Shopping in the diversity supermarket; using big data to bring diversity to breeding

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Big Data in Agriculture
14th May 2018

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Seeds of Discovery (SeeD) 2010 (MasAgro Biodiversidad)

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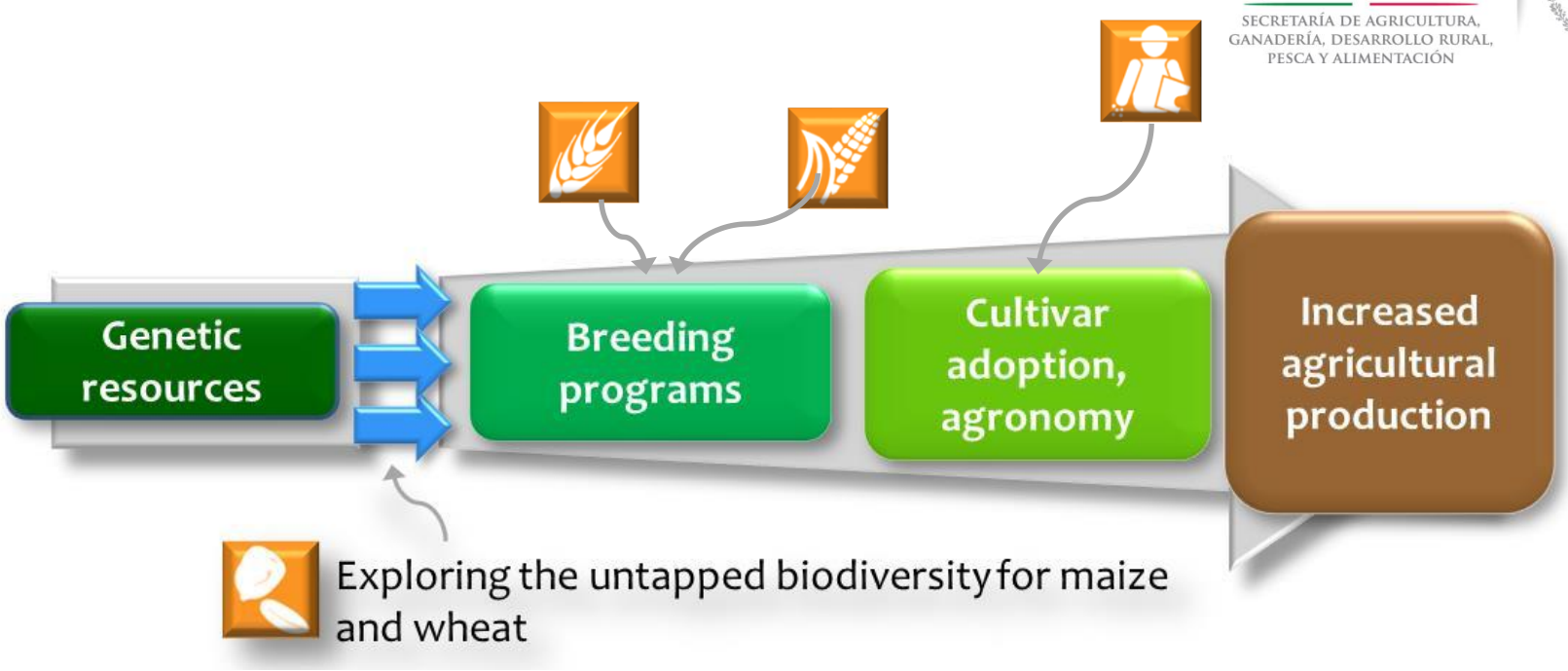

Genotypic characterization of germplasm banks and public elite germplasm

Phenotyping and Marker-trait associations

Pre-breeding

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Diversity, diversity everywhere but not a drop to drink

Inbred donors and elite lines- basis of breeding in public and private sector

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Barriers to use

Adaptation, linkage drag

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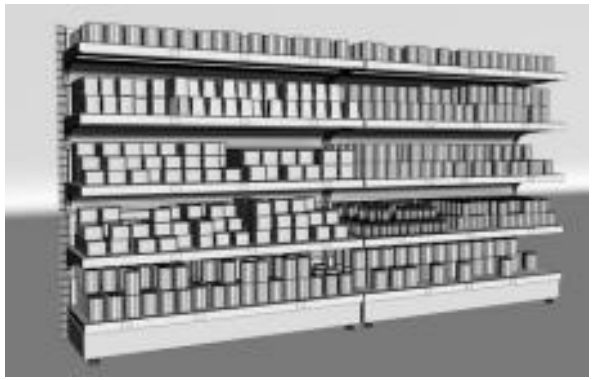
Barriers to use



Where does Big Data fit?

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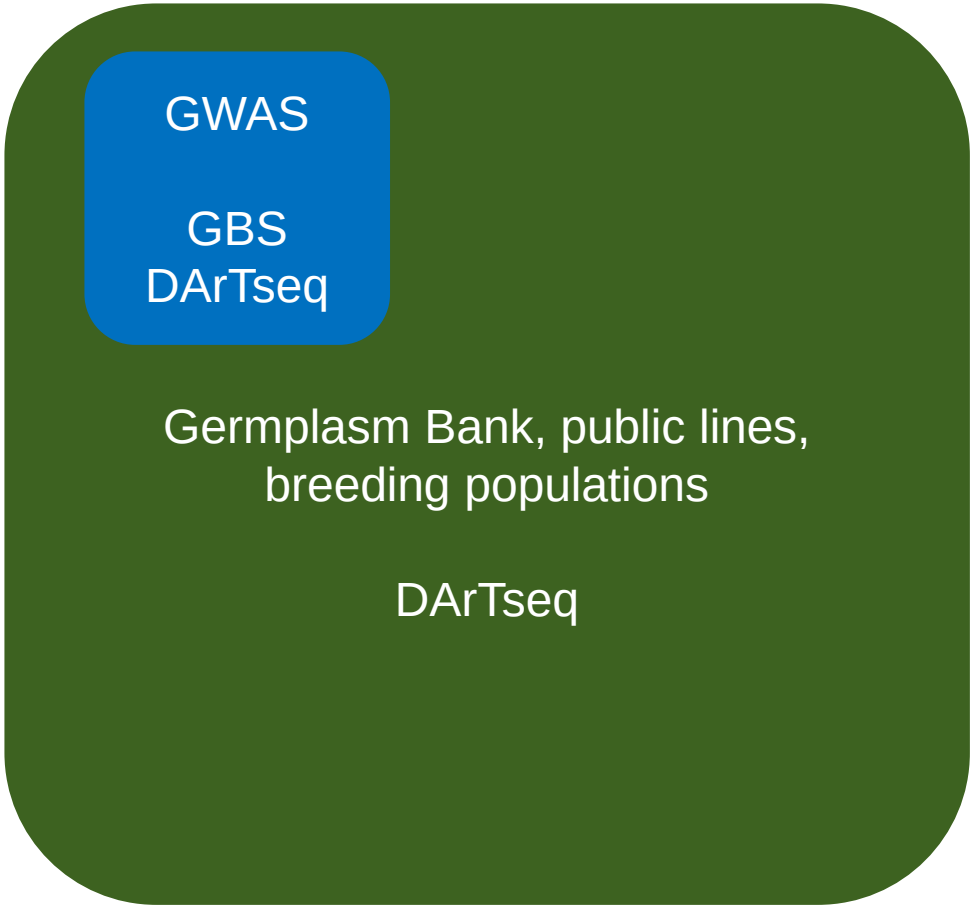
Genotyping of germplasm



GBS
1M ref genome aligned SNP
Imputation
QC filtered to ~350k

DArT seq
GWAS:- 110k SNP
~50%mapped to ref genome
No imputation

Bank: 1M markers, 650k SNP
filtered to 350-470k SNP (5x)
Allele frequencies
~45% mapped to ref genome

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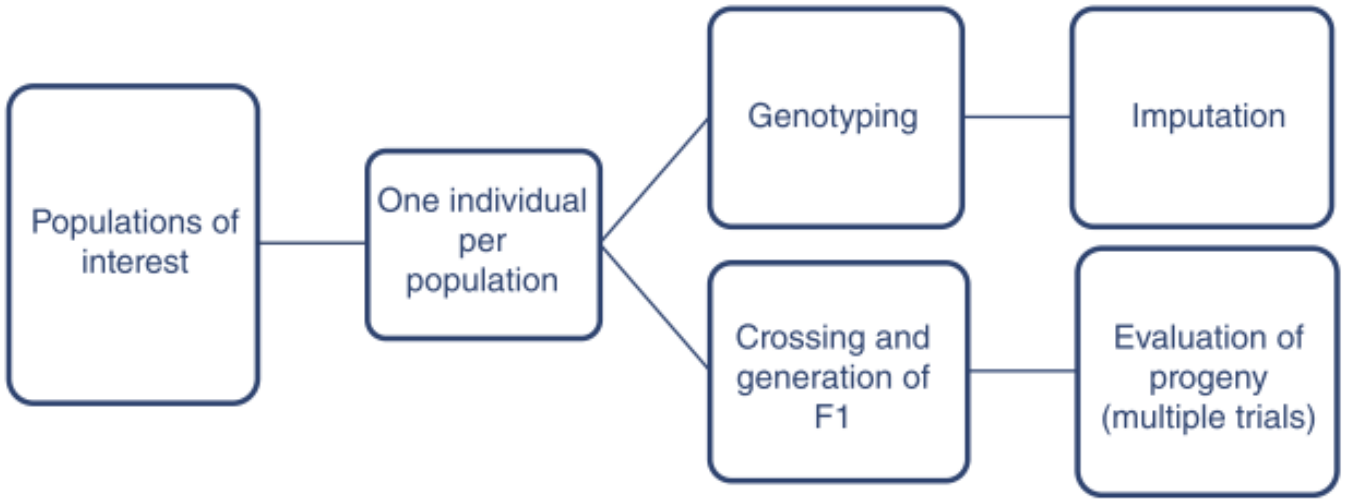
Marker trait associations - GWAS

F1 association mapping (FOAM)



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

34 trials

Romero et al 2017, Nature Genetics

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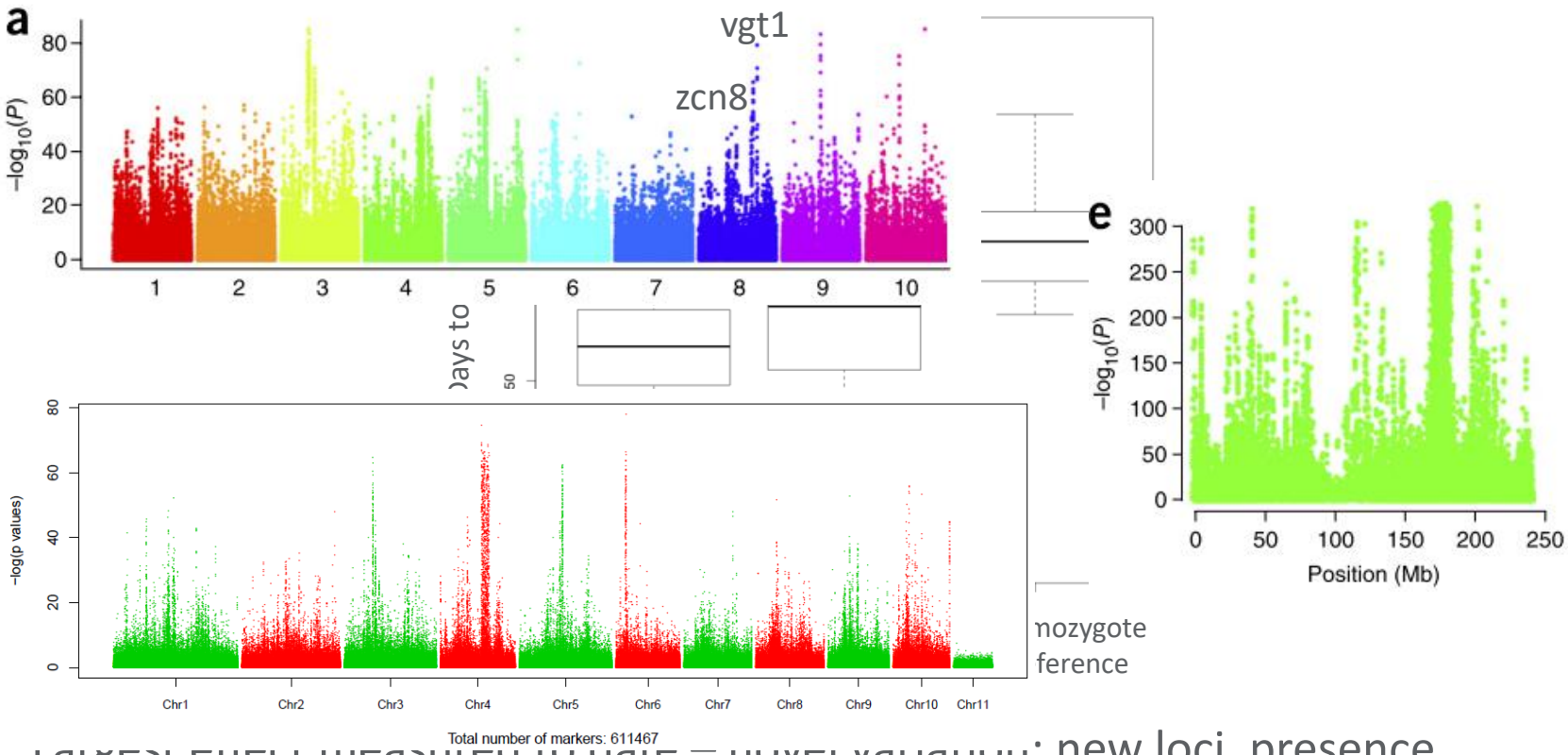
GWAS - flowering

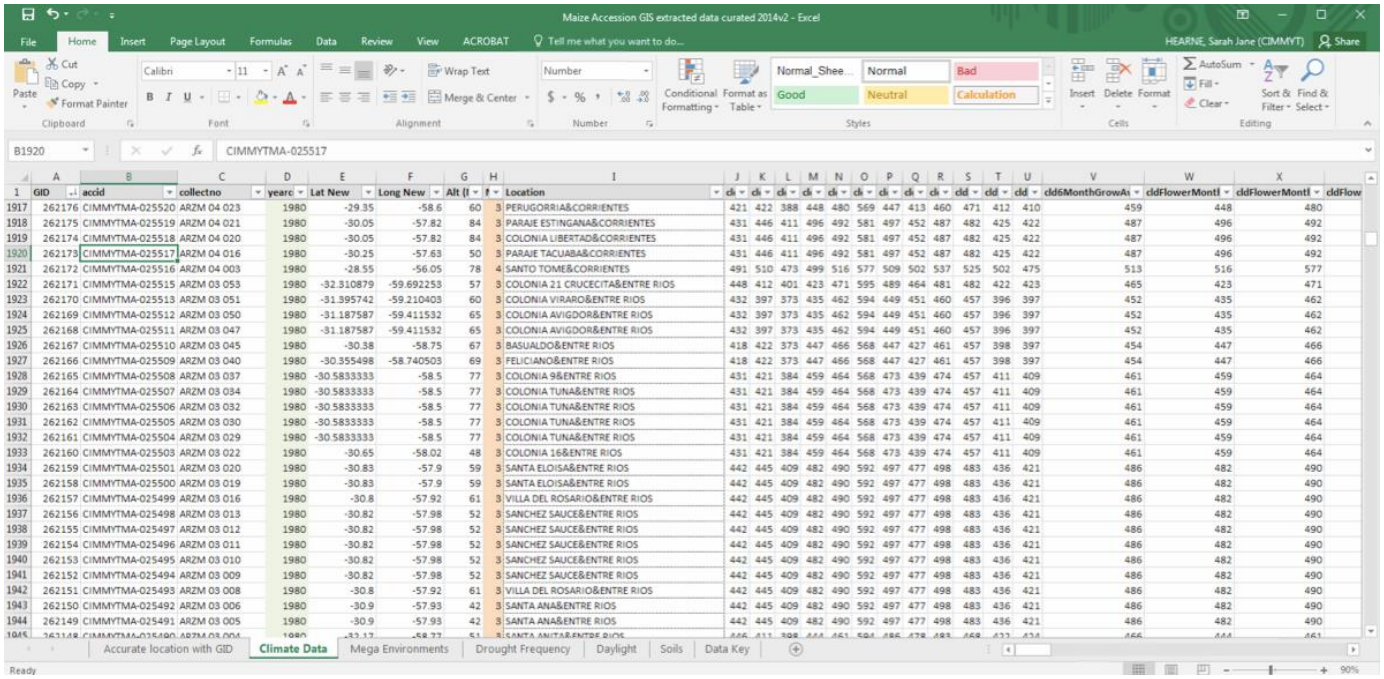


Largest effect measured to date – novel variation; new loci, presence in elite tropical material (CMLs) varies– ~1000 genes

Romero et al 2017, Chen, Palacios, Willcox, Burgueno, Hearne unpublished

Extending and expanding germplasm bank data

- ~17500 landrace accessions with collection site “data”
- 2y curation effort
- Derive GIS climate variables from collection sites



Kai Sonder

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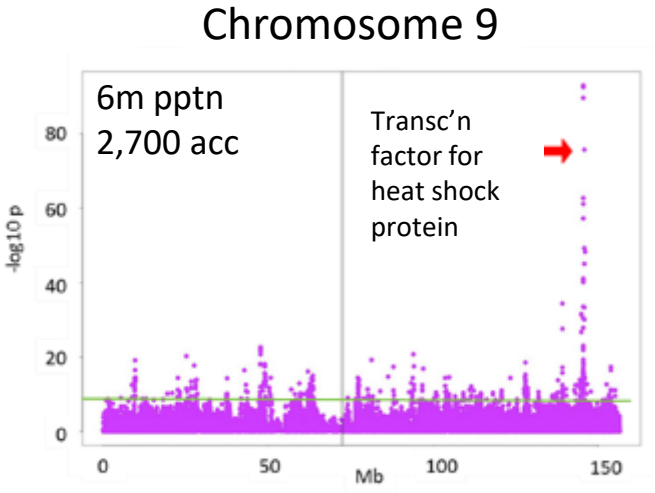
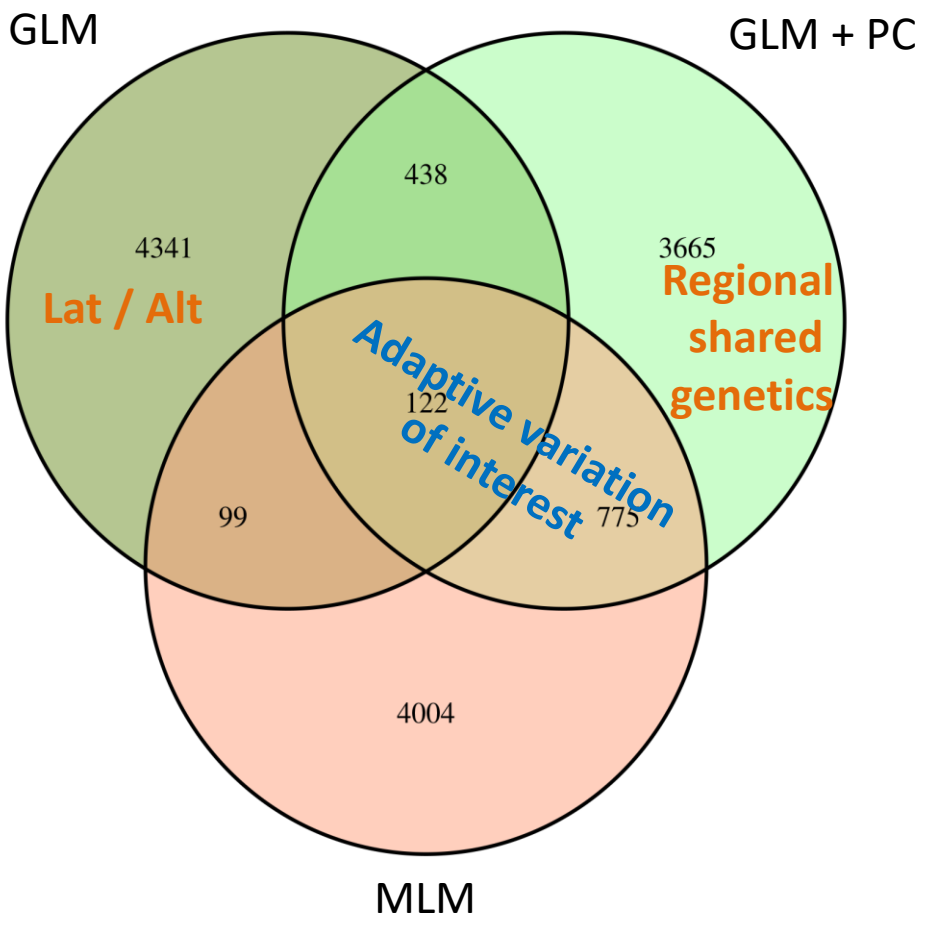
Environmental GWAS





Alberto Romero, Arcadio Valdes- unpublished, HuiHui Li, Jorge Franco, Jose Crossa

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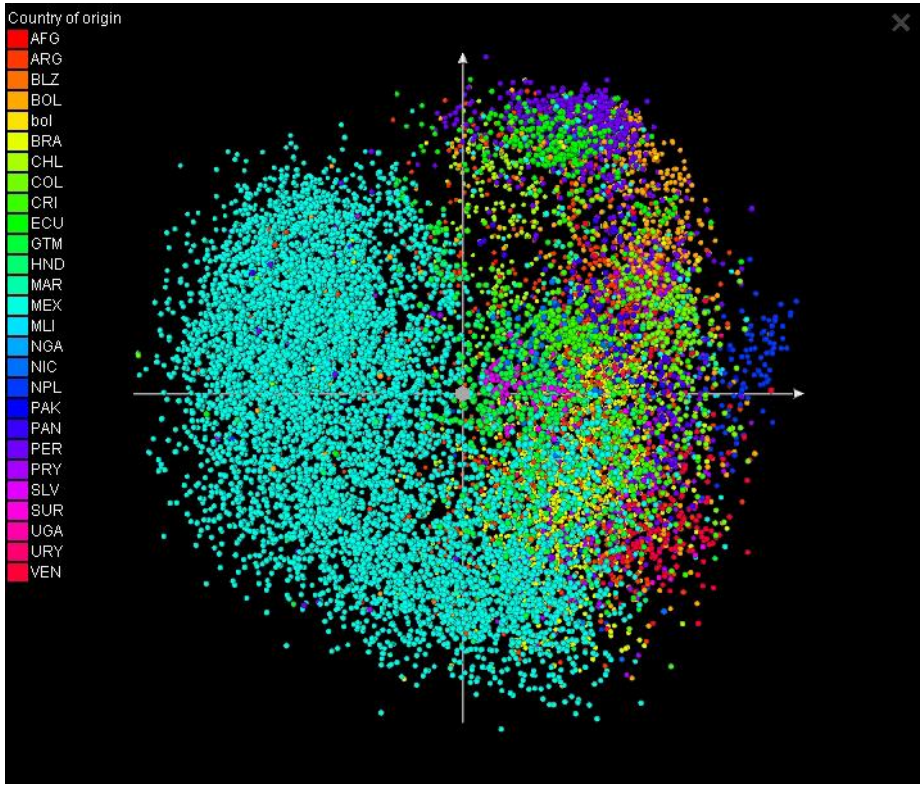
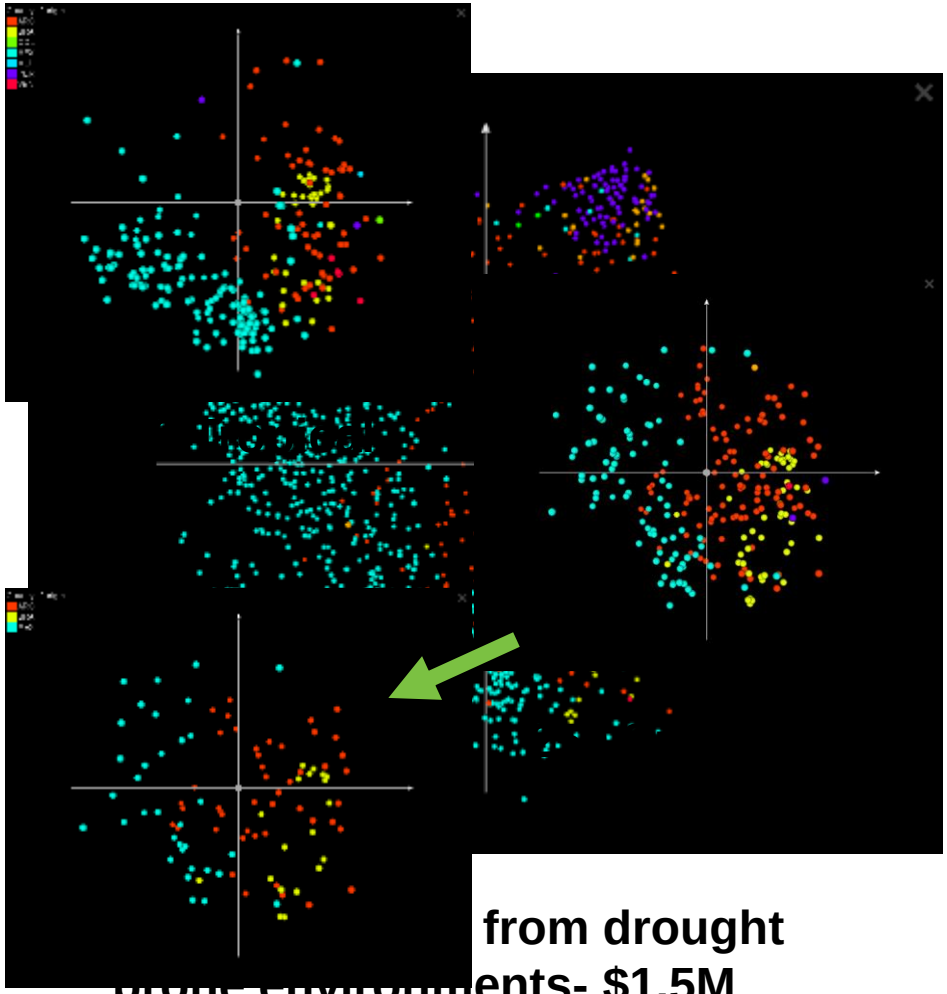
Molecular and environmental diversity – shift from cores to breeder panels

MDS euclidian genetic distances





15,384 landraces

from drought

prone environments- $1.5M

100 Sub-tropical

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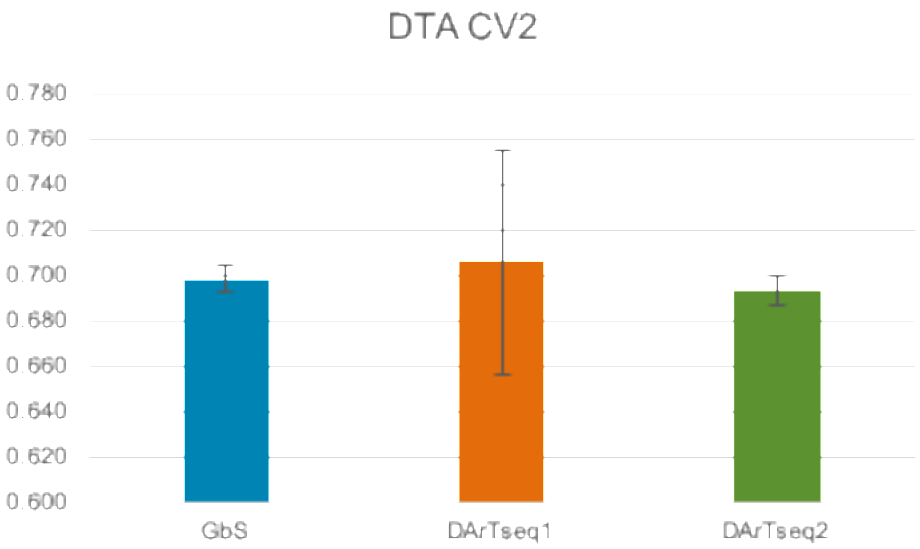
Smarter selection?

GS with landraces

Look in GWAS panel



Marker	Before QC	After QC
GBS	(1M) 352048	335319
DArTseq1	110698	40880
DArTseq2	94644	**5027**

Gorjanc *et al* 2016 BMC Genomics

Crossa and Hearne unpublished

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MORE?

Phenotypes

Genotypes

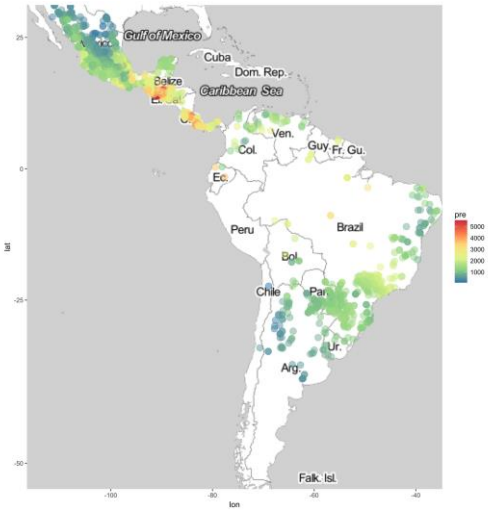
Environments

Environmental GS

Predict landrace collection site environments?

Genotype Matrix Genotype Effects

Landrace Origin Climatic Data (precip|frost|temp|…) = $\mu + X_{Genotype} B_{Genotype} + error$



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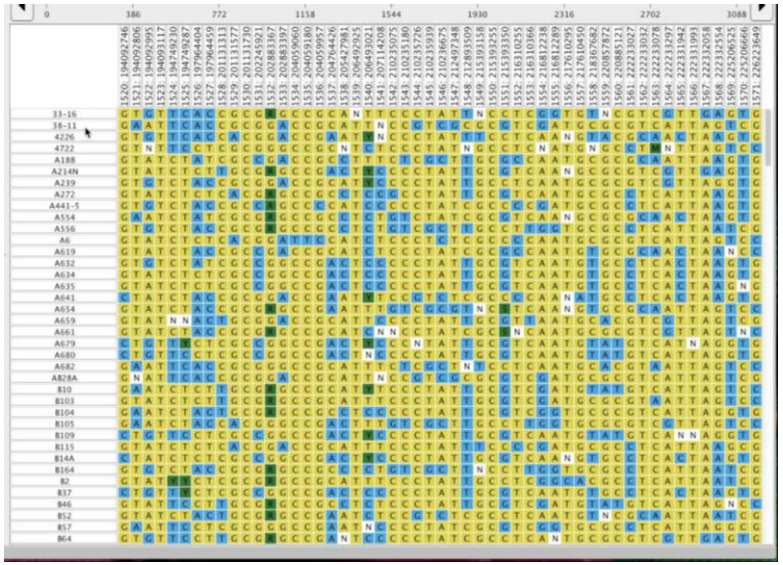

Arcadio Valdes, 2700 acc GWAS panel,120k markers (single SNP 50bp window) imputed GBS

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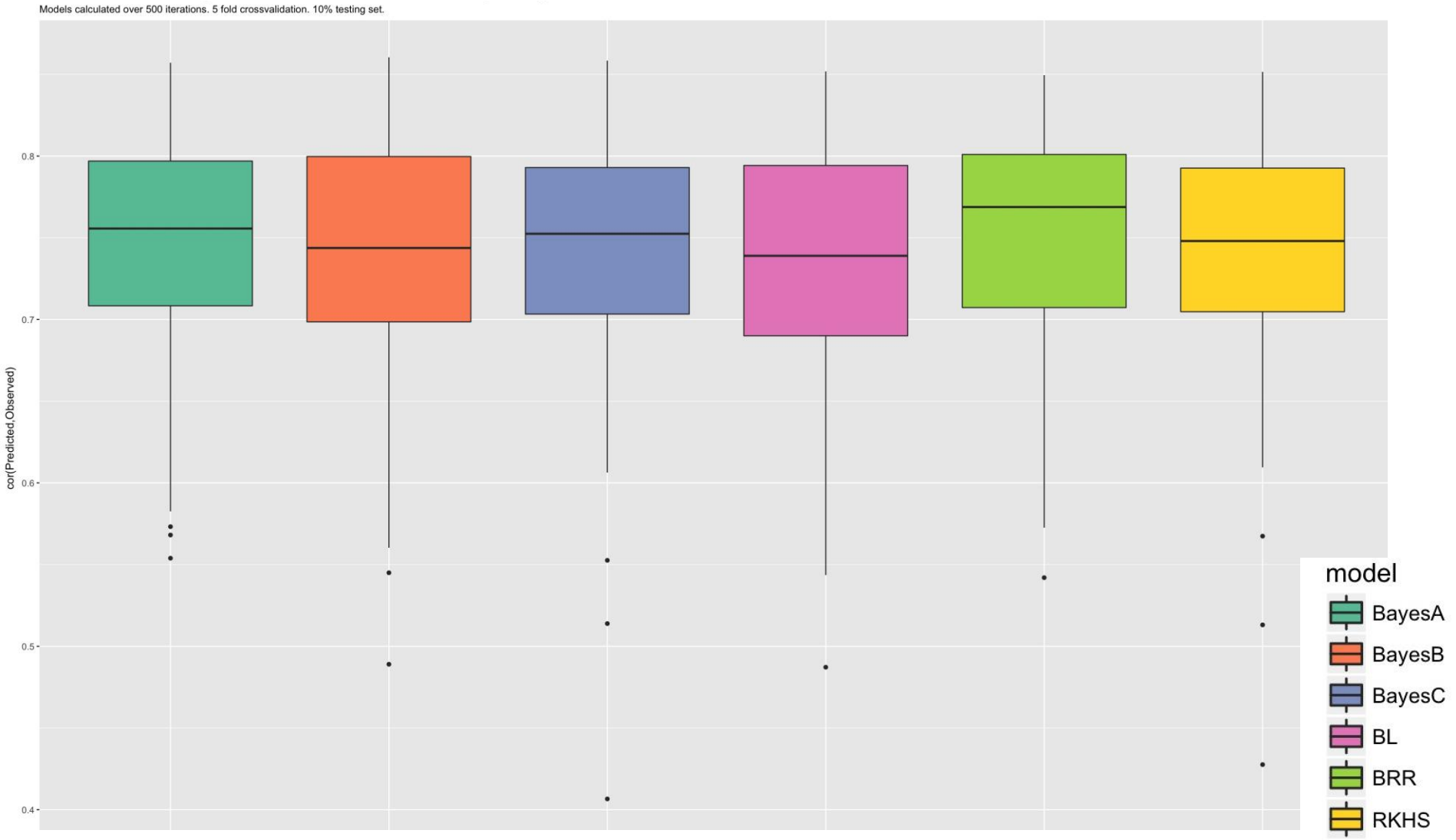
Environmental GS

Landrace origin environment



Models calculated over 500 iterations. 5 fold crossvalidation. 10% testing set.

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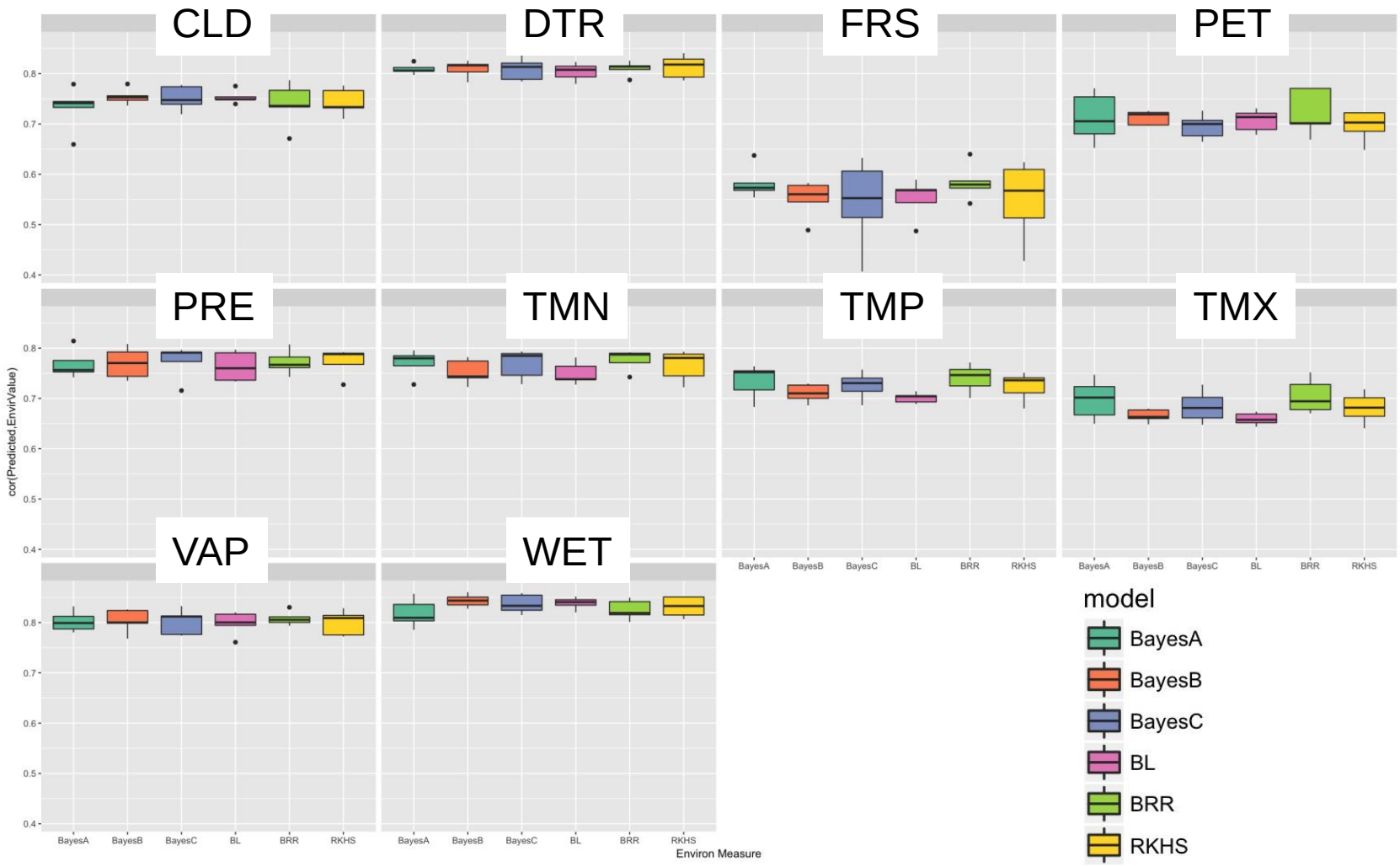
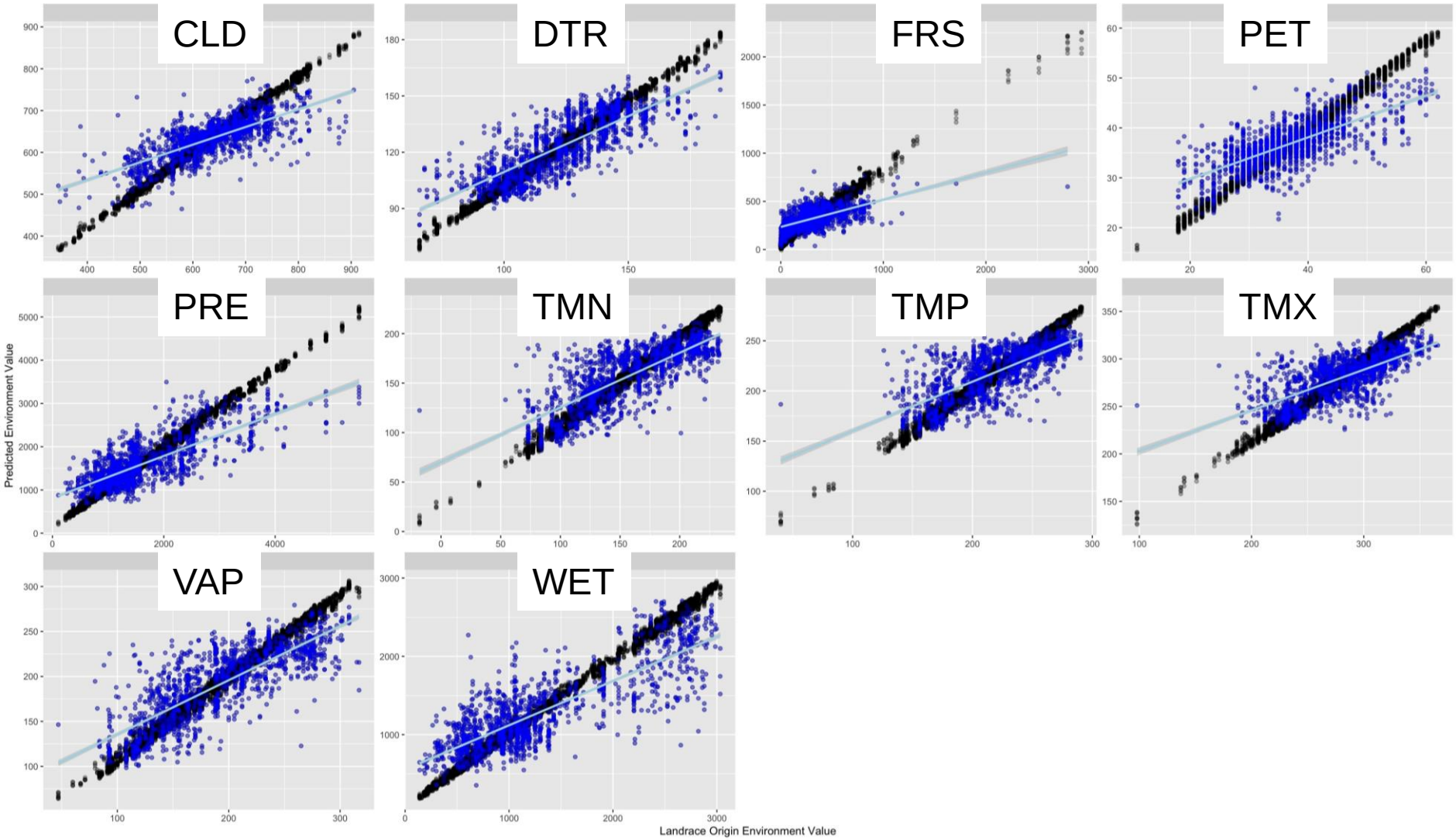
Environmental GS



Environmental GS

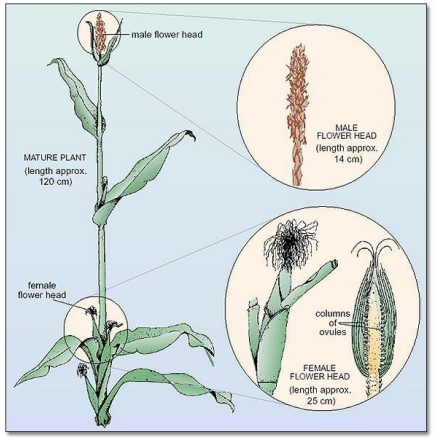


Environmental GS

Predicting Flowering Time from Landrace collection site environment?

Field Trial Phenotype (DTA) = Landrace Origin Climatic Data

$$\mu + X_{precip}B_{temp} + X_{temp}B_{temp} + \ldots + X_{env}B_{env} + error$$



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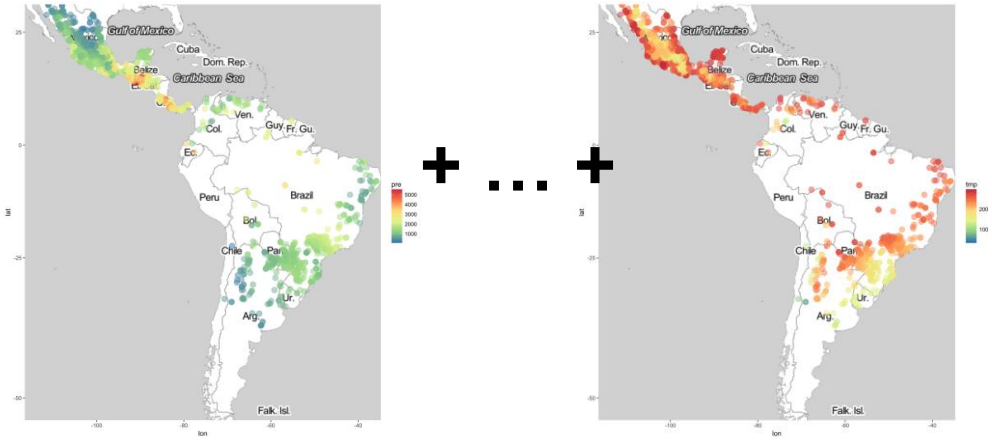

Landrace Origin Climatic Data GBLUP

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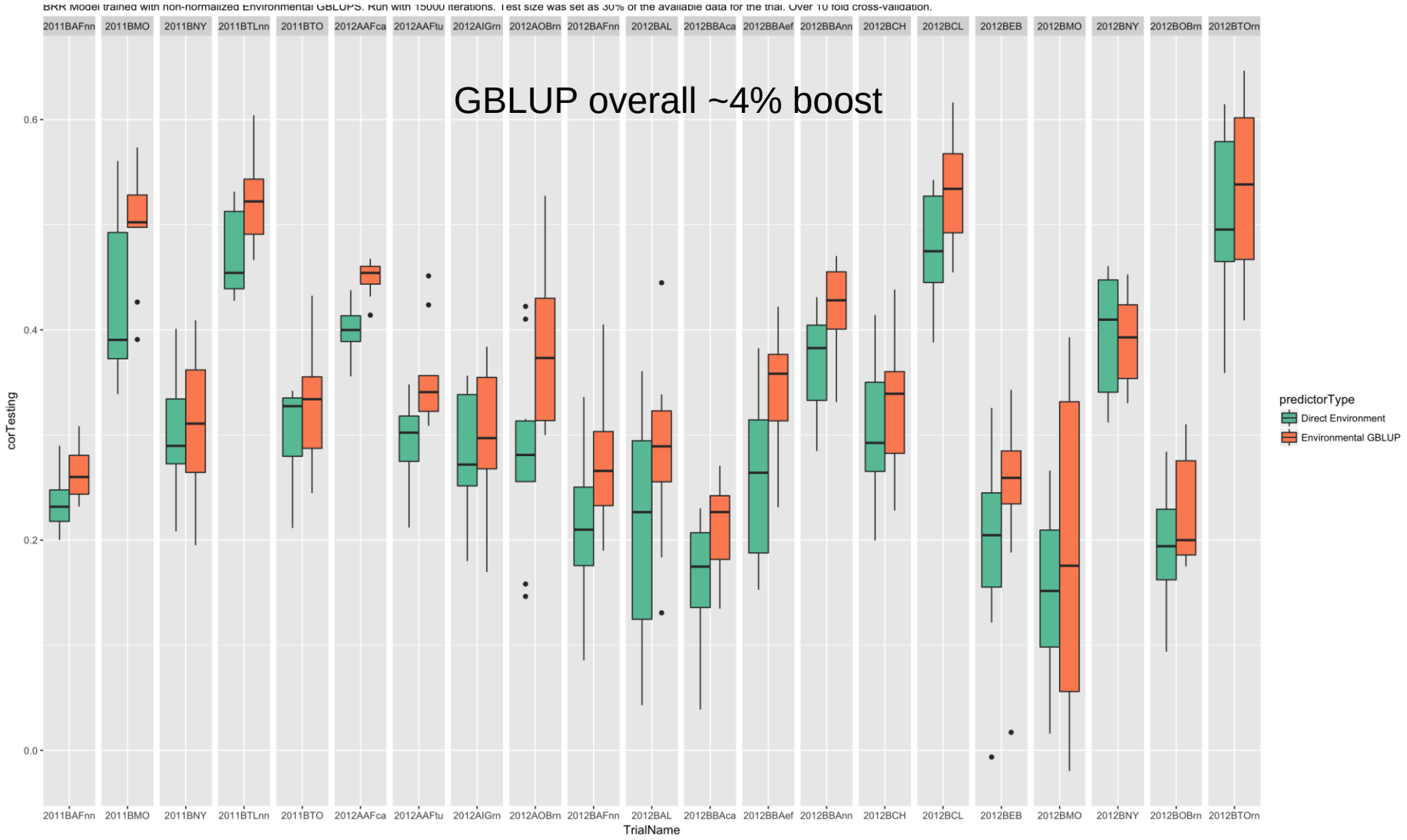
Environmental GS

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



Extend from GWAS panel to MGB

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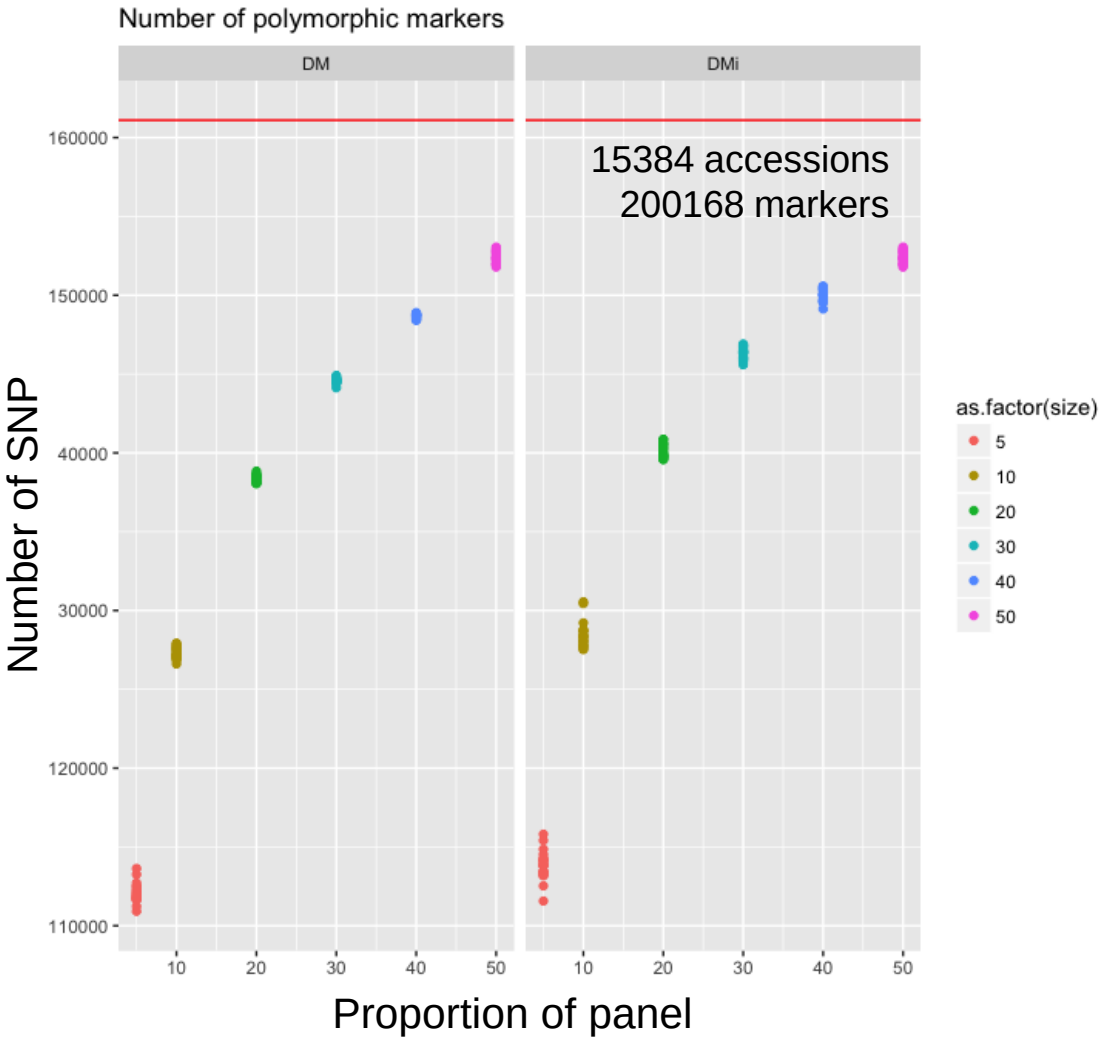
Where now?

Genotypes
24,500 LR
28,500 MGB

Environments
17,500

Phenotypes
?



EnvGS: Best bets – highest potential value (soc-econ links)

EnvGWAS: What is potentially novel

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Thank you to fantastic, colleagues, collaborators and students

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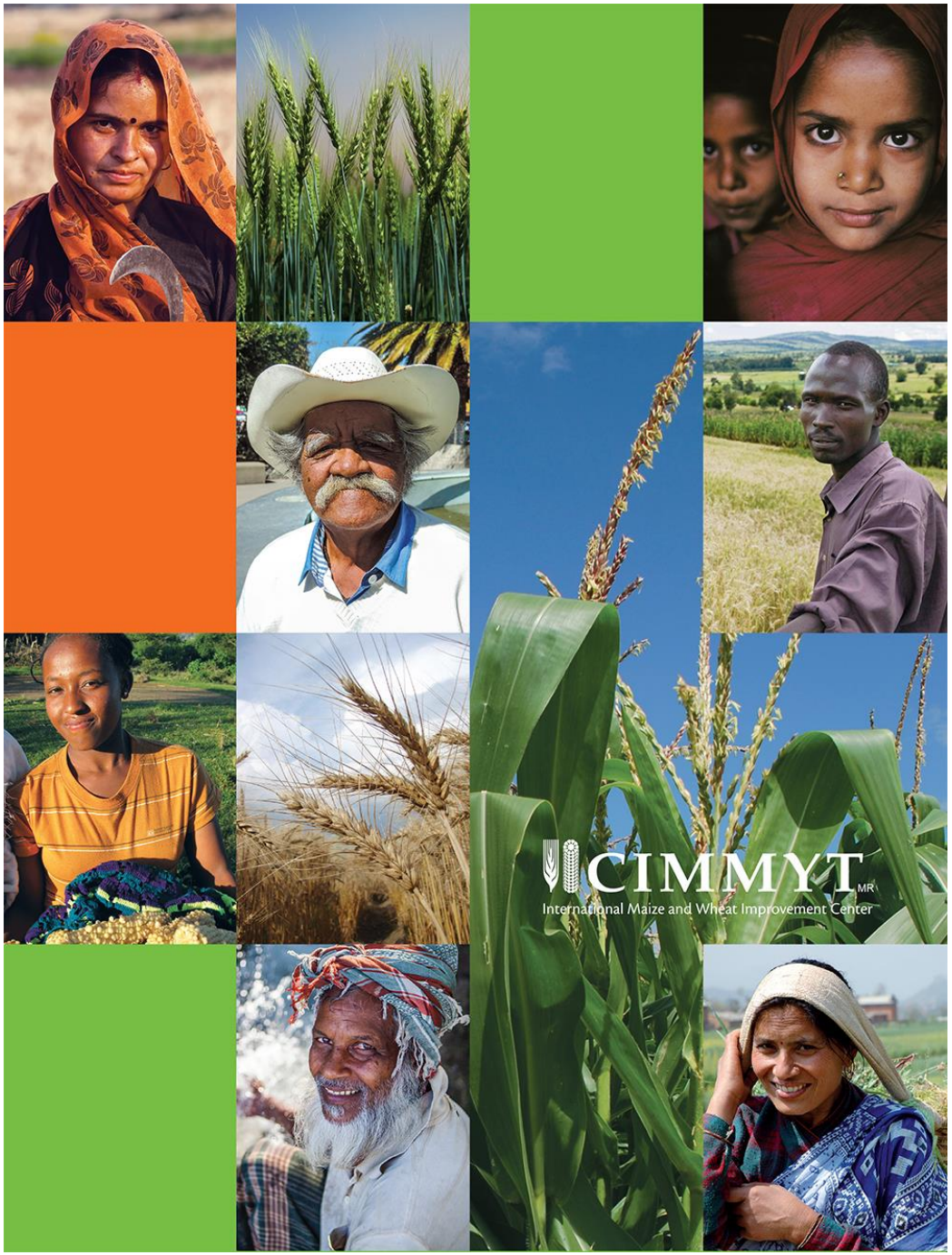

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Thank you for your interest!

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