

Seeds of Discovery (SeeD)- Maize MasAgro-Biodiversidad - Maíz

An initiative to systematically explore and
mobilize novel genetic variation into
maize breeding programs



“Genebanks are not museums”

- Most of the requests to banks with maize germplasm holdings are for described elite lines or landraces / wild relatives with some publication history



- Most breeders would not “touch” an un-described landrace and would have to be “desperate” to use one with very good characterisation

Bridging the divide



Information
Knowledge
Germplasm



Maize strategy

Partners: Mexican genebanks (INIFAP, UAAAN, UdeG, UACH), Langebio, DArT, AMAIZING

Partners: Cornell Univ., INIFAP, UAAAN, UdeG

Molecular Atlas

Small and large effect alleles

GWAS of 4500 testcrosses

Information

**Breeding programs
(line and landrace improvement)**

Per-se
evaluation

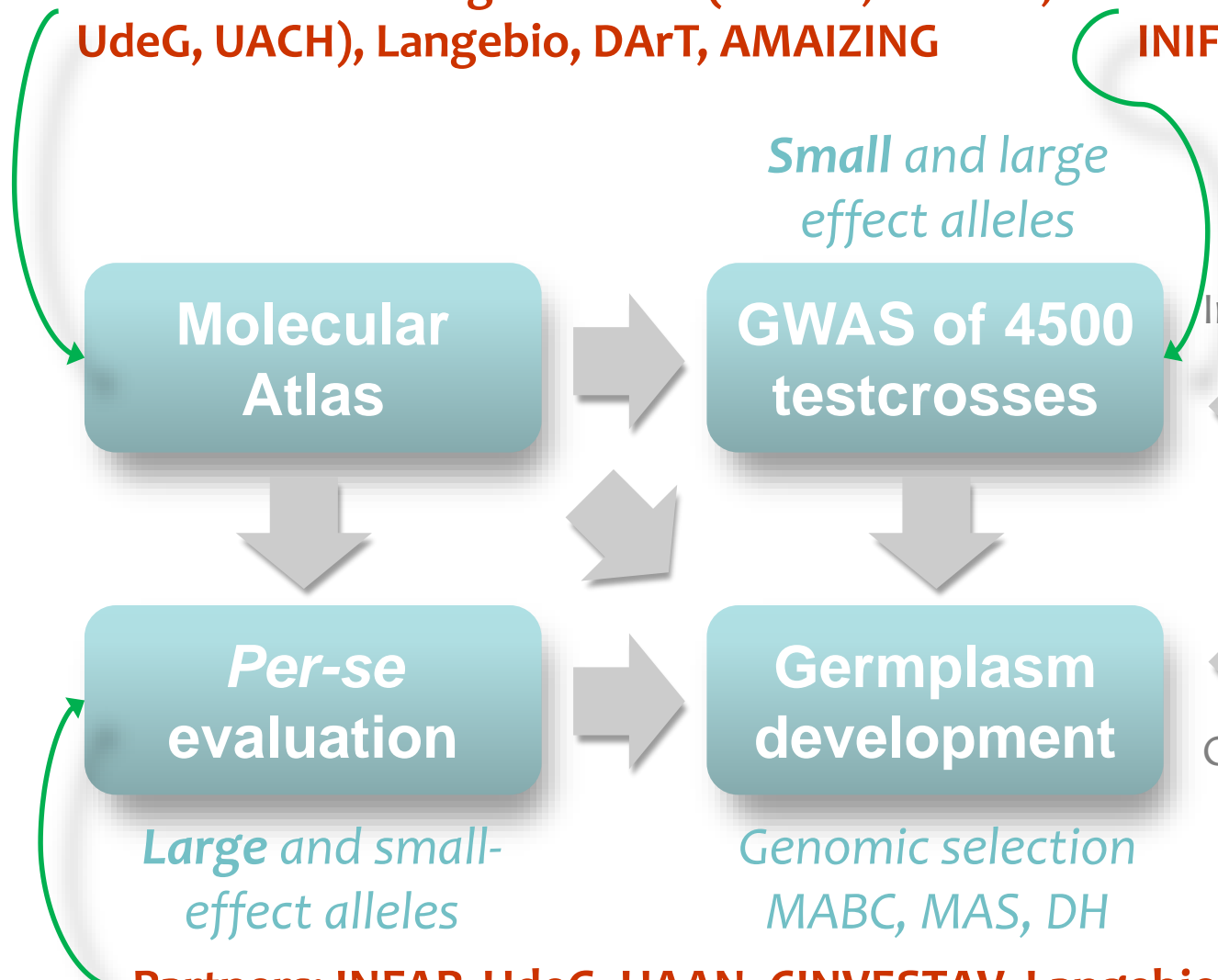
Germplasm development

Germplasm

Large and small-effect alleles

*Genomic selection
MABC, MAS, DH*

Partners: INFAP, UdeG, UAAN, CINVESTAV, Langebio



What is GWAS

- Genome wide association studies (also called whole genome association studies) describe the evaluation of regions of the genome common across unrelated individuals to see if these shared variants in the genome are associated with common traits such as response to diseases
- This kind of study has been successfully used in human studies for close to a decade; by 2009 there were more than 1200 studies identifying an excess of 4000 associations of SNP with over 200 human diseases and conditions

Benefits of GWAS

- For the study of human conditions GWAS was a breakthrough – we can not ethically conduct crosses in humans and selfing in mammalian systems is not possible
- GWAS tends to identify variants present in reasonably high frequency in populations under study with the ability to identify variants with small effects relative to other methods of analysis e.g. genetic linkage within families and QTL approaches

GWAS in Maize

- Successfully used for a number of traits – flowering time, plant architecture, disease resistance, grain quality...
- At CIMMYT we have used for drought tolerance, low N tolerance, disease tolerance.
- In all cases these studies populations are based on advanced breeding lines – while diverse these are bottlenecked materials



GWAS in Seed

- Unique as we use landraces as starting material not lines
- 4000 diverse landraces represented in the panel of materials evaluated
- Largest publically funded association mapping panel in maize in the world to date

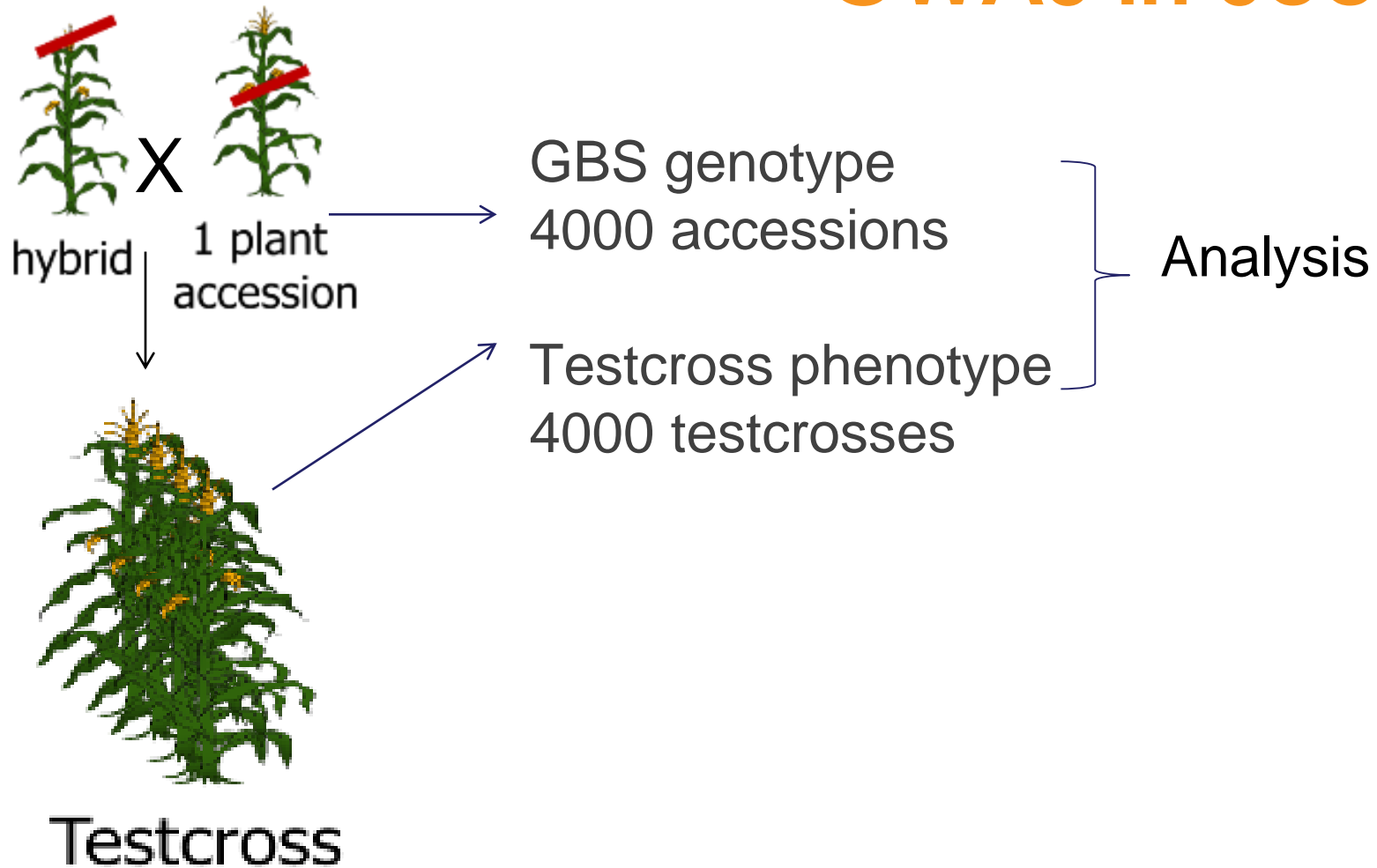


GWAS in Seed

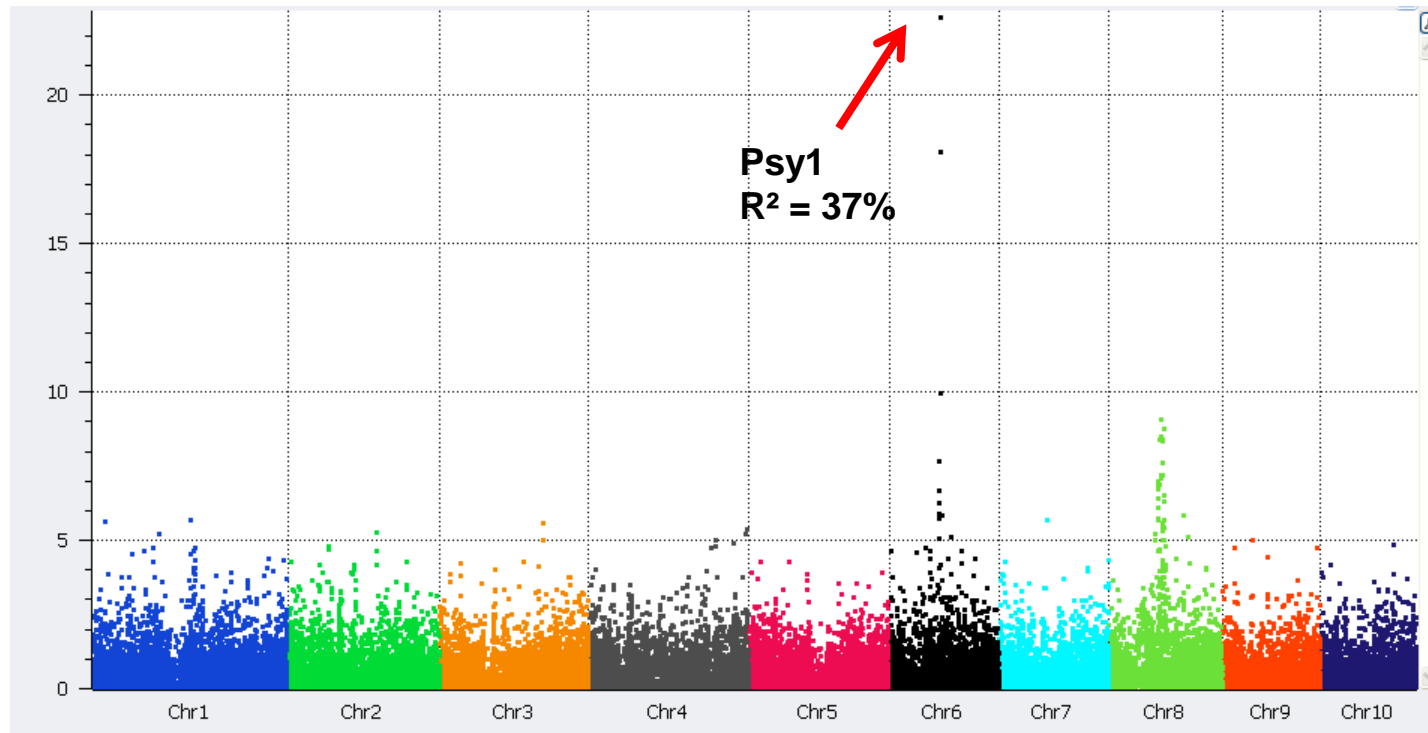
- With Mexican collaborators we have evaluated for multiple traits across many locations, adaptations and environments



GWAS in SeedD



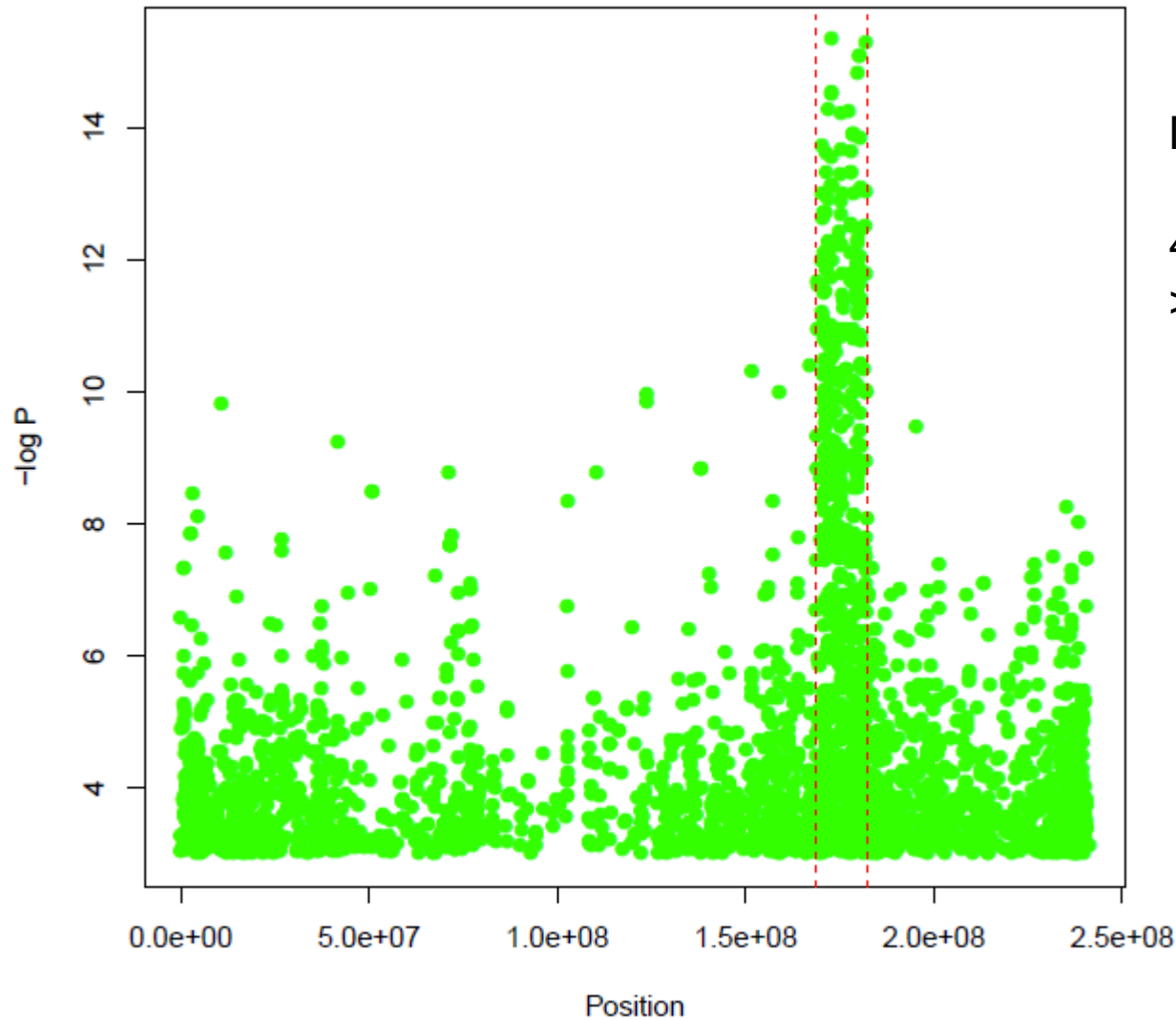
GWAS in SeeD



DTMA panel, grain colour, 55k markers and 178 lines. SNP with largest significant association with grain color located within one of the exons of Phytoene Synthase1 (psy1) on chr.6

Babu Raman

GWAS in Seed



Male flowering Chr 4

4000 individuals
>1M markers

GWAS in Seed

- With international and Mexican collaborators we are currently conducting GWAS analysis on
 - ▶ Flowering
 - ▶ Drought
 - ▶ Low N
 - ▶ Tar spot
 - ▶ Fusarium ear and stalk rots
 - ▶ Grain quality traits
 - ▶ Lodging



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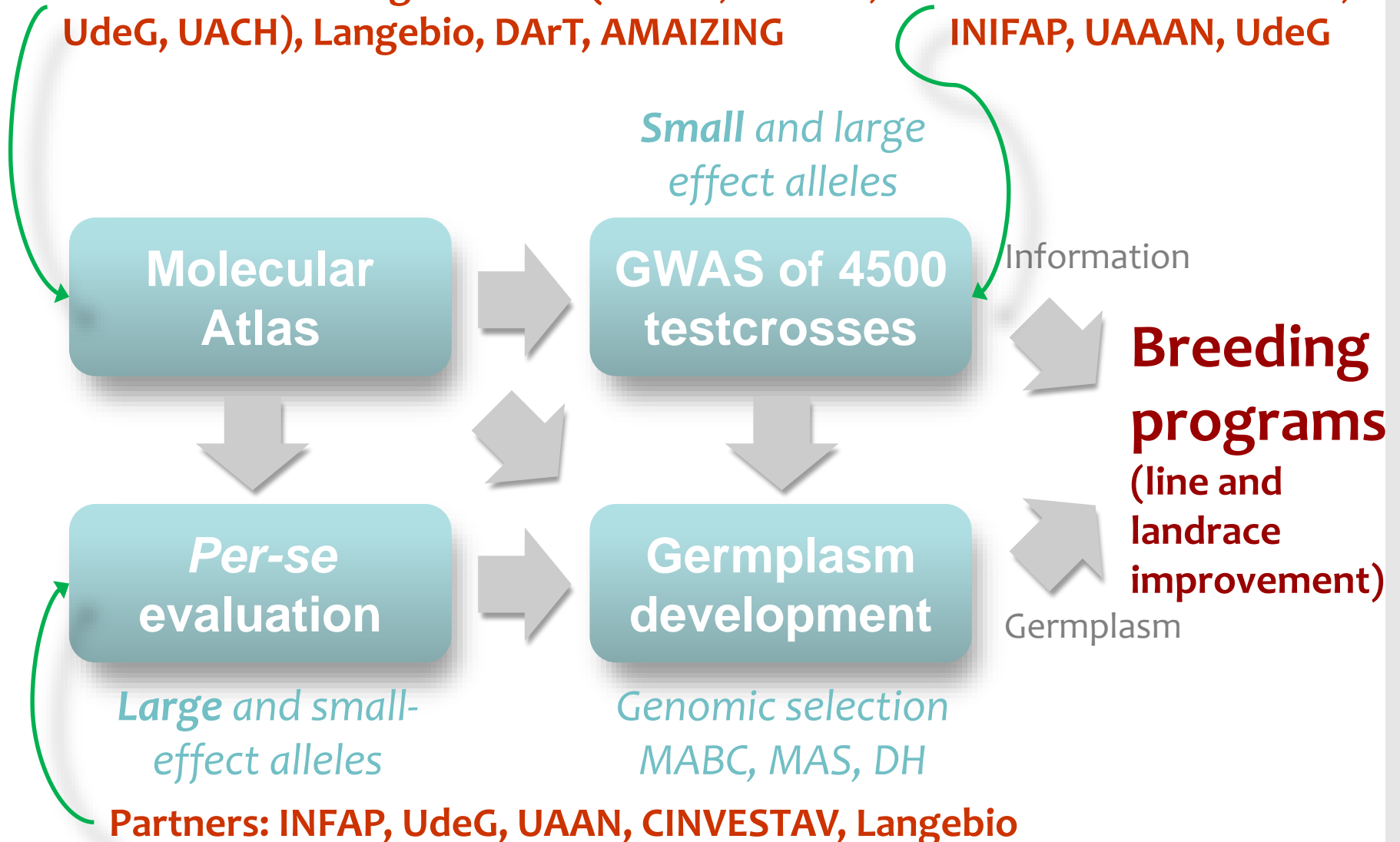
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Thank you

Flowering time:-

Ed Buckler (Cornell): GWAS analysis

Armando Espinosa (INIFAP): maize GWAS field trials

Andrzej Kilian (DArT): DArT GBS for structure

Sharon Mitchel (IGD Cornell): GBS

Ernesto Preciado (INIFAP): maize GWAS field trials

Alberto Romero (Cornell): SeeD PhD student

Arturo Terron (INIFAP); maize GWAS field trials

Humberto Vallejo (INIFAP): maize GWAS field trials

Victor Vidal (INIFAP): maize GWAS field trials

Juan Burgueño: GWAS field trial design and phenotypic data analysis

Huihui Li: imputation

Ivan Ortíz: maize GWAS field trials

Samuel Trachsel: maize GWAS field trials

Martha Willcox: maize phenotyping coordinator, maize GWAS field trials

Sarah Hearne: SeeD-maize lead, GWAS coordinator

Peter Wenzl: project lead