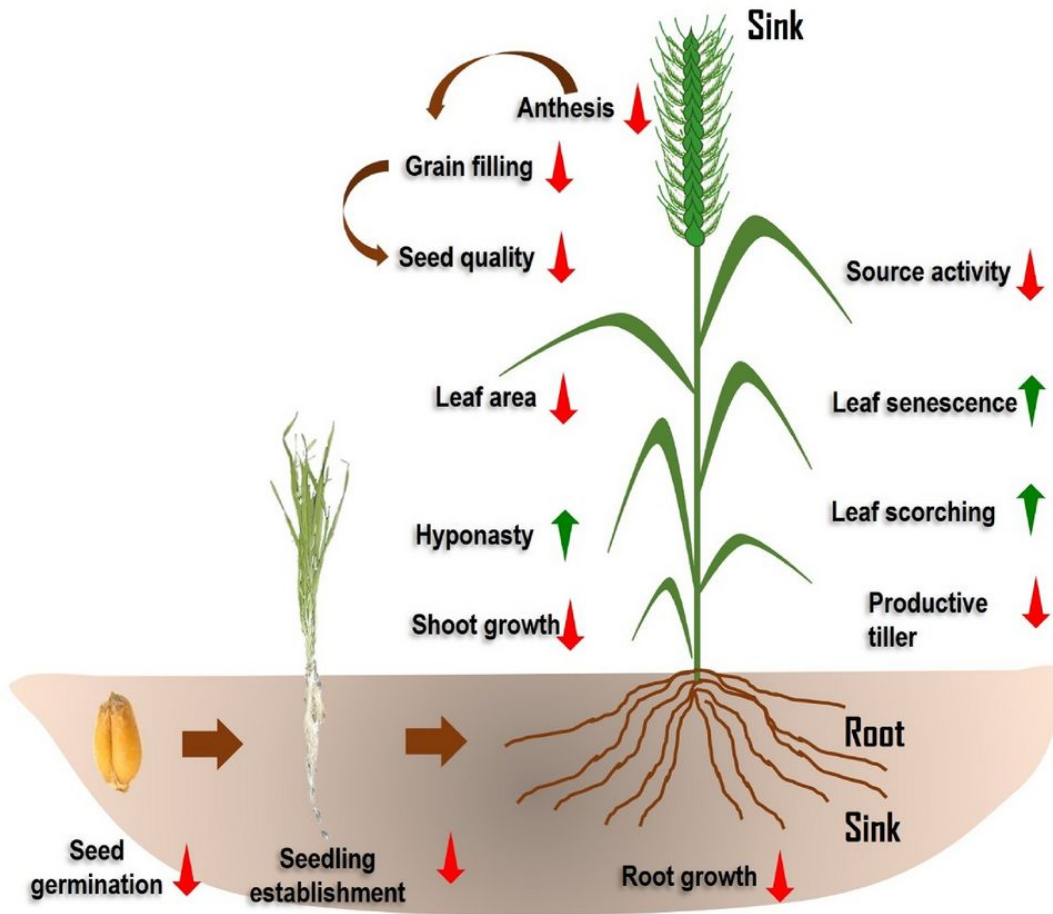


# Genomics-assisted breeding for heat tolerance in the CIMMYT Global Wheat Program

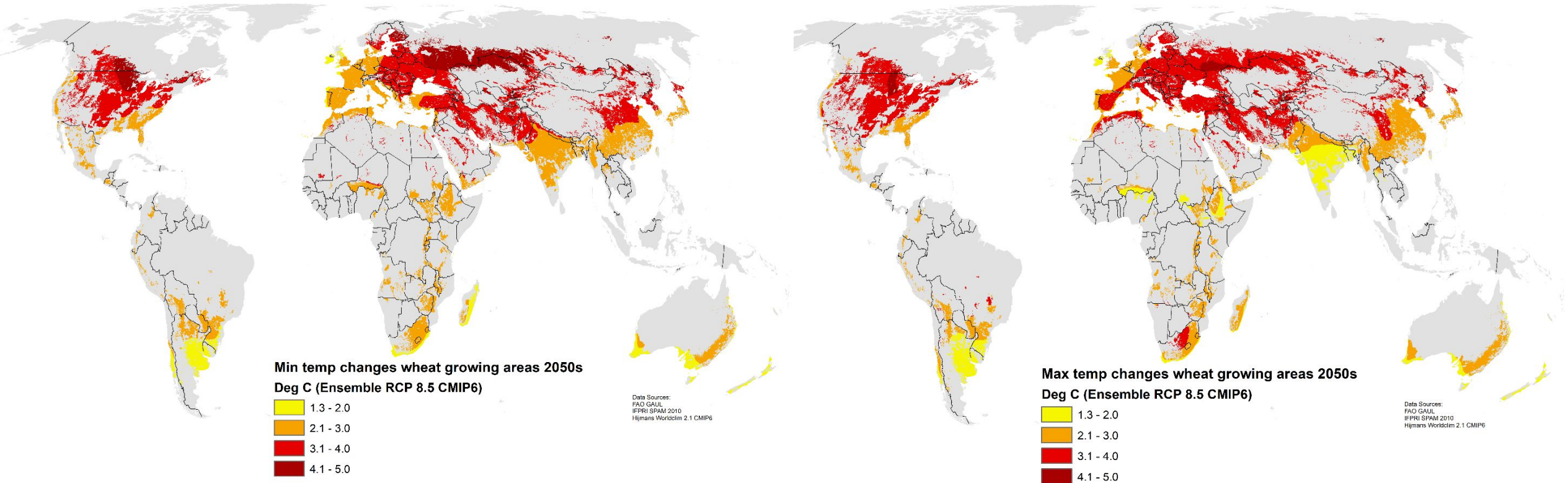
Susanne Dreisigacker & Matthew Reynolds

# Heat is a major environmental stress limiting wheat productivity

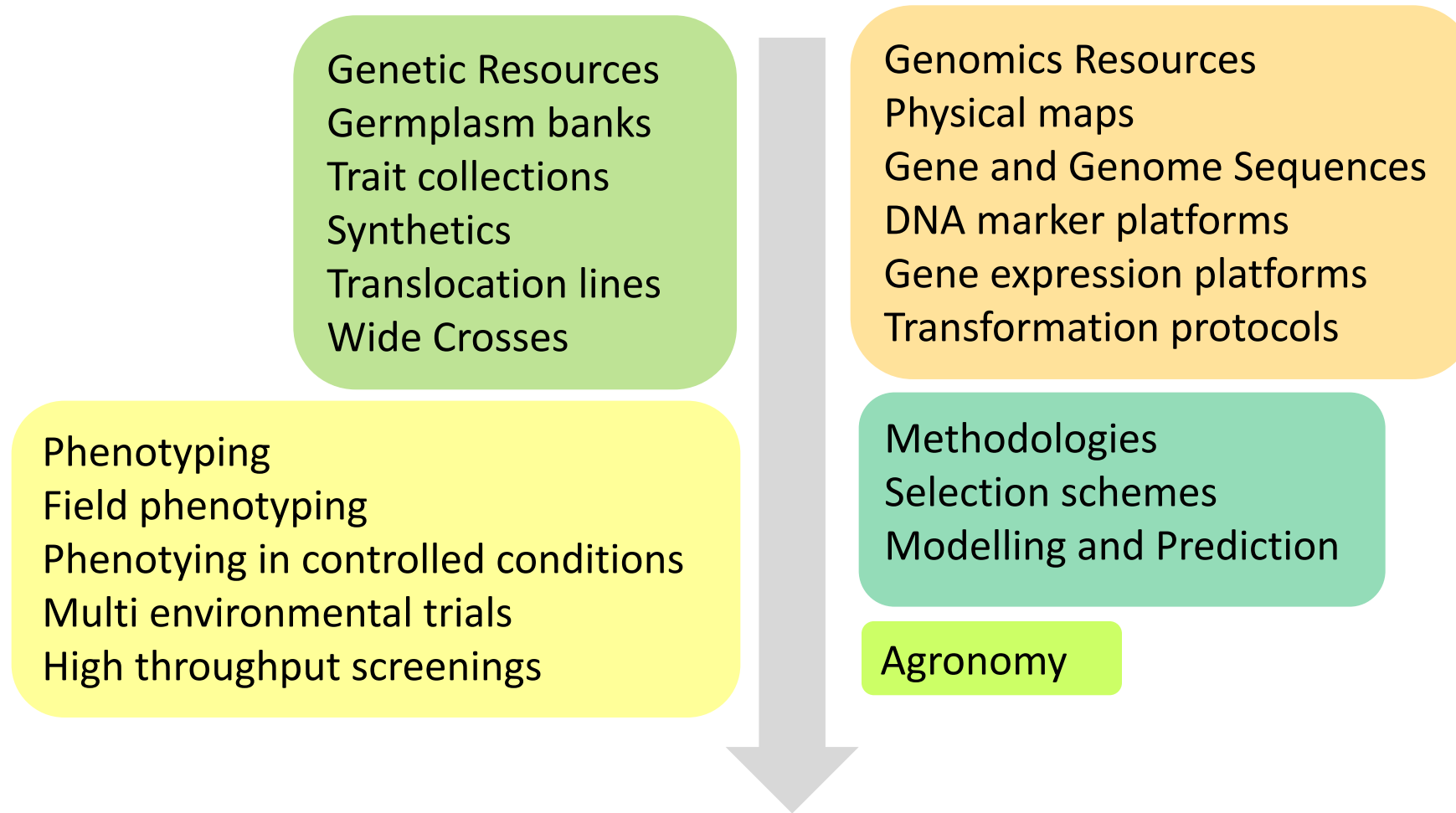


- Inhibits seed germination and seedling establishment.
- Inhibits photosynthesis -> reduction in growth of productive tillers and reproductive organs at anthesis
- Increased leaf senescence and scorching
- Decrease in leaf area -> less photo-assimilates -> reduction of shoot and root growth.
- Reduced grain filling and seed qualities
- Reduction in overall yield

# Simulated changes of min and max temperatures in wheat growing areas globally

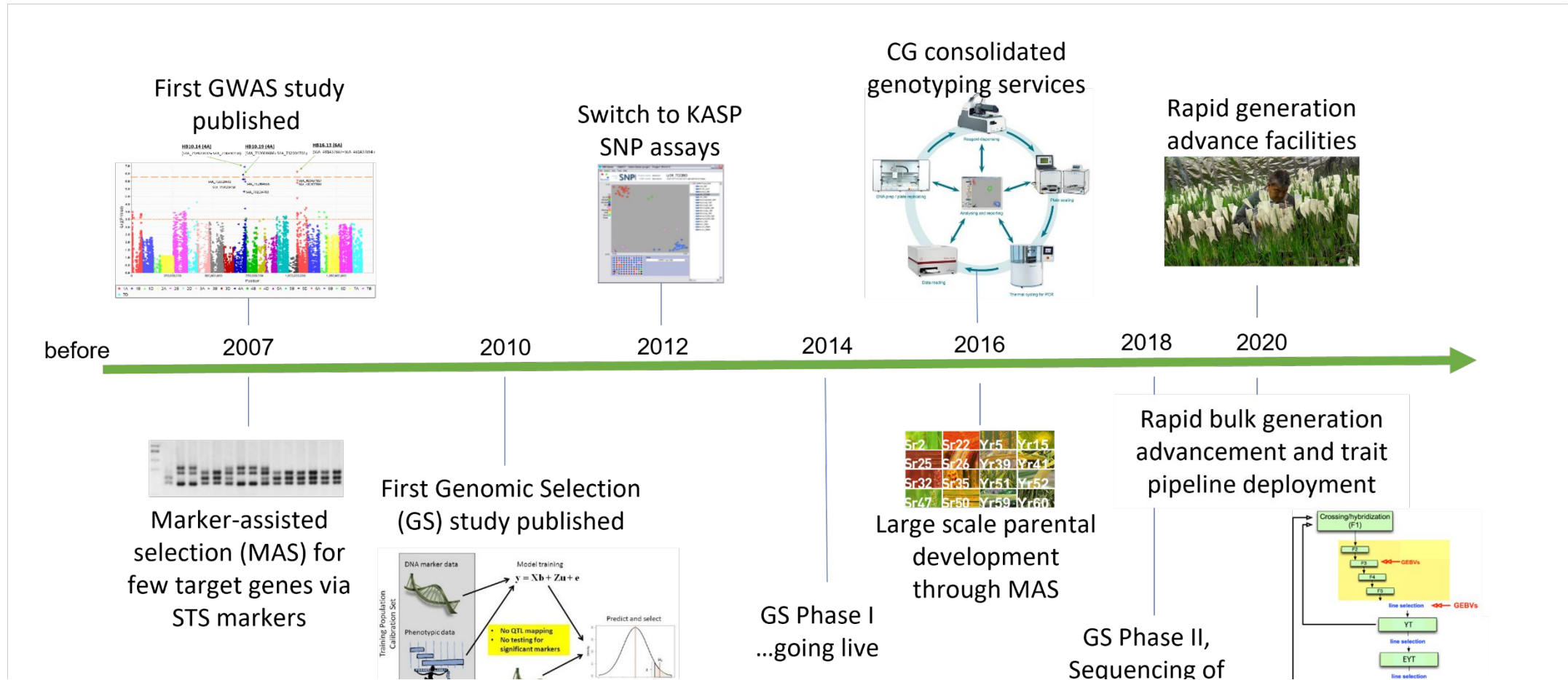


# Multidiscipline - Wheat Breeding



Improved wheat varieties

# Integration of genomics-assisted breeding tools in the CIMMYT GWP

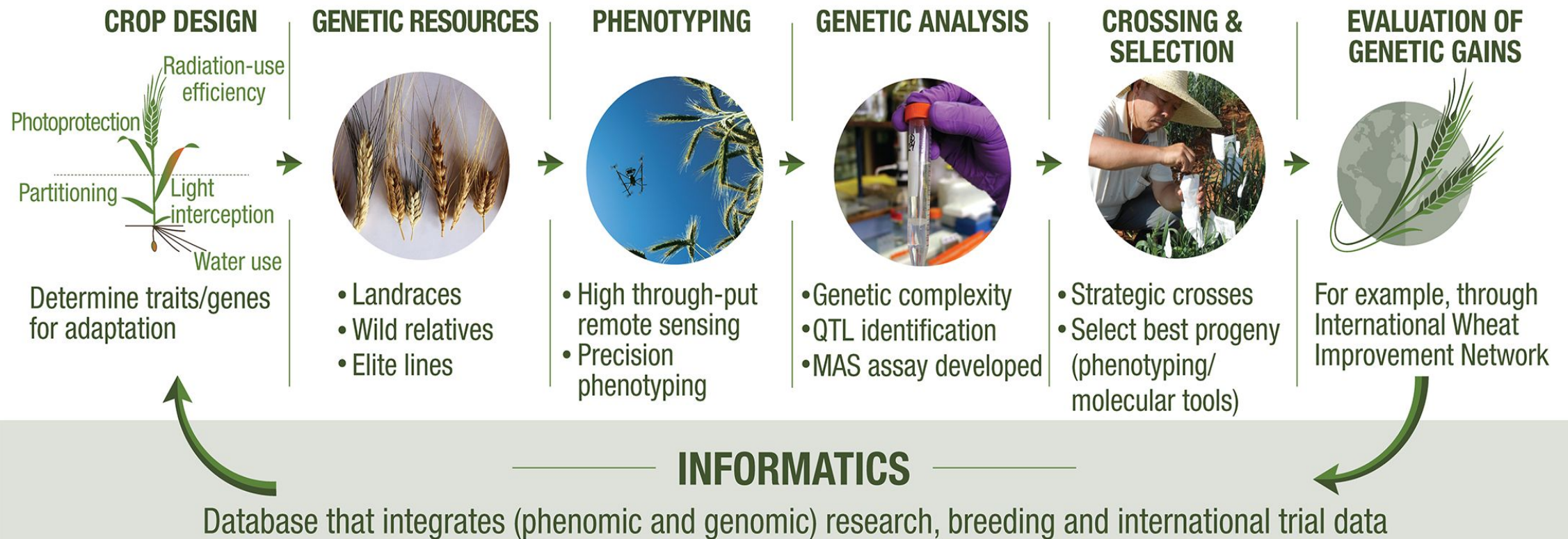


# Genomics-assisted breeding tools to improve heat tolerance

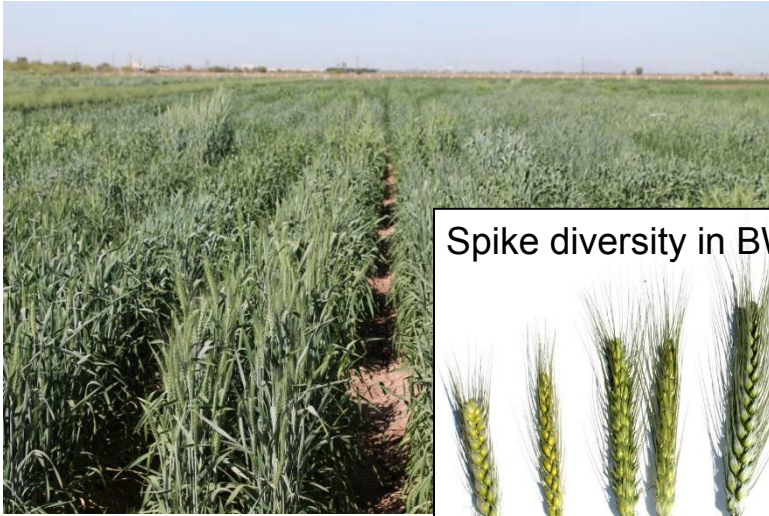
- Identify improved sources of heat tolerance in untapped genetic resources to broaden the wheat gene pool
- Elucidate the genetic bases of heat tolerance across diverse germplasm panels
- Describe and summarize known and novel genomic regions related to heat adaptation in a QTL catalogue
- Introgress novel sources of heat/drought resilience from wild relatives and ancestral genomes into adapted wheat
- Use of genomic-estimated breeding values in parent selection and generation advance

# Translational research & pre-breeding for complex traits

## PHYSIOLOGICAL PRE-BREEDING PIPELINE



# Evaluation of new sources for stress tolerance



Spike diversity in BW panel



## Bread wheat diversity panel (370)

Includes best performing lines from:

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

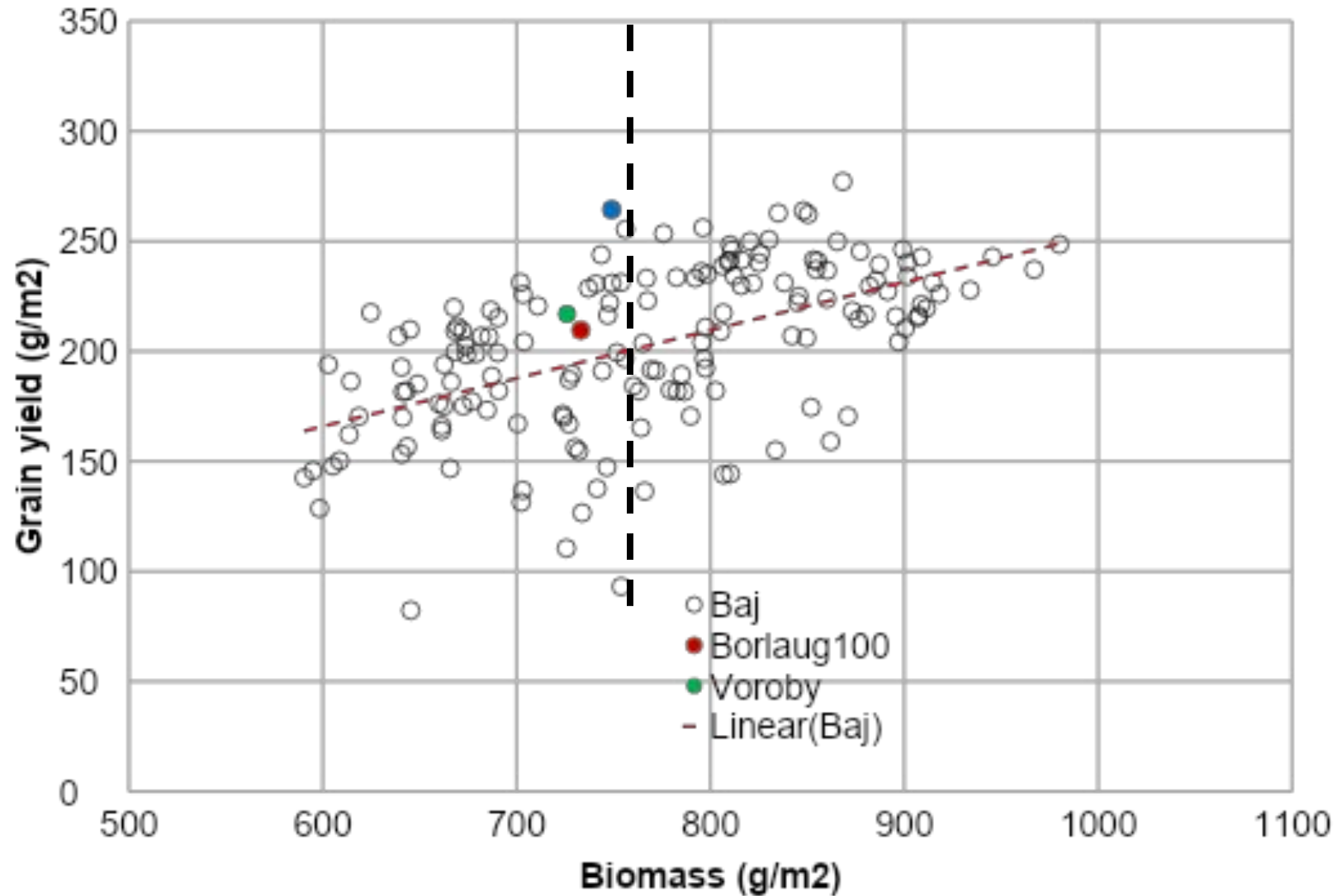


## Elite primary synthetic panel (160)

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

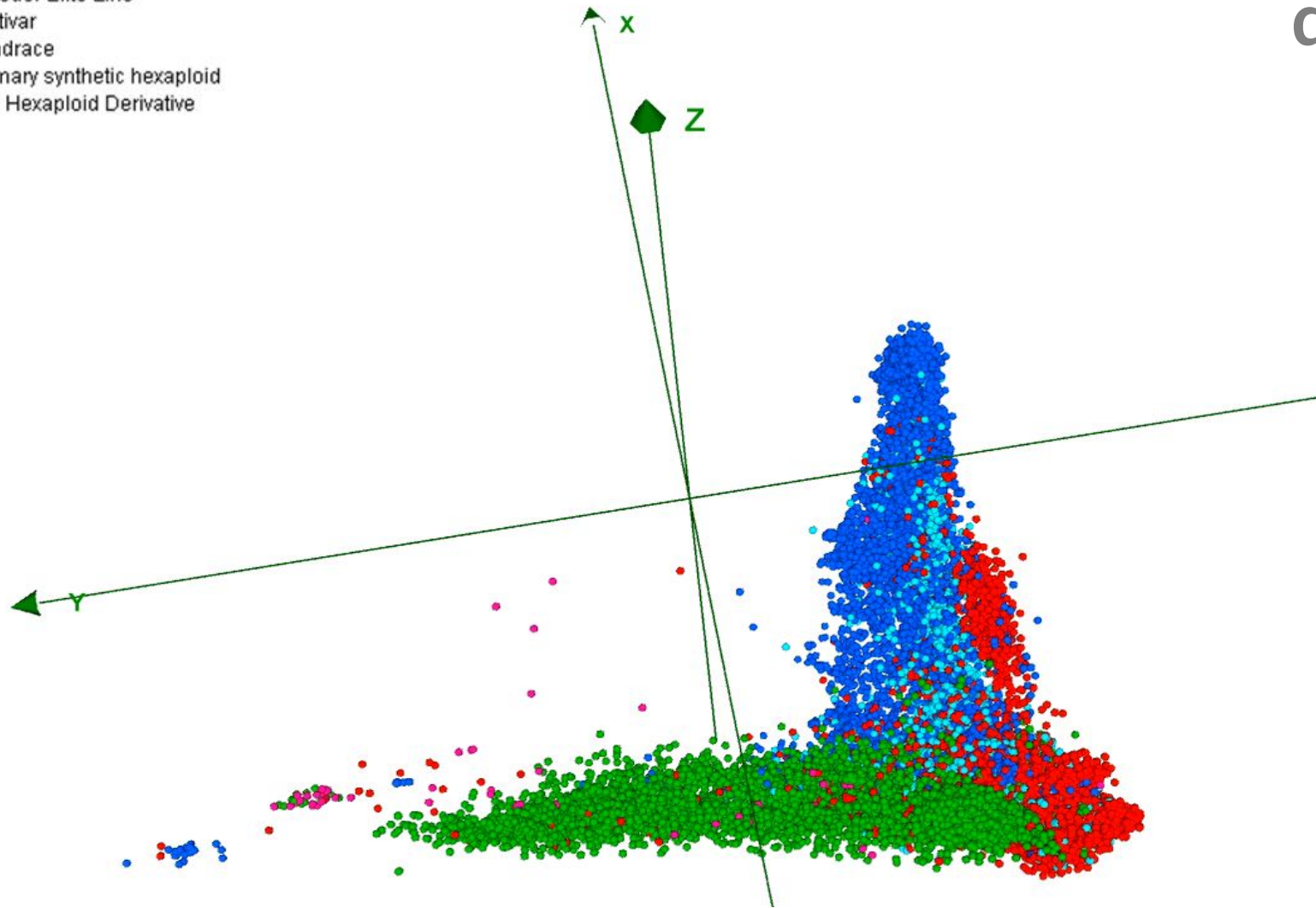


# Genetic variation in synthetic hexaploid wheat (heat stress) NW Mexico, 2016 & 2017



# 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,

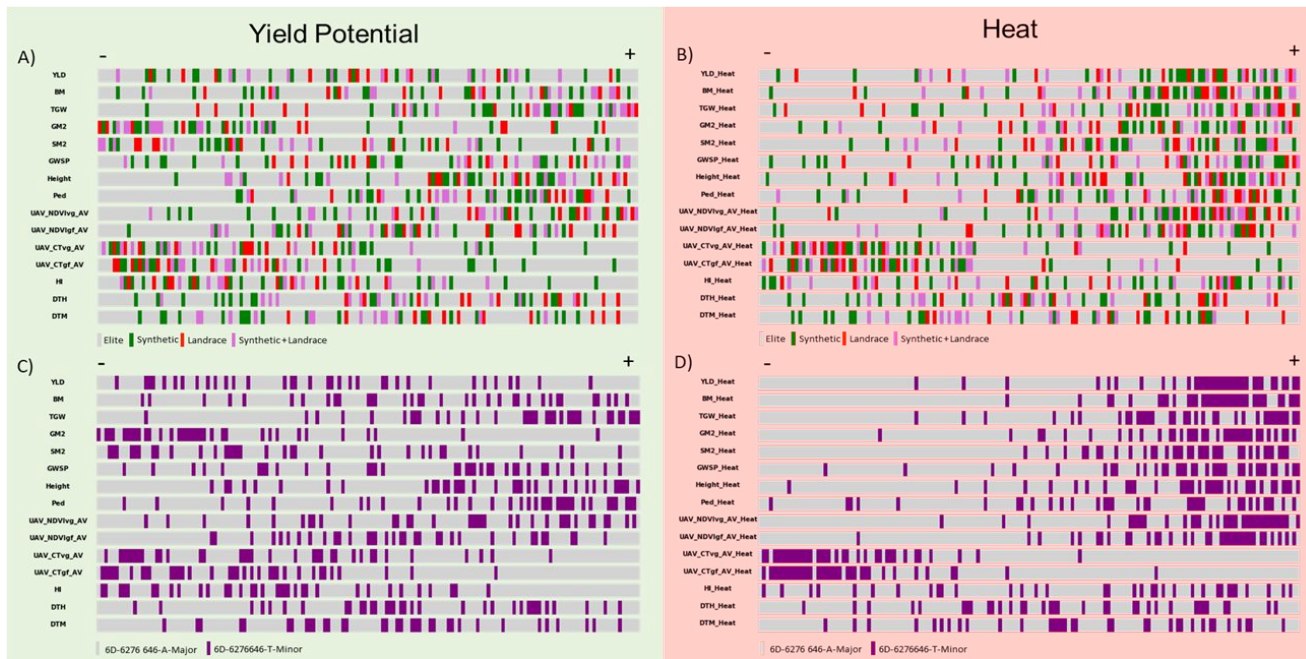
105 countries

26,500 SilicoDArT

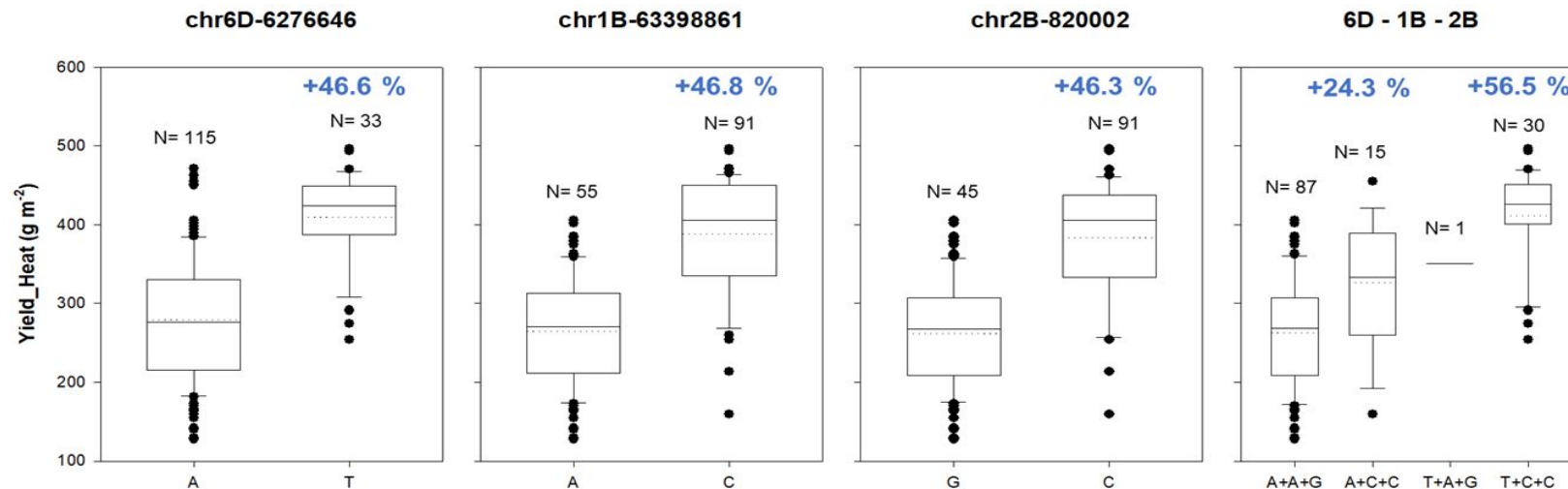
85,500 SNP's

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

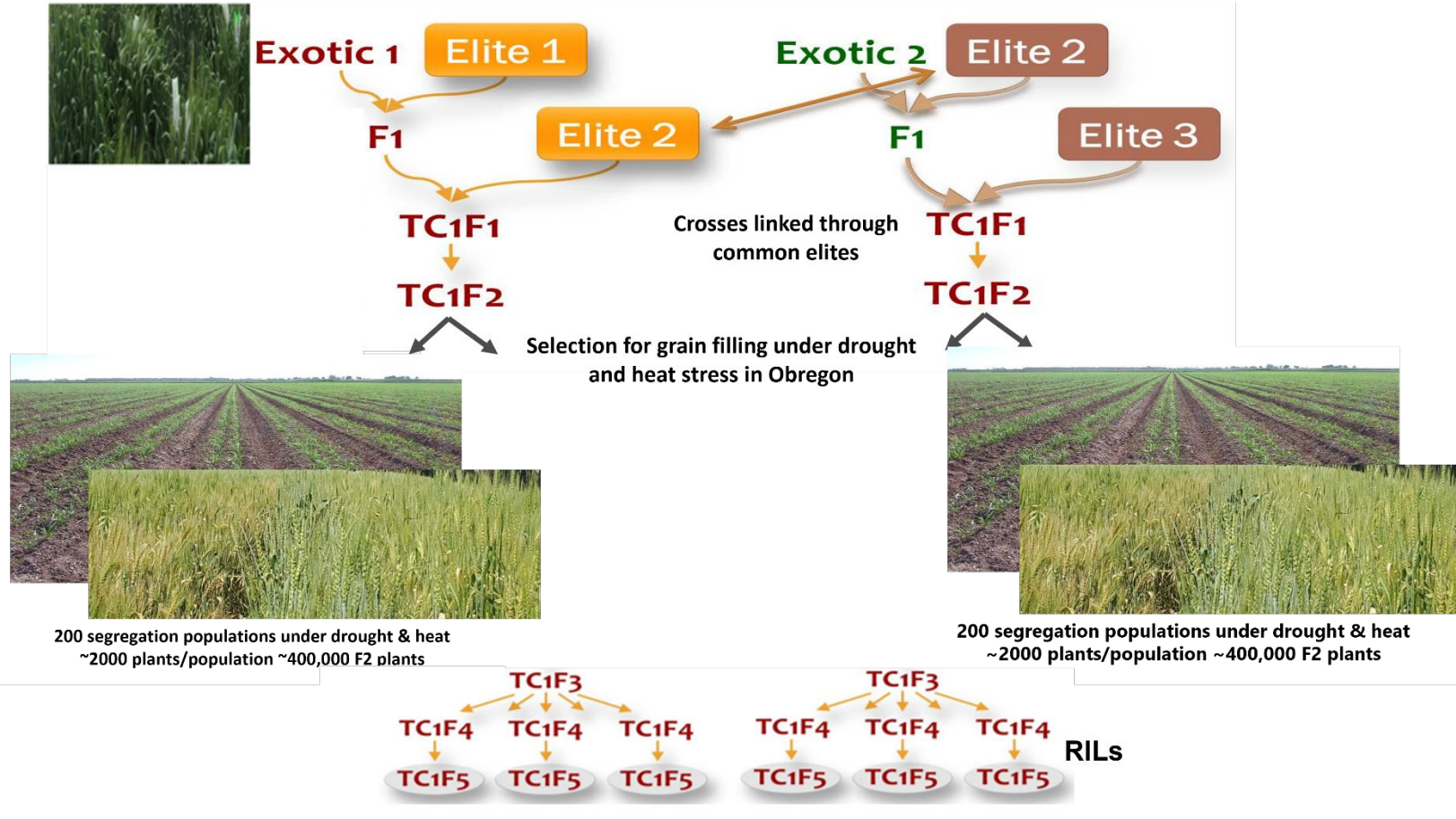
# Identification of genomic regions derived from novel sources



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

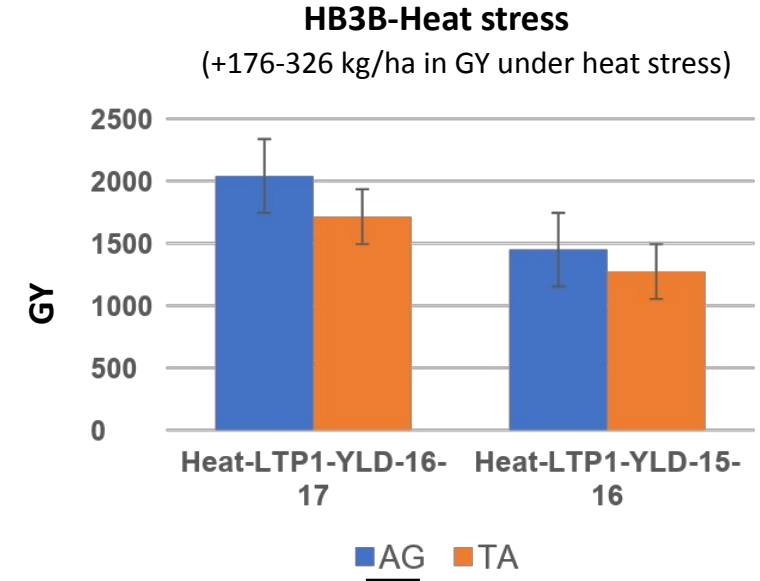
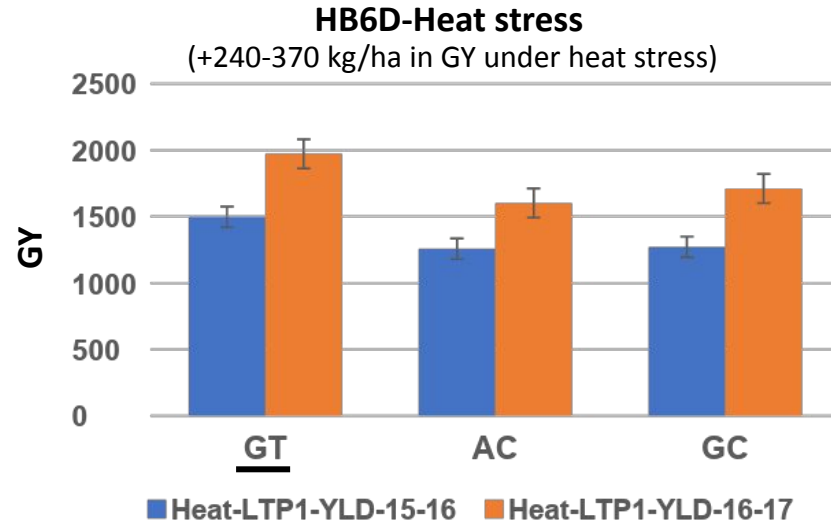
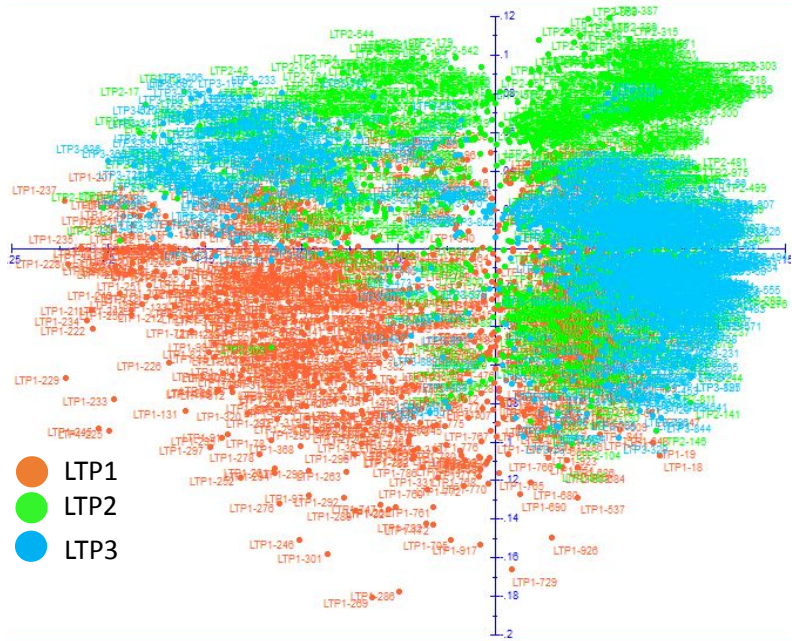


# Identification of genomic regions derived from novel sources

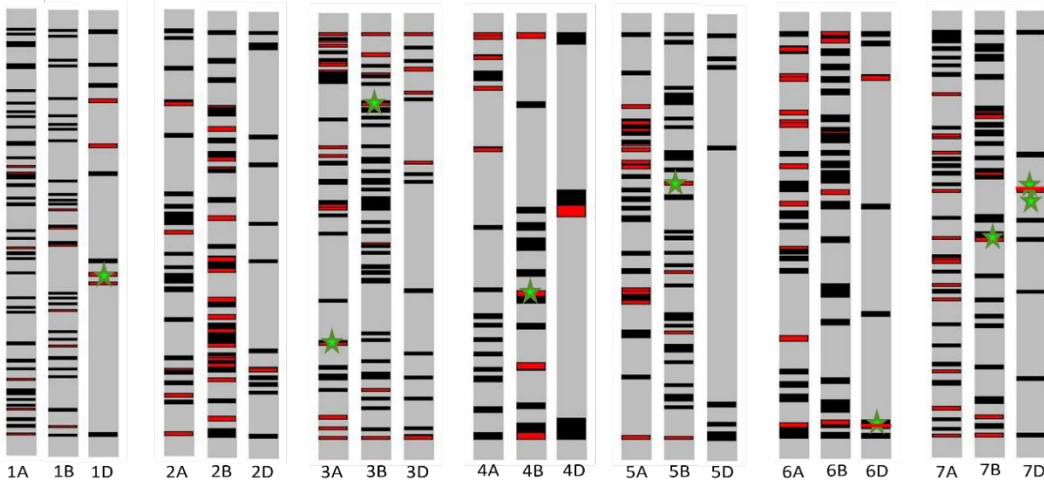


- Three-way crossing scheme of linked top-cross populations (LTP) in the Seed of Discovery project
- Exotic parents include synthetic hexaploidy and landraces selected via FIGS
- Elite parent include lines from the spring BW breeding program

# Quantification of the contribution of the exotic parents in LTPs

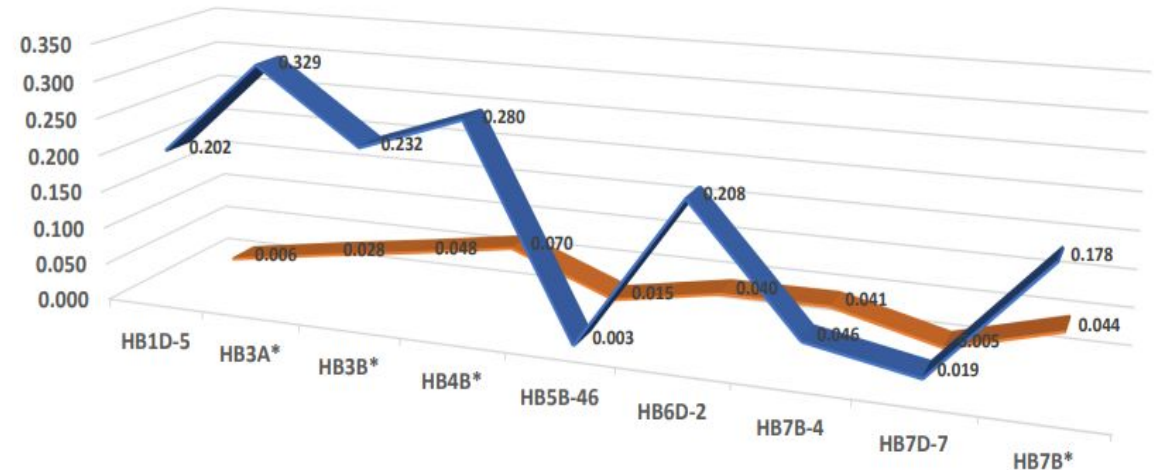


## ★ Exotic specific associations

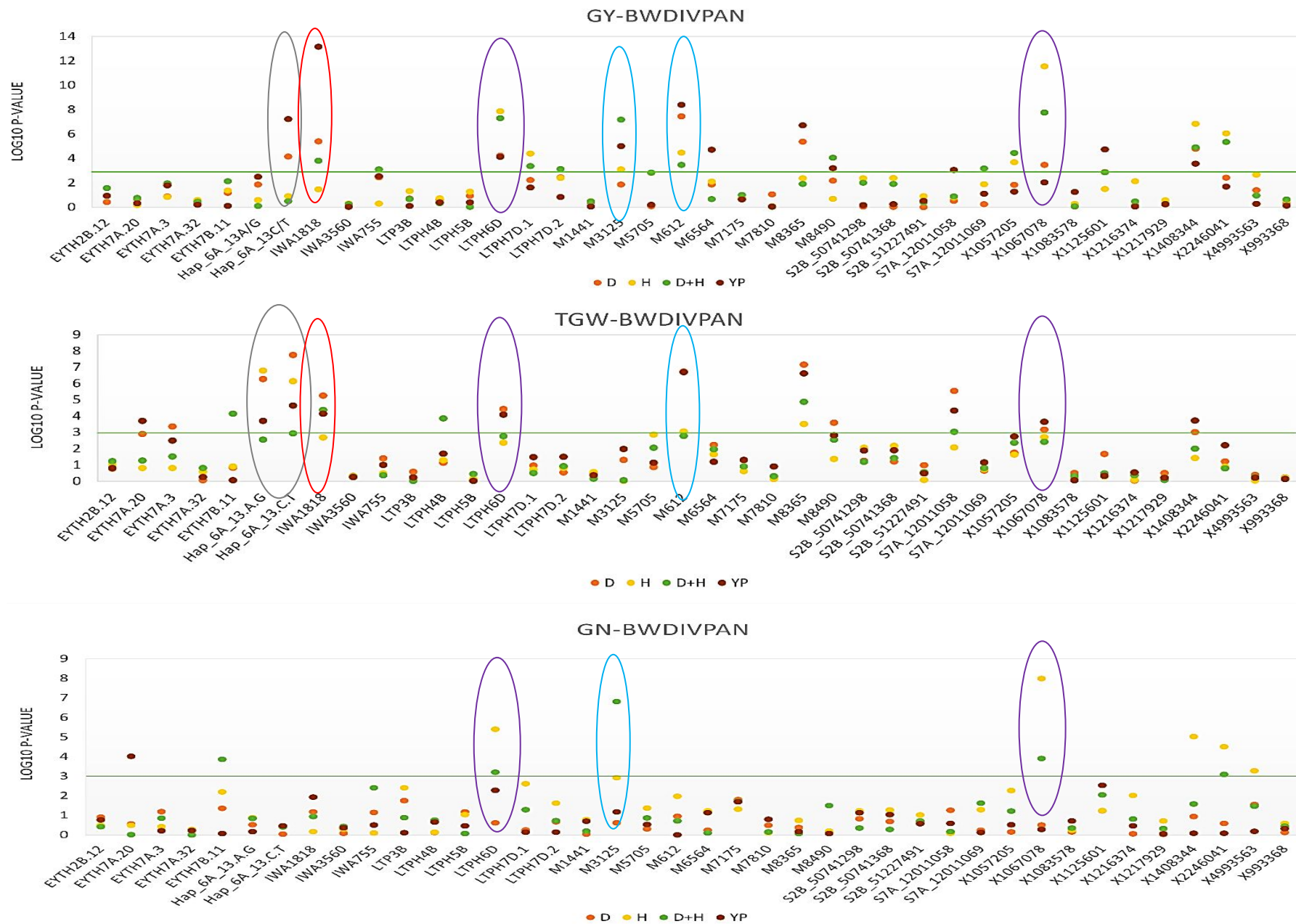


Introgressed genomic regions from exotics are shown as red bars

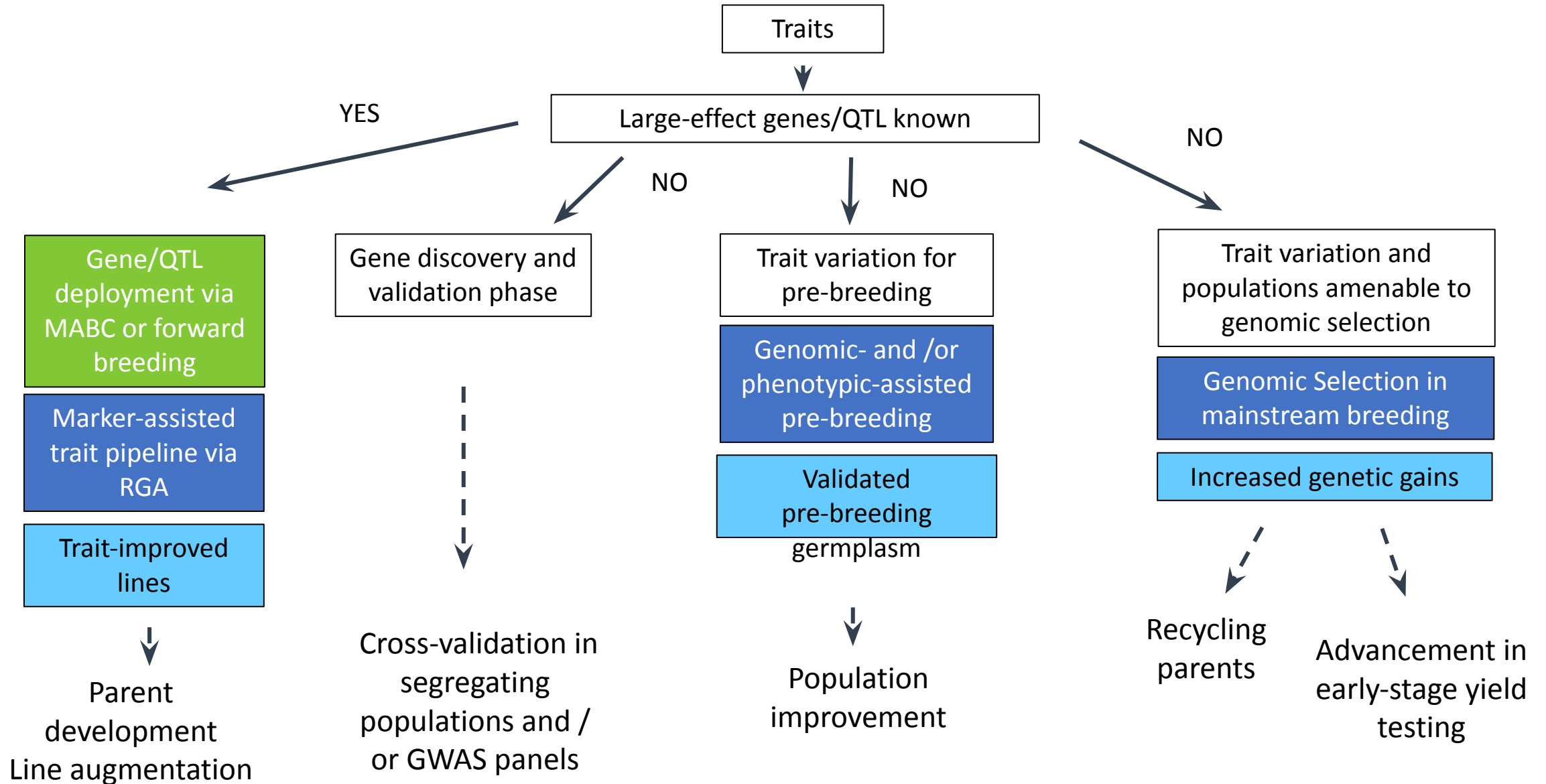
## Haplotype frequencies in exotic parents and 16K genebank accessions



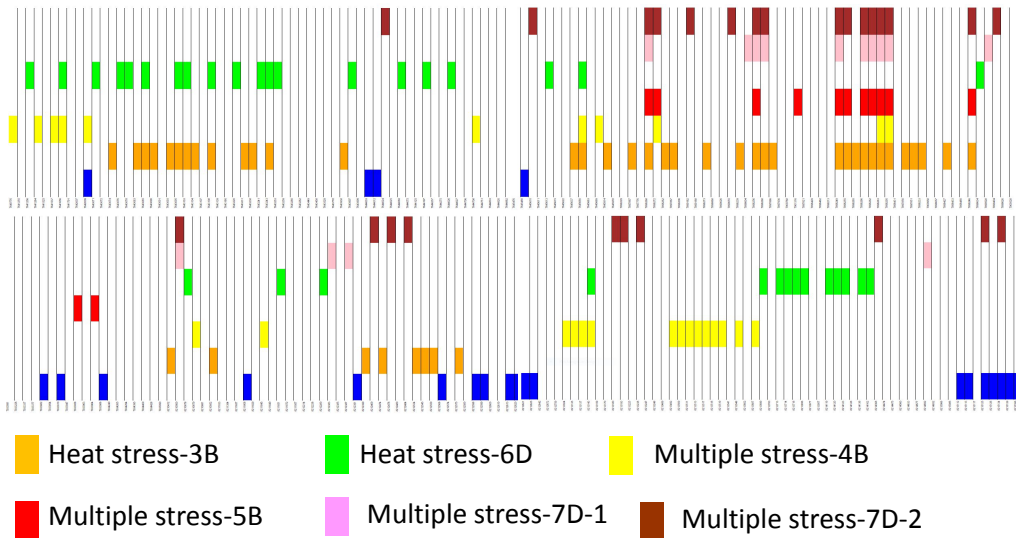
# QTL validation across germplasm panels (e.g., BWDIVPAN)



# Deployment of identified genomic regions in breeding

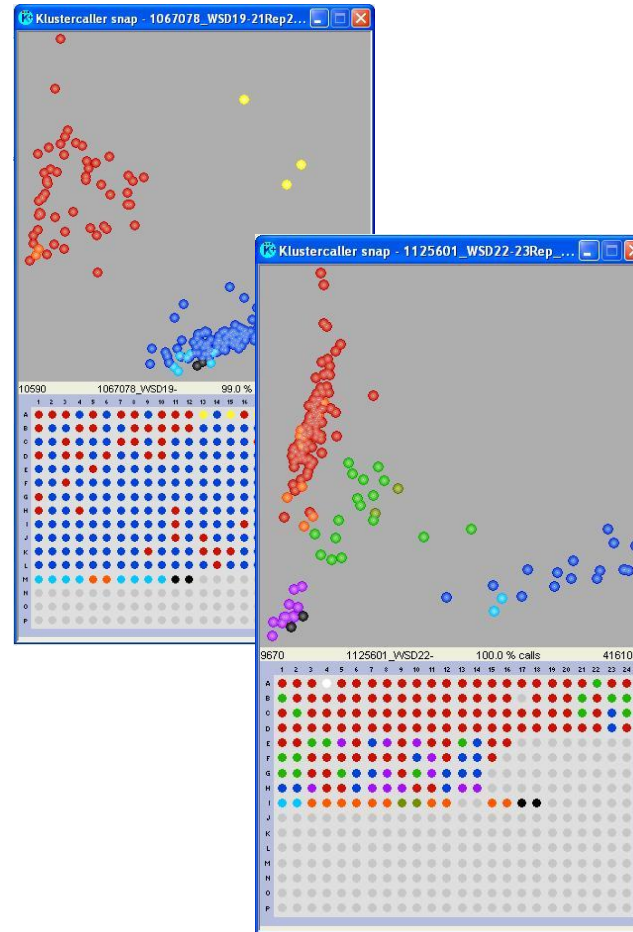


# Introgression of exotic-specific associations in additional elite backgrounds



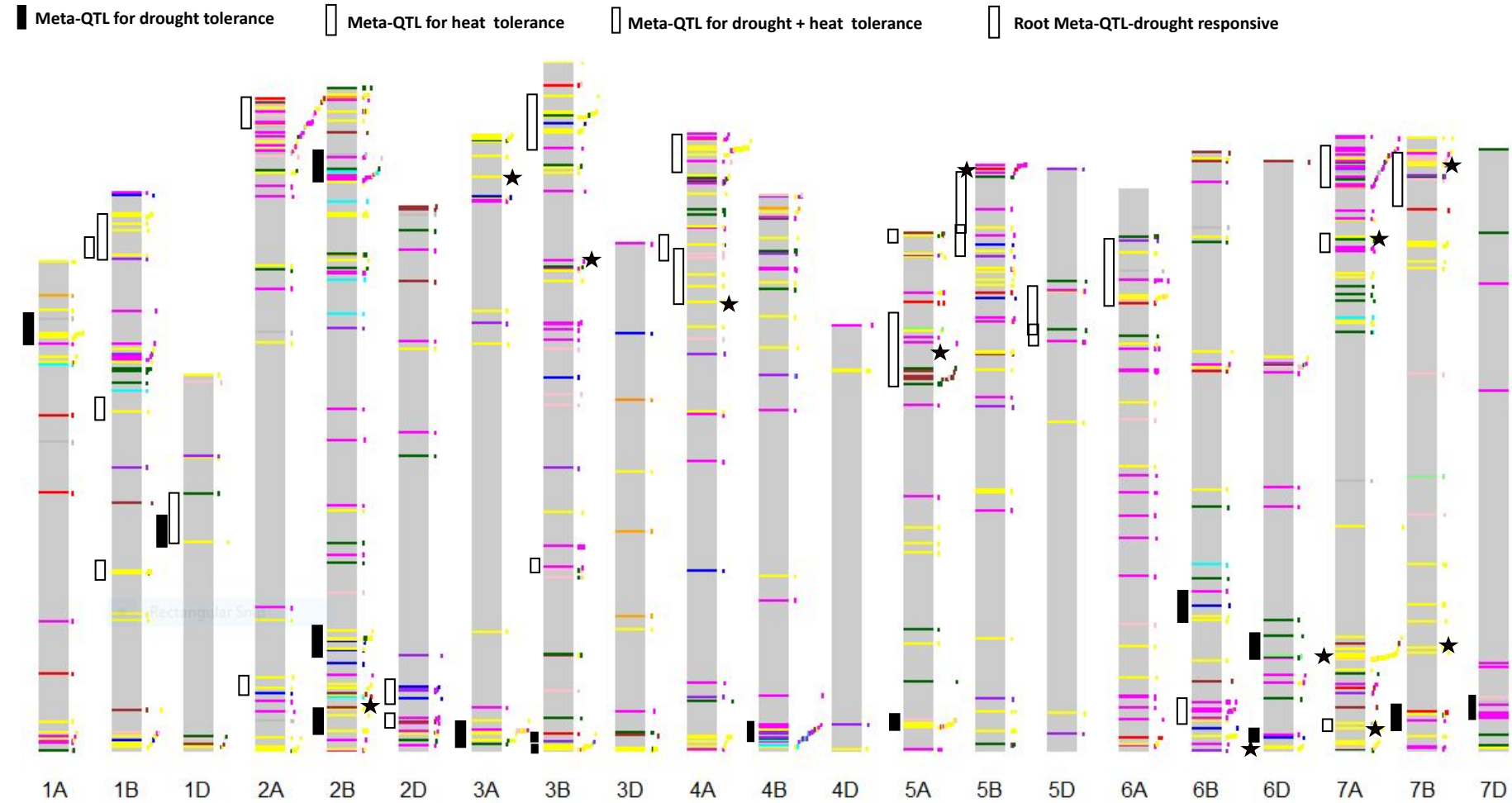
Selected donor parents are

- Evaluated in additional yield and physiological trials
- Integrated in the breeders conventional crossing block
- Integrated in trait improvement pipelines for accelerated trait augmentation in elite germplasm





# Summary catalogue for the identification of MetaQTL

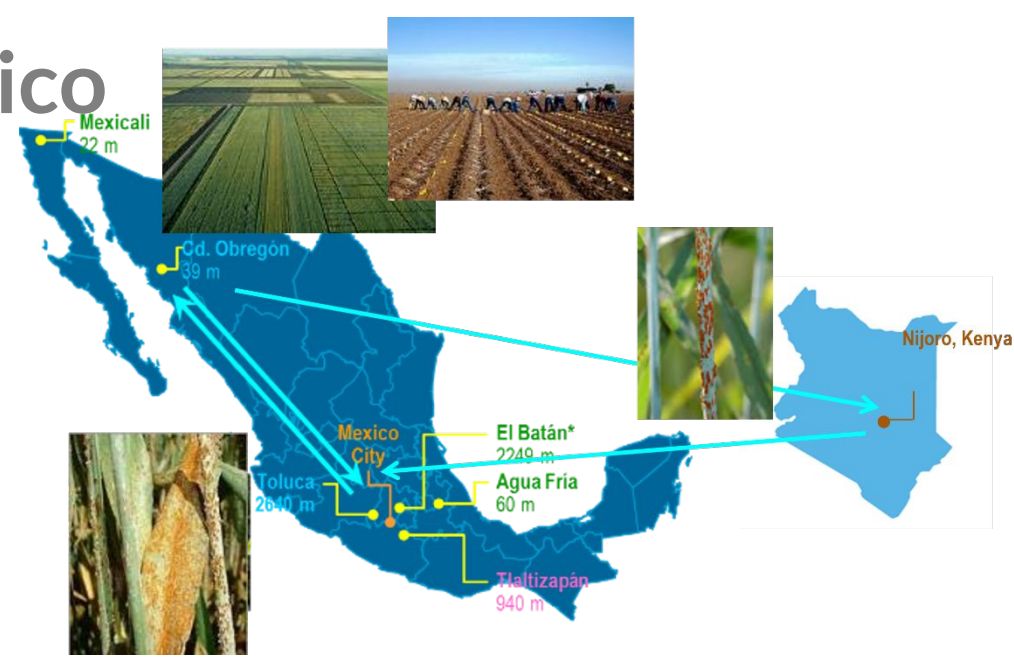


GY	
GN/GNS/GNP/GPS/GSP (Grain no./Grains per spike/Grain no per spike)	
BM	
SPS/SPLKSP (number spikelets per spike)	
SM2/SM (Spikes per m2)	
SL (Spike length)	
TGW/TKW/HSITGW	
GWSP/GWS (Grain weight per spike)	
TN (Tiller no/Fertile tiller no.)	
SPP/ESNP (spike per plant, Effective spikes per plant)	
HI	
SDW	
GM2 (Grain per m2)	

# CIMMYT Global Wheat Program - Mexico

## Centralized breeding approach

Shuttle breeding and evaluation of fixed lines in preliminary multi-environment yield trials in Mexico, including heat stress phenotyping



Heat stress phenotyping



Water use efficiency phenotyping



Yield potential evaluation

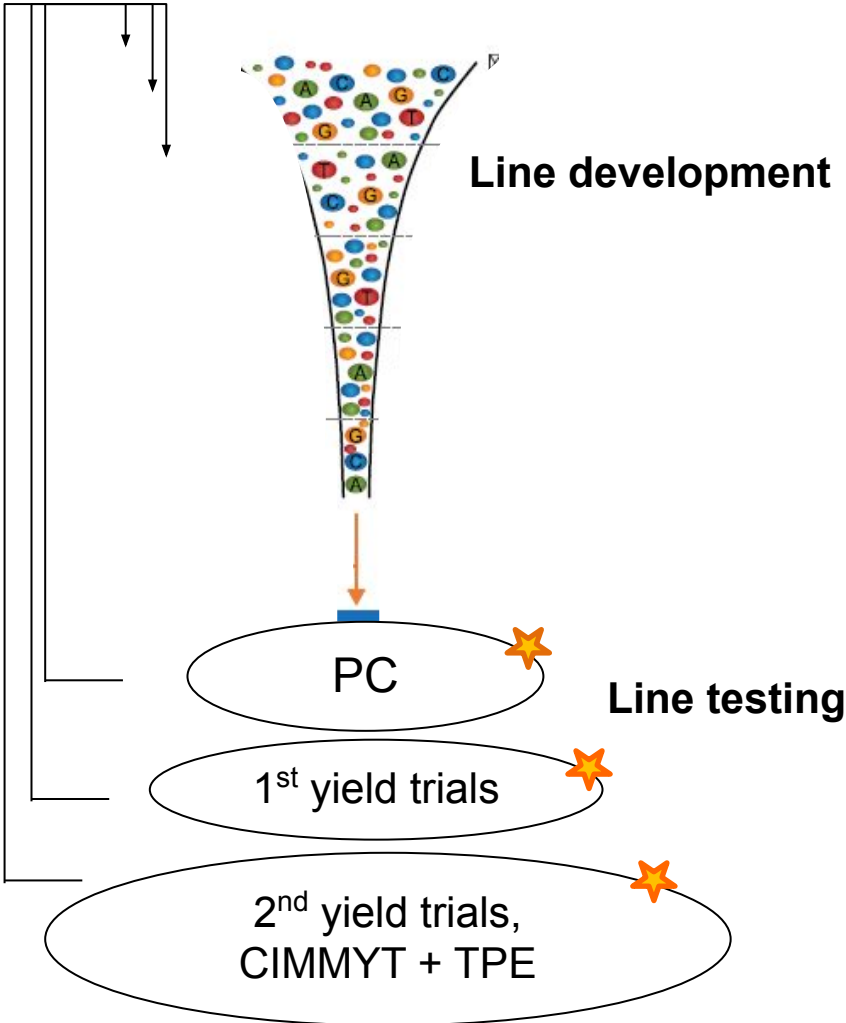


Yield stability

Market segment- Bread Wheat	Area, million ha	Average Grain yield, t/ha	Total Wheat Production (million ton)	Value of the crop (billion USD) <sup>2</sup>	Farming family (mio)	Food for people in market segment (mio)
1. Hard White-Optimum Environment (HW-OE)	32.0	4.1	131.2	24.4	24.0	1093.0
2. Hard White- Heat Tolerant Early Maturity (HW-HTEM)	9.6	2.5	24.0	4.5	9.1	300.0
3. Hard White- Drought Tolerant Normal Maturity (HW-DTNM)	10.0	1.8	18.0	3.3	3.3	100.0
4. Hard White-Drought Tolerant Early Maturity (HW-DTEM)	7.0	2.7	18.9	3.5	4.6	236.0
5. Hard White- High Rainfall (HW-HR)	2.8	2.7	7.6	1.4	3.1	125.0
6. Hard Red-High Rainfall (HR-HR)	0.35 <sup>1</sup>	1.9	0.7	0.1	0.2	2.5
Total	61.8	3.25	200.3	37.3	44.3	1856.5

# Grain yield under heat estimated using Genomic Selection

## Genomic prediction in the line testing phase to enhance field trial selection



**Approx. 18,000 PC lines** being genotyped in 2021 (USAID supported Feed the Future Innovation Lab for Applied Wheat Genomics at KSU) for selecting lines going into the 1<sup>st</sup> stage yield trials

Training set: Lines in 2<sup>nd</sup> stage yield trials (2014-2020), ~ 8,000 lines

*Pre-testing stage (PC): ~ 18,000 lines*

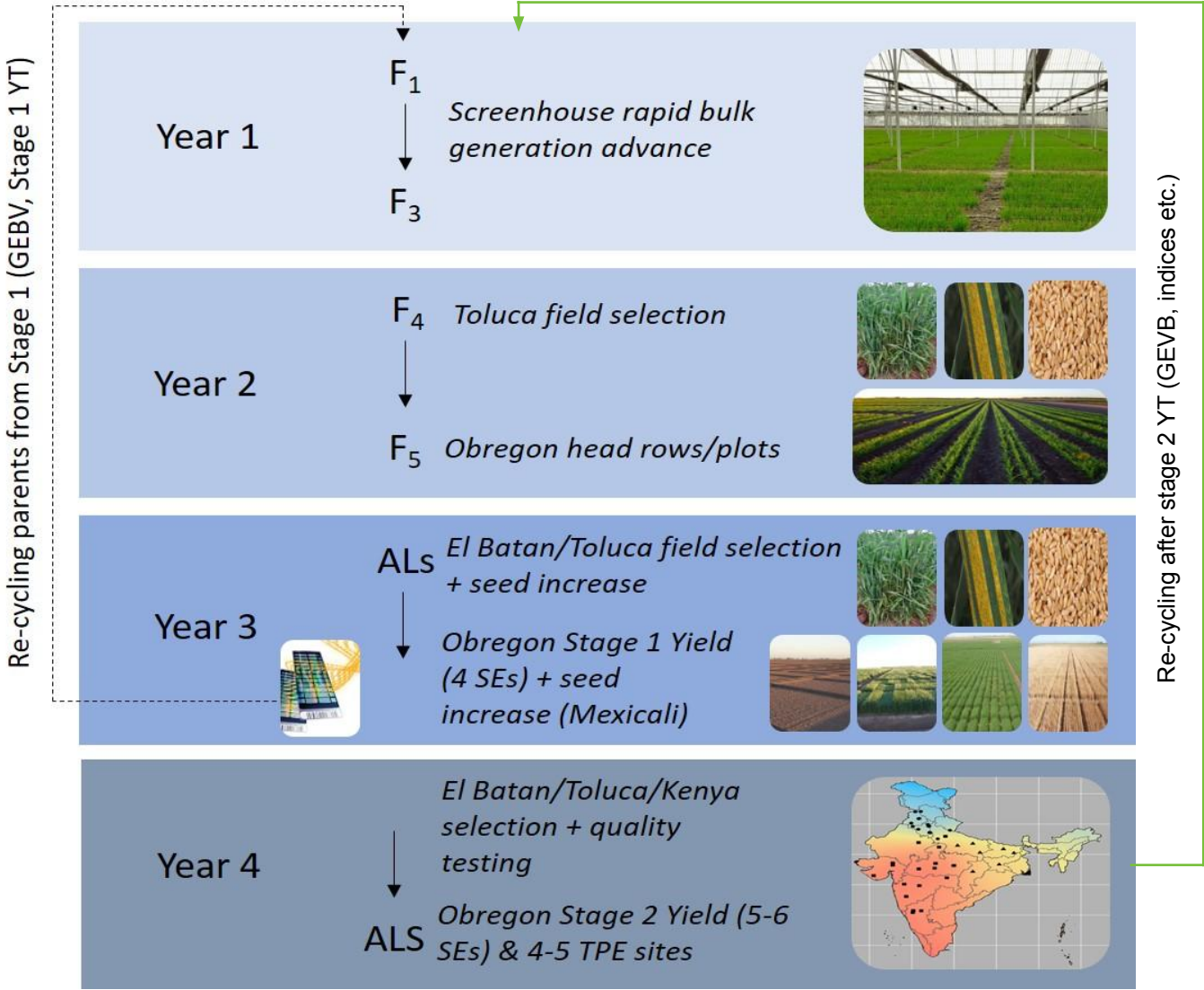
*Discard low performing genotypes (phenotypic data for disease and agronomic type)*

*Stage 1 yield trials (YT): ~ 4,500 lines, 1 reps, ~ 4 envr. at CENEB*

*Stage 2 yield trials (EYT): ~ 600-700 lines, 6 envr. at CENEB and 5-6 TPE sites*

# Optimizing the breeding schemes by reducing cycle time

## Rapid Bulk Generation Advancement (RBGA) optimization and implementation



# In summary

- ✓ A series of phenomics and genomics tools are used at CIMMYT to elucidate the genetic basis of complex traits such as heat tolerance
- ✓ The genetic basis of the traits is increasingly described to maximize its use and allow to develop adequate deployment strategies in the breeding programs
- ✓ New genetic variation is incorporated into the elite breeding pool using physiological pre-breeding and marker-assisted trait-development pipelines
- ✓ Mainstream breeding for heat tolerance is increasingly assisted by Genomic Selection



# Acknowledgements

The CGIAR Research Program WHEAT receives W1&W2 support from the Governments of Australia, Belgium, Canada, China, France, India, Japan, Korea, Netherlands, New Zealand, Norway, Sweden, Switzerland, U.K., U.S., and the World Bank.



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Ravi P. Singh  
Sue Mondal

Excellence in Breeding  
(EIB) Platform

WMB team