

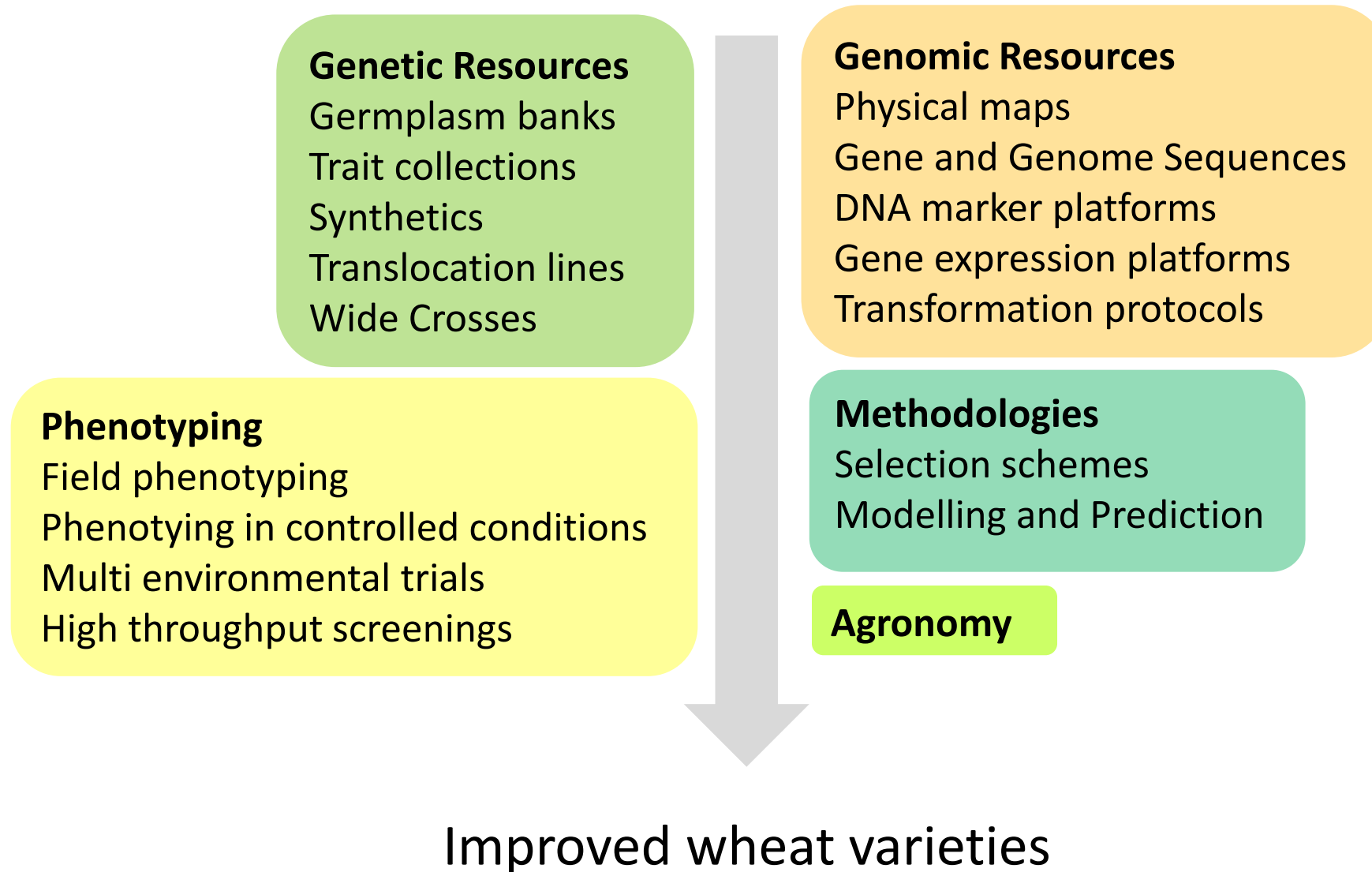


Harnessing Genomics Outputs for Accelerating Genetic Gains: The CIMMYT Global Wheat Program

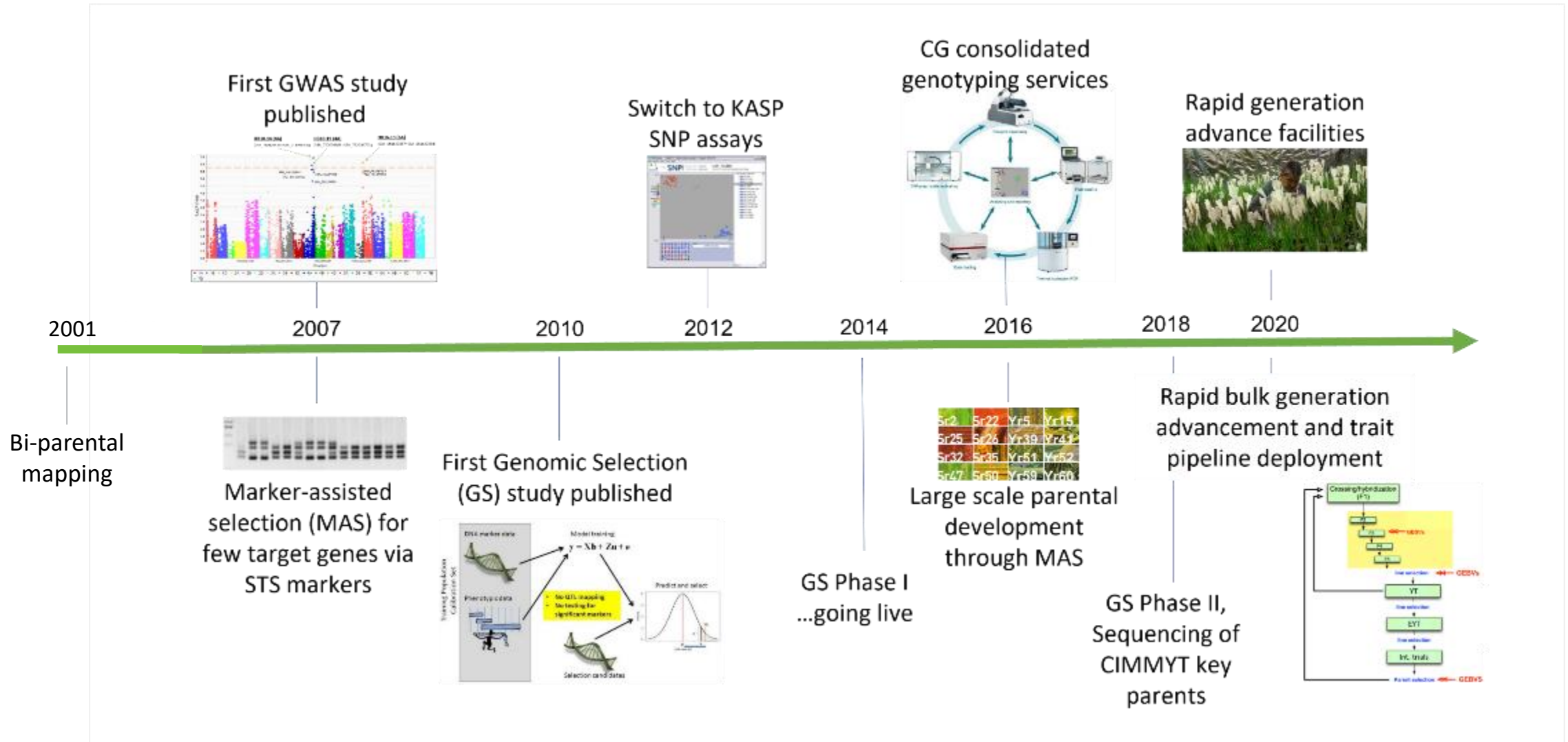
Susanne Dreisigacker, Matthew Reynolds & the CIMMYT Global Wheat Program



Multidiscipline - Wheat Breeding

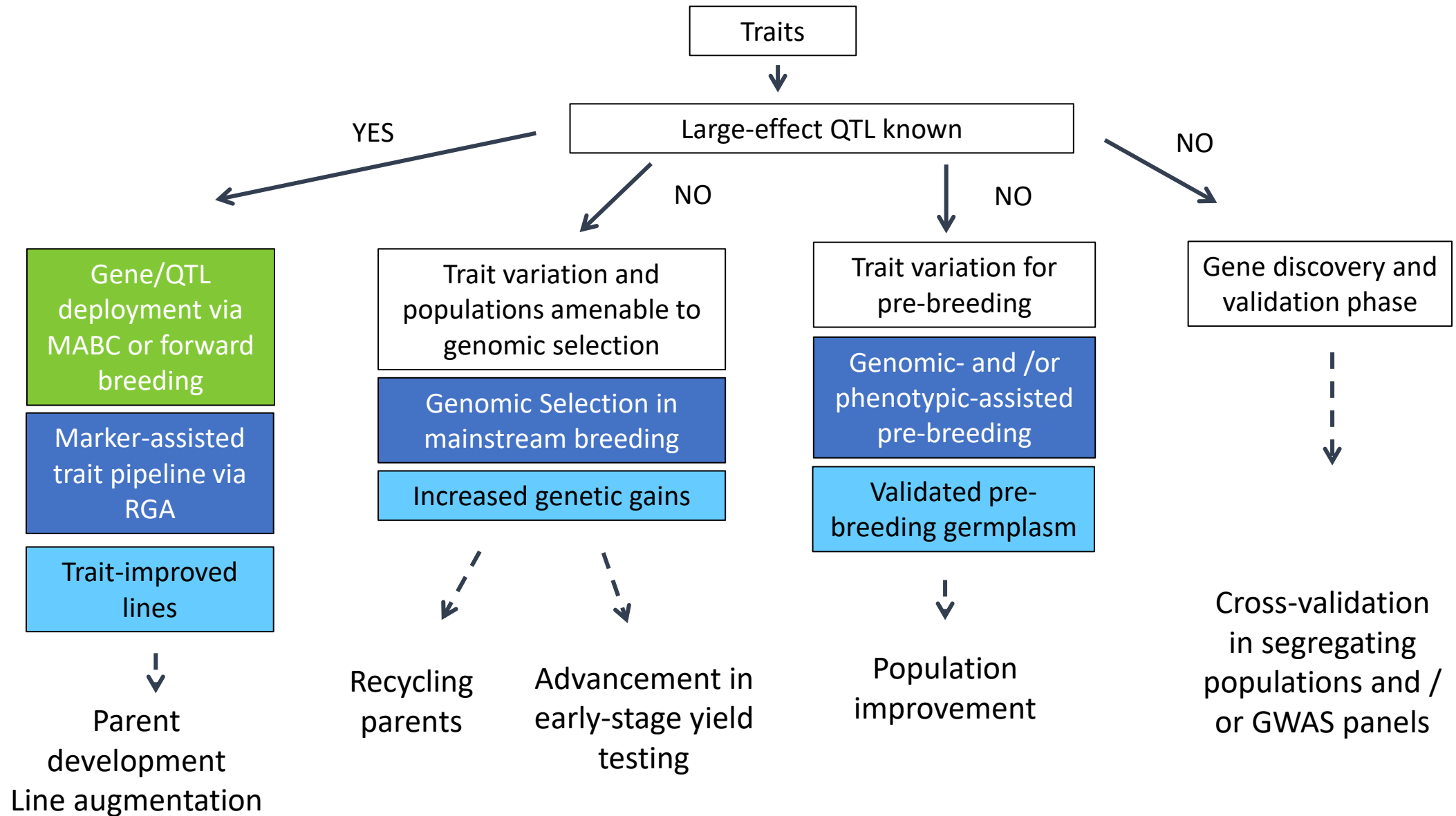


Integration of genomics tools in the CIMMYT GWP



How to funnel genomics outputs into breeding improvements?

Genomics-assisted test designs and deployment strategies



Genomics-assisted trait development pipelines

Germplasm improvement stream (diseases, nutritional traits, physiology)

Hypothesis and objectives

Line augmentation

Variant deployment, product development

Parent development

Marker design variant introgression

Discovery

New donors, new genetic variants

Running parent development pipelines

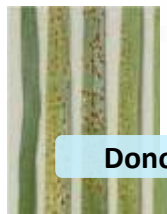
Grain yield

Heat and drought tolerance

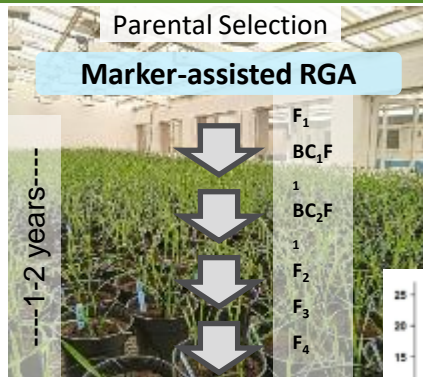
Yield components

 Trait-pipeline Advancement Committee

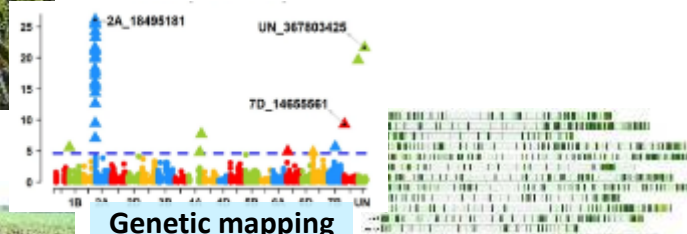
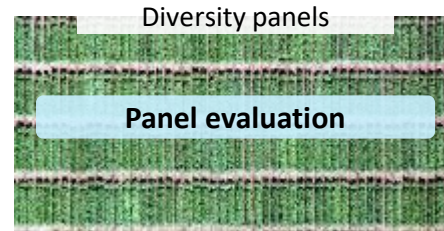
Trait-pipeline activities toolkit



Donor identification



Phenotyping



Genotyping

Running line augmentation pipelines

Stem rust

Yellow rust

Fusarium head blight

Septoria tritici blotch

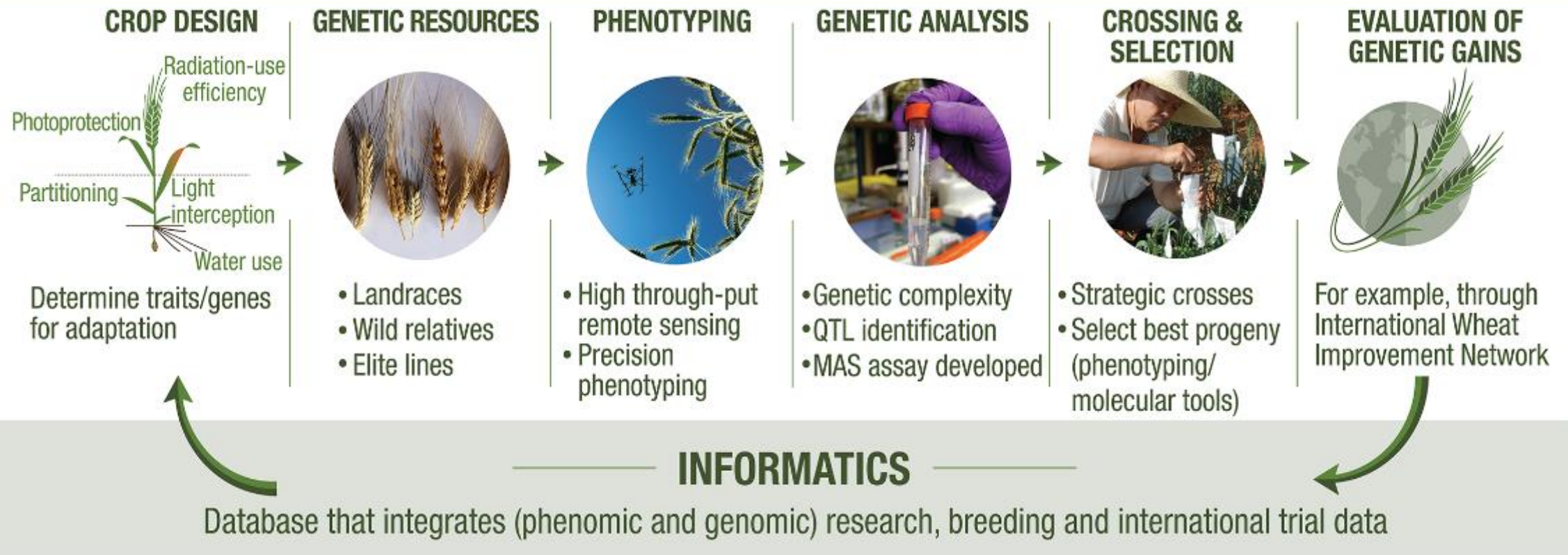
Insect resistance (greenbug)

Grain weight

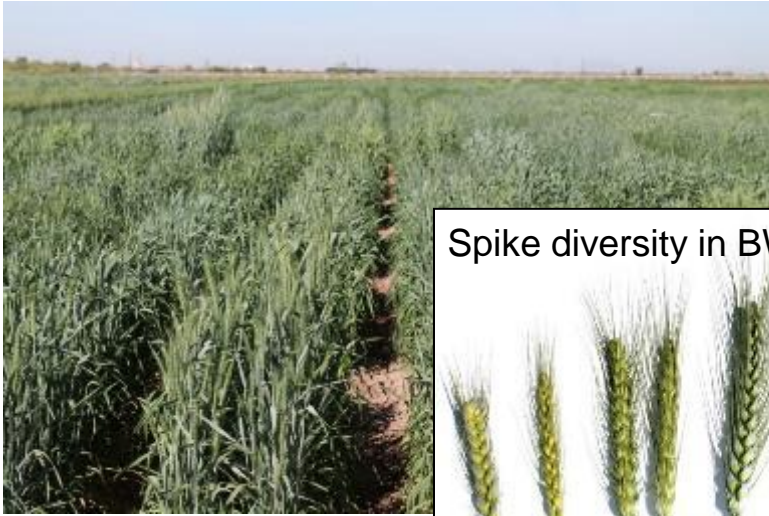
Support Services: New data base structures, genotyping, decision support tools

Translational research & pre-breeding for complex traits

PHYSIOLOGICAL PRE-BREEDING PIPELINE



Evaluation of new sources for stress tolerance or yield potential



Bread wheat diversity panel (370)

Includes best performing lines from:

- International nurseries
- Derivatives from landraces/FIGS panels
- Lines derived from inter-specific hybridization

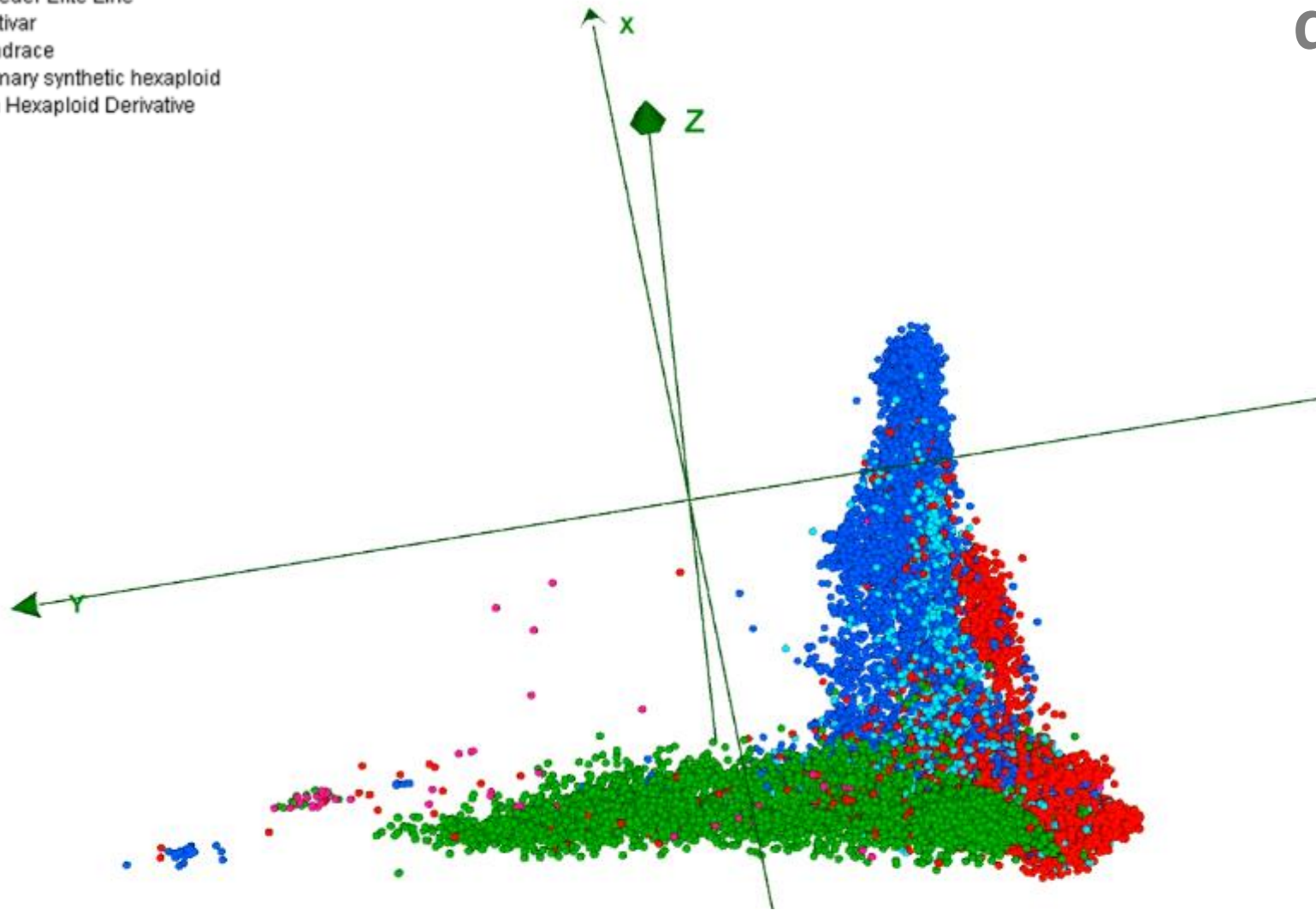


Elite primary synthetic panel (160)

Selected from 2,000 lines (i.e. with brand new hexaploid genomes) for adaptation to heat, drought and favorable conditions

DNA fingerprinting for diversity subsets

- Breeder Elite Line
- Cultivar
- Landrace
- Primary synthetic hexaploid
- Syn Hexaploid Derivative



Hexaploid diversity

60,000 accessions,

8 domesticated species:

T. aestivum subs. *aestivum*,
T. aestivum subs. *spelta*,
T. aestivum subs. *compactum*,
T. aestivum subs. *sphaerococcum*,
T. aestivum subs. *macha*,
Triticum hybrid,
x Aegilotriticum
x Triticosecale

ABD genomes,

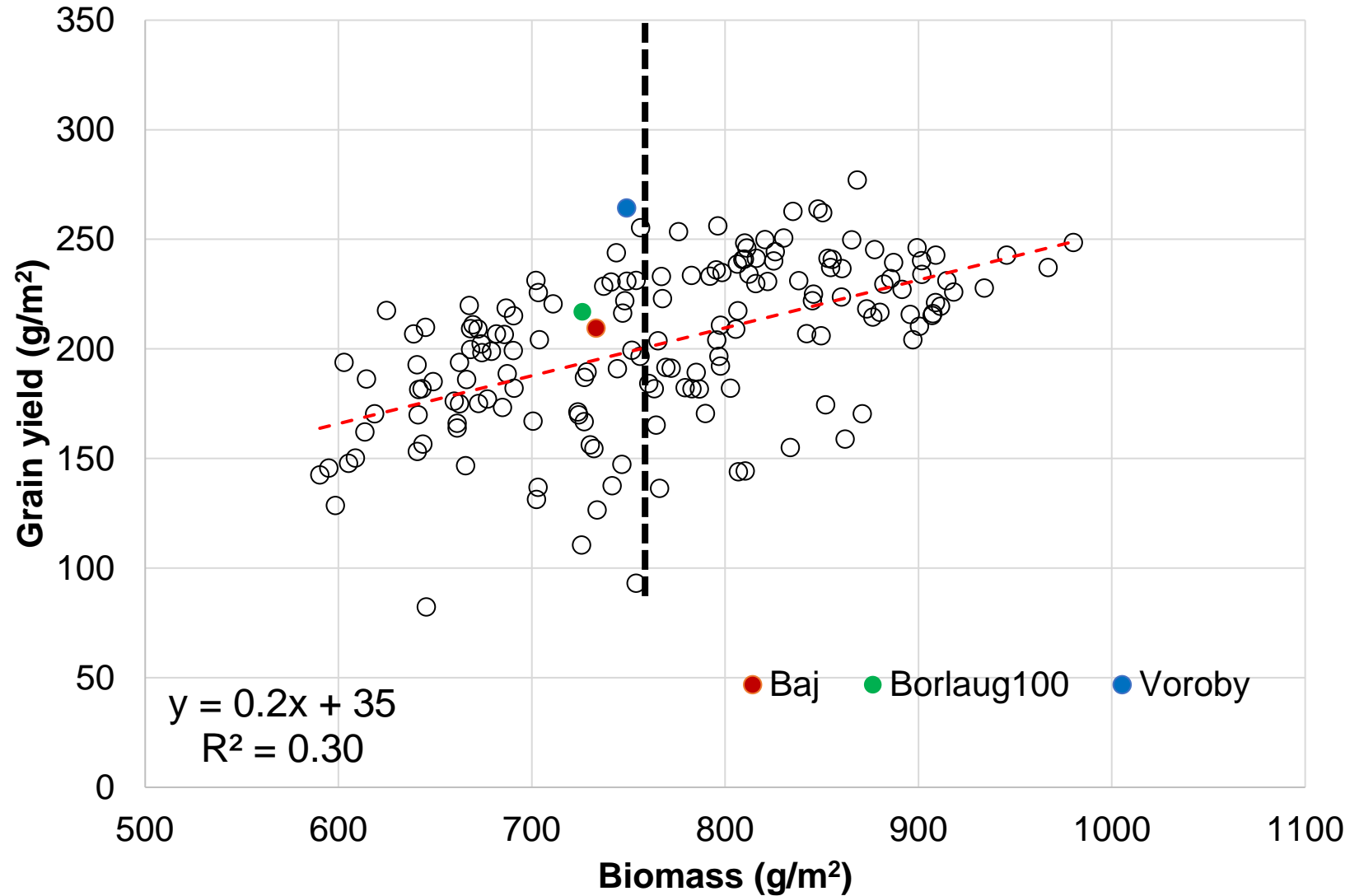
105 countries

26,500 SilicoDArT

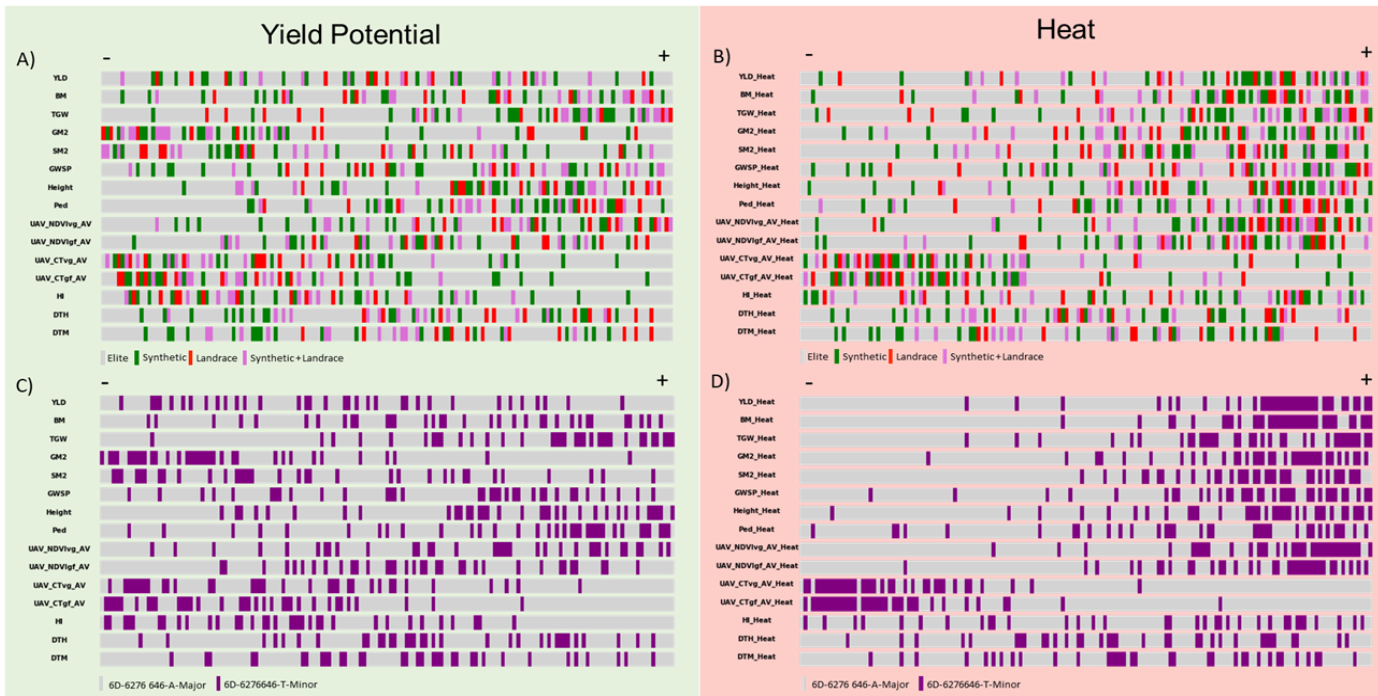
85,500 SNP's

Modified Roger distance of 60,000 hexaploid accessions displayed in a multidimensional scaling plot.

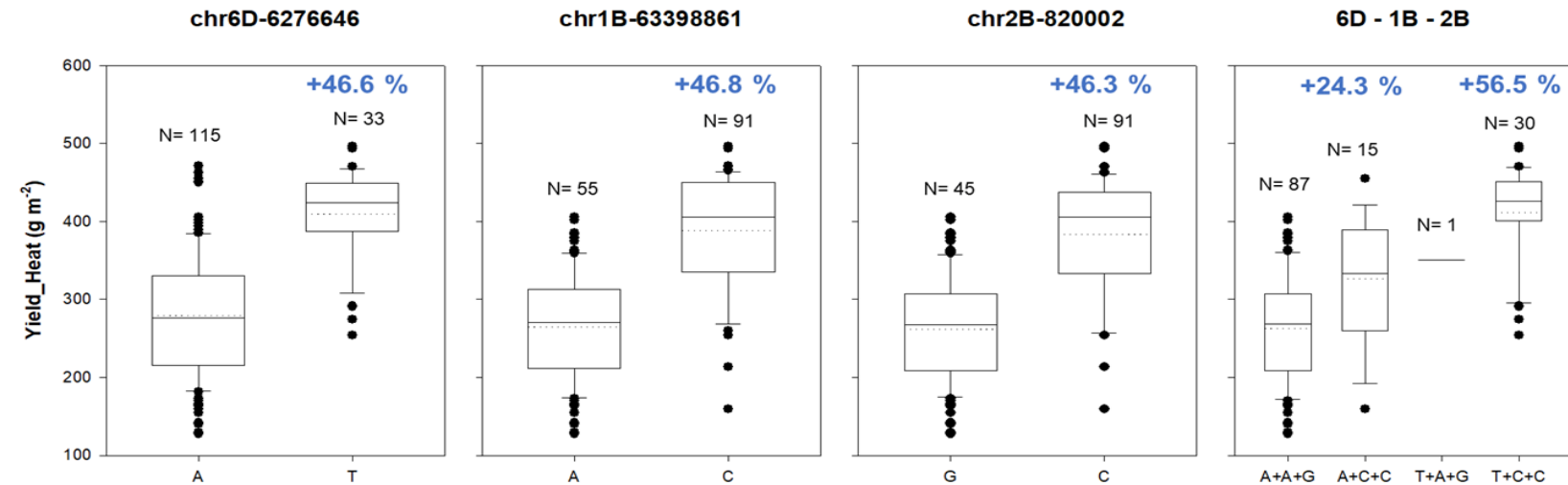
Genetic variation in synthetic hexaploid wheat (heat stress) NW Mexico, 2016 & 2017



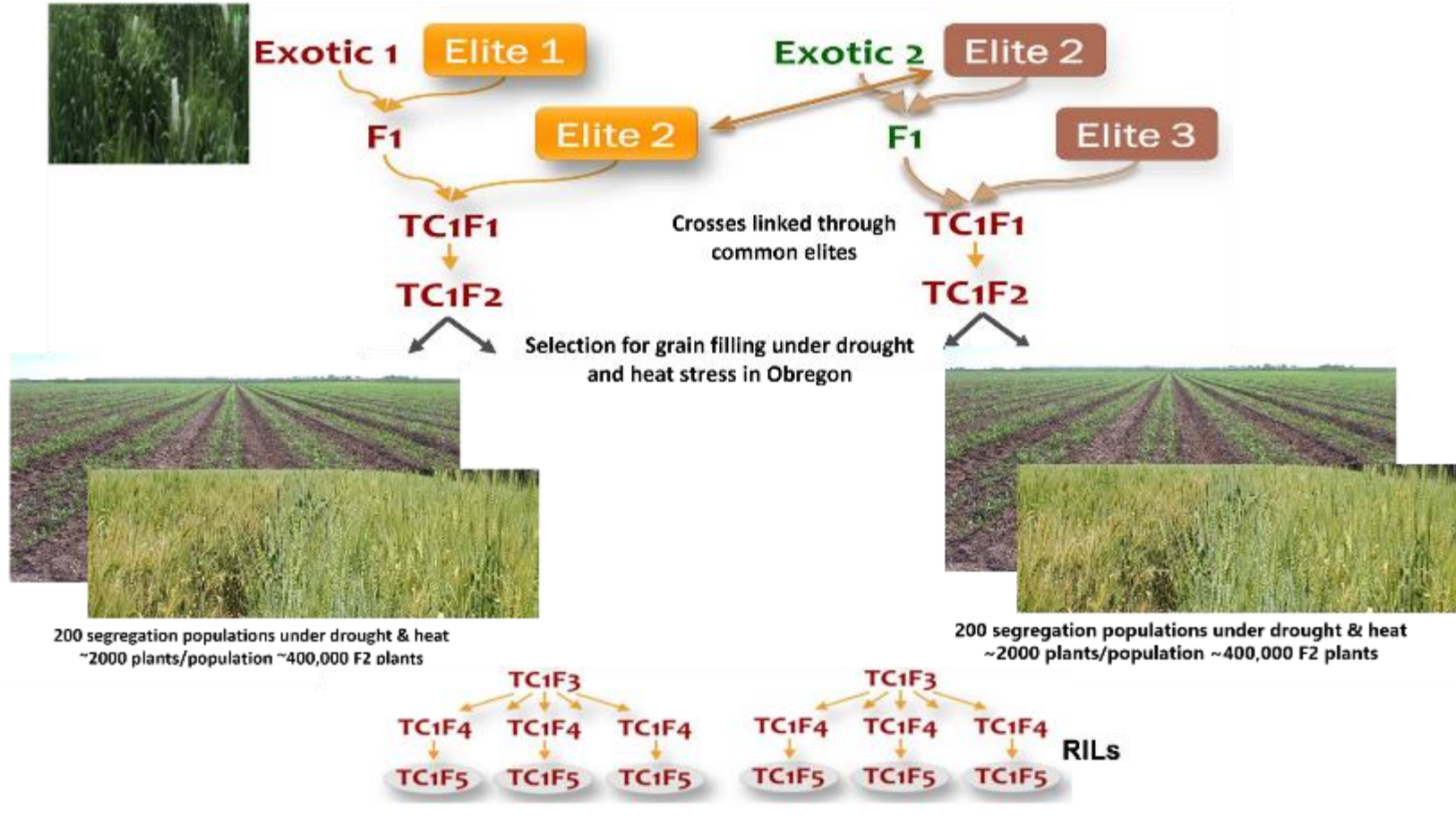
Identification of genomic regions derived from novel sources



- Selected genetic resources (Synthetic hexaploid wheat and landrace) performed better under heat in the High Biomass Association Panel (HIBAP, 150 entires)
- Exome capture sequencing identified three QTL with large effect for heat tolerance, likely derived form genetic resources

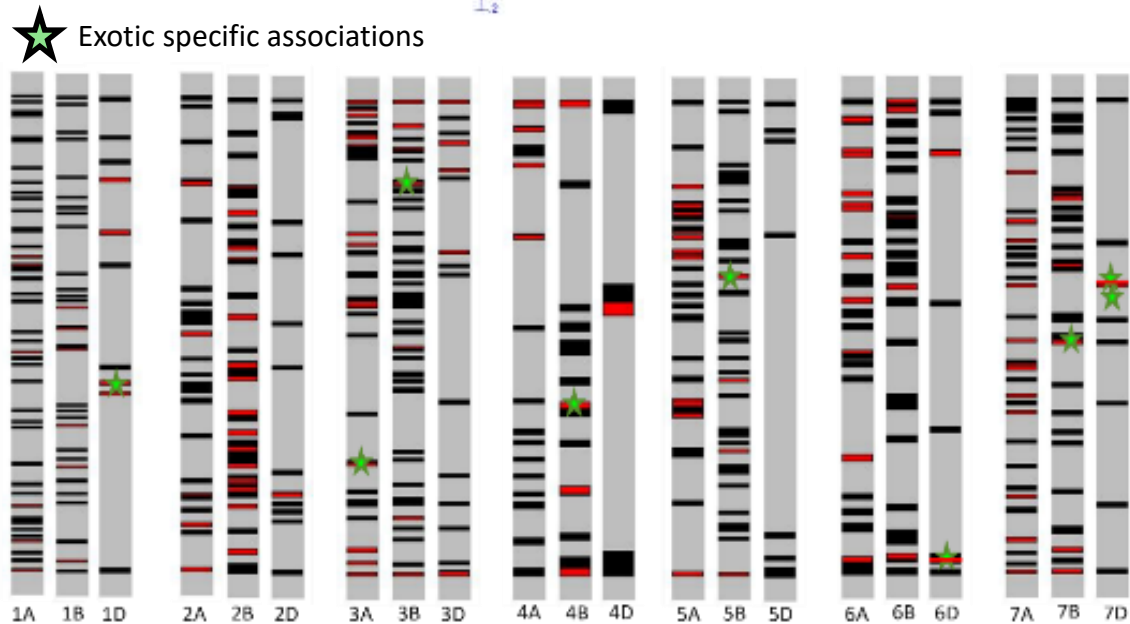
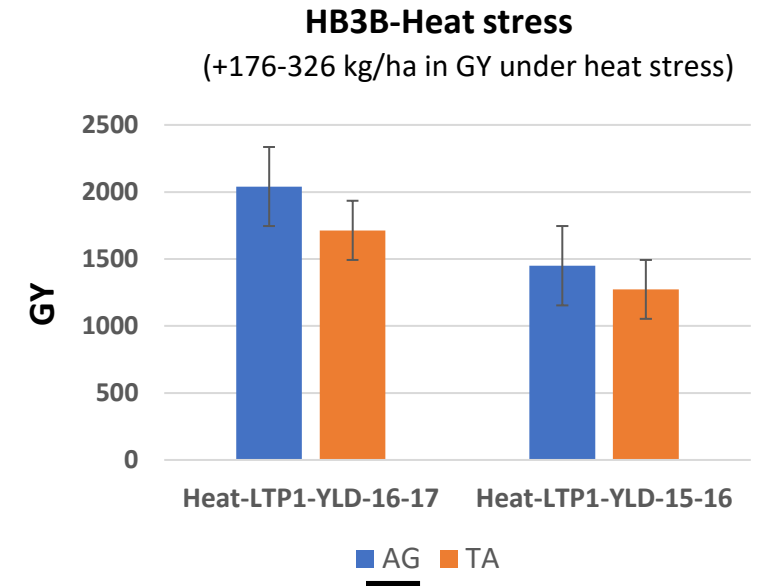
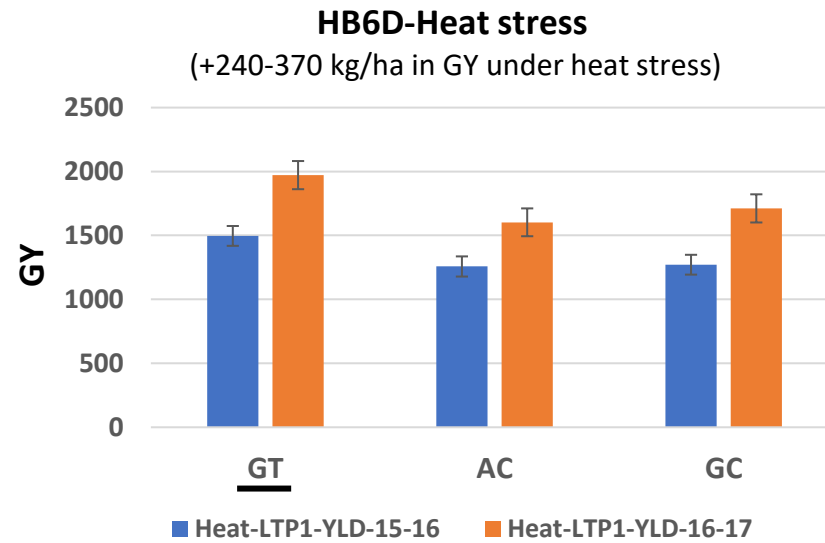
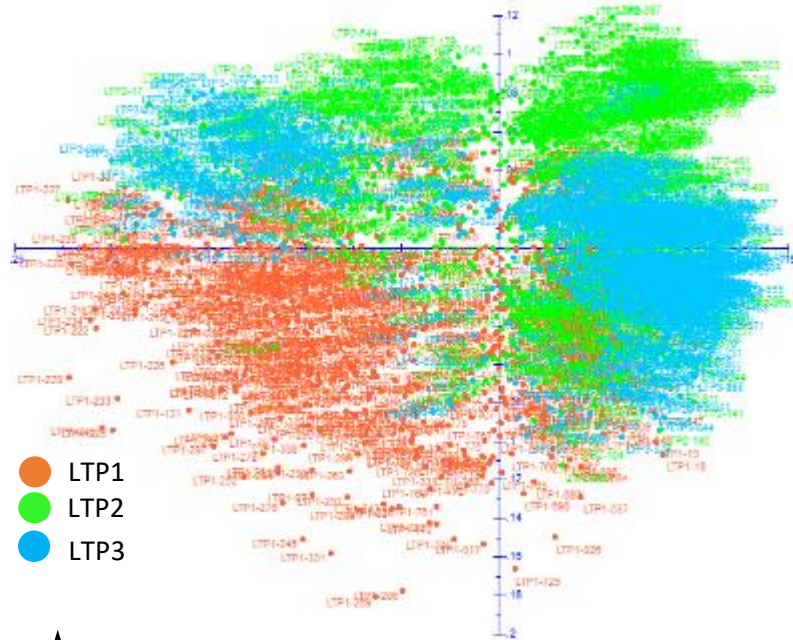


Identification of genomic regions derived from novel sources



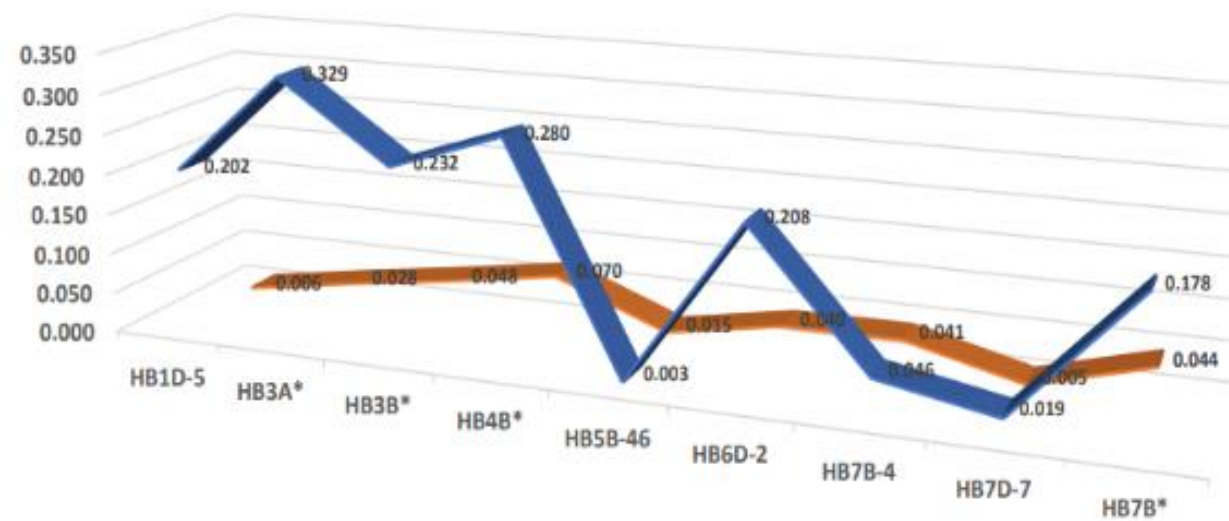
- Three-way crossing scheme of linked top-cross populations (LTP) in the Seed of Discovery project
- Exotic parents include synthetic hexaploidy and landraces selected via FIGS
- Elite parent include lines from the spring BW breeding program

Quantification of the contribution of the exotic parents in LTPs

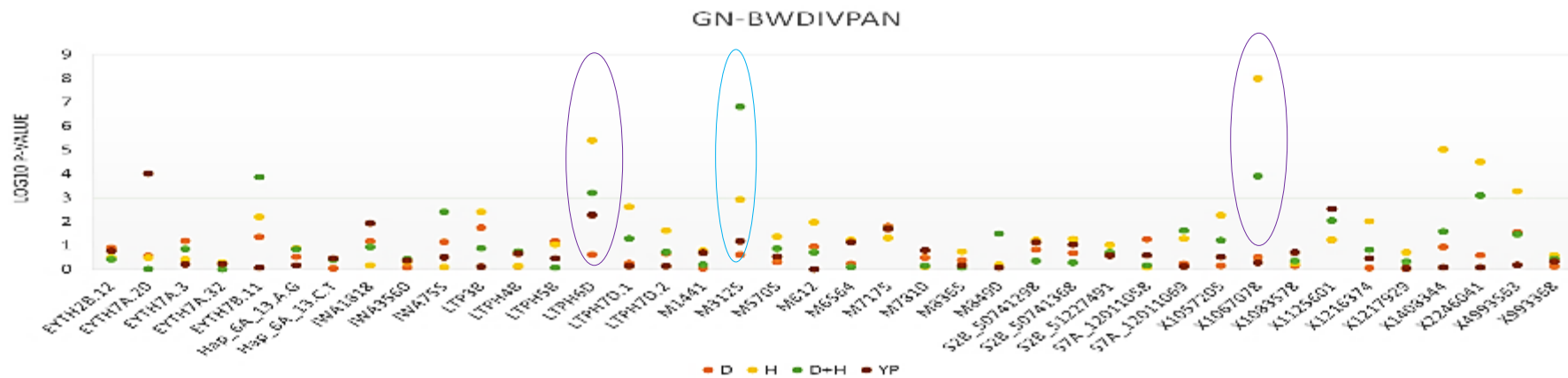
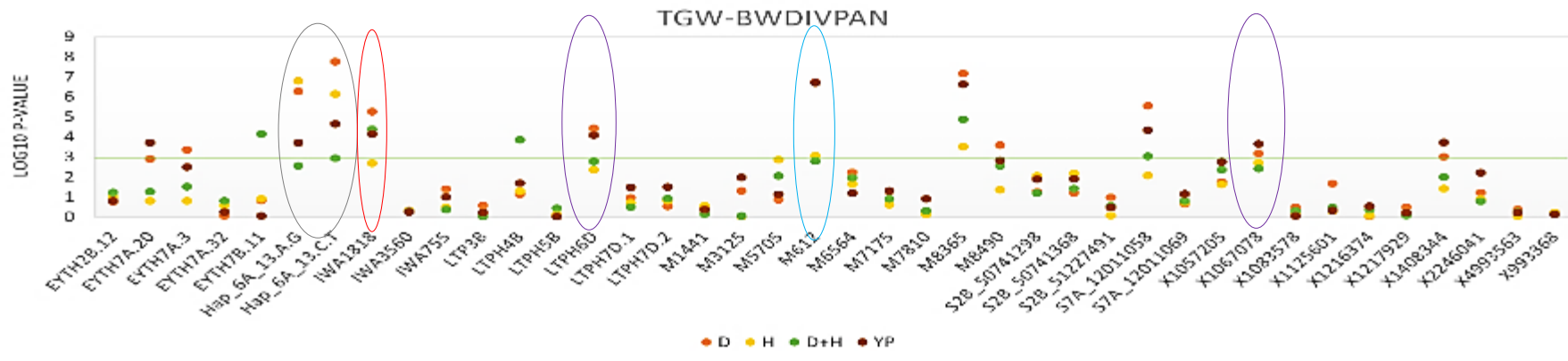
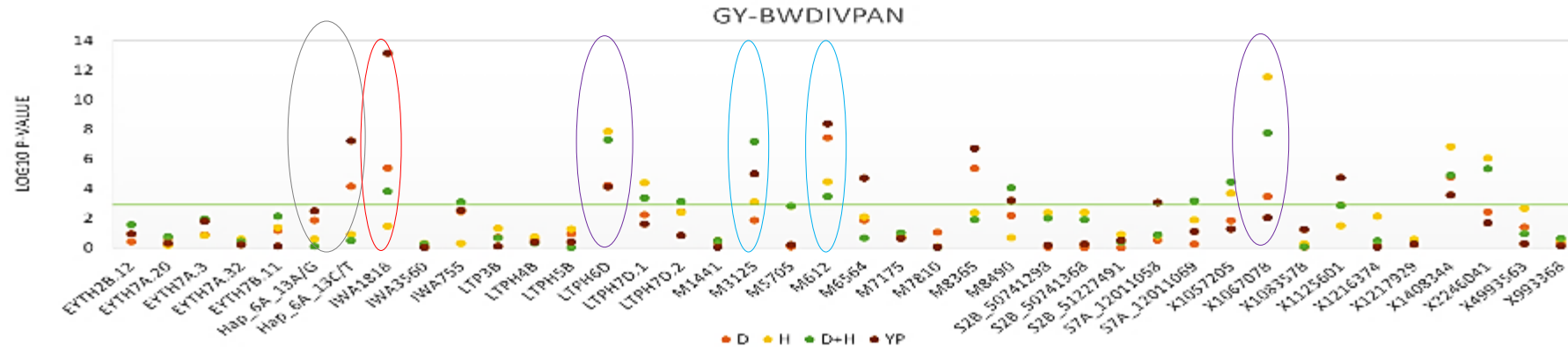


Introgressed genomic regions from exotics are shown as red bars

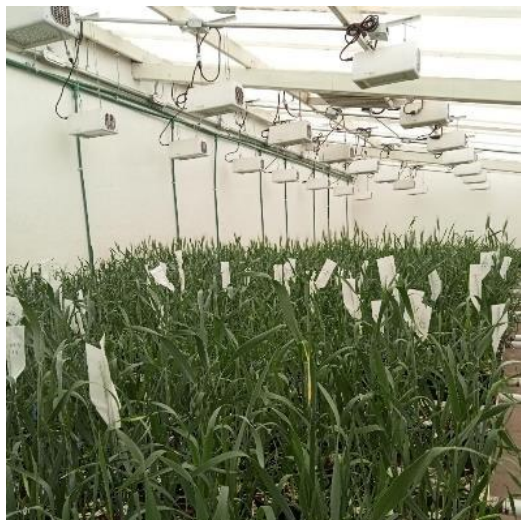
Haplotype frequencies in ■ exotic parents and ■ 16K genebank accessions



QTL validation across germplasm panels (e.g., BWDIVPAN)



Cycles of rapid generation advance in screen- and greenhouses

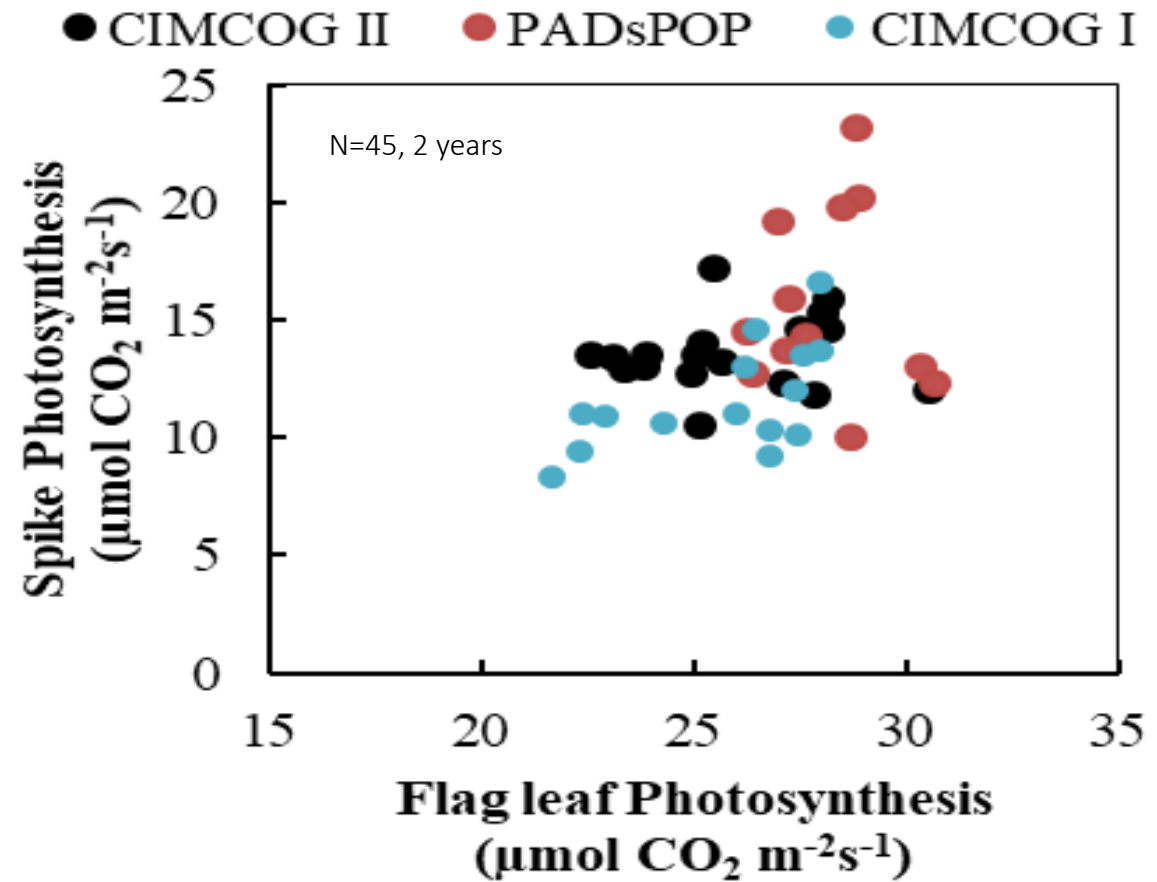
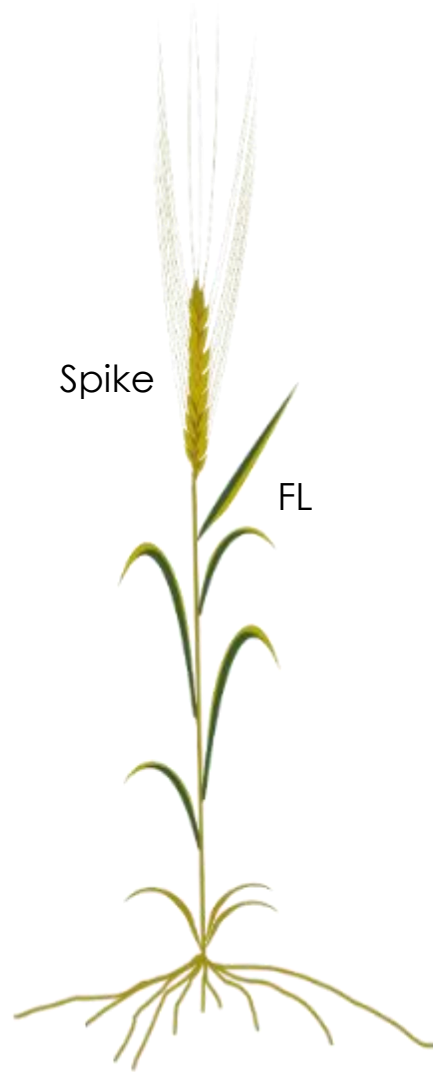


Rapid generation advance facilities in Toluca led by Suchismita Mondal

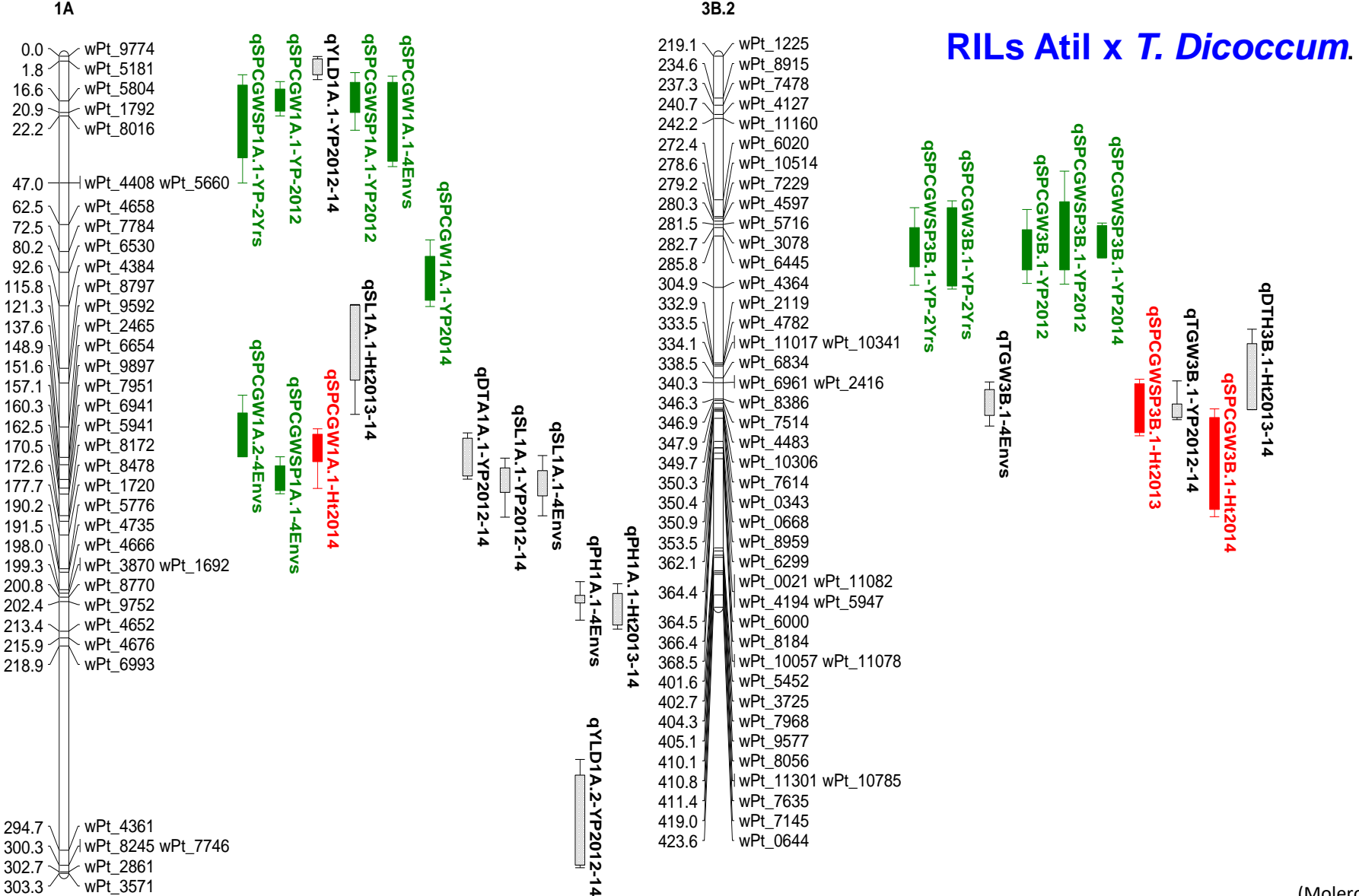
Summary catalogue for the identification of MetaQTL



New traits - Spike photosynthesis, not linked to leaf photosynthesis

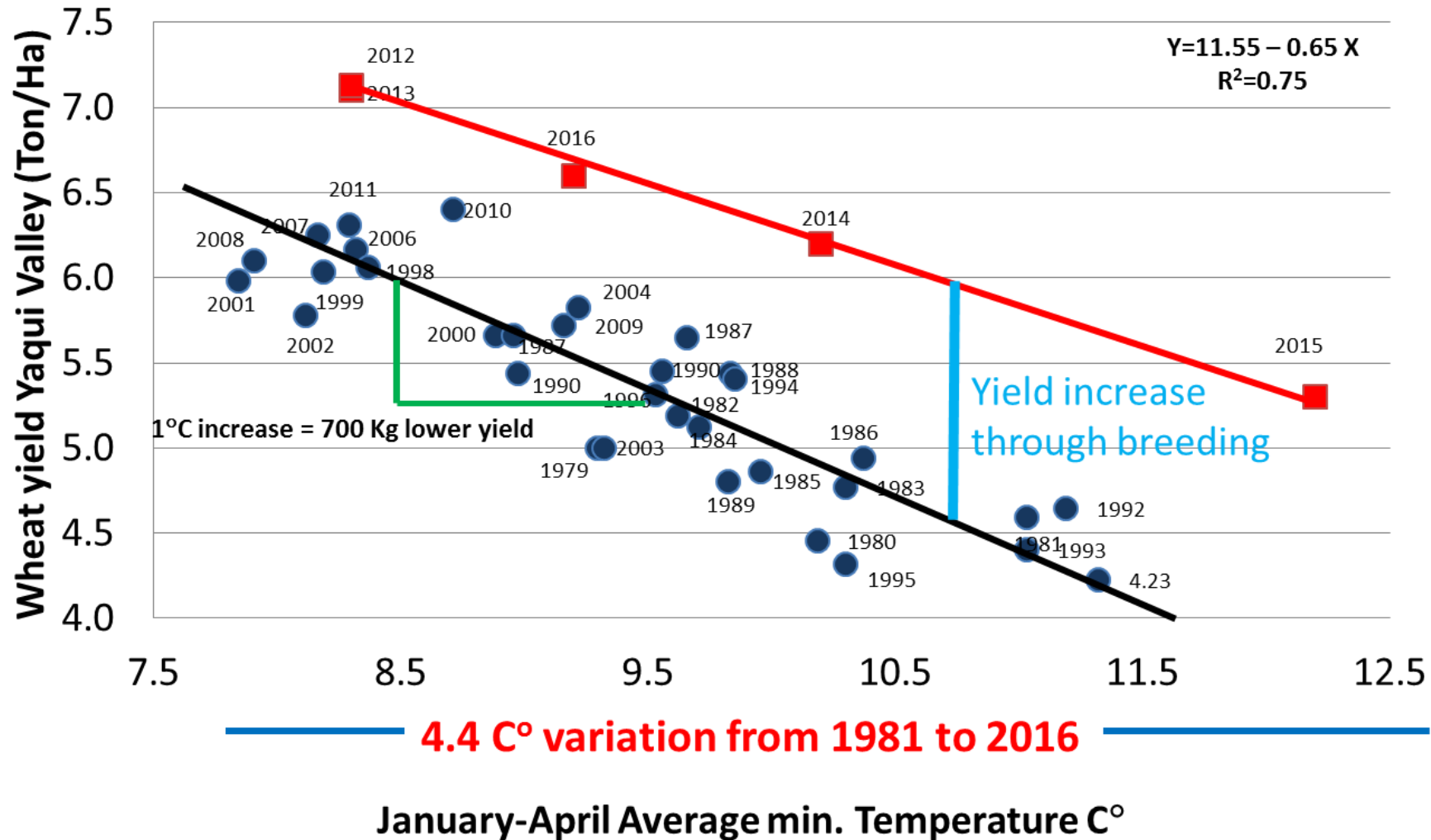


Identifying QTL for spike photosynthesis contribution under yield potential and heat stress



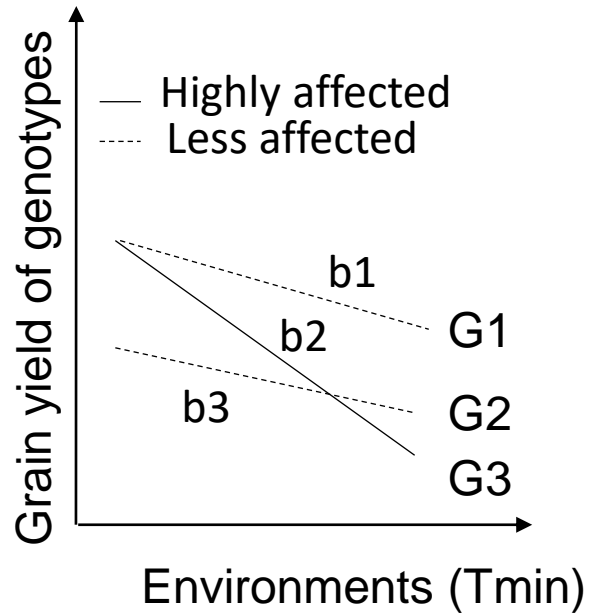
(Molero, Sukumaran, Reynolds, 2015)

New traits - Effect of night temperature



Effect of night temperature

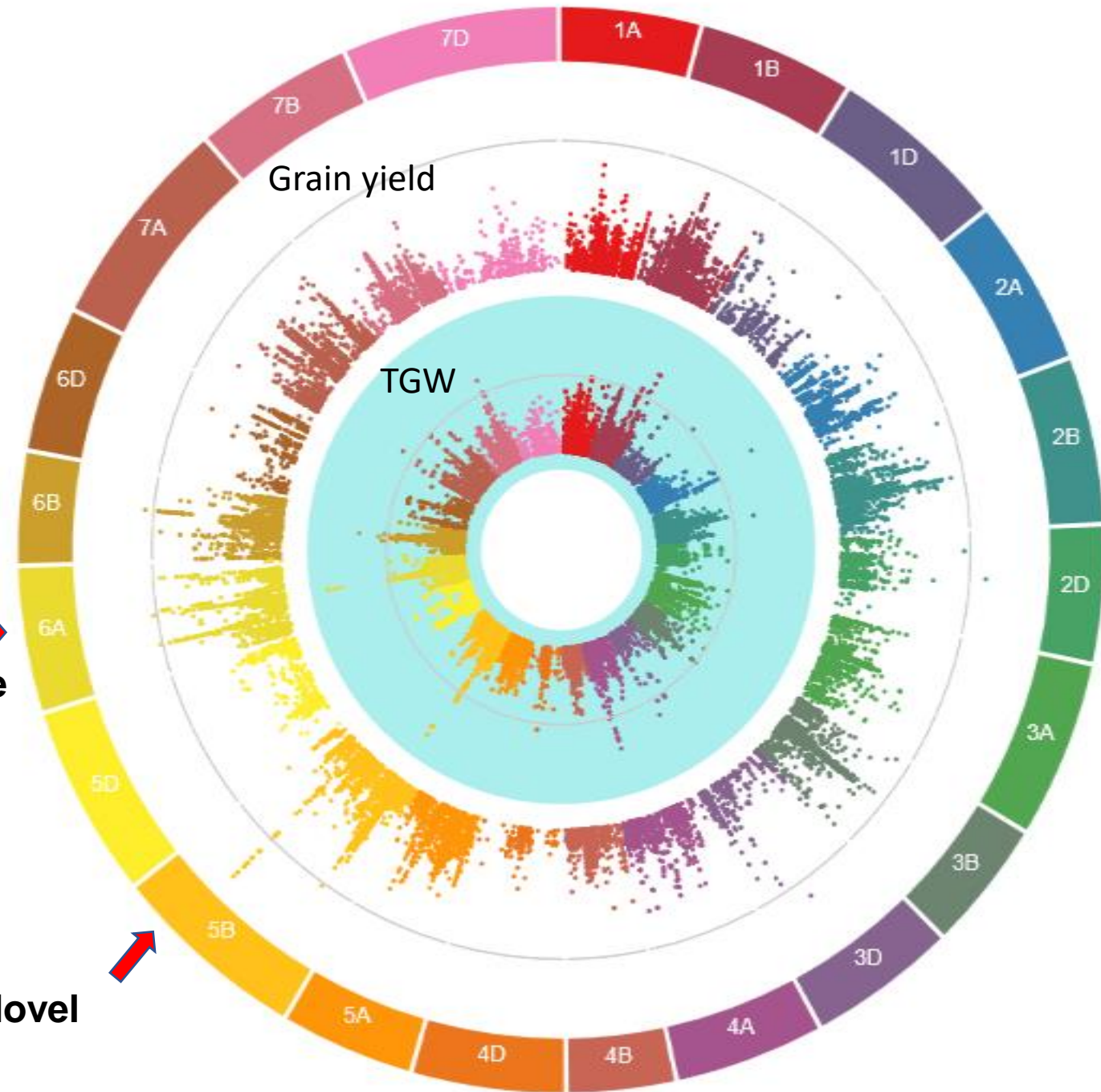
Slope of reaction of genotypes to Tmin



TaGW2 gene is involved in trait variation, response to nighttime temperature, and phenotypic plasticity

Novel →
TaGW2 gene →

Novel →



In summary

- ✓ Genomics technologies are increasingly used also in public sector wheat breeding
- ✓ The development and implementation of well-defined, effective deployment strategies for the many genomics outputs depending on trait complexity is becoming a significant component in breeding
- ✓ Validation of genomics outputs is time consuming and costly, often underestimated and insufficiently funded
- ✓ Evaluation of diverse germplasm remains key for future progress and genetic gain



Acknowledgements

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