



Genomics-assisted breeding in the CIMMYT Global Wheat Program

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CIMMYT Global Wheat Program - Mexico

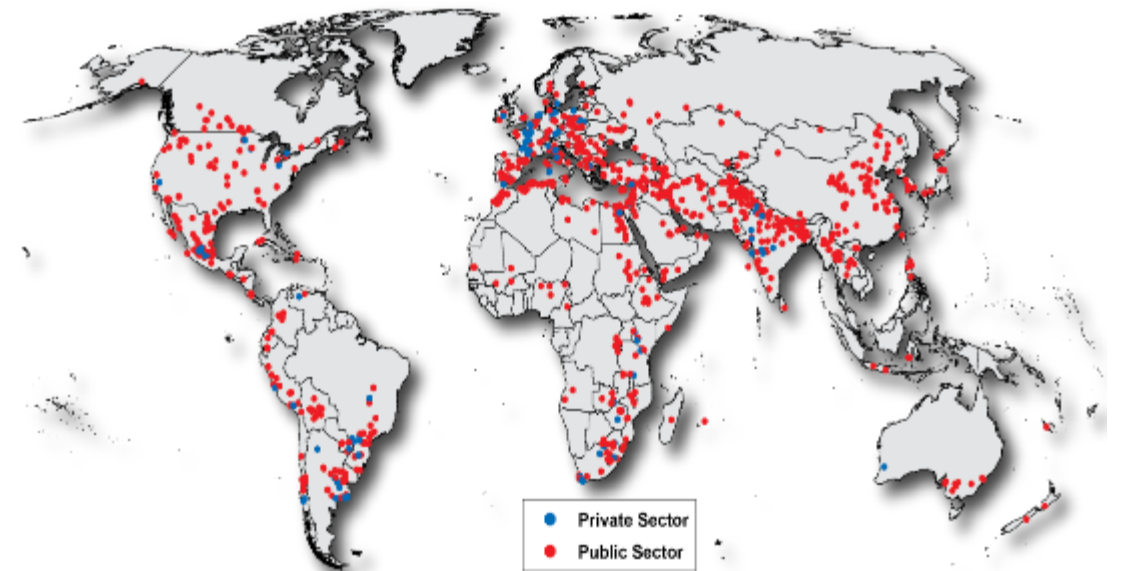


Centralized breeding approach

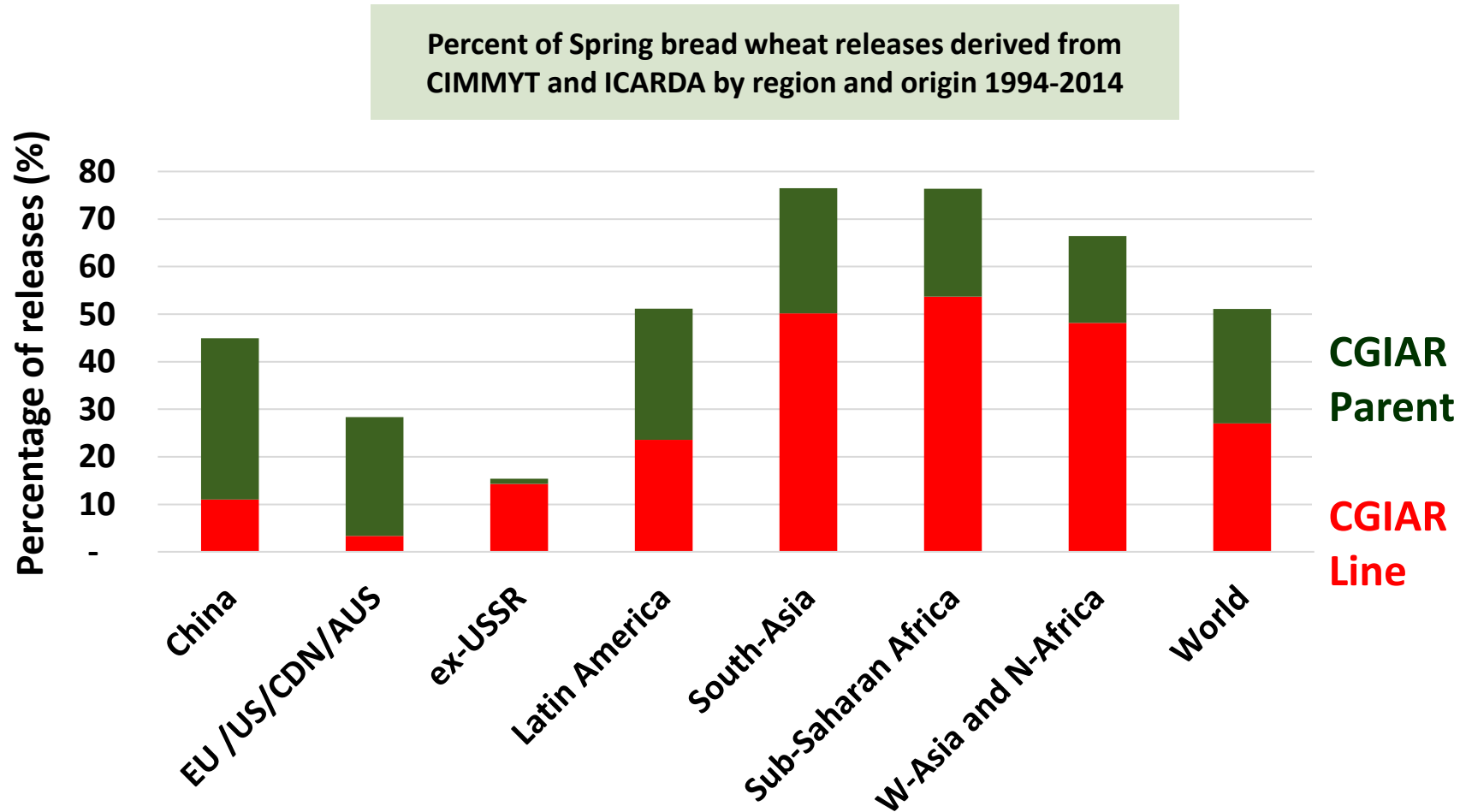
Shuttle breeding and evaluation of fixed lines in preliminary multi-environment yield trials in Mexico

Germplasm distribution

Annual seed shipments of approx. 200 000 wheat lines to approx. 450 breeding programs

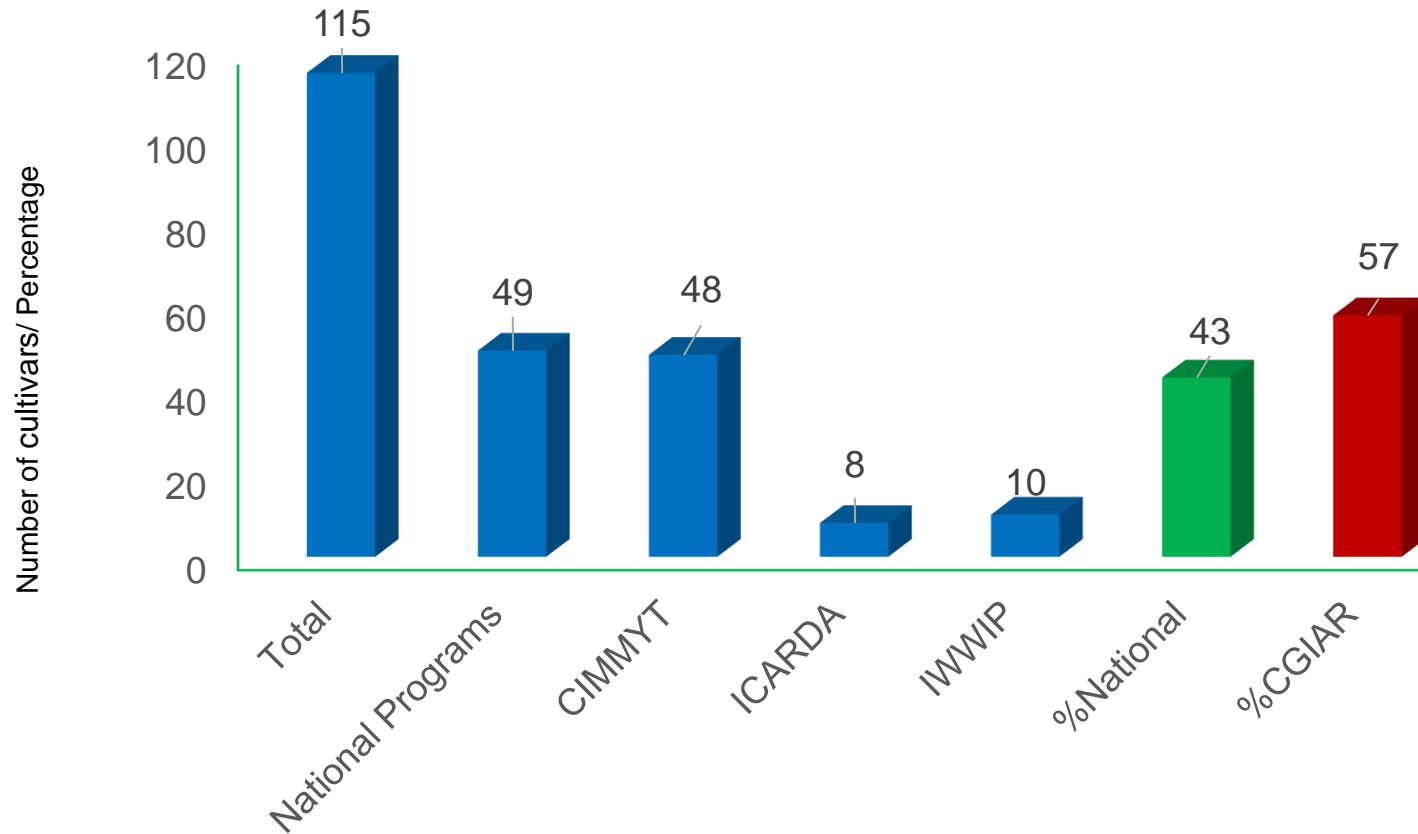


Impact of CGIAR Wheat Breeding Germplasm



Note: Percent release roughly represents area sown to CIMMYT derived wheat varieties

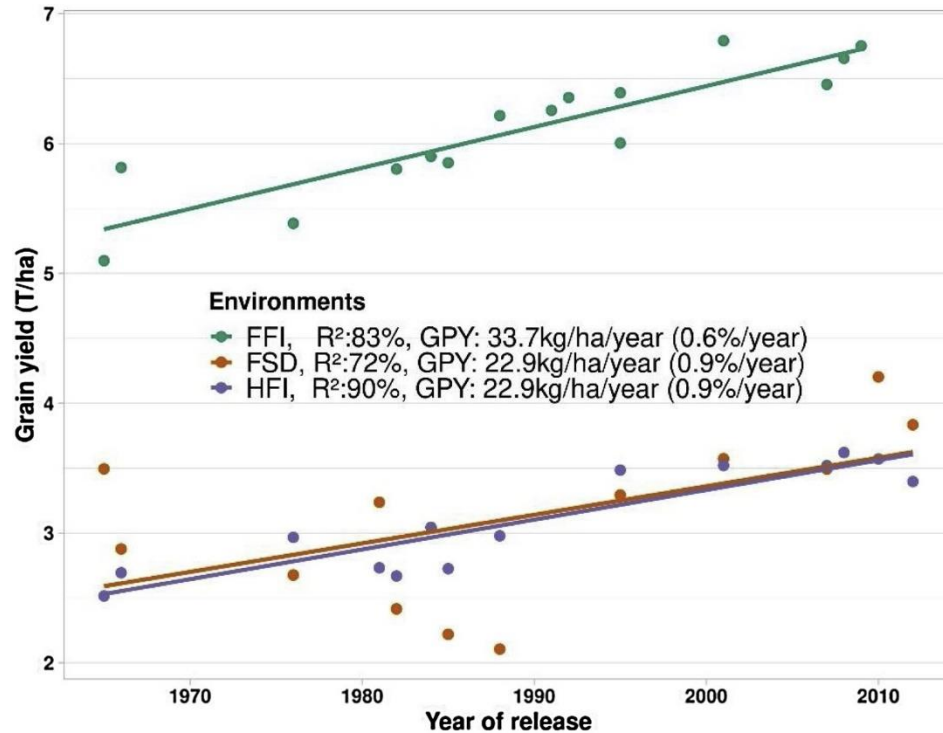
Origin of Wheat Cultivars (Bread Wheat & Durum Wheat) released from 2001-2021 in Iran



Note: Bread wheat cultivars bred by the national wheat breeding programs have at least one parents from CIMMYT germplasm in their background.

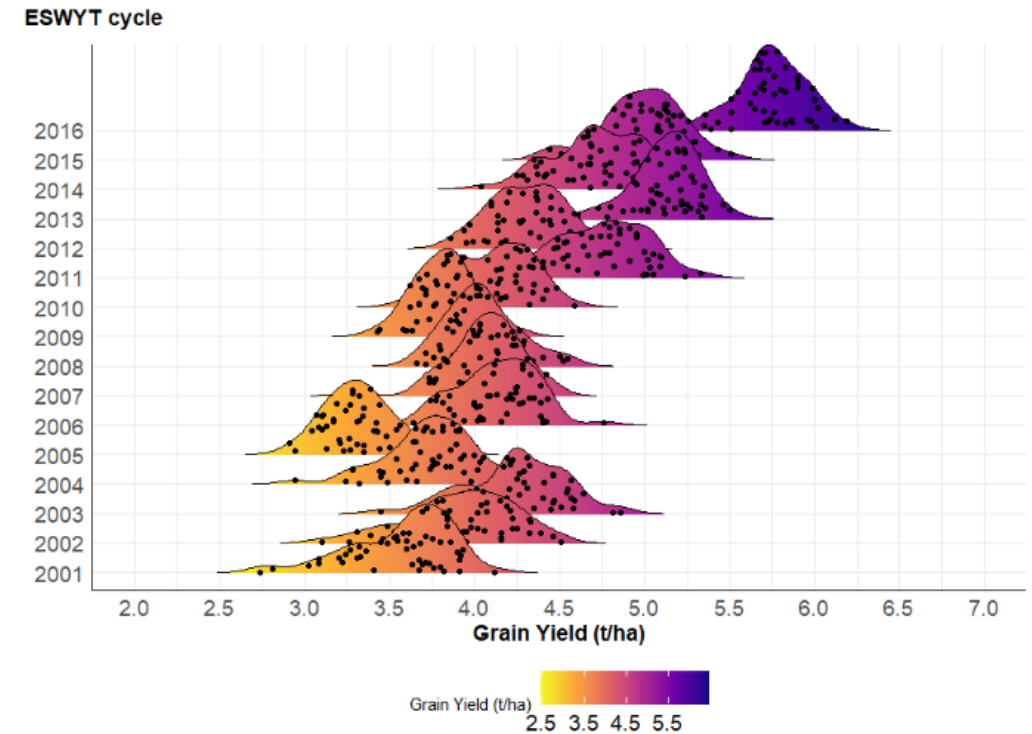
Continuous breeding progress for grain yield

1965–2014 in simulated environments (Cd. Obregón)



Mondal *et al.* (2020) Fifty years of semi-dwarf spring wheat breeding at CIMMYT: Grain yield progress in optimum, drought and heat stress environments. *Field Crops Research* doi: 10.1016/j.fcr.2020.107757.

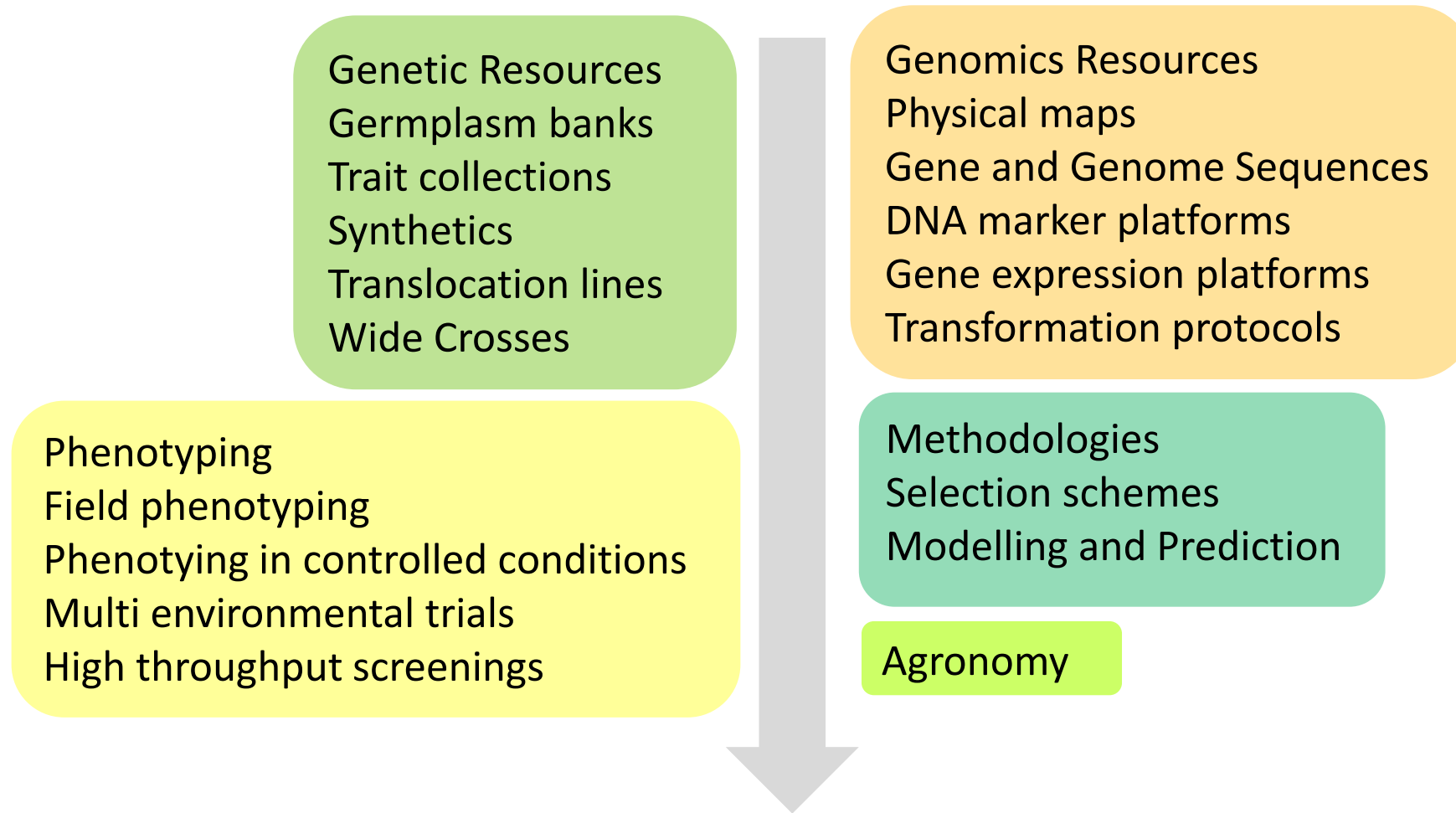
2001–2016 across Indian TPEs



Crespo-Herrera *et al.* (2021) Target population of environments for wheat breeding in India: definition, prediction and indirect genetic gains. *Frontiers in Plant Science* doi: 10.3389/fpls.2021.638520

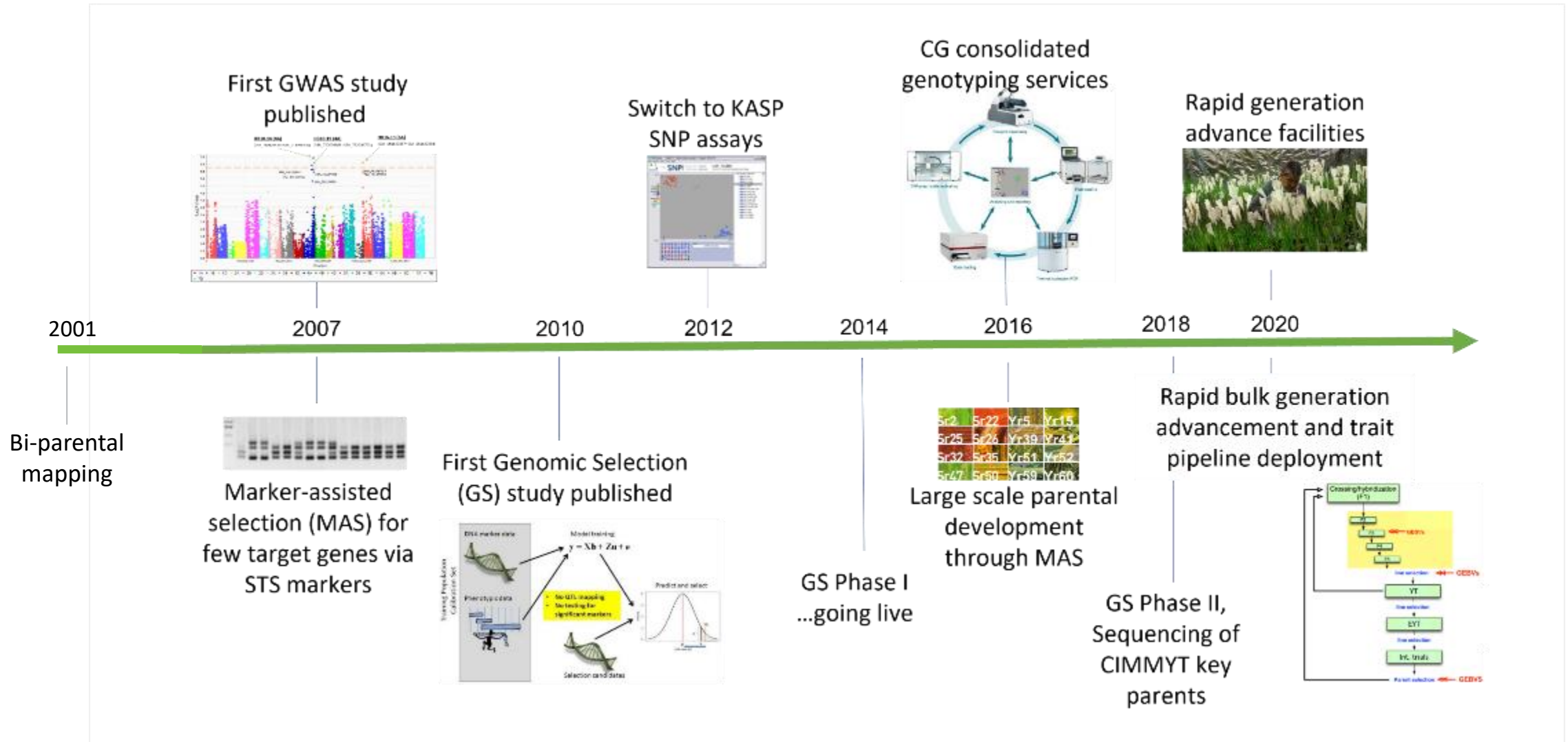


Multidiscipline - Wheat Breeding



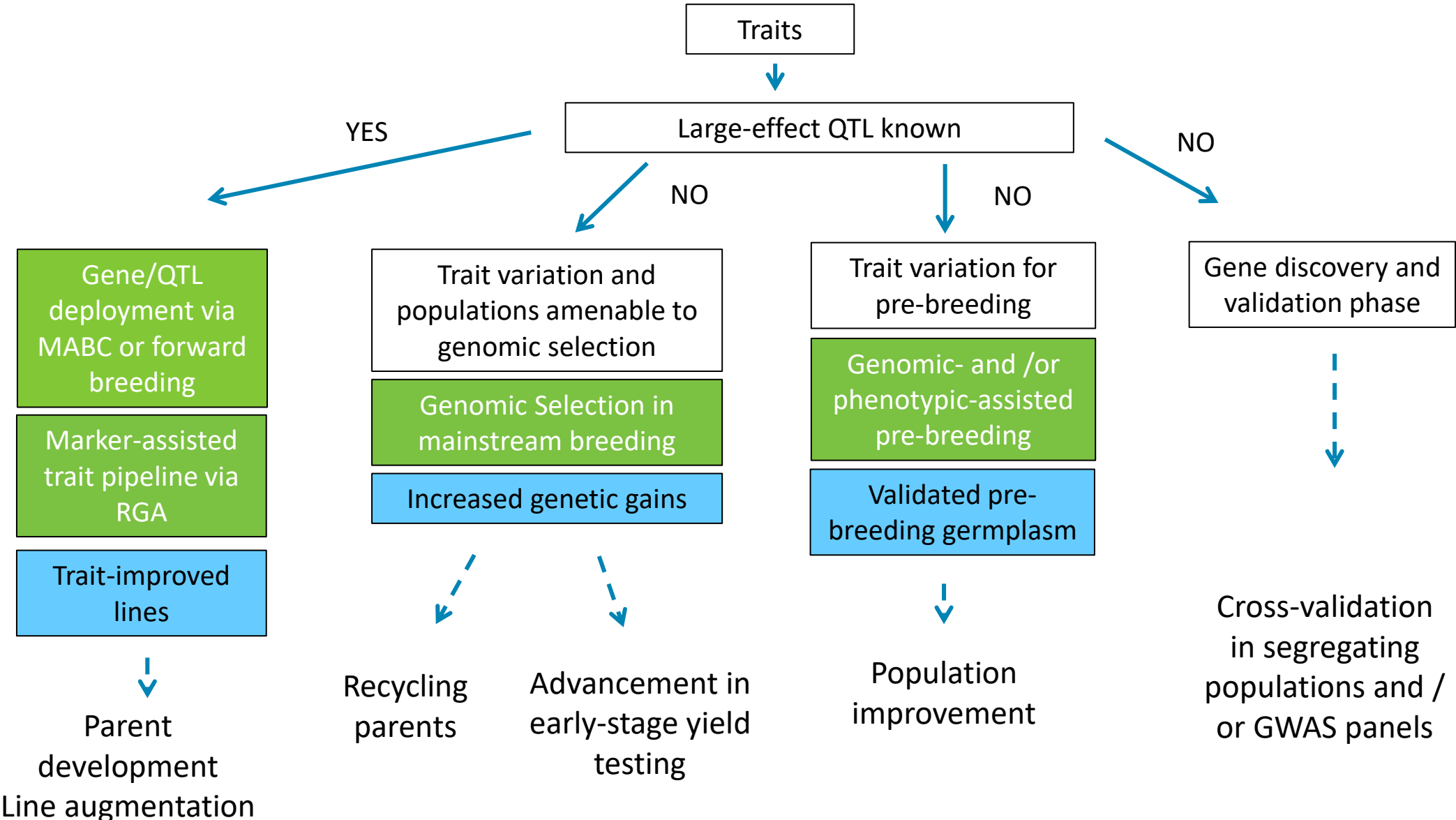
Improved wheat varieties

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

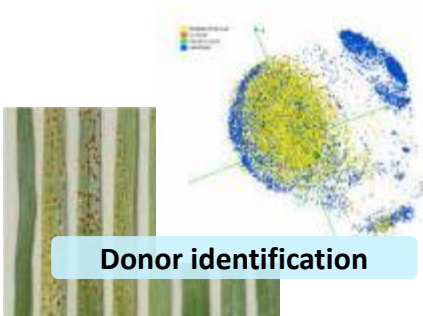
Discovery

New donors, new genetic variants

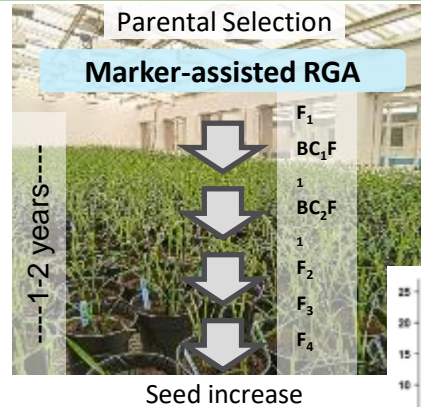


Trait-pipeline Advancement Committee

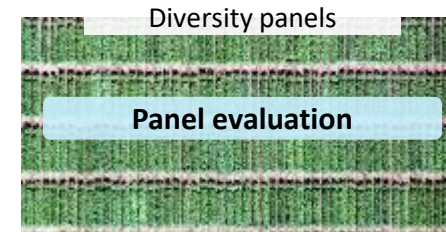
Trait-pipeline activities toolkit



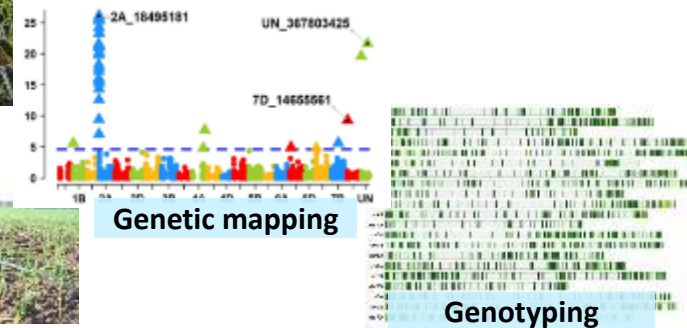
Donor identification



Phenotyping



Panel evaluation



Genetic mapping

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

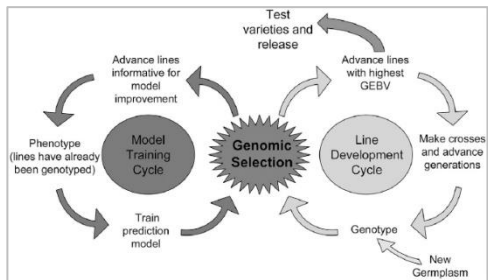
Examples



Parental development and line augmentation pipelines for disease resistance



Trait validation design for more complex stress adaptive traits



Genomic selection in mainstream breeding



Introgression of disease resistance genes

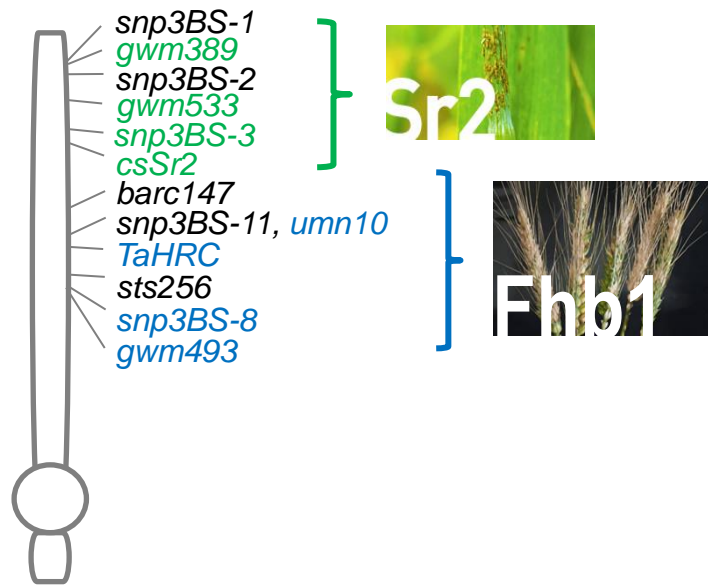
Source	Gene	Type
RL6077/AOC-YR SUJATA	<i>Lr67/Yr46/Sr55/Pm46</i> <i>Lr67/Yr46/Sr55/Pm46, YrSuj-7BL</i>	Pleiotropic APR
H-S A/2*MUNAL #1	<i>Sr2 + Fhb1</i>	FHB
SWSR22T.B. KACHU/3/WHEAR//2*PRL/2*PASTOR SHORT SR26 TRANS./4/3*CHIBIA//... SR32 W3763-SR35 SR47 SR50	<i>Sr22</i> <i>Sr25</i> <i>Sr26</i> <i>Sr32</i> <i>Sr35</i> <i>Sr47</i> <i>Sr50</i>	Stem rust resistance genes
ALPOWA CHUAN NONG 19 BLANCA GRANDE 515 SUMMIT 515 YR51#5515-1 KOELZ W 11192:AE YR57#5474-6 IRAGI LALBMONO1*4/PVN	<i>Yr39</i> <i>Yr41</i> <i>Yr5, Yr15</i> <i>Yr5, Yr15</i> <i>Yr51</i> <i>Yr52</i> <i>Yr57</i> <i>Yr59</i> <i>Yr60</i>	Stripe rust resistance genes
SERI//T.DIC. PI94623/AE.SQ. (1027)	<i>Gba, QRp.slu-5AL, QRp.slu-5BL</i>	Insect resistance
PI592729 PI572542	<i>H25</i> <i>H26</i>	Hessian fly resistance

Parental line development with new rust genes

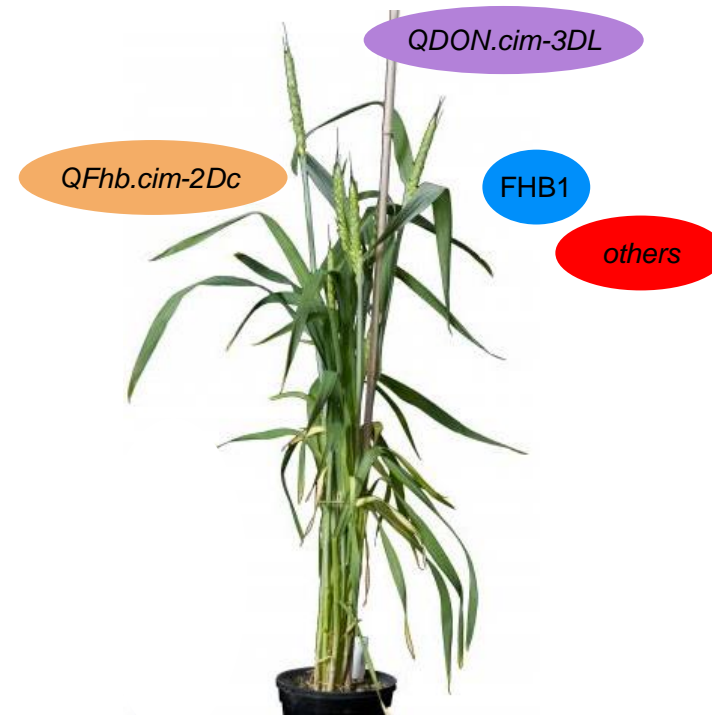
Cross	Gene	# lines YT18-19
BOKOTA*3//RL6077/AOC-YR	Lr67	1
BORL14*3/SUJATA	Lr67 + QTL.7BL	1
HARTOG_SUMAI3 (LINE B)/2*NAVJ07/5/KIRITATI//HUW234+LR34/PRINIA/3/FRANCOLIN #1/4/BAJ #1/6/2*TAM200/PASTOR//TOBA97/3/FRNCLN/4/WHEAR//2*PRL/2*PASTOR	Sr2 + Fhb1	2
HARTOG_SUMAI3 (LINE B)/2*NAVJ07/4/MUTUS//KIRITATI/2*TRCH/3/WHEAR/KRONSTAD F2004/5/2*TAM200/PASTOR//TOBA97/3/FRNCLN/4/WHEAR//2*PRL/2*PASTOR	Sr2 + Fhb1	1
SWSR22T.B.//TACUPETO F2001*2/BRAMBLING/3/2*TACUPETO F2001*2/BRAMBLING/4/MUNAL #1/5/2*MUNAL*2/WESTONIA	Sr22	1
SWSR22T.B.//TACUPETO F2001*2/BRAMBLING/3/2*TACUPETO F2001*2/BRAMBLING/4/SUP152/BAJ #1/5/2*KUTZ	Sr22	1
SWSR22T.B./FRANCOLIN #1//2*FRNCLN/3/3*WBLL1*2/BRAMBLING*2//BAVIS	Sr22	2
MUTUS*2/HARIL #1*2/3/SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU/4/MUCUY	Sr22	4
SWSR22T.B.//TACUPETO F2001*2/BRAMBLING/3/2*TACUPETO F2001*2/BRAMBLING/4/3*KACHU/3/WHEAR//2*PRL/2*PASTOR	Sr22 + Sr25	2
BORL14*3/4/KACHU/3/WHEAR//2*PRL/2*PASTOR	Sr25	3
SHORTENED SR26 TRANSLOCATION/4/3*CHIBIA//PRLII/CM65531/3/MISR 2/5/2*BAJ #1	Sr26	1
SHORTENED SR26 TRANSLOCATION//2*WBLL1*2/KKTS/3/BECARD/4/3*BORL14	Sr26	1
FRANCOLIN #1*2//ND643/2*WBLL1/3/SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU/5/SHORTENED SR26 TRANSLOCATION/4/3*CHIBIA//PRLII/CM65531/3/MISR 2/6/SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU	Sr26 + Sr22	4
BORL14*2/SR50	Sr50	7
BORL14*3/SR50	Sr50	7
BORL14*3/BLANCA GRANDE 515	Yr5 + Yr15	13
BORL14*2/BLANCA GRANDE 515	Yr5 + Yr15	6
BLANCA GRANDE 515/2*BAJ #1	Yr5 + Yr15	4
BORL14*3/KOELZ W 11192:AE	Yr52	3
YR57#5474-6/3*BAJ #1	Yr57	2
BORL14*3/IRAGI	Yr59	2
BORL14*2/IRAGI	Yr59	1
BORL14*3//LALBMONO1*4/PVN	Yr60	3
BORL14*2//LALBMONO1*4/PVN	Yr60	1
LALBMONO1*4/PVN//3*BAJ #1	Yr60	1

Combining genes for fusarium head blight resistance

Sr2-Fhb1 recombinants
introgressed in CIMMYT elite
backgrounds



Pyramiding of complementary
genes

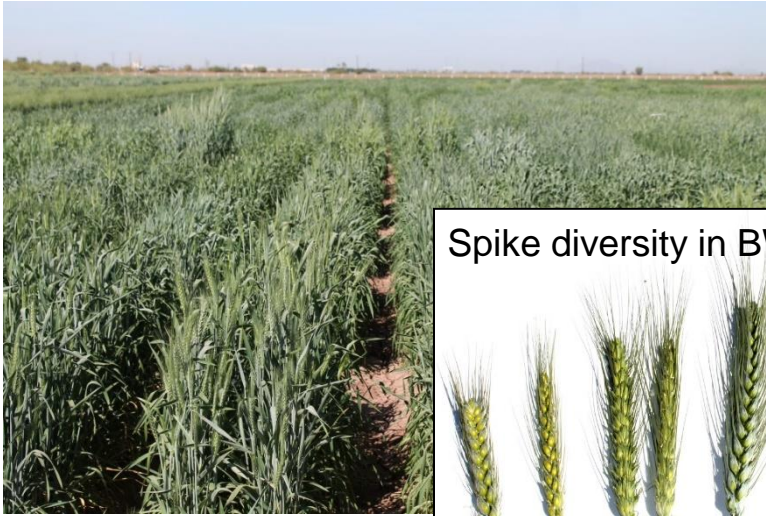


Trait augmentation pipelines

Crop*	Project Value	Product Profile	Trait	Genes
BW	Improved and diversified rust resistance	HW-OE-NM, HW-DT-NM	Stem and yellow rust	<i>Sr22, Sr50, Sr2, Yr57, Yr59, Sr35, Yr15, Yr5, Sr47, Sr25, Sr13</i>
BW	Enhanced Fhb resistance	HW-OE-NM, HW-DT-NM	Fusarium head blight	<i>Fhb1, Qfhb.cim-2DLc</i>
BW	Improved STB resistance	HW-OE-NM, HW-DT-NM	<i>Septoria tritici</i> Blotch	<i>Stb6, Stb16</i>
BW	Improved insect resistance	HW-OE-NM, HW-DT-NM	Green bug	<i>Gb7/Gba, Gb5, QRp.slu-5AL, QRp.slu-5BL-R</i>
BW	Novel diversity for stress tolerance (heat drought)	-	Heat/drought tolerance	LTP haplotypes from genetic resources (six haplotypes)
DW	Novel stem rust resistance gene combinations	ADW-DT+IR, ADW-HTEM	Stem rust	<i>Sr22 + Sr25</i>
DW	Improved grain weight/yield	ADW-DT+IR, ADW-HTEM	Grain weight	<i>TaGW2</i>



Evaluation of new sources for stress tolerance in physiological pre-breeding



Bread wheat diversity panel (370)

Includes best performing lines from:

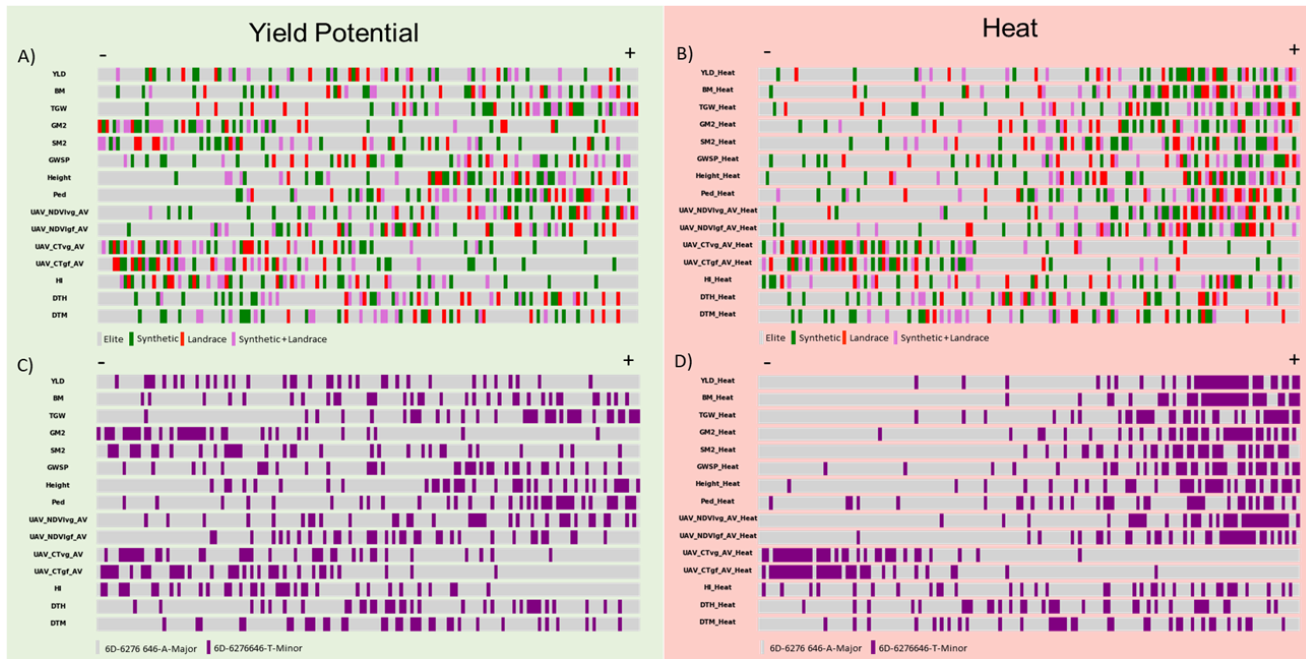
- International nurseries
- Landraces/FIGS panels
- Lines derived from inter-specific hybridization



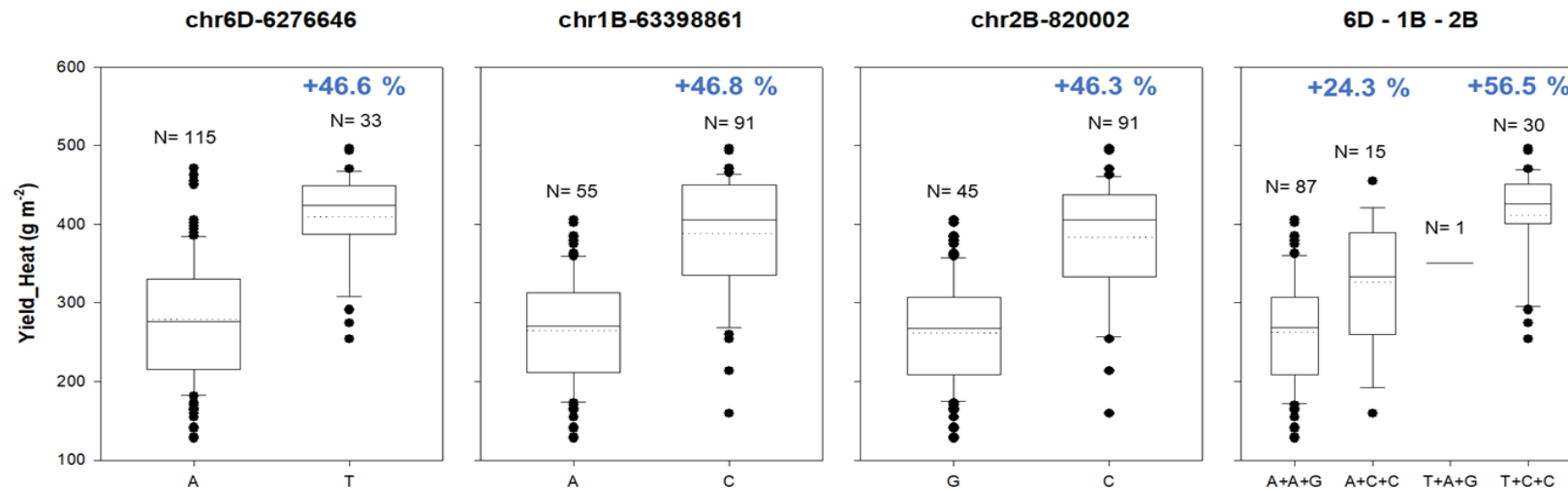
Elite primary synthetic panel (160)

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

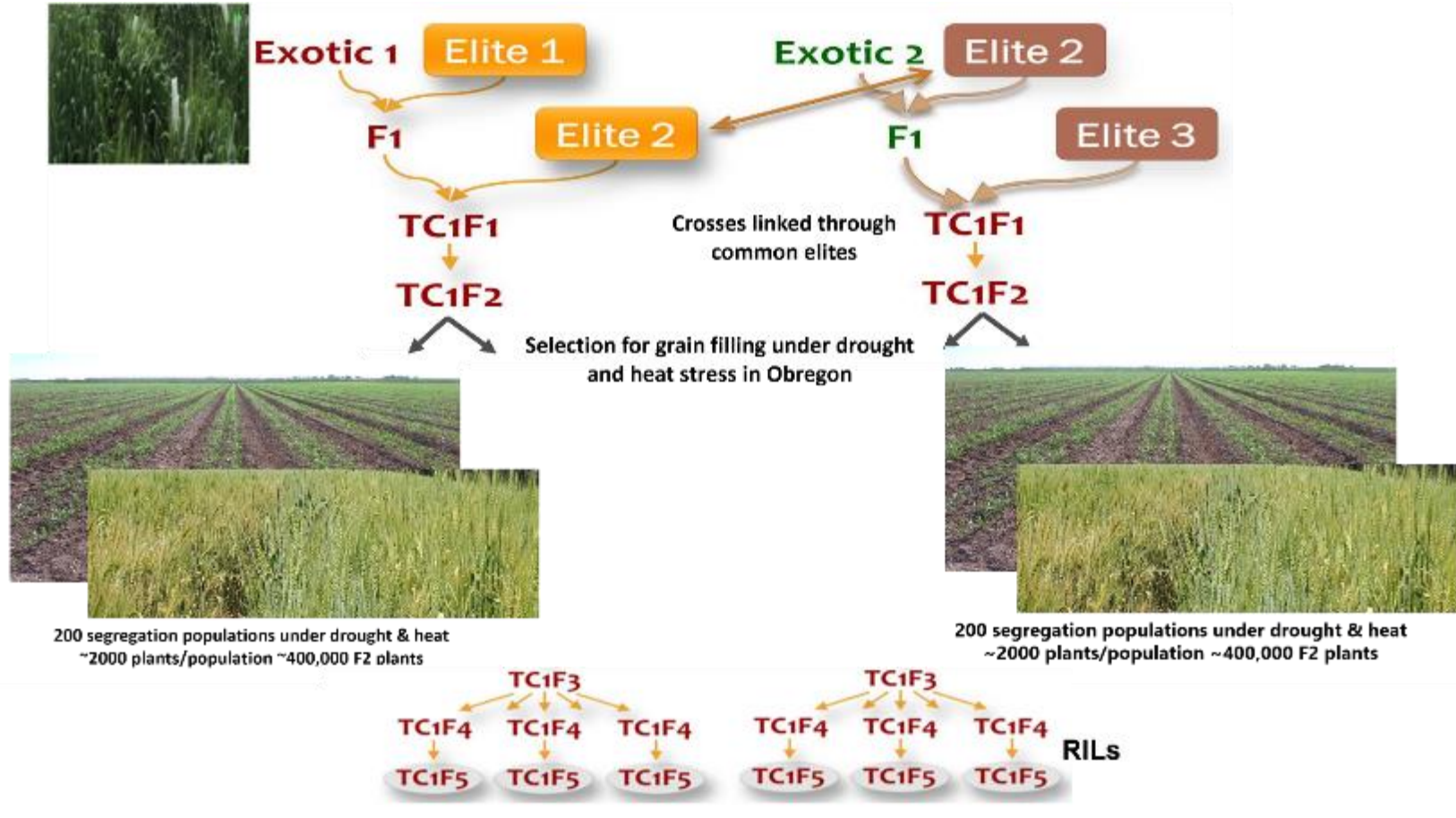
Identification of genomic regions derived from novel sources



- 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

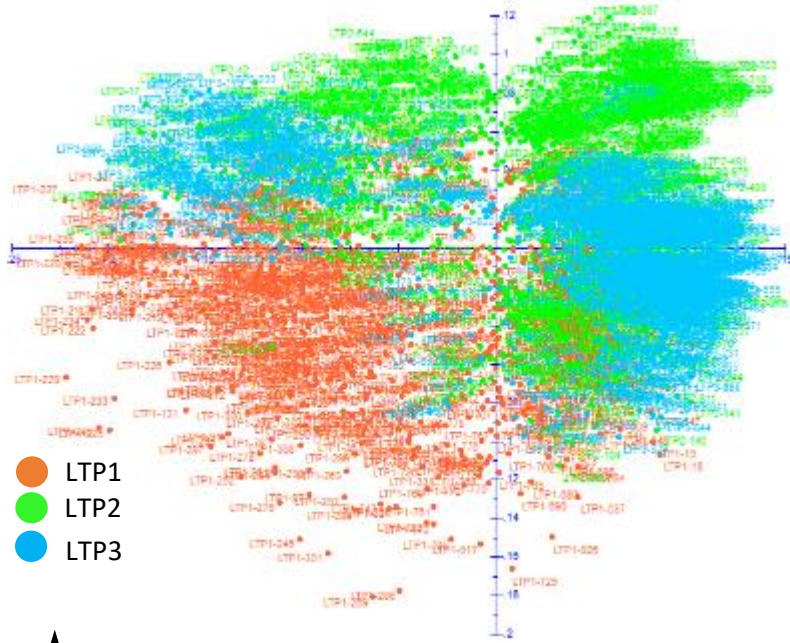


Identification of genomic regions derived from novel sources

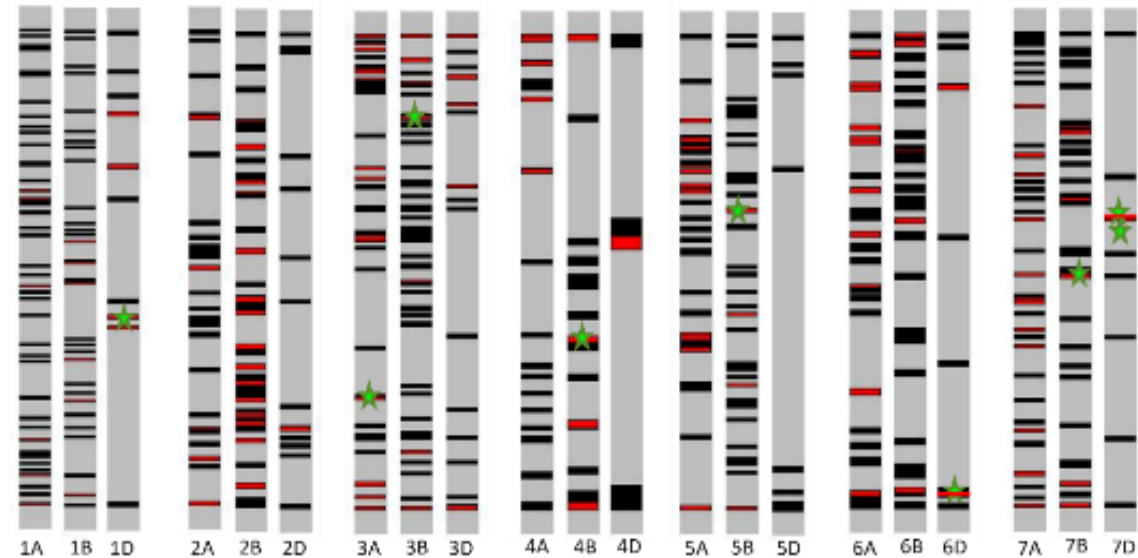


- Three-way crossing scheme of linked top-cross populations (LTP) in the Seed of Discovery project
- Exotic parents include synthetic hexaploidy and landraces selected via FIGS
- Elite parent include lines from the spring BW breeding program

Quantification of the contribution of the exotic parents in LTPs

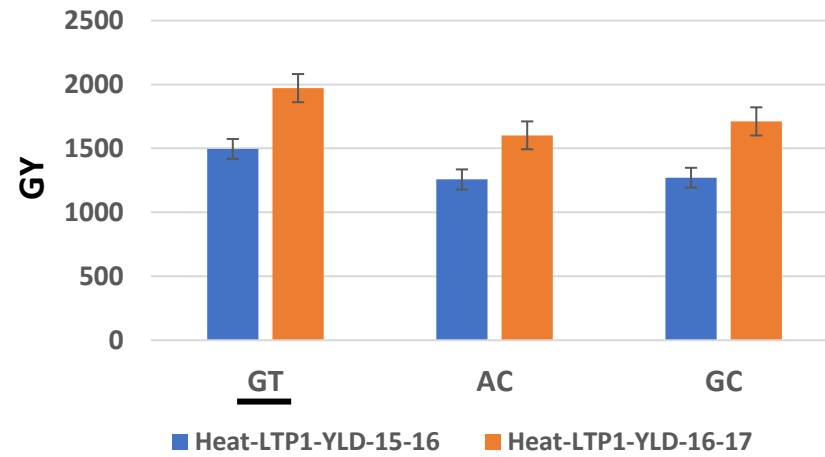


★ Exotic specific associations

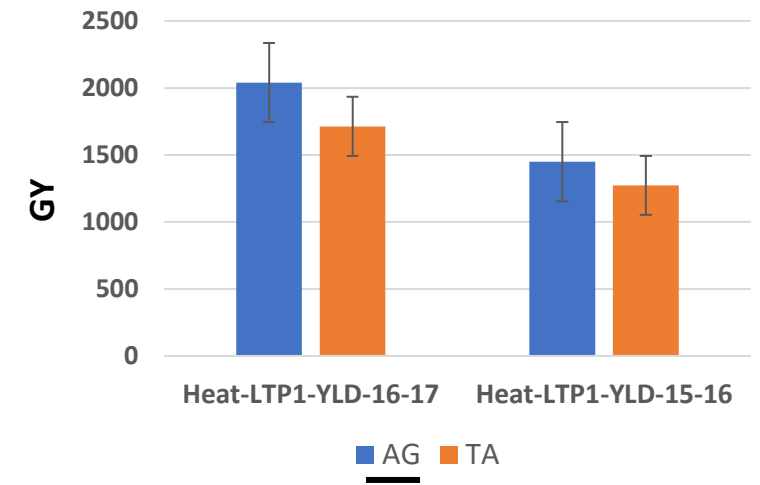


Introgressed genomic regions from exotics are shown as red bars

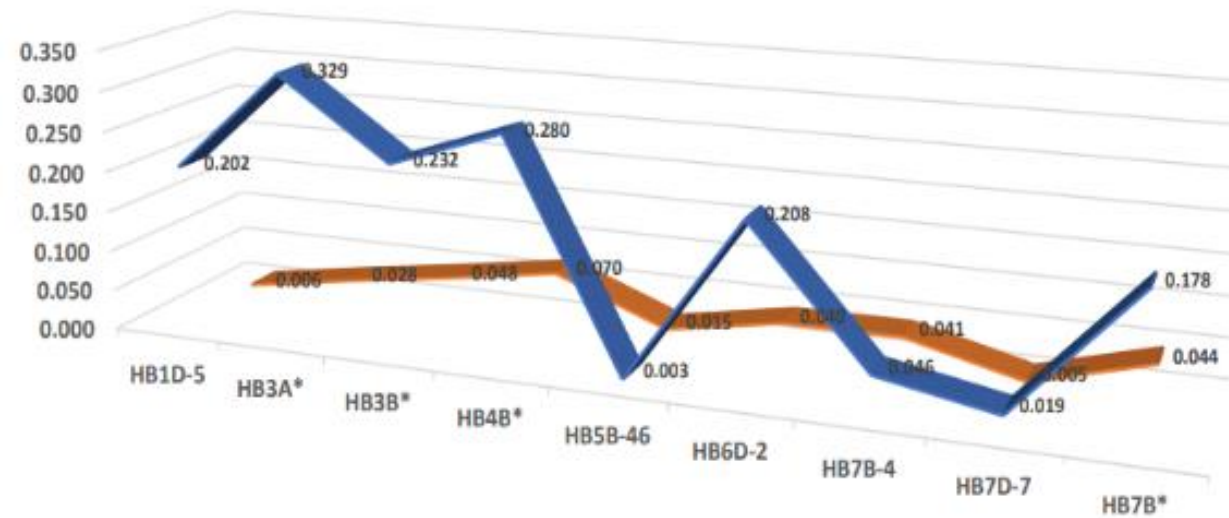
HB6D-Heat stress
(+240-370 kg/ha in GY under heat stress)



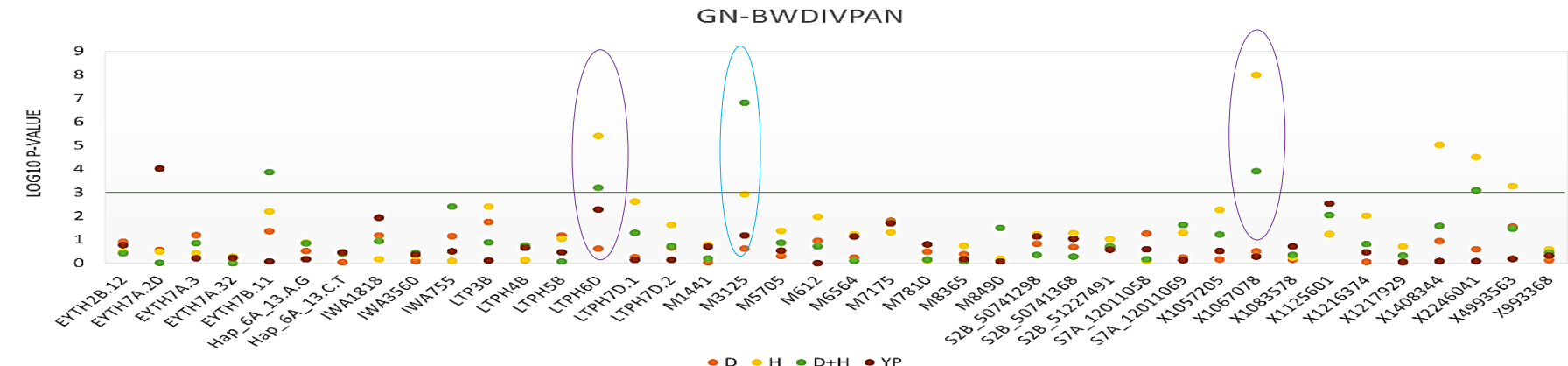
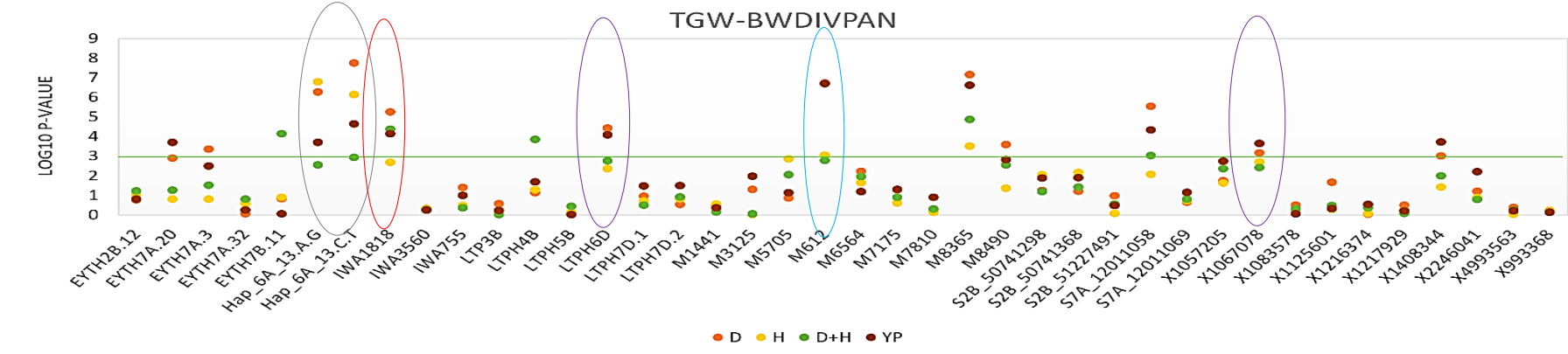
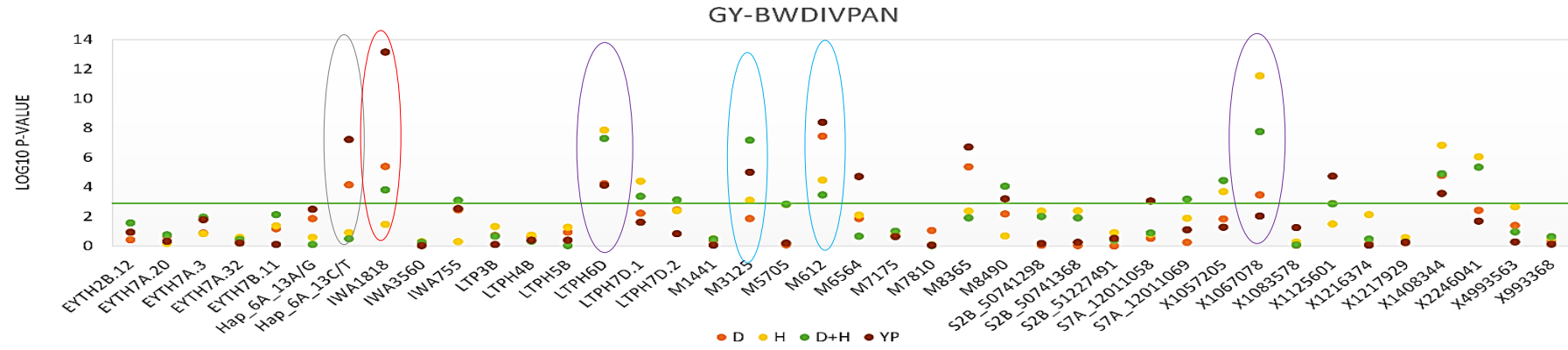
HB3B-Heat stress
(+176-326 kg/ha in GY under heat stress)



Haplotype frequencies in exotic parents and 16K genebank accessions

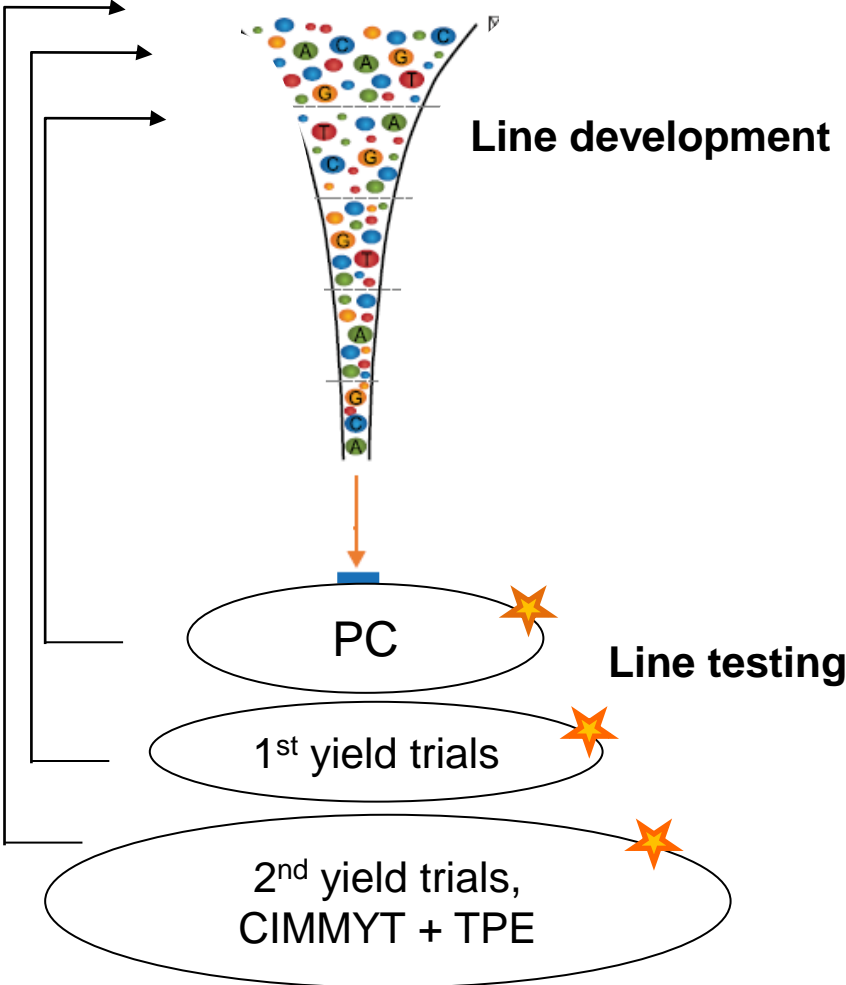


QTL validation across germplasm panels (e.g., BWDIVPAN)



Genomic Selection in mainstream breeding

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 1st stage yield trials

Training set:
Lines in 2nd 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

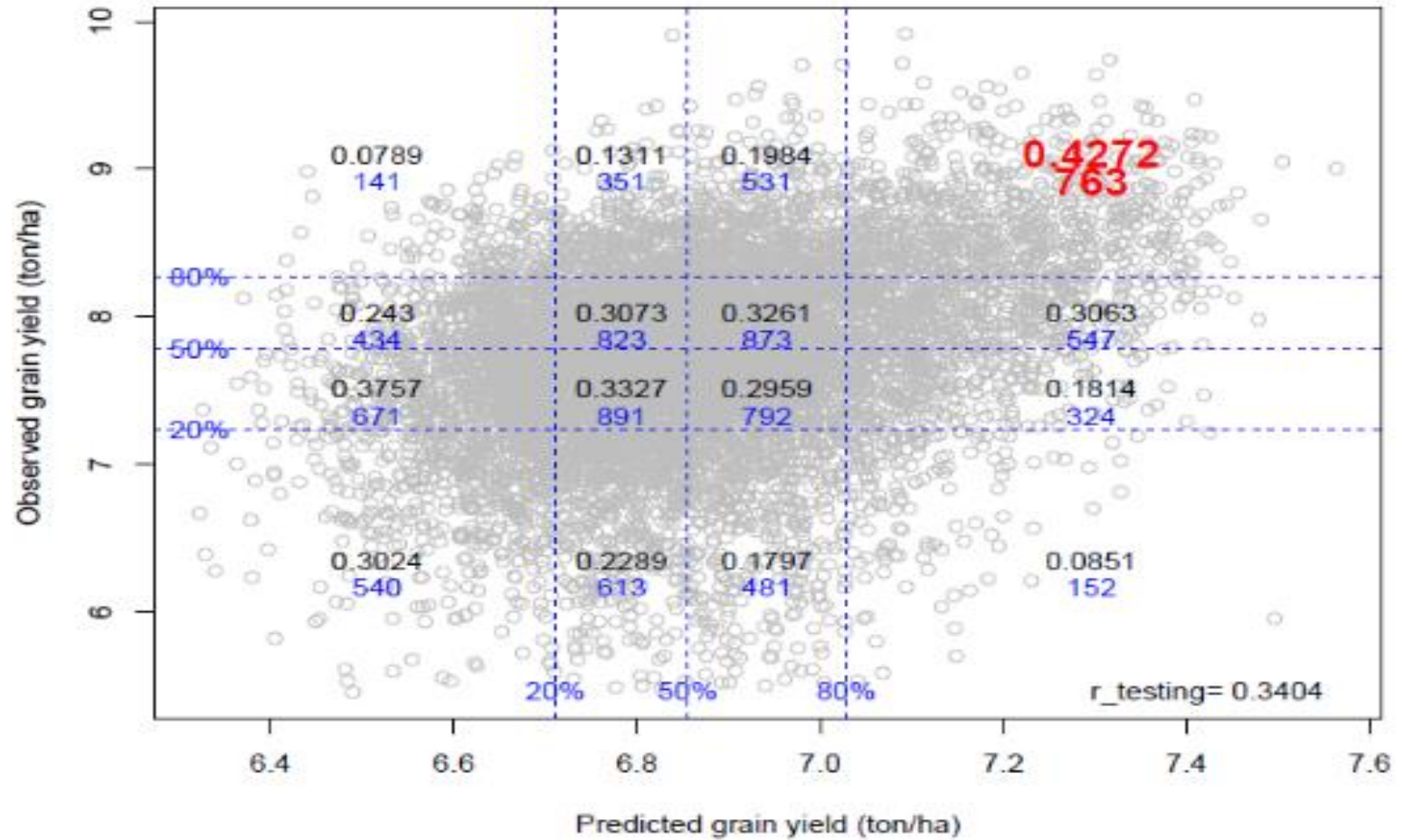
Stage 2 yield trials (EYT): ~ 600-700 lines, 6 envr. at CENEB and 5-6 TPE sites

Genomic prediction ability of elite lines in the stage 1 yield trials

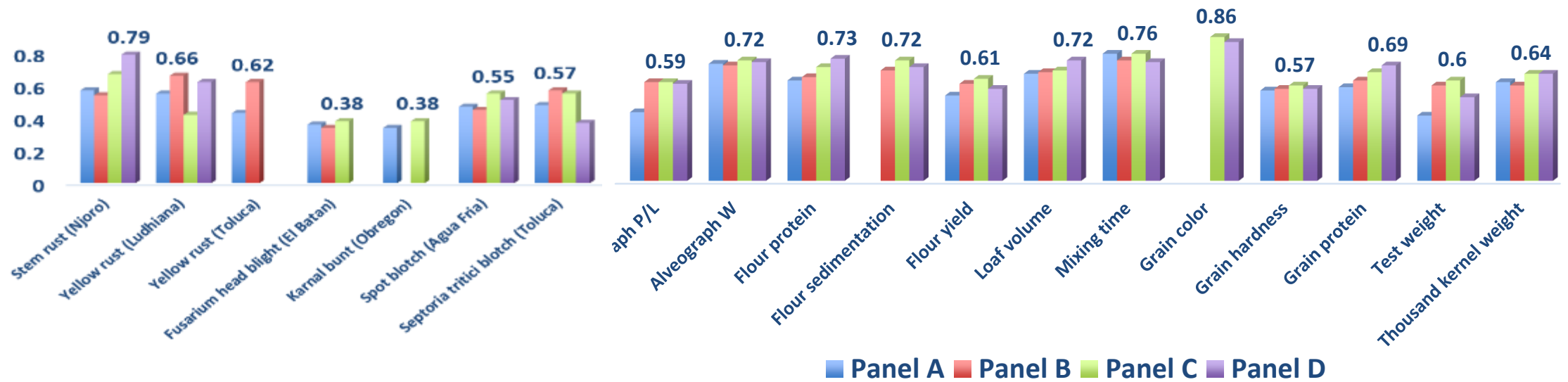
Phenotypic and genotypic data

YT trials

Env	Number of lines
13-14	7406
14-15	8936
15-16	9276
16-17	9394
17-18	8311
18-19	8927 ← To be predicted



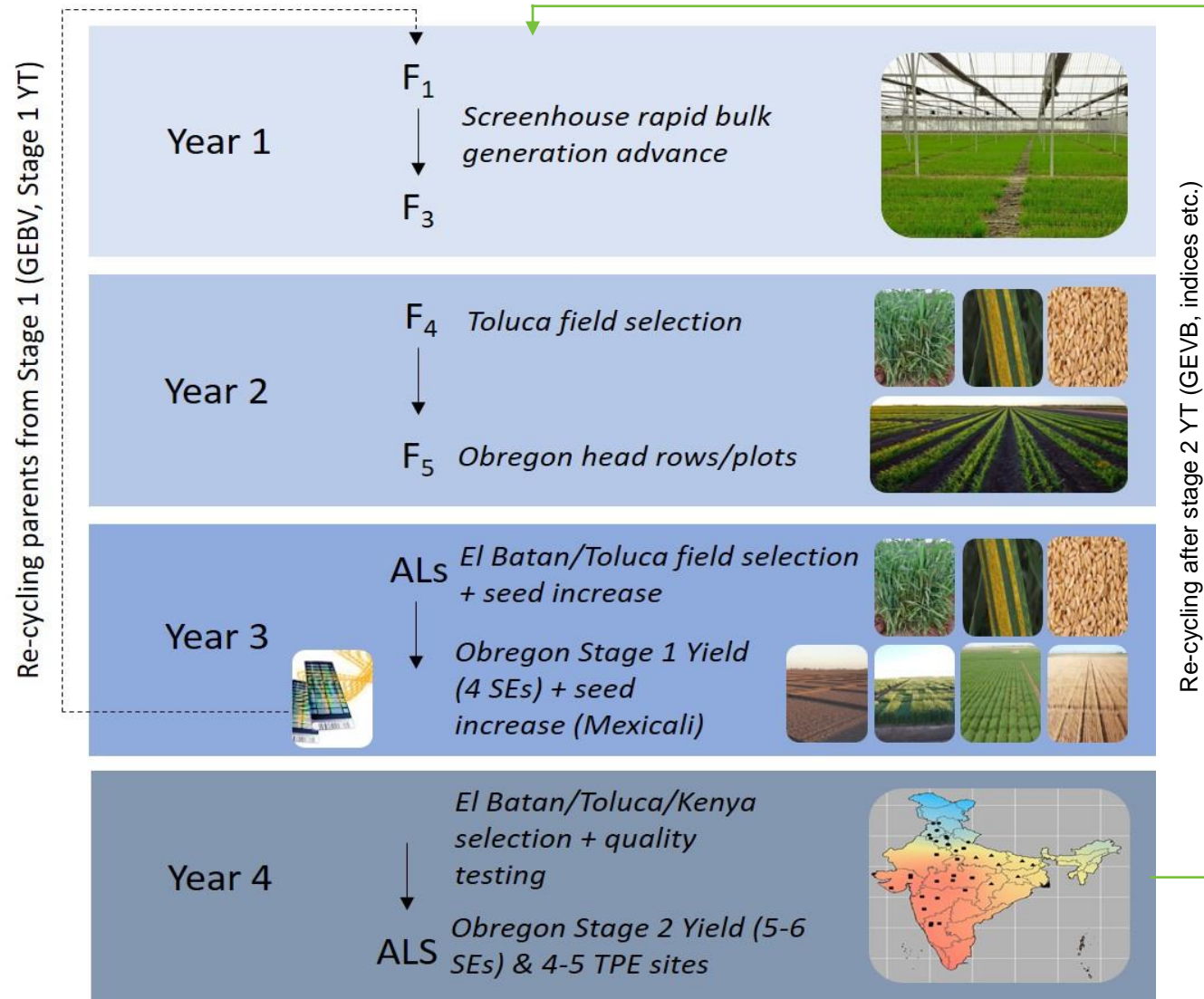
Genomic prediction for more than yield in the Stage 2 yield trails



Scaling-up selections in the Stage 1 yield trails using the Stage 2 yield trails as training population for more than grain yield and stem rust

Optimizing the breeding schemes by reducing cycle time

Rapid Bulk Generation Advancement (RBGA) optimization and implementation



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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