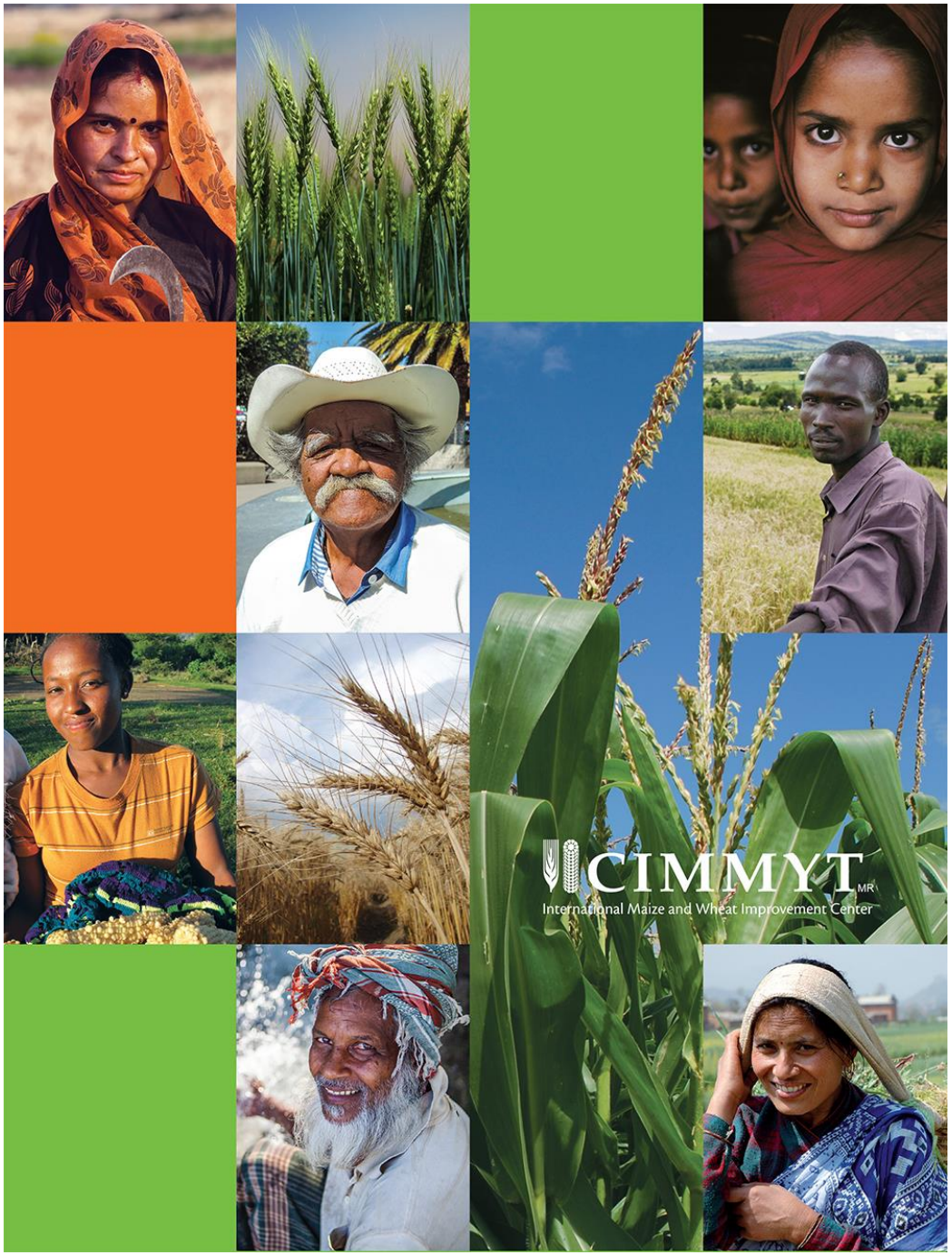
- Deploy a computing hardware and software platform
- Integrate computing resources and expertise at Earlham, CIMMYT and NIAB
- Facilitate data-intensive bioinformatics analyses leveraging data generated by SeeD for the genetic improvement of wheat.
- Data will be available via public and open resources (Wheat Information System; Ensembl Plants browser).
- Add value to SeeD and IWYP, and enhance their benefits to the wheat research community.

Data integration across genotyping platforms



EiB linkages

- **Data-** genotypic, phenotypic, GIS, passport.
- **Knowledge-** marker-trait associations, germplasm panels, protocols, “how to”.
- **Tools-** data collection software, online query tools, data visualization tools and software, statistical analysis methods, training links.
- **SAGA, training**



Thank you for your interest!

CGIAR RESEARCH PROGRAM ON Maize

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