Maize Seeds of Discovery (SeeD)

Finding potential in the haystack: new approaches and ideas to identify and move breeder-relevant variation from the germplasm bank to breeding programs.

Sarah Hearne

CIMMYT

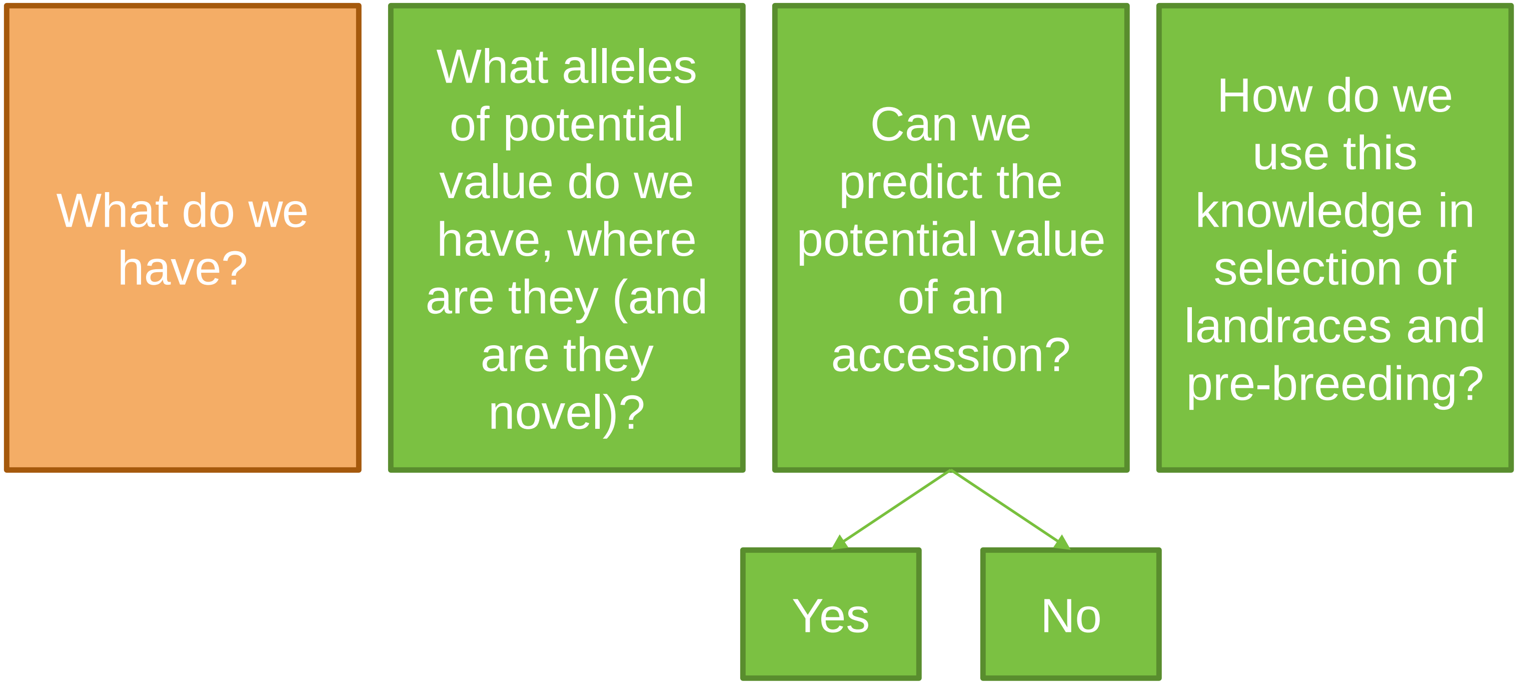
Four pillars of work

Genotypic characterization of germplasm banks and public elite germplasm

Phenotyping, trait discovery and predictions

Pre-breeding

Capacity Development, IT & Data Management



What do we have?

What alleles of potential value do we have, where are they (and are they novel)?

Can we predict the potential value of an accession?

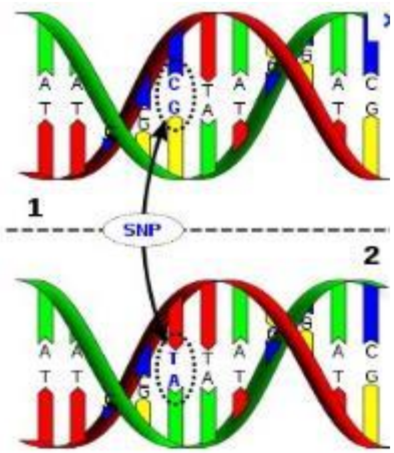
Yes

No

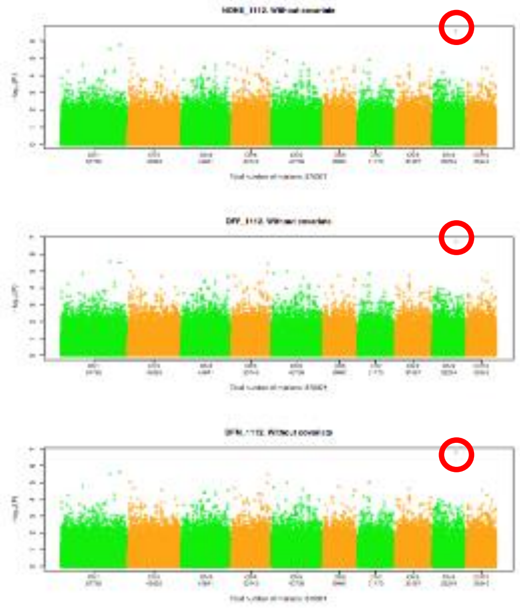
How do we use this knowledge in selection of landraces and pre-breeding?

What alleles of potential value do we have, where are they (and are they novel)?

Genome-wide association studies “GWAS”



~3500 accessions



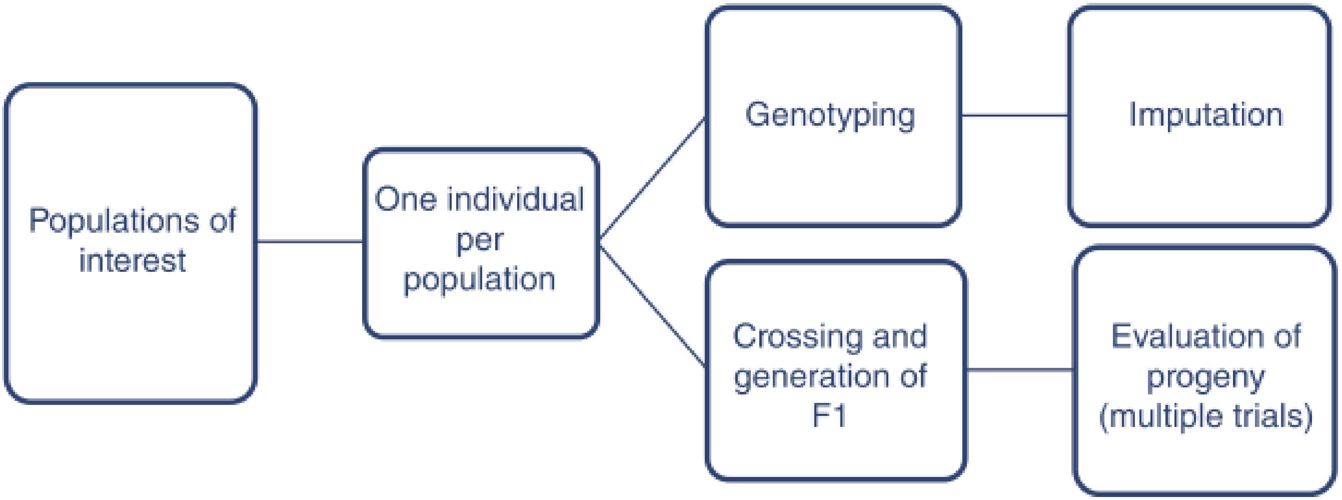
Molecular markers associated with phenotype of interest

3 to 14 % of the landraces

Martha Willcox, Juan Burgueño, Charles Chen, Sarah Hearne, Ed Buckler, INIFAP, UAAAN, Pioneer

Marker trait associations - GWAS

F1 association mapping (FOAM)

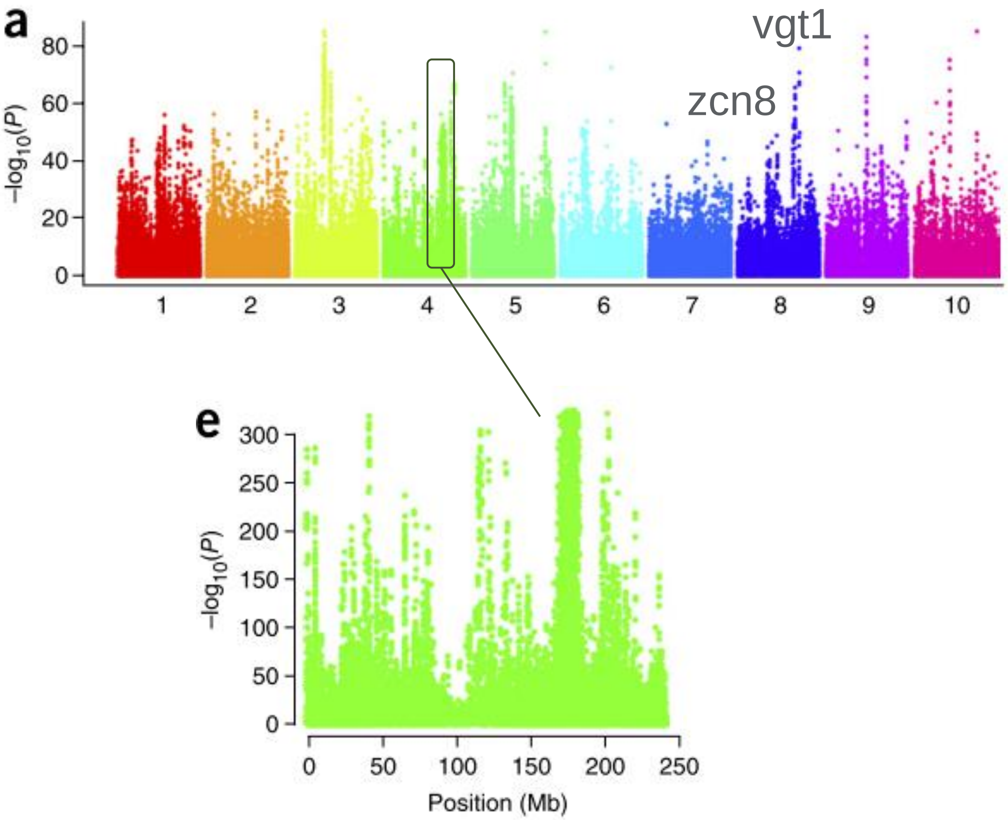


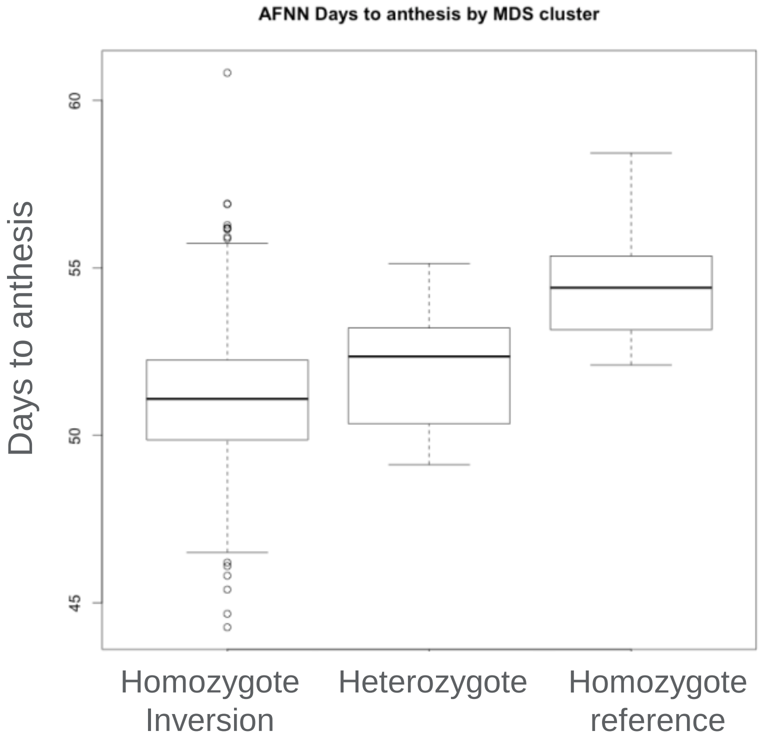
3500 accessions, flowering, plant & ear height…..

34 trials

Romero et al 2017, Nature Genetics

GWAS - flowering



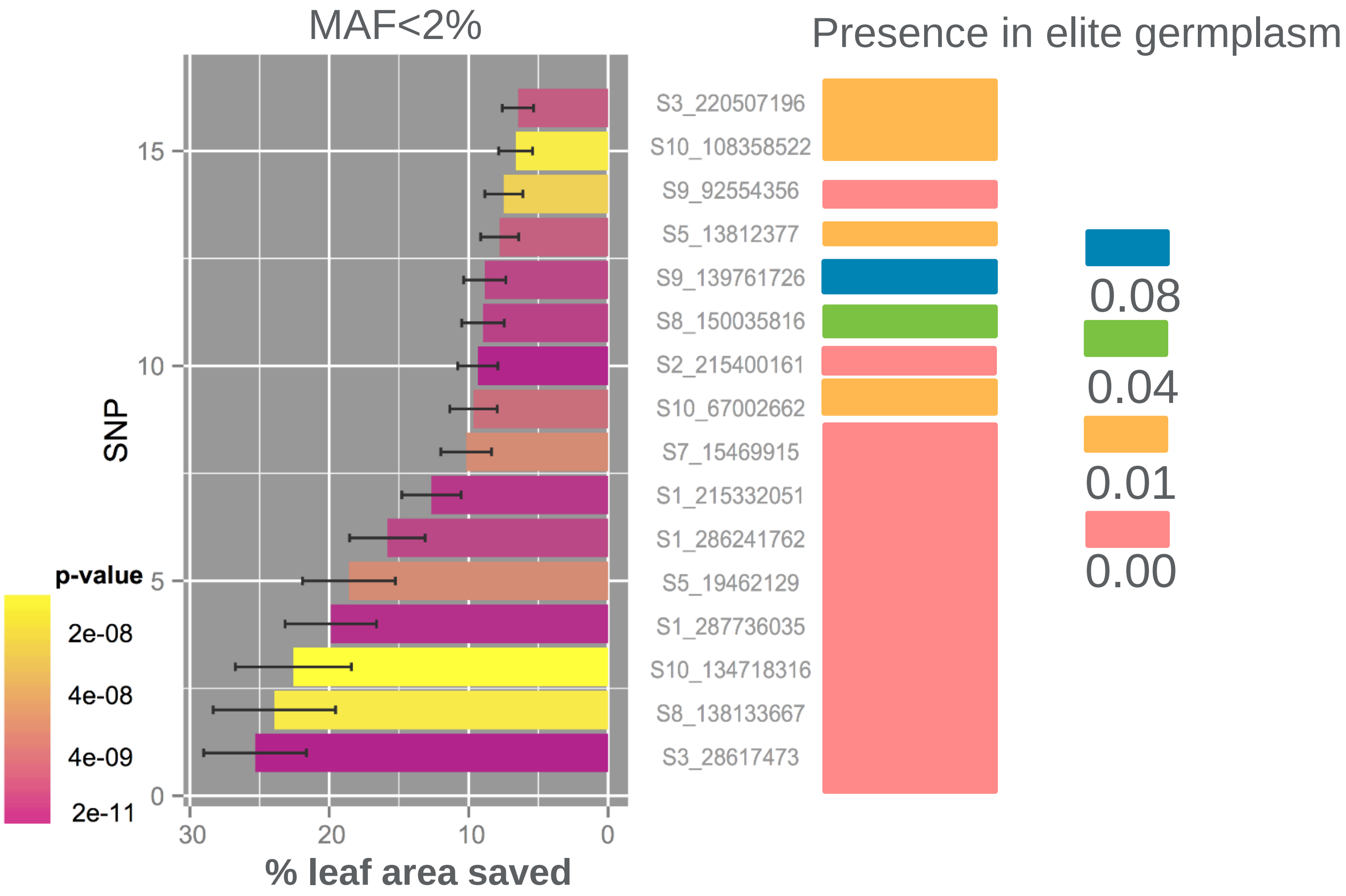


Largest effect measured to date – novel variation; new loci, presence in elite tropical material (CMLs) varies– BUT ~1000 genes

Romero et al 2017, Nature Genetics

GWAS – Tar Spot Complex

912 landrace TCs
41 QTL

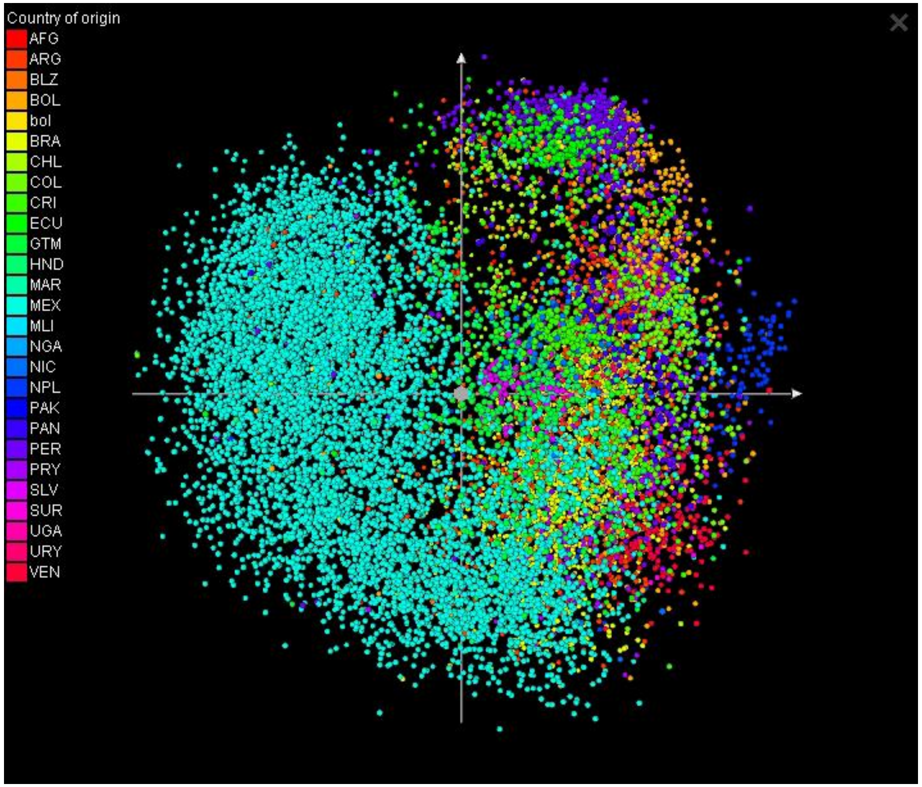


Response to virus and bacteria, stress response pathogen recognition specificity for R genes, LRR – all QTL are different to those identified in 495 and 451

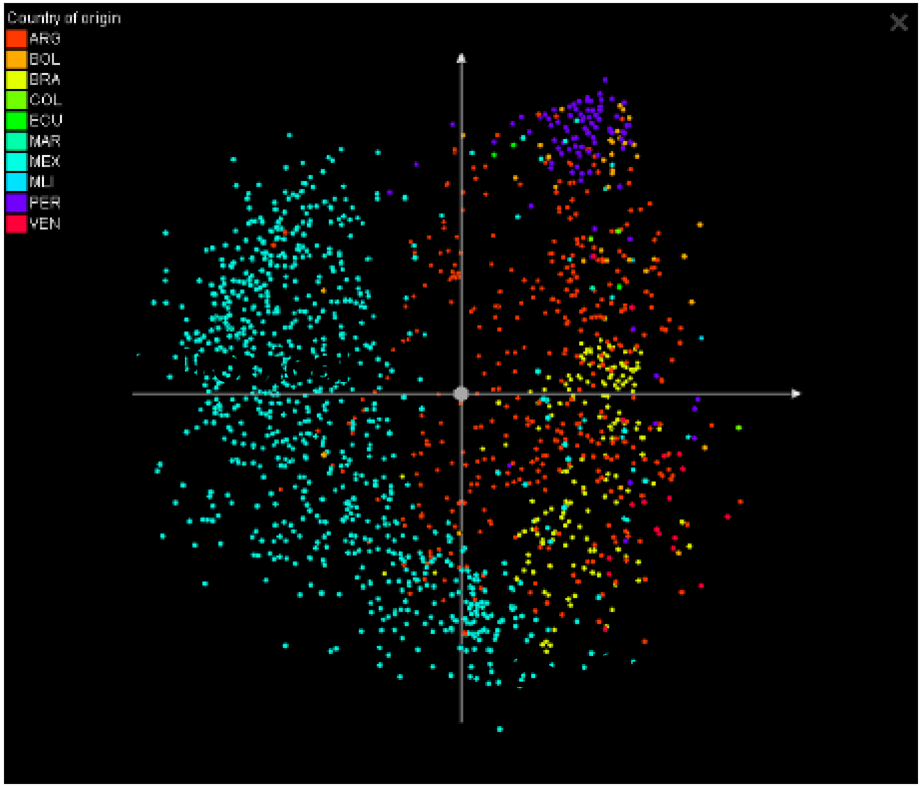
Charles Chen, Martha Willcox, Juan Burgueño, Sarah Hearne

Molecular and environmental diversity – shift from cores to breeder panels

MDS euclidian genetic distances



15,384 landraces

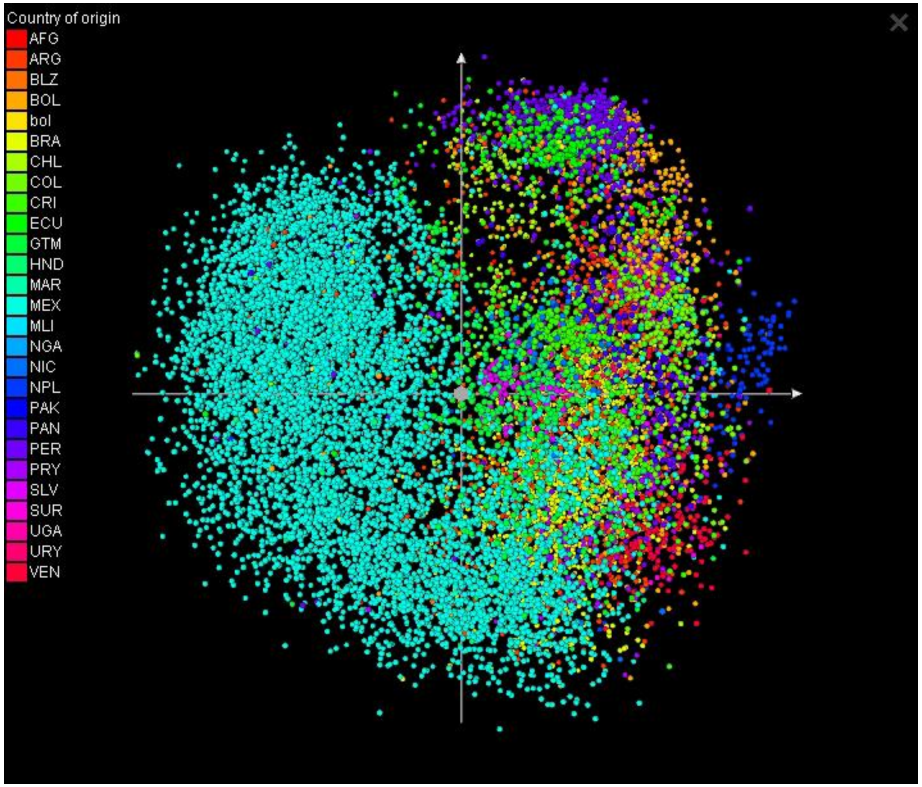


1,549 landraces from drought prone environments- $1.5M

Jorge Franco, Universidad de la Republica, Uruguay

Molecular and environmental diversity – shift from cores to breeder panels

MDS euclidian genetic distances



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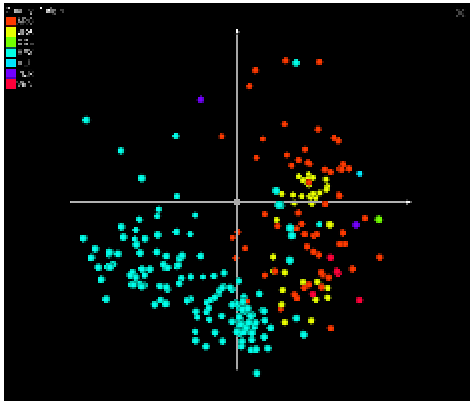
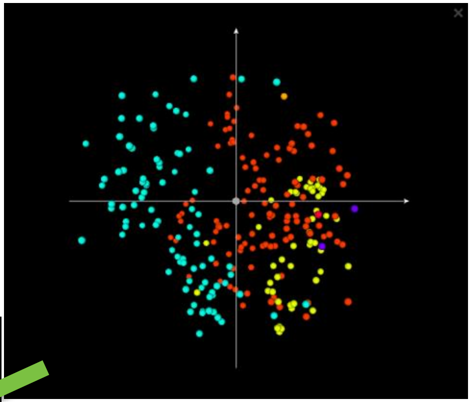
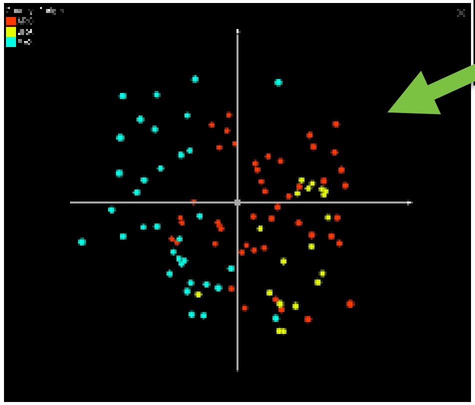


250 Tropical



250 Sub-tropical

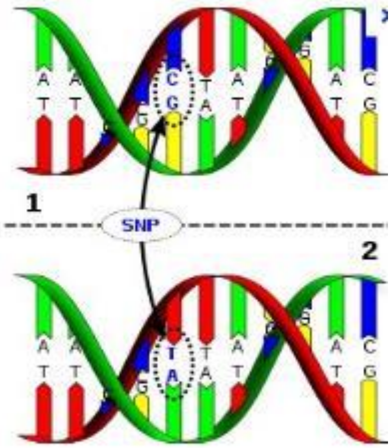


100 Sub-tropical

Jorge Franco, Universidad de la Republica, Uruguay

Finding genetic variation of breeding value

Environmental Genome-wide Association Studies “EnvGWAS”



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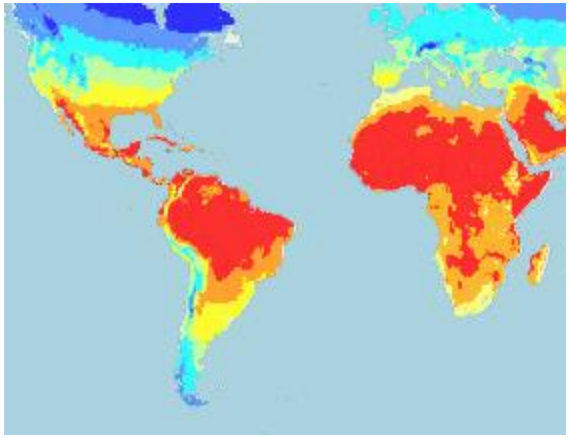

GIS-derived collection site data; ~17500 maize accessions

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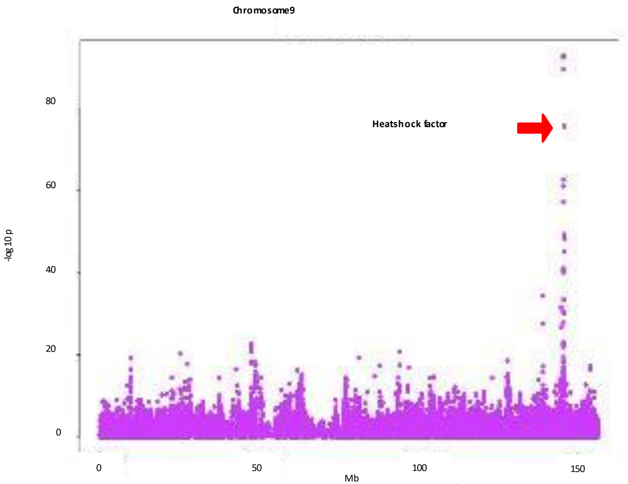


Alberto Romero

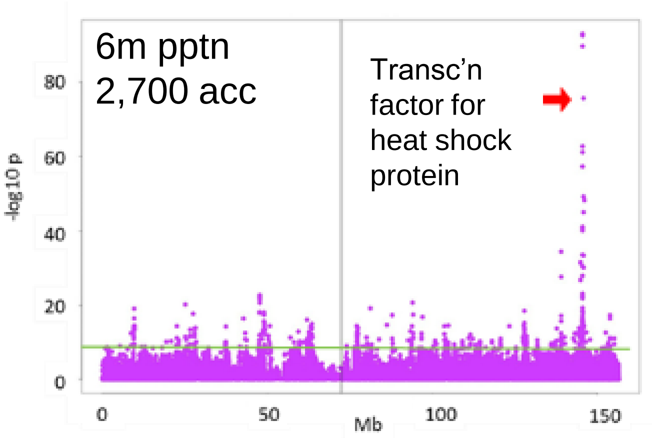
Molecular markers associated with adaptive variation of breeding relevance

GIS data is “virtually” free – 2.5x10^{-14}%

Sarah Hearne, Ed Buckler. Jeff Ross Ibarra, Alberto Romero, Arcadio Valdez

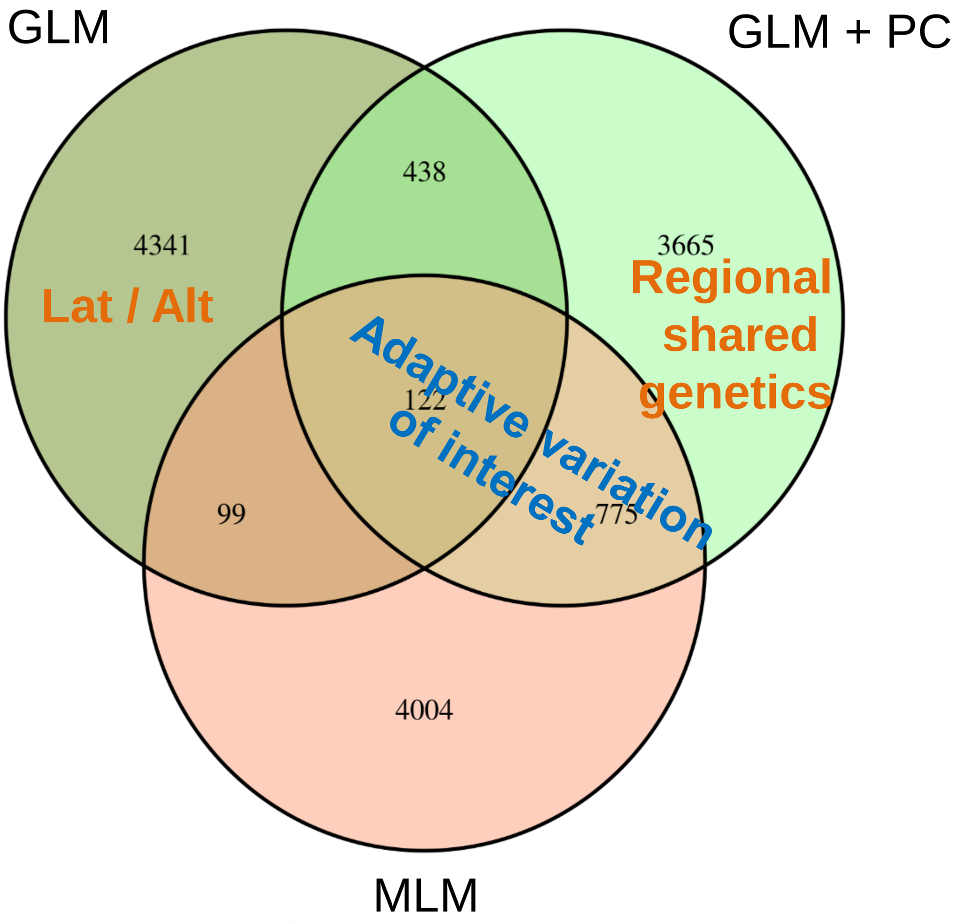
Finding genetic variation of breeding value

Chromosome 9



6m pptn
2,700 acc

Transc'n factor for heat shock protein



GLM

GLM + PC

MLM

Lat / Alt

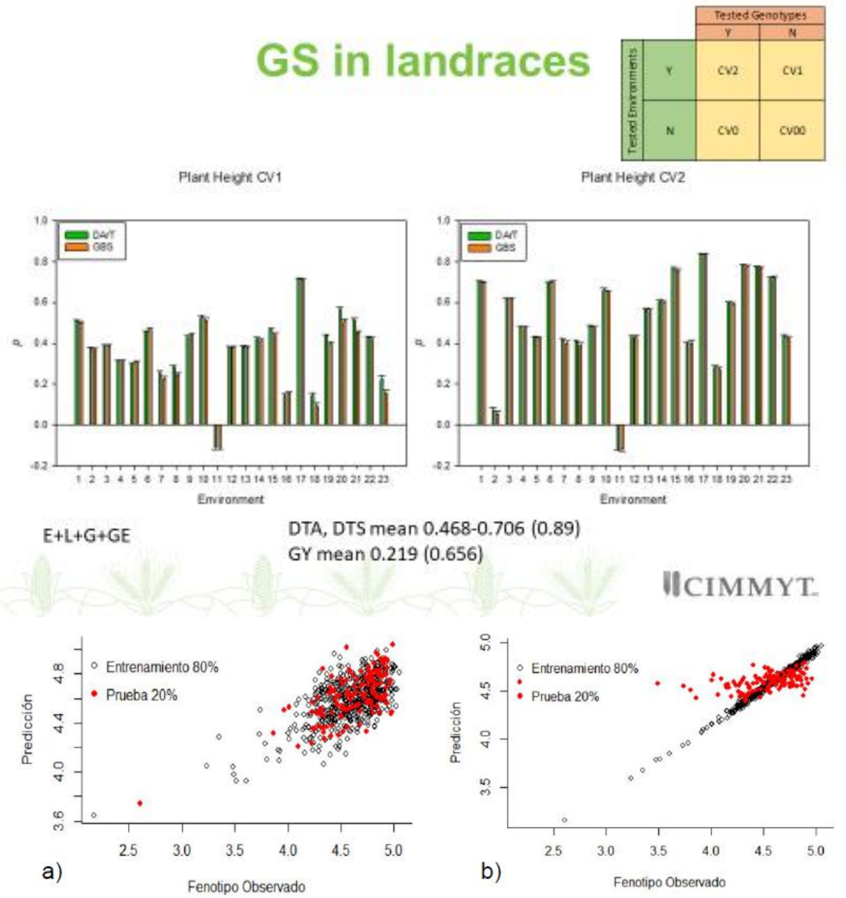
Regional shared genetics

Adaptive variation of interest

You have QTLs…so what

From QTL to Value (GEBV +)

- Finding QTLs is “easy”
- Breeding with many QTLs of small effect for complex traits is not recommended
- What to do with them?
    - Identify the QTLs new/novel to existing breeding material
        - *CML and donor line genotypes*
    - Finding QTLs which work across backgrounds
        - *Look to broader QTL complementarity across landraces and use landrace passport*
    - There are 10s to 100s how can we effectively use this information?
        - *Combination with genomic prediction when fewer loci*



		Tested Genotypes	
		Y	N
Tested Environments	Y	CV2	CV1
	N	CV0	CV00

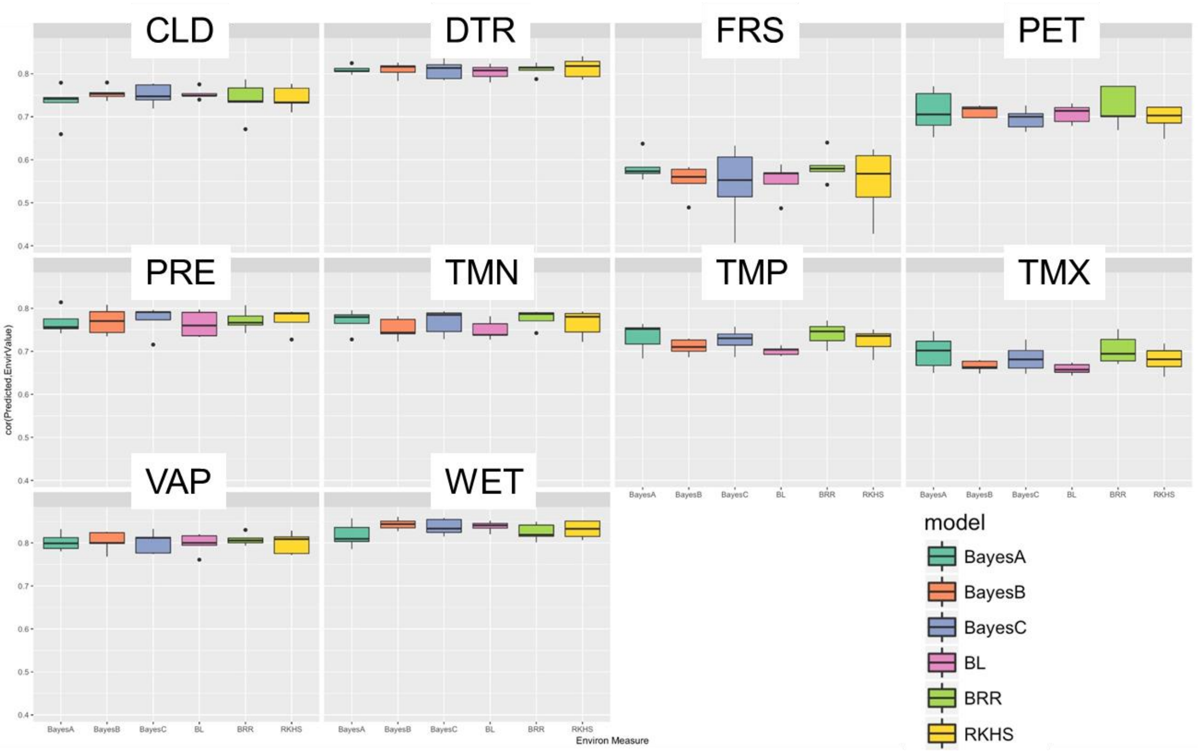
DTA, DTS mean 0.468-0.706 (0.89)
GY mean 0.219 (0.656)

Jose Crossa, David Gonzalez, Terry Molnar, Martha Wilcox

Predicting the value of an accession using environmental data

Prediction using phenotype well established

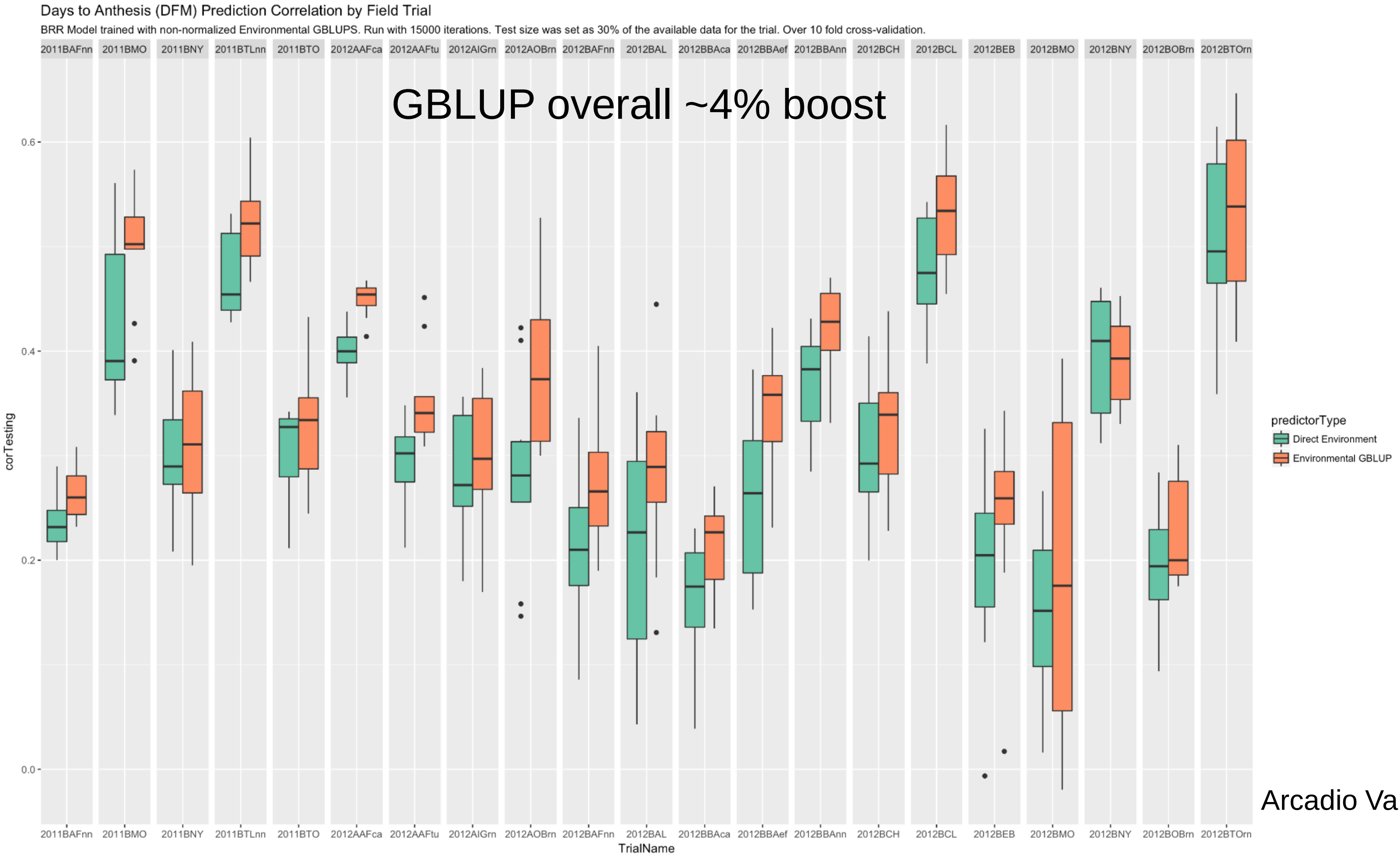
- We can’t phenotype all the collection for relevant characteristics
- Can we use a proxy for phenotype?
- Use the GIS derived climate data



Arcadio Valdez

Predicting the value of an accession

Days to Anthesis predicted using landrace collection site environment- cross trials



GBLUP overall ~4% boost

Arcadio Valdez

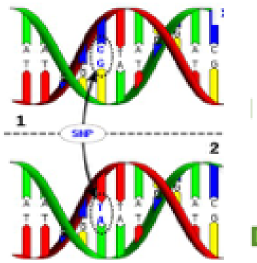
Extend from GWAS panel to maize germplasm bank

Selecting germplasm without and phenotypic or GIS proxies

- Knowledge and data
    - e.g. a specific disease
        - Accessions from locations with disease prevalence, historic outbreaks
        - Genotypic data to develop a panel representative of the diversity present

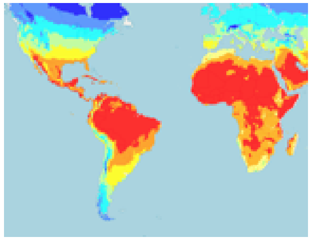
    - Other knowledge- race (use), historic environmental likelihood of disease etc.
    - In the absence of any information start with a representative diverse panel adapted to the environment of evaluation

How do we use this knowledge in selection of landraces and pre-breeding?



Classical GWAS

Identify specific novel genetic variation of breeding relevance



Environmental GWAS

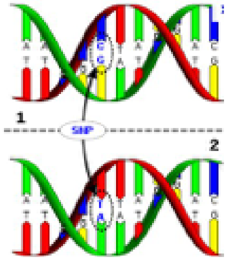
Identify novel genetic variation for adaptive variation of breeding relevance

Environmental Genomic Prediction

Identify which accessions are most likely to have highest potential novel value for breeding?

Select and phenotype materials

How do we use this knowledge in selection of landraces and pre-breeding?



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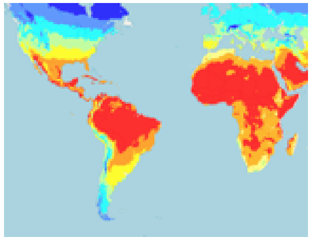


Knowledge

Identify diverse accessions representing our best estimate of a target environment?

→

Select and phenotype materials

“Pre-breeding”

Realizing promise- pre-breeding

- Development of inbred and semi-inbred germplasm which contains high value exotic alleles in elite backgrounds
  - This kind of germplasm is the most flexible germplasm- amenable to use by breeders interested in both landrace improvement and hybrid development

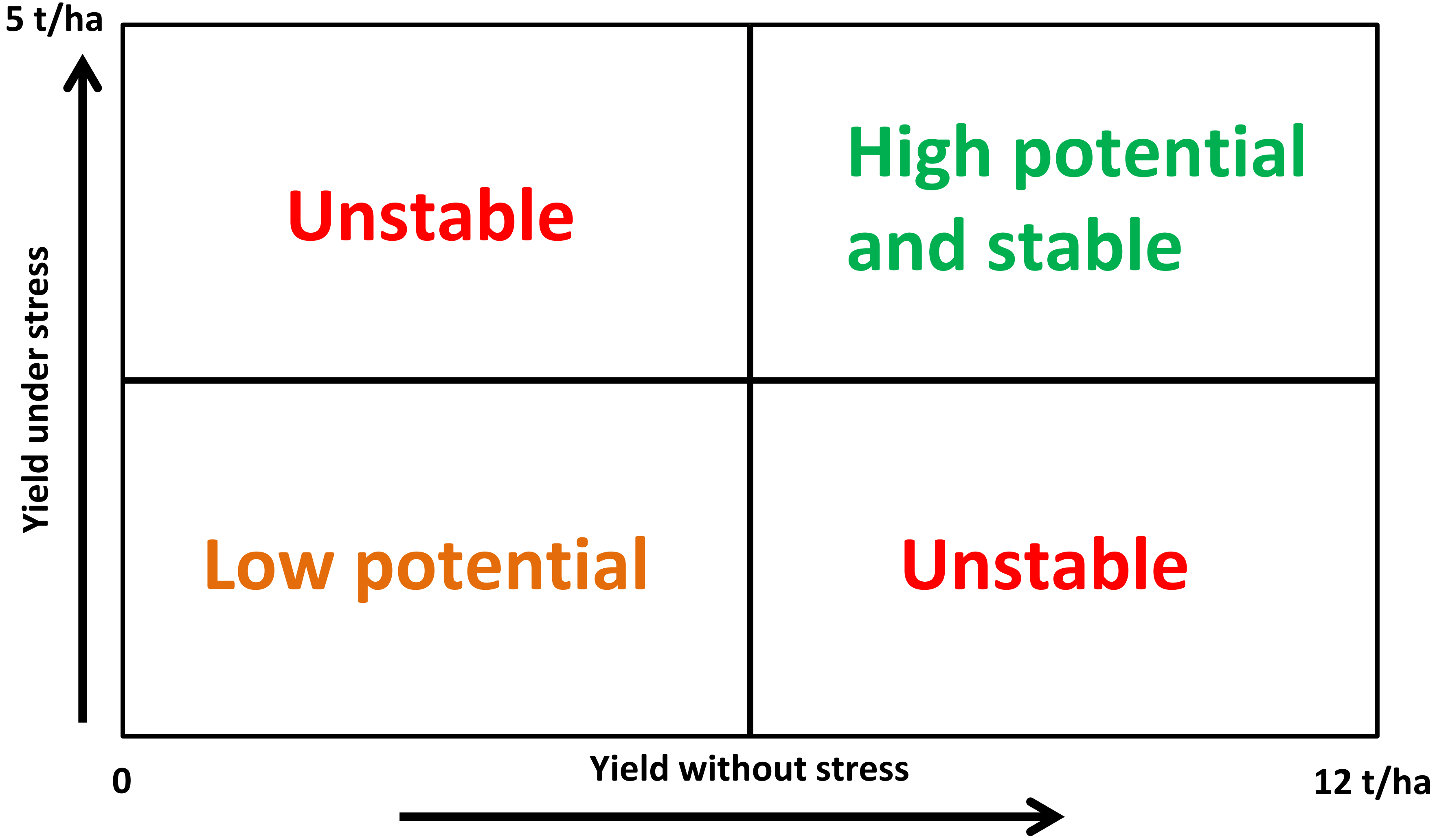
- Good agronomic performance is needed in addition to novel genetic variation
  - Poorly performing lines will not be used by breeders- the easier to use more stable donor germplasm is the easier it is for a breeder to assess its value to their breeding and adopt it for use

Pre-breeding

- Drought tolerance at flowering
- Heat tolerance (>38° C) at flowering & during grain fill
- Resistance to the Tar Spot Disease Complex
- Maize with high-anthocyanin kernel content.

Per-se testing, BC breeding, GS

GIS and molecular selection of accessions drought and heat



5 t/ha

Yield under stress

Unstable

High potential and stable

Low potential

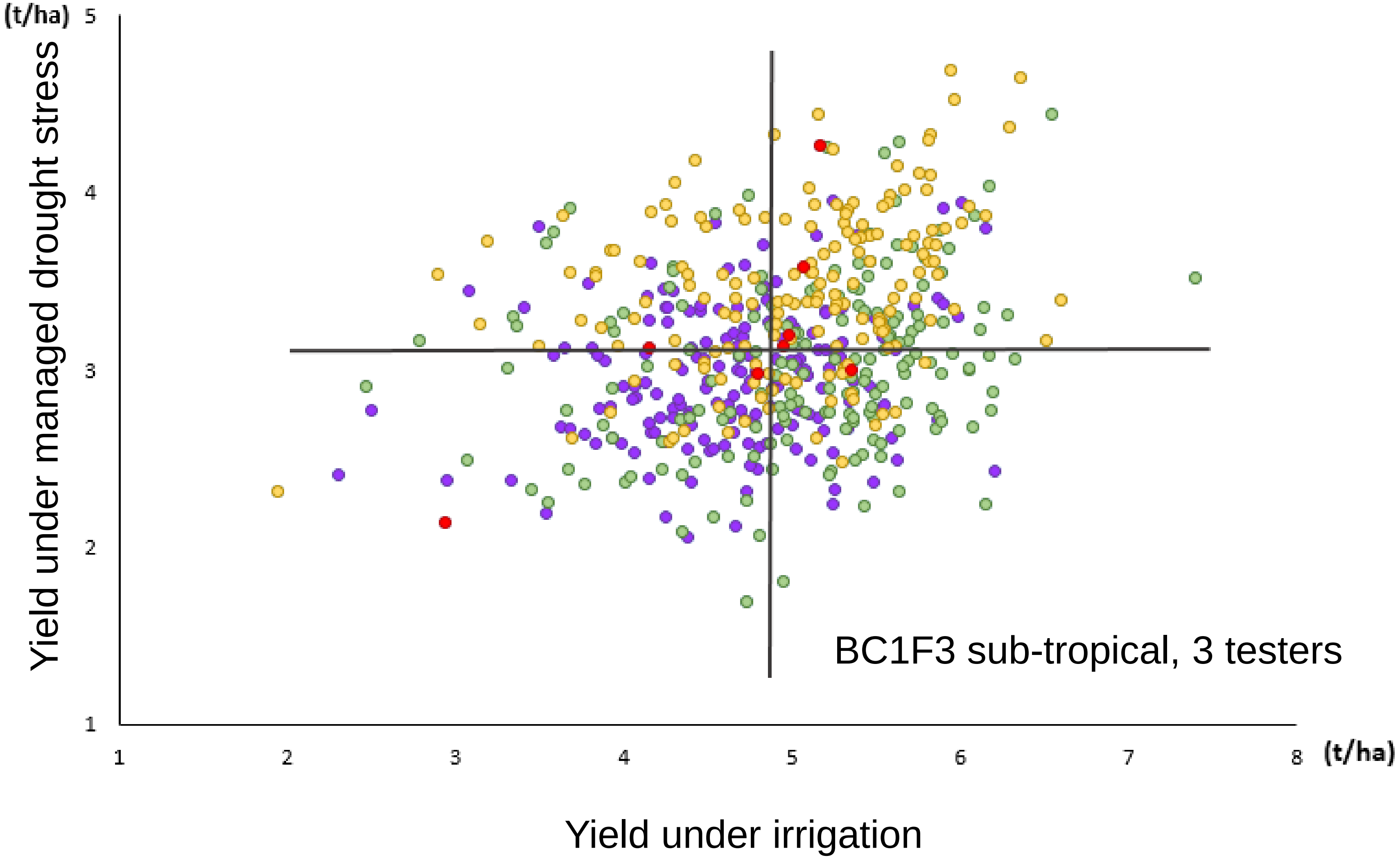
Unstable

0

Yield without stress

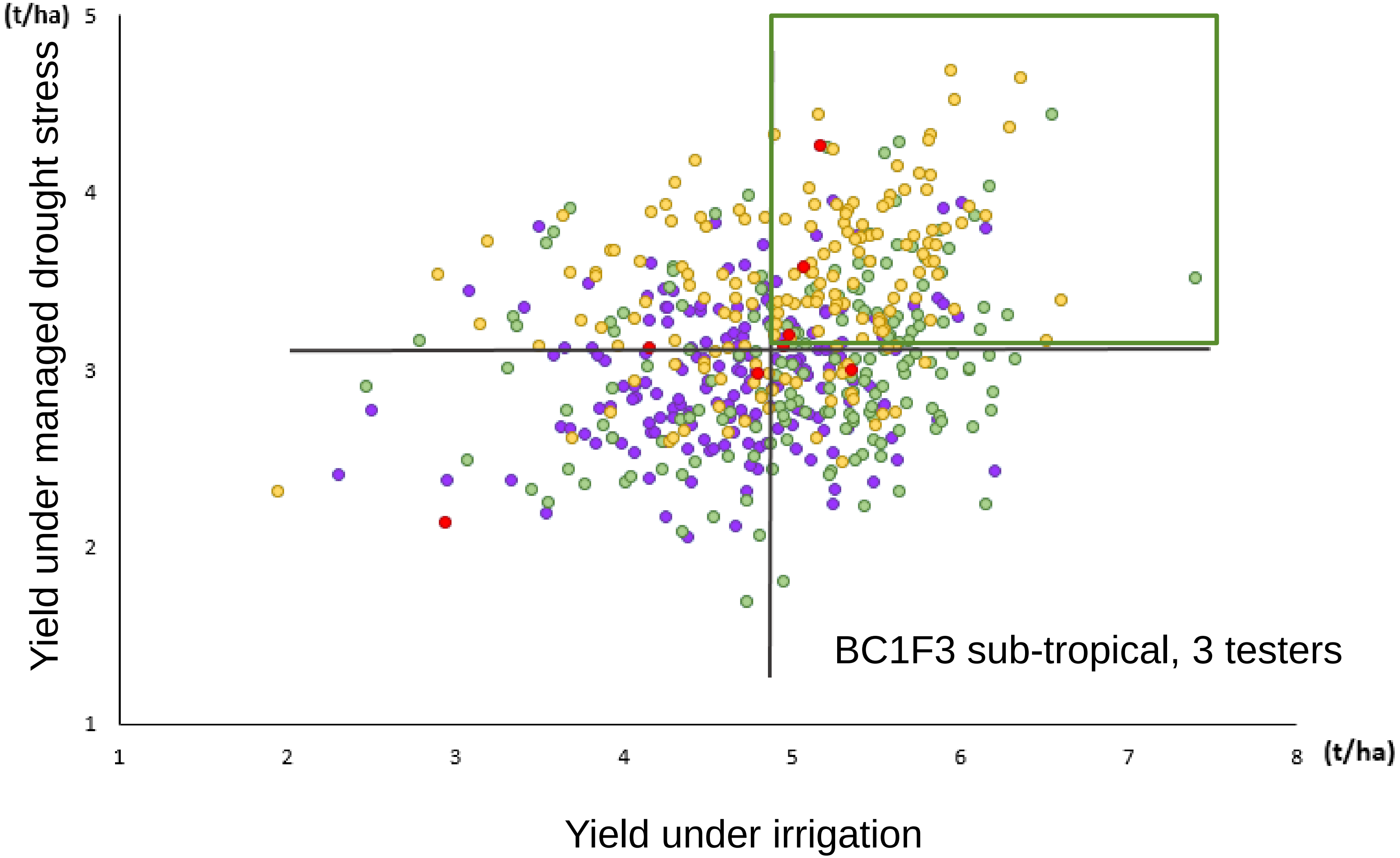
12 t/ha

Drought tolerant germplasm development



Tester 1 yellow, tester 2 green, tester 3 purple. Red = hybrid checks

Drought tolerant germplasm development



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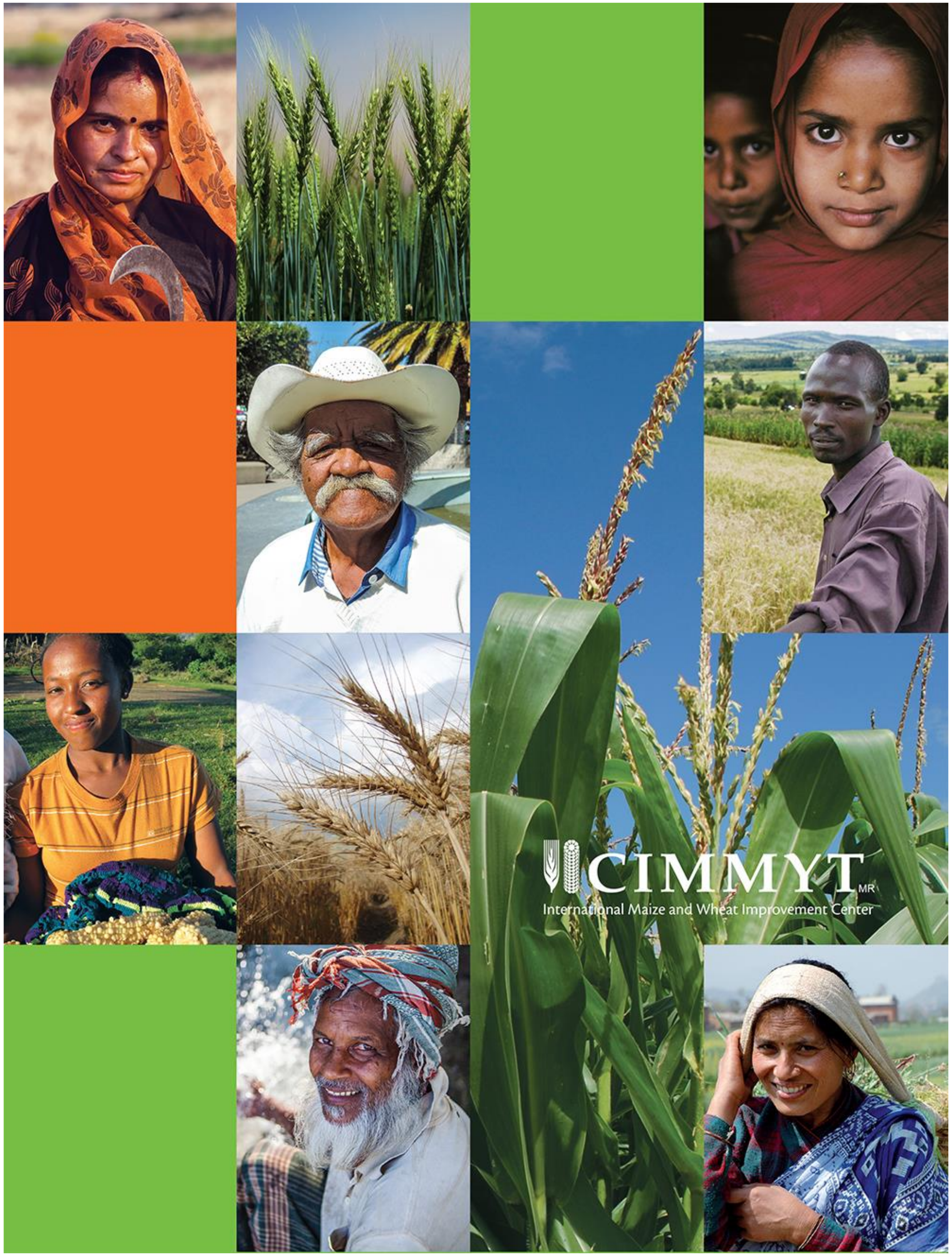

Thank you for your interest!