Wheat to eat

Accelerating plant breeding to address global food & nutrition security

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IWGSC Webinar - 24th September 2021

Accelerating Genetic Gains in Maize and Wheat

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Wheat is essential to global food security

Global wheat area ~220 million ha

Average farm size: 1-3 ha vs. 40-5000 ha

Genetic resources

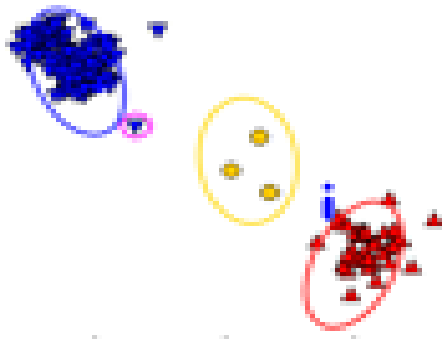
Elite germplasm

Multi-environments

Phenotyping methods

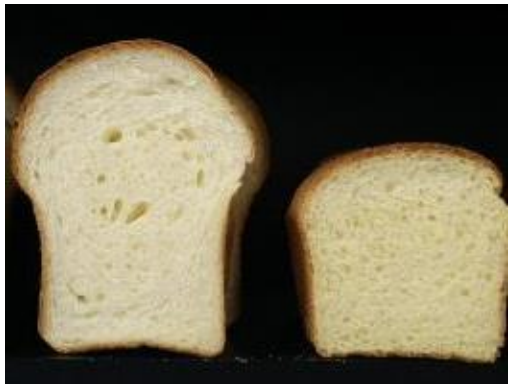
Remote sensing

A vast array of available breeding tools & resources



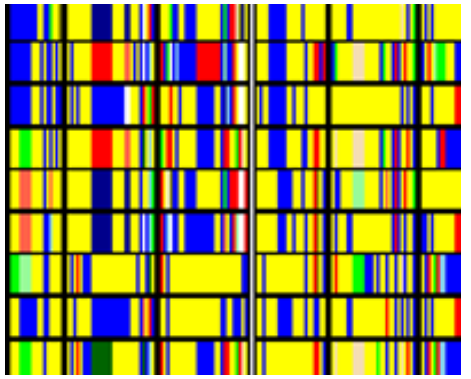
Marker-assisted selection

Pan-genomes



Quality traits

Biotechnology



Genomic selection

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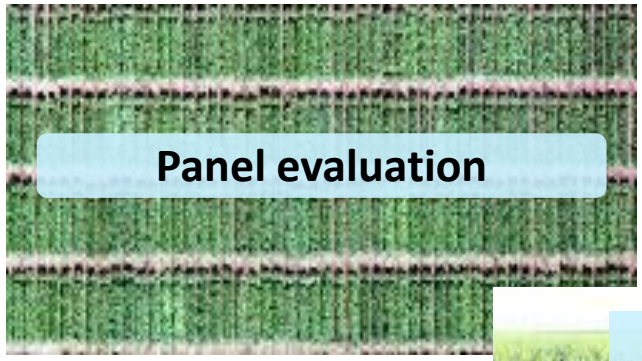
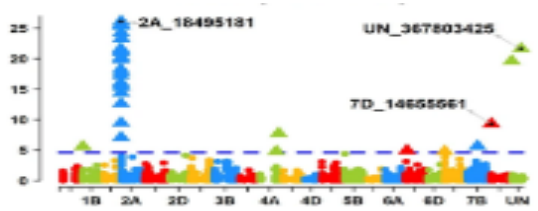
Challenge: how to funnel multiple outputs into breeding improvements?

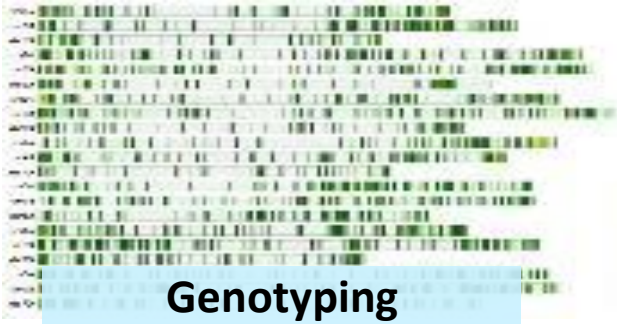


Panel evaluation

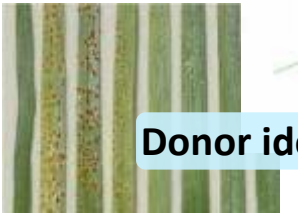


Genetic mapping

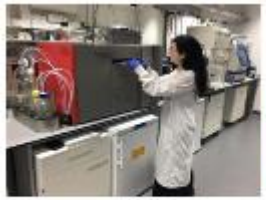
Phenotyping

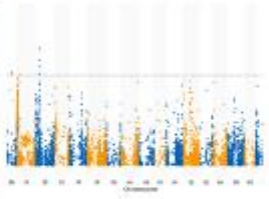


Genotyping



Donor identification





Trait-linked markers

International germplasm evaluation

Search:

Trait Name	Trait Description	Marker Name(s)	Marker Discovery Platform	Marker Conversion Technology	Validated?	Potential / Known IP?	References
Grain weight	Thousand grain weight	GW2-A		KASP	Yes	None	Simmonds et al 2016
Grain weight	Thousand grain weight	GW2-B		KASP	Yes	None	Wang et al 2018
Grain weight	Thousand grain weight	GW2-D		KASP	Yes	None	Wang et al 2018
5A gene	Thousand	GL-1		KASP	Yes	Only	unpublished

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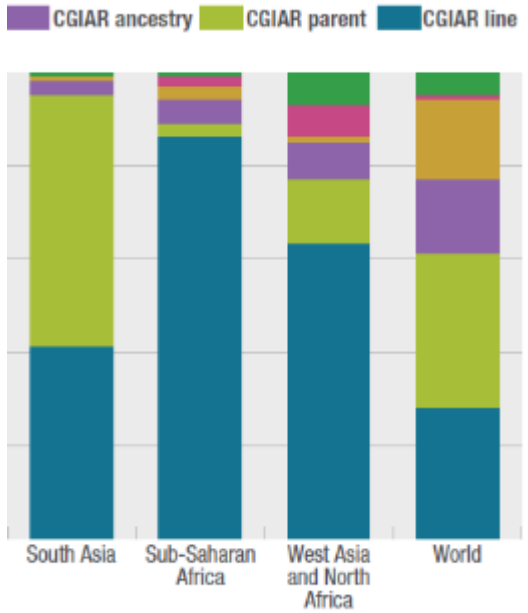
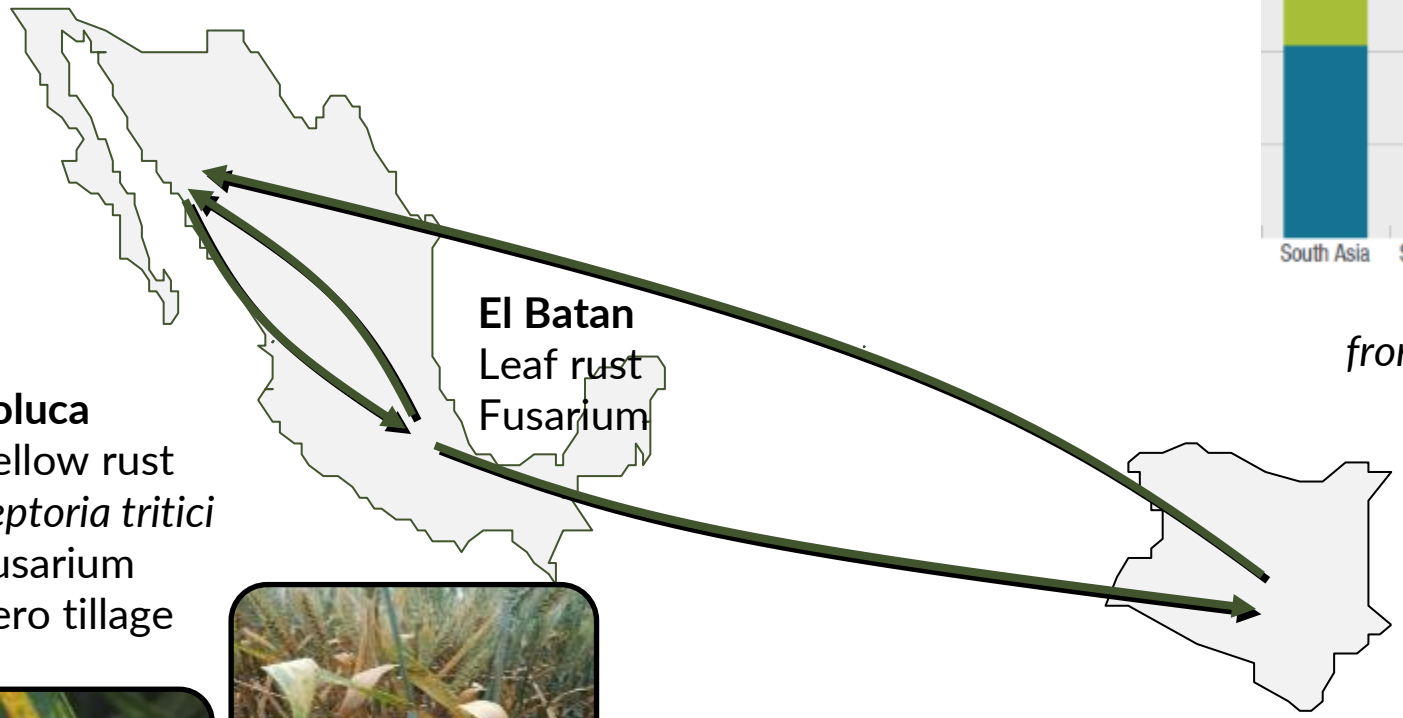
Context: *achieving large impact worldwide through provision of improved germplasm from centralized breeding.*



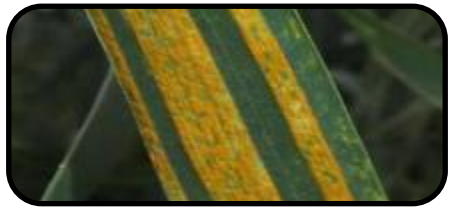
from Lantican, 2016

Cd Obregon
High yield (irrigated)
Water-use efficiency
Heat tolerance
Leaf rust
Stem rust (not Ug99)



El Batan
Leaf rust
Fusarium

Toluca
Yellow rust
Septoria tritici
Fusarium
Zero tillage



Njoro, Kenya
Stem rust (Ug99 group)
Yellow rust

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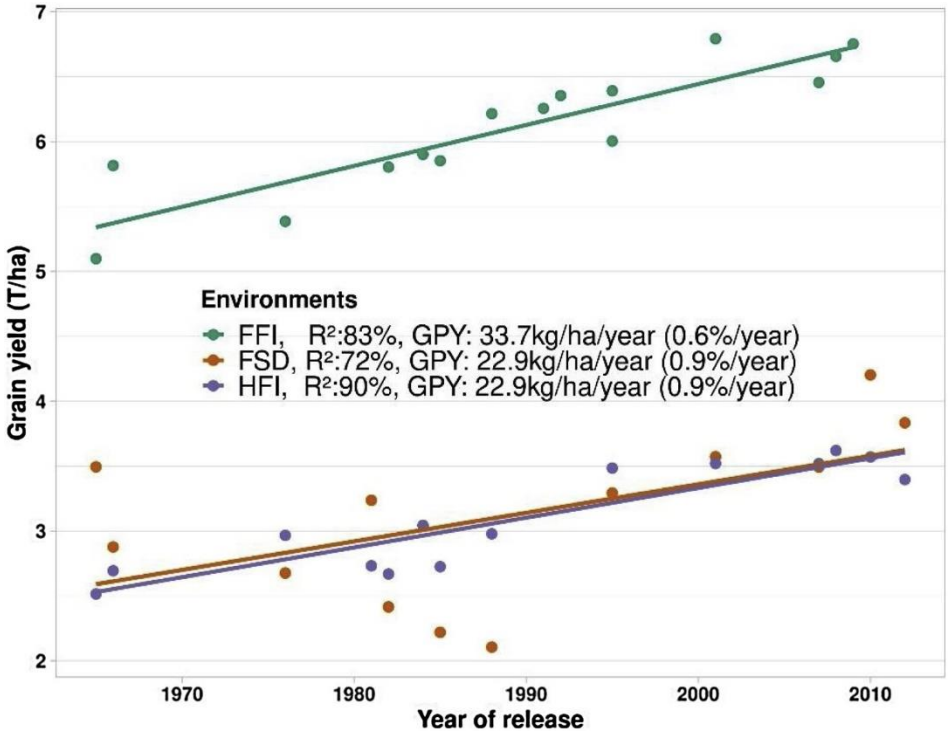
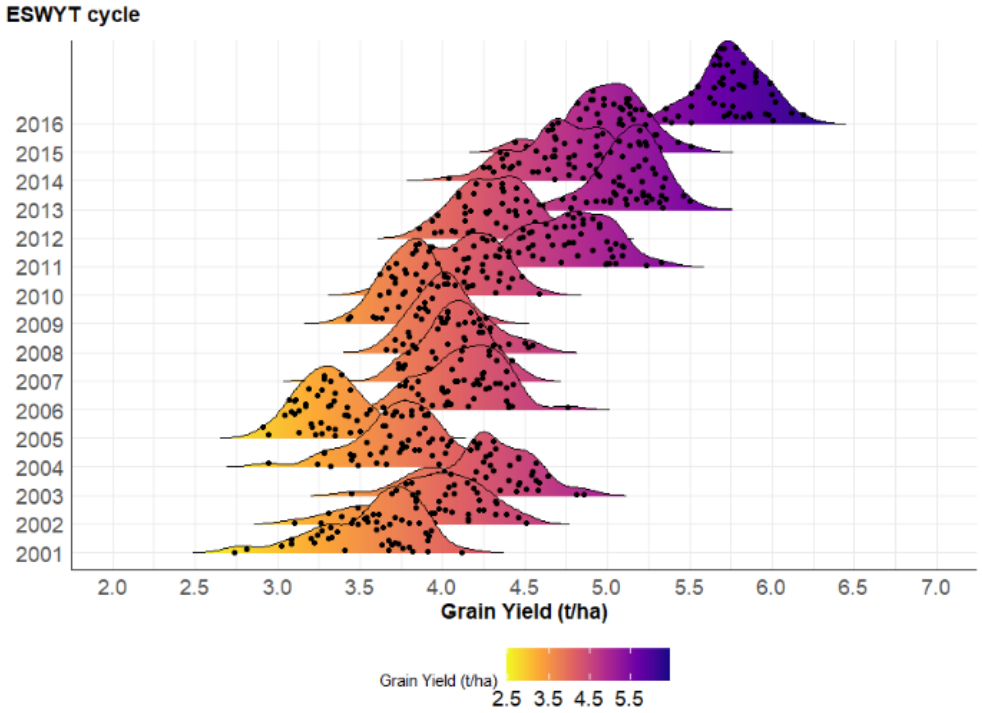
Continuous breeding progress for grain yield

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

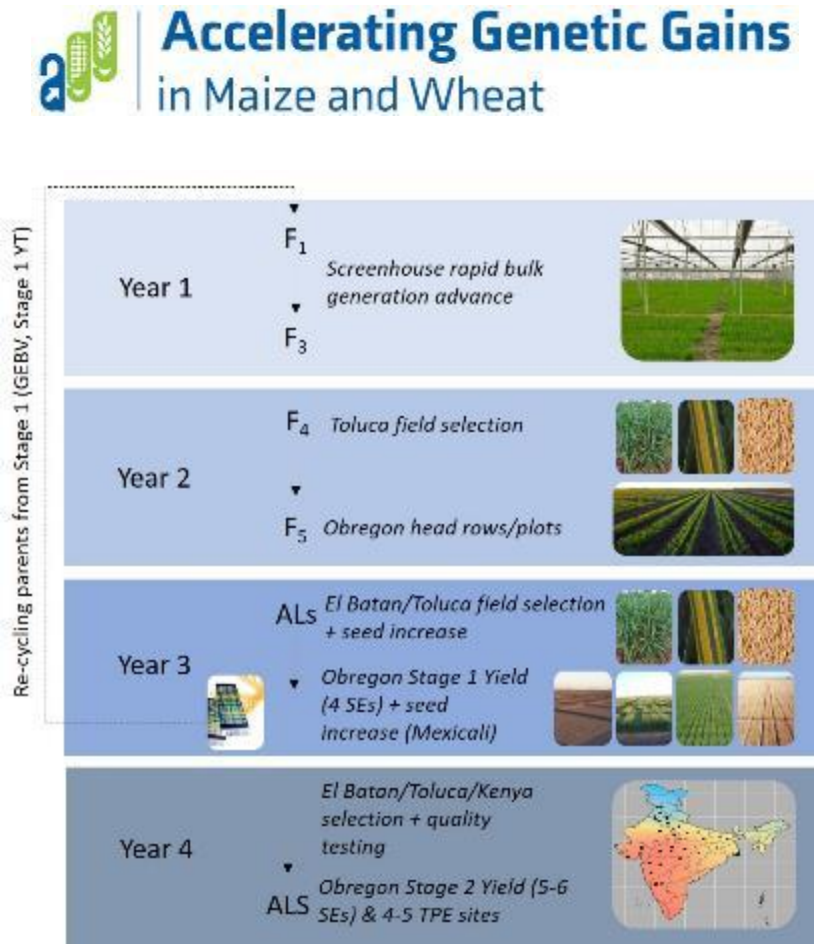


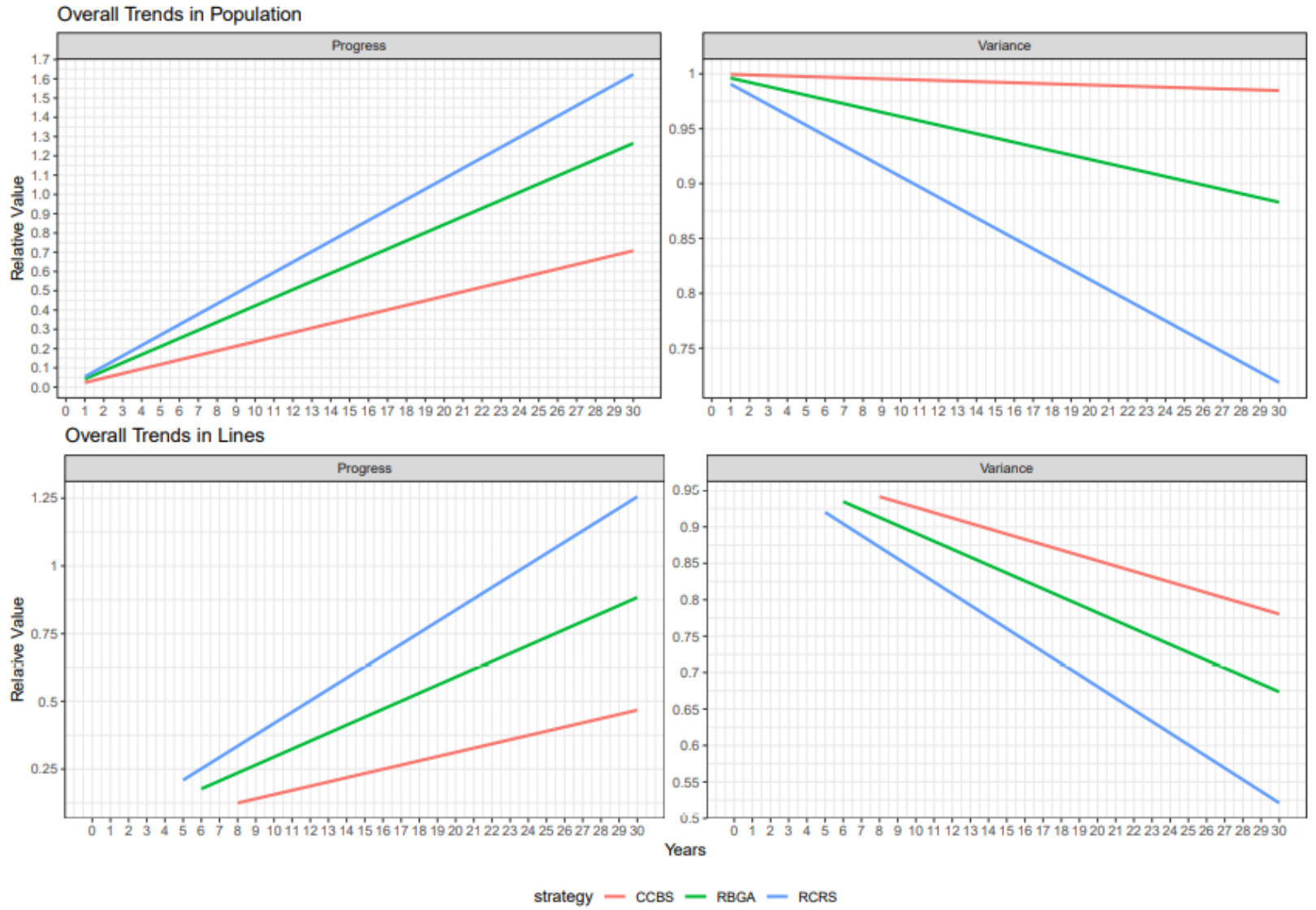
Crespo-Herrera *et al.* (2021) Target population of environments for wheat breeding in India: definition, prediction and indirect genetic gains. *Frontiers in Plant Science* doi: 10.3389/fpls.2021.638520

Accelerating genetic gains in wheat breeding

Adoption of rapid-generation breeding methods to reduce breeding cycle time

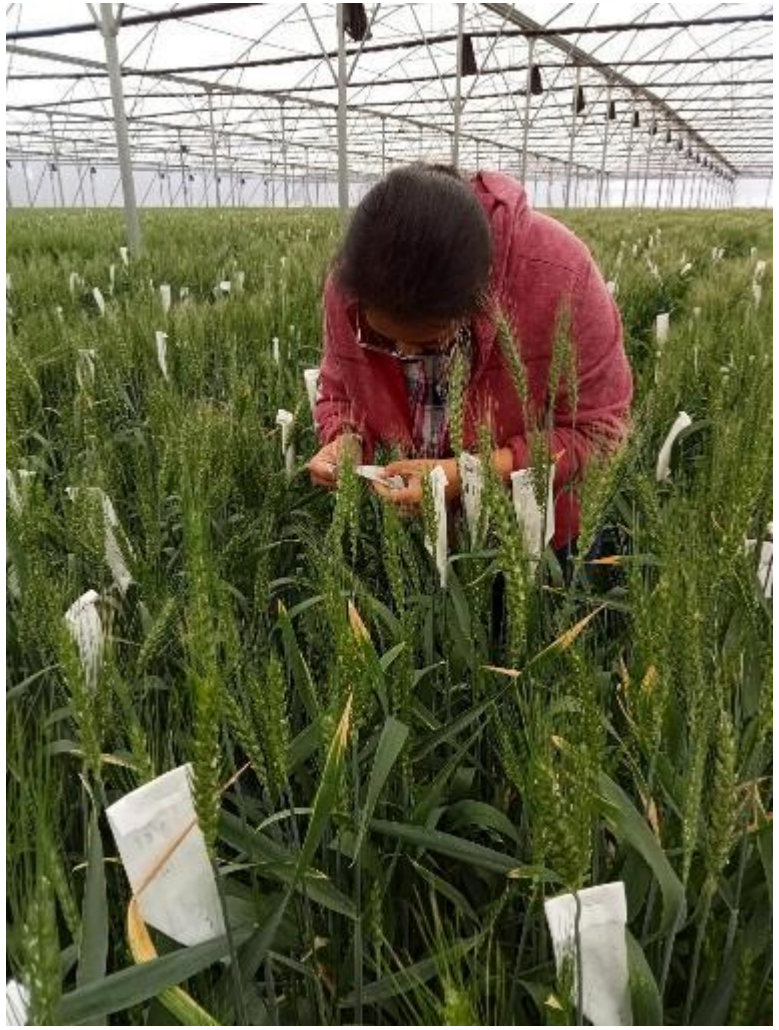
- **Faster breeding:** new screenhouse infrastructure in Toluca is being used to reduce breeding cycle time from ~6 to 3 years per cycle
- **Innovative methods:** genomic selection is being implemented for rapid recycling of parents.
- **Novel trait introgression:** speed breeding has been initiated for rapid trait introgressions of race-specific genes and QTLs for disease resistance into elite lines.





AGG-Wheat simulations led by FH Toledo

First cycle of crossing complete (August, 2021)



AGG-Wheat breeding scheme optimization led by Suchismita Mondal

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Marker-assisted trait development pipelines

Trait-pipeline advancement process

Assess current pipeline demand, initiation of trait advances and augmentation (internal and external), future pipeline demand

Line augmentation

Variant deployment, Product development

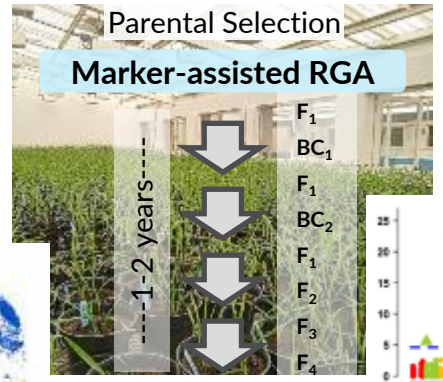
Parent development

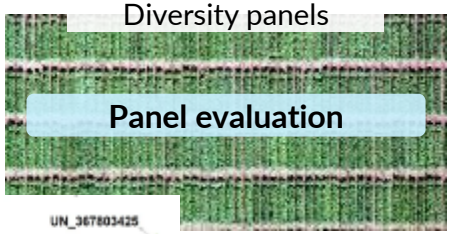
Marker design variant introgression

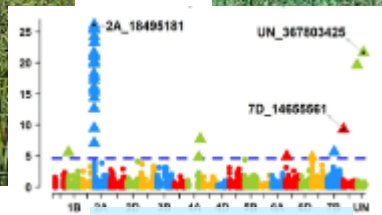
Discovery

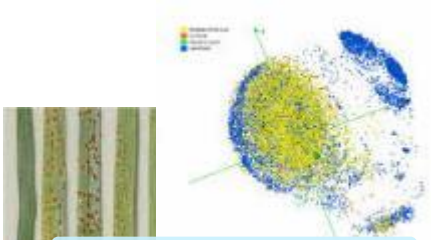
New donors, new genetic variants

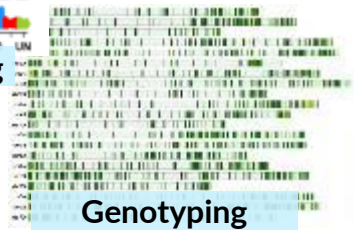
Trait-pipeline activities toolkit











Support Services: New database structures, genotyping, decision support tools

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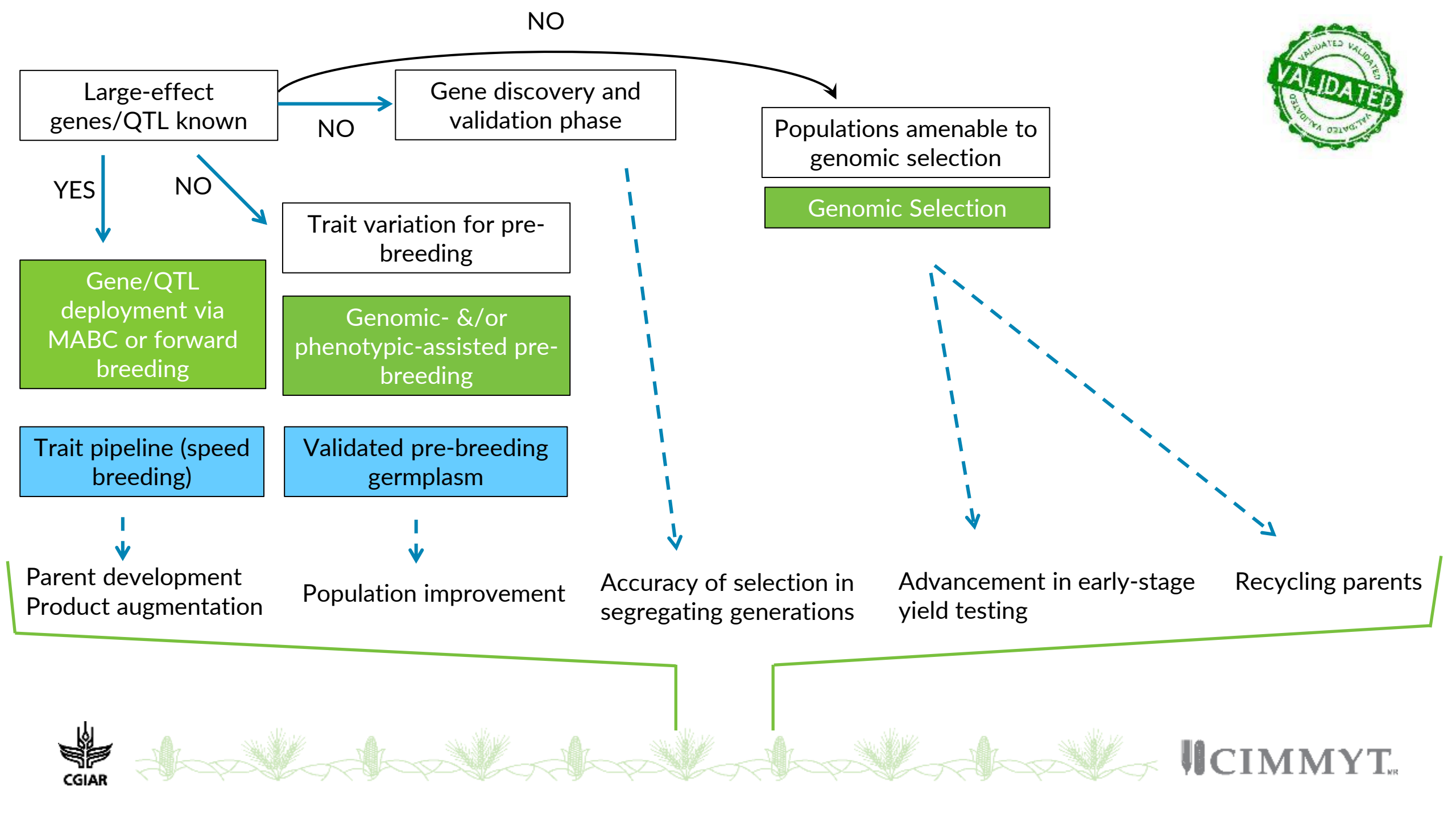
NO
Large-effect genes/QTL known
NO
Gene discovery and validation phase
Populations amenable to genomic selection
Genomic Selection
YES
NO
Trait variation for pre-breeding
Gene/QTL deployment via MABC or forward breeding
Genomic- &/or phenotypic-assisted pre-breeding
Trait pipeline (speed breeding)
Validated pre-breeding germplasm
Parent development
Product augmentation
Population improvement
Accuracy of selection in segregating generations
Advancement in early-stage yield testing
Recycling parents

Current line 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	*Sr22*, *Sr50*, *Sr2*, *Yr57*, *Yr59*, *Sr35*, *Yr15*, *Yr5*, *Sr47*, *Sr25*, *Sr13*, *YrSP*
BW	Enhanced Fhb resistance	HW-OE-NM, HW-DT-NM	Fusarium head blight	*Fhb1*, *Qfhb.cim-2DLc*
BW	Improved STB resistance	HW-OE-NM, HW-DT-NM	*Septoria tritici* Blotch	*Stb6*, *Stb16*
BW	**Improved insect resistance**	**HW-OE-NM, HW-DT-NM**	**Green bug**	**Gb7/Gba, Gb5, QRp.slu-5AL, QRp.slu-5BL-R**
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	Sr22 + Sr25
DW	Improved grain weight/yield	ADW-DT+IR, ADW-HTEM	Grain weight	TaGW2

Crop* BW = bread wheat; DW = durum wheat

AGG-Wheat marker-trait introgression from Susanne Dreisigacker & Suchismita Mondal

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Genotyping workflow

From sampling to data analysis

Sampling of leave tissue in the field or greenhouse

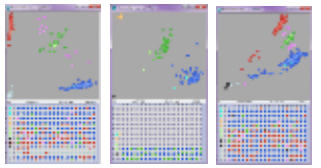
Sample shipment when outsourcing

DNA extraction

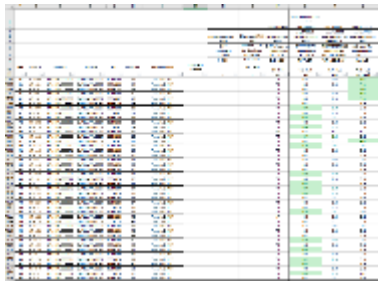
Project planning and genotyping preparation (sample managing and tracking)

Genotyping service

intertek



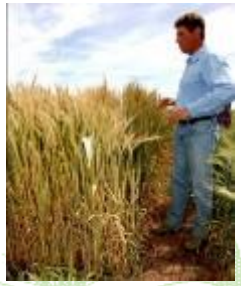
Genotyping



Data QC and decision support tools

GOBii

Data storage



Field selection based on MAS and phenotypic data

CIMMYT Wheat Molecular Biology lab led by Susanne Dreisigacker

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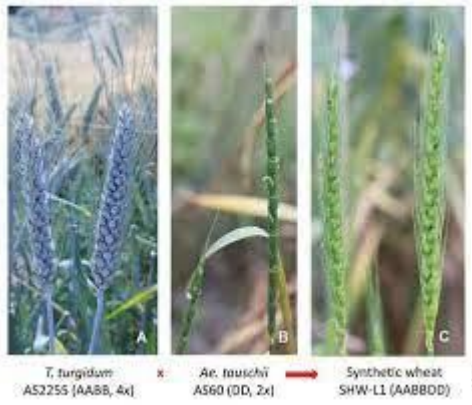
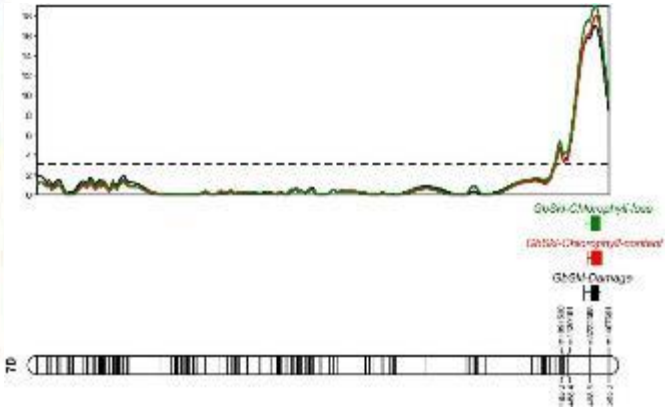
Native genetics for insect resistance

Current pyramiding of four loci in a single background using speed breeding & MAS

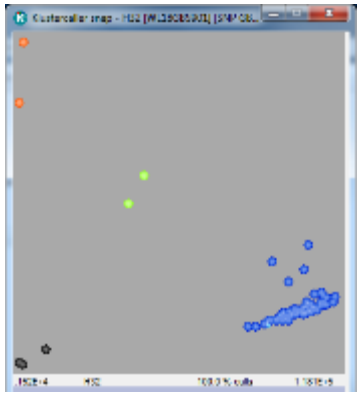
Synthetic wheat



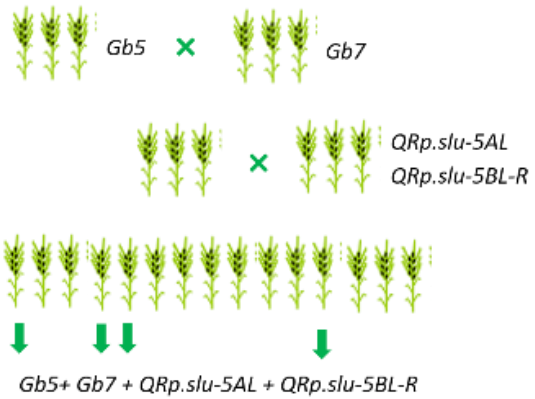
Major QTL on chr7B



Breeding marker



Gene pyramiding



Aphid resistance work led by Leo Crespo & Susanne Dreisigacker

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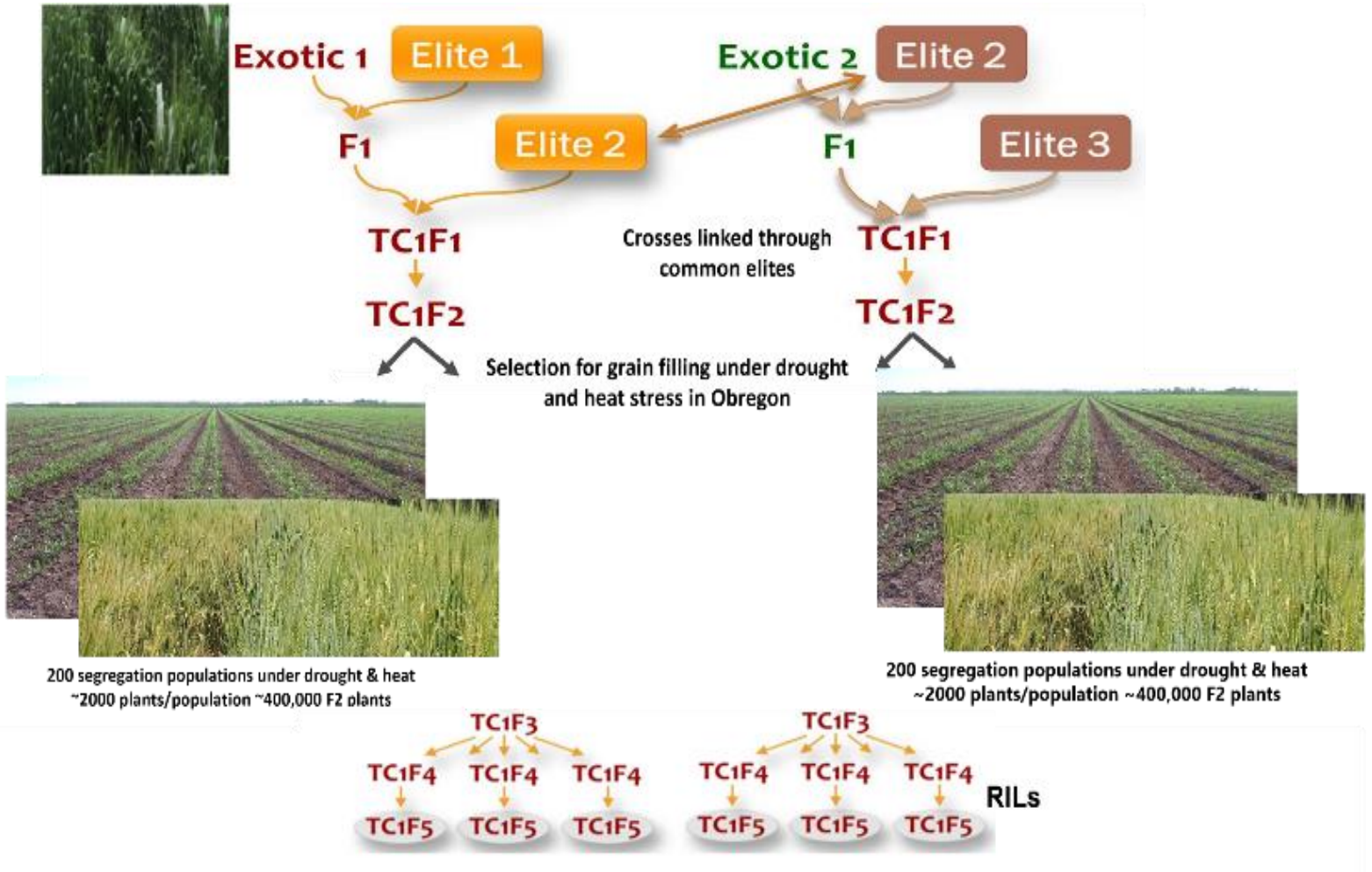
Novel genomic regions derived from genetic resources



- 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

LTP discovery work led by Deepmala Sehgal & Susanne Dreisigacker

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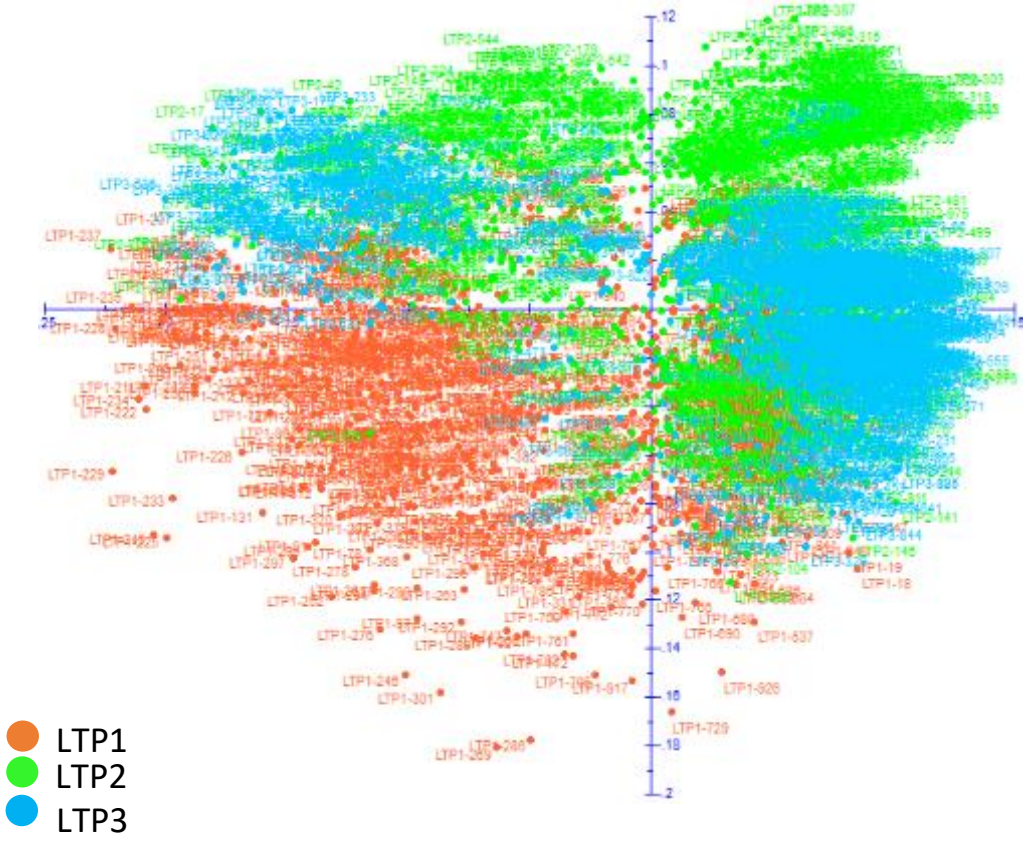
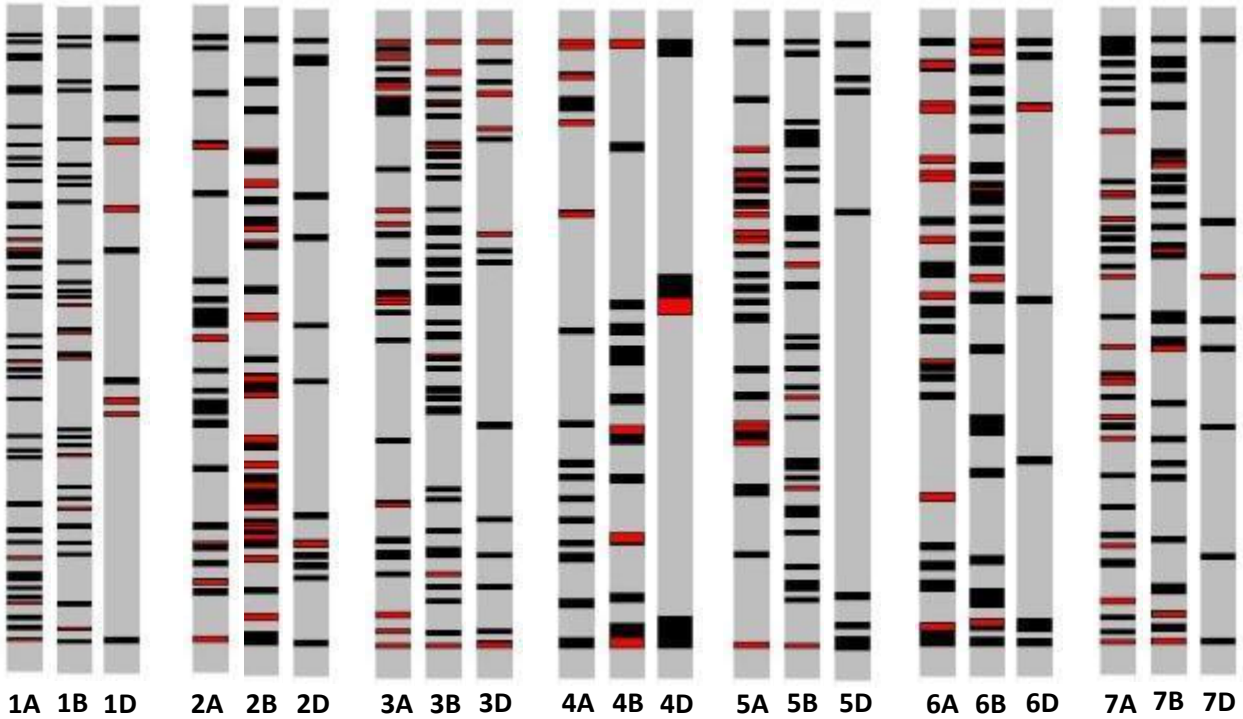
Quantification of the contribution of the exotic parents in LTPs

Genetic diversity of three LTP populations used for genetic analysis (2,867 pre-breeding lines)



Haplotype map of the exotic genome contribution to the pre-breeding lines (approx. 17%)

Introgressed genomic regions from exotics are shown as red bars



LTP discovery work led by Deepmala Sehgal & Susanne Dreisigacker

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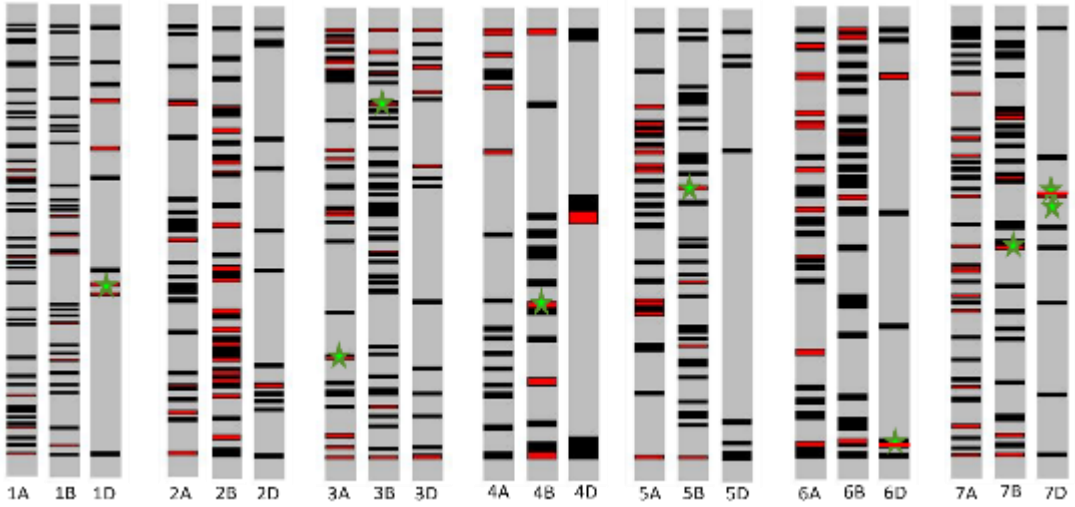
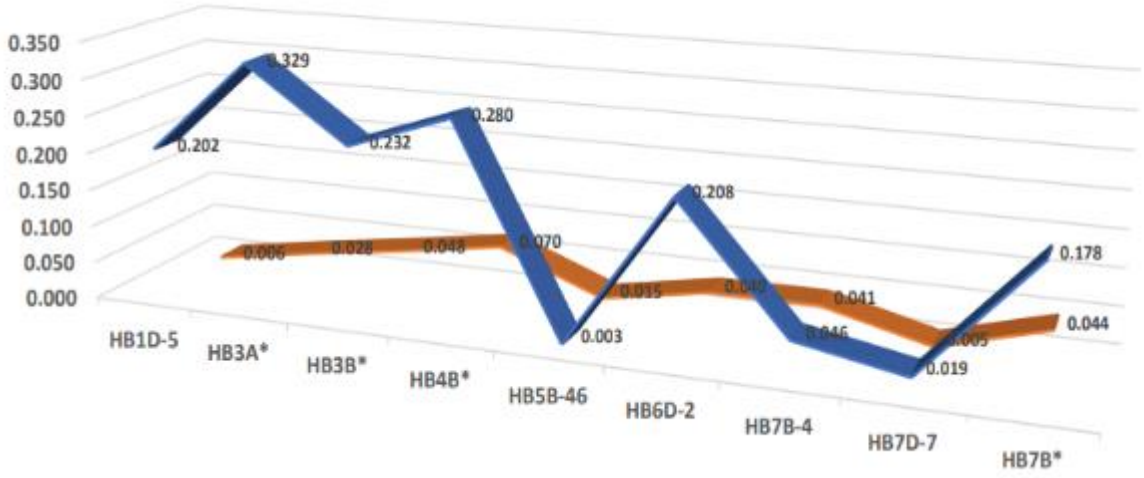
Exotic-specific association derived by GWAS

Exotic specific associations

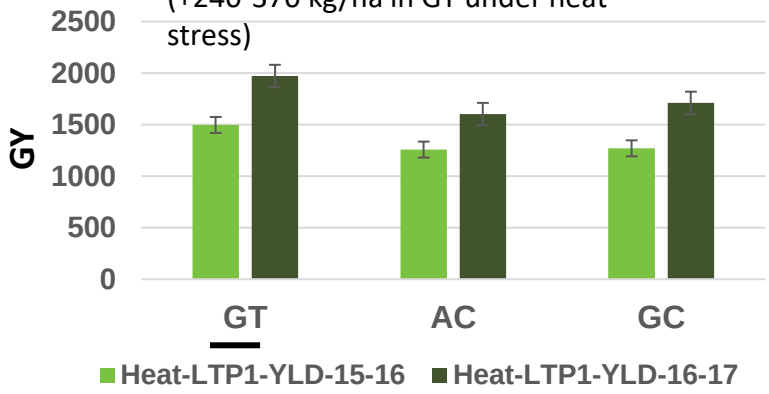


Haplotype frequencies in exotic parents and 16K genebank accessions



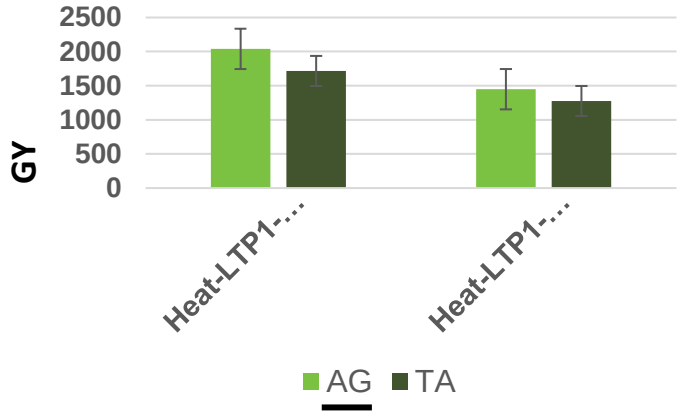
HB6D-Heat stress

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

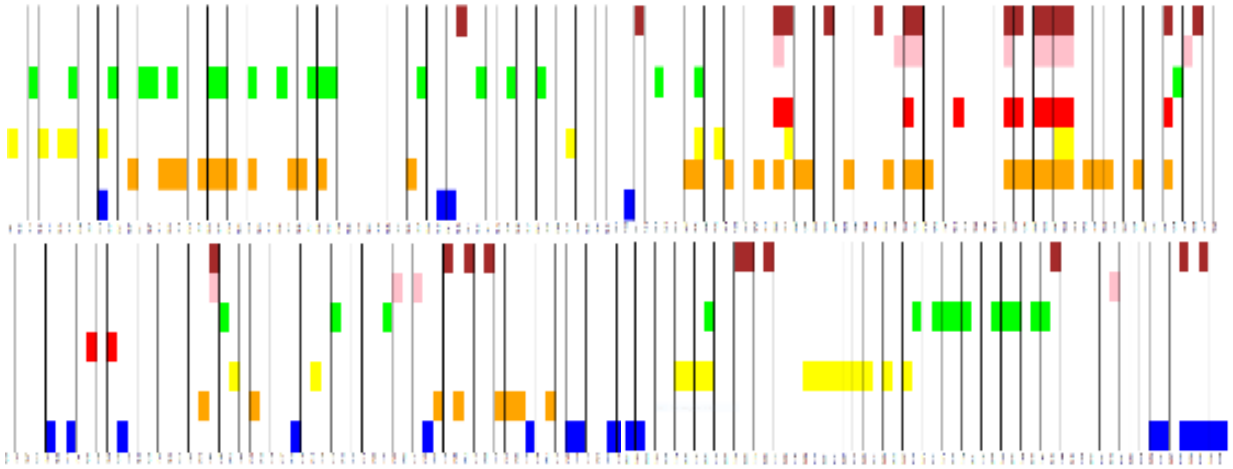


HB3B-Heat stress

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



Evaluation & introgression of exotic-specific associations in 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

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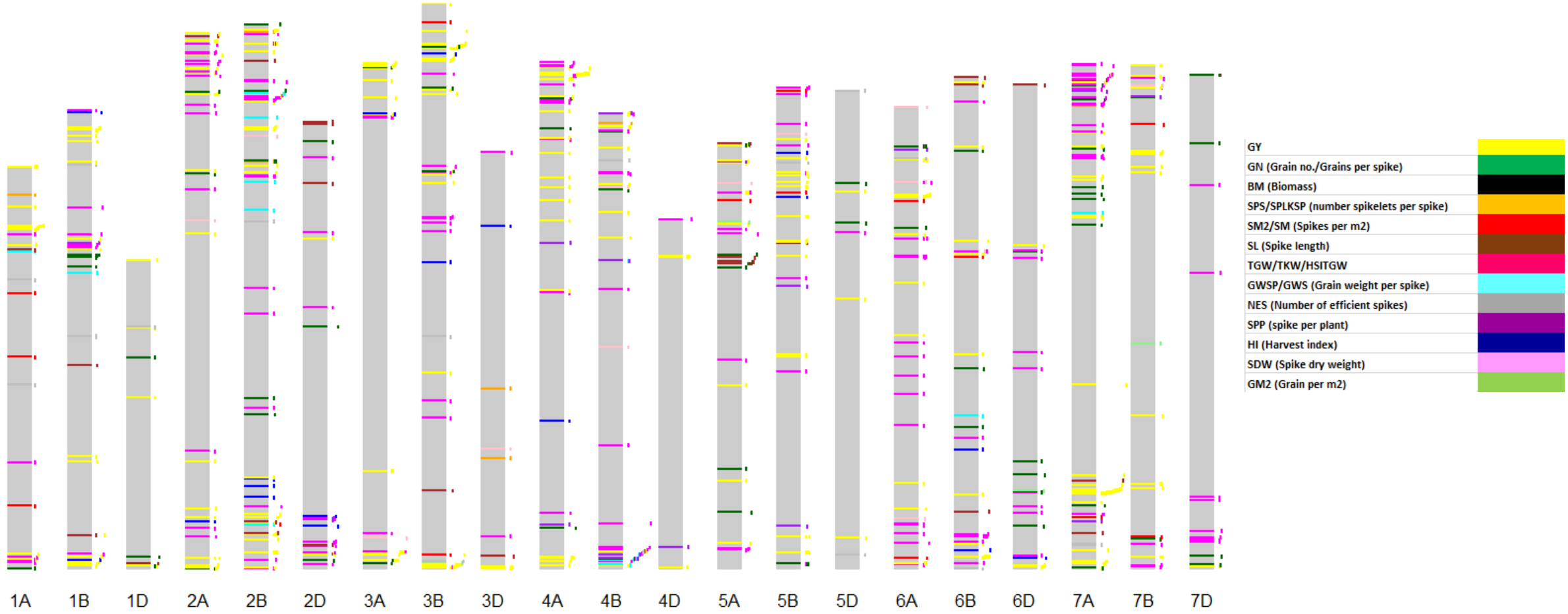
Catalogue of QTLs aligned to the wheat reference genome



CIMMYT QTL catalogue led by Deepmala Sehgal

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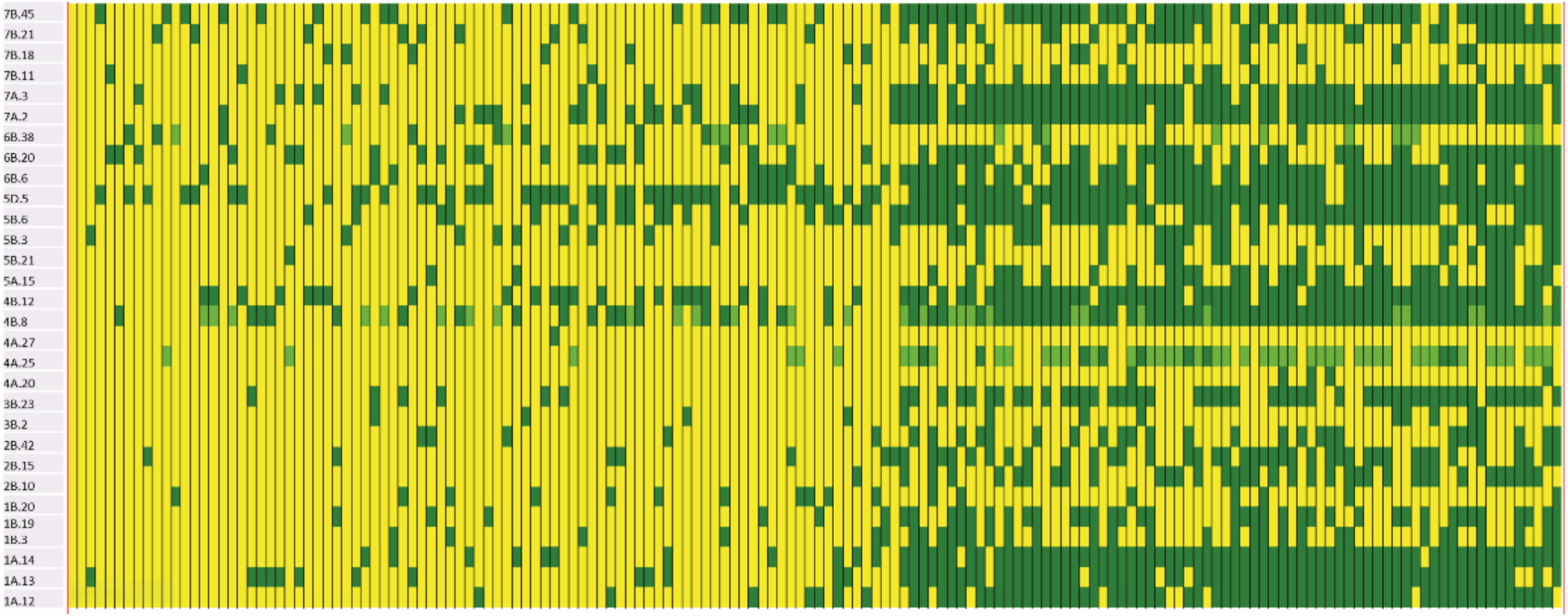
From QTLs to haplotypes

In collaboration with Uauy group, John Innes Centre



https://www.cimmyt.org/news/cimmyt-and-john-innes-centre-announce-strategic-collaboration-on-wheat-research/

Mid-density, low-cost genotyping service platform

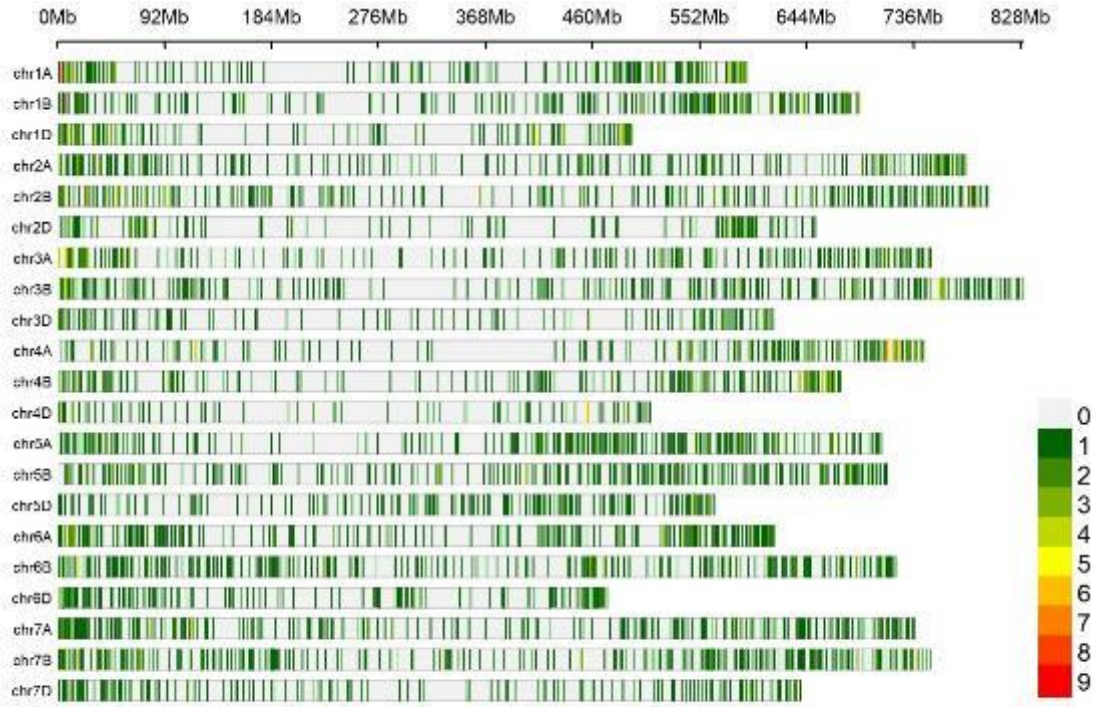
Panel optimization: second design phase , maximizing overall SNPs

Excellence in Breeding Platform

DArTAG – wheat panel vs. 02

- A total of 3900 SNPs.
- Includes more gene and QTL related sequences (469), full QC marker set (125), in CIMMYT germplasm highly polymorphic, genome-wide distributed SNPs (1802)
- Connectivity to the KSU exome sequence capture platform (500 common SNPs)
- Connectivitiy to the ongoing development of UK Axiom Breeders Chip/s (1005 common SNPs)

Genome distribution of the 3900 SNP in DArTAG – wheat panel vs 02.



DArTAG wheat development led by Susanne Dreisigacker

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But what about nutrition?

Agricultural & social sciences

Cereals production environment

- breeding & biofortification for improved grain nutrient quality
- systems productivity, resource-use efficiency & ecological sustainability
- climate- & gender-smart innovation

Food sciences, political & industrial economy

Processing & manufacturing

- product & process innovation for reduced losses & enhanced nutritional quality & food safety
- socially responsible pro-nutrition regulation of product formulation & packaging
- incentives for & capacities of businesses to enhance the nutritional content of manufactured foods

Economics & behavioural psychology

Food distribution

- pro-nutrition regulation of labelling & promotion
- efficient & profitable value chains for wholesale, retail & targeted institutional outlets & networks
- enhanced consumer choice through education, awareness & empowerment

Balanced diets

- redressing deficiencies of vitamins, minerals, proteins, fats, carbohydrates & bioactive food components

➢ ***increasing human health & well-being***

› Food Policy. 2020 Sep 18;10

Agri-nutrition r
of maize and wh

Nigel Poole [1], Jason Donovan

inable health and

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Mainstreaming micronutrient biofortification

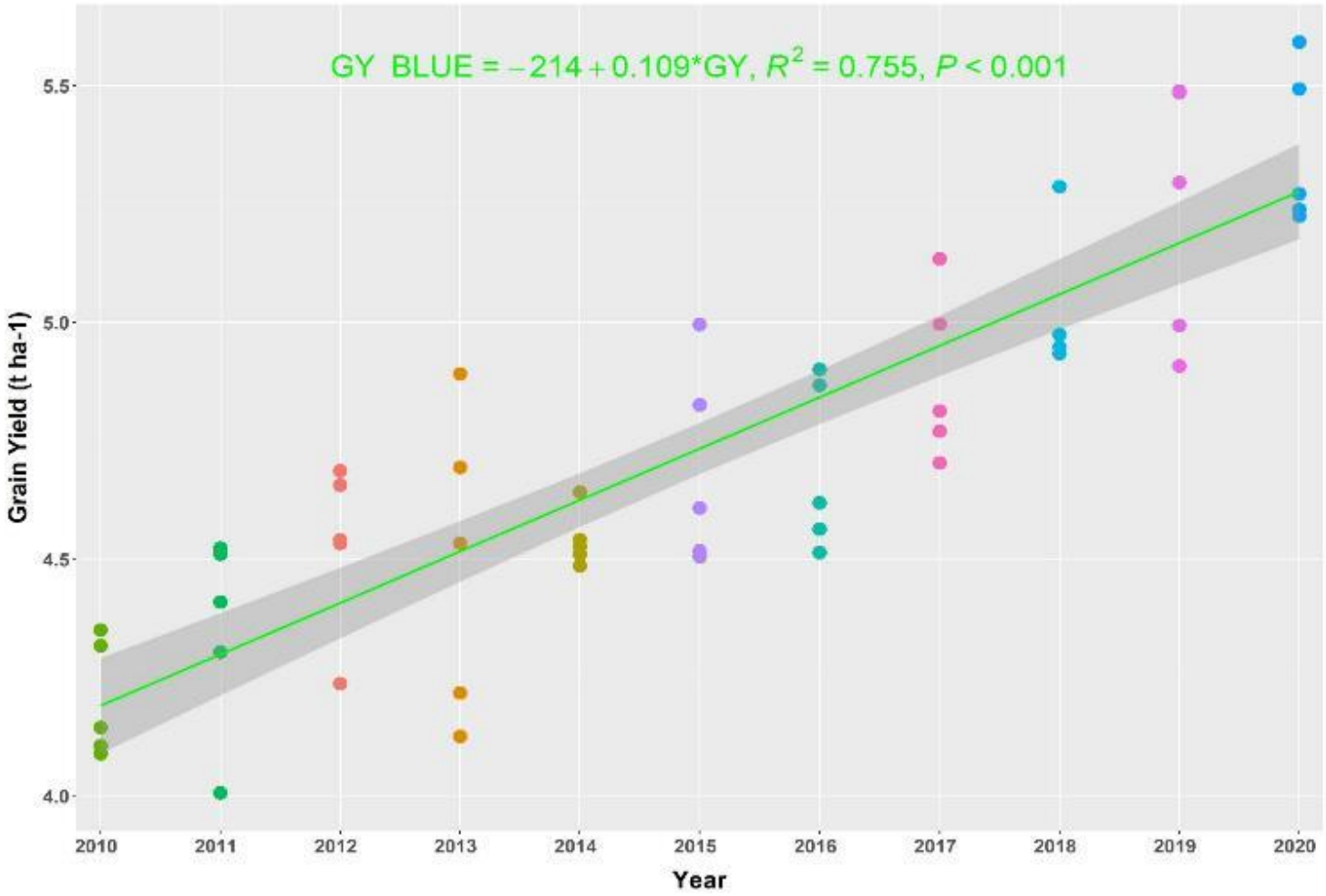
Selection for Zn in all CIMMYT wheat breeding pipelines to address malnutrition

https://www.reuters.com/business/healthcare-pharmaceuticals/exclusive-new-zinc-fortified-wheat-set-global-expansion-combat-malnutrition-2021-04-15/

Yield gain progress for Zinc breeding pipeline

- HarvestPlus Yield Trial material produced by CIMMYT.
- Data analysed across international environments from 2010-2020.
- Annual yield gain of 0.755% and grain yield progress of 109 kg/ha/yr

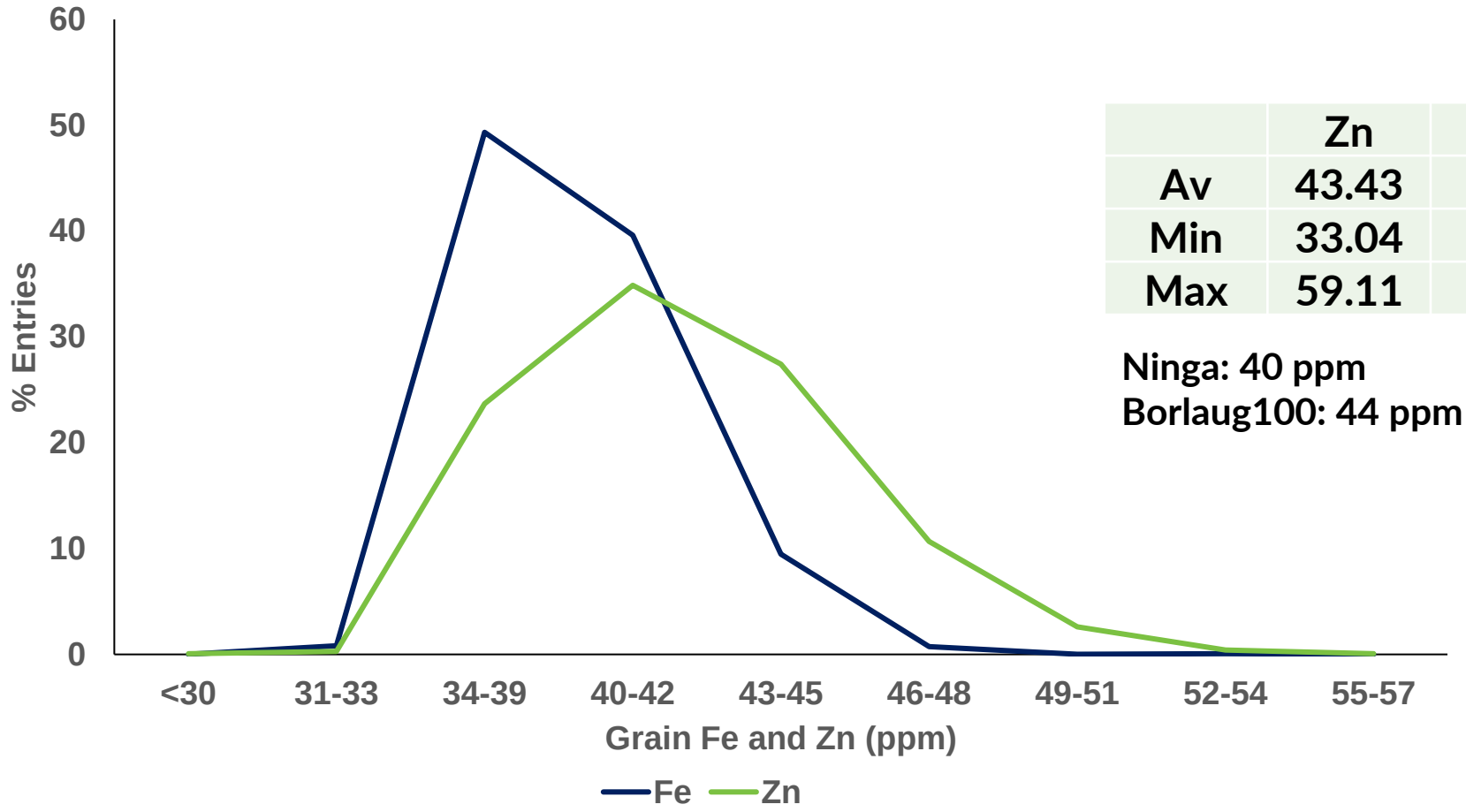
- Yield gains are on par with core breeding material, whilst also having > 6 ppm average Zn increase.



Zn breeding led by Velu Govindan

Zn mainstreaming: assessment in Stage 1 BW materials (1500 lines)

Variation for Zn in core breeding pipelines



	Zn	Fe
Av	43.43	39.34
Min	33.04	29.35
Max	59.11	48.90

Ninga: 40 ppm
Borlaug100: 44 ppm

Zn breeding led by Velu Govindan

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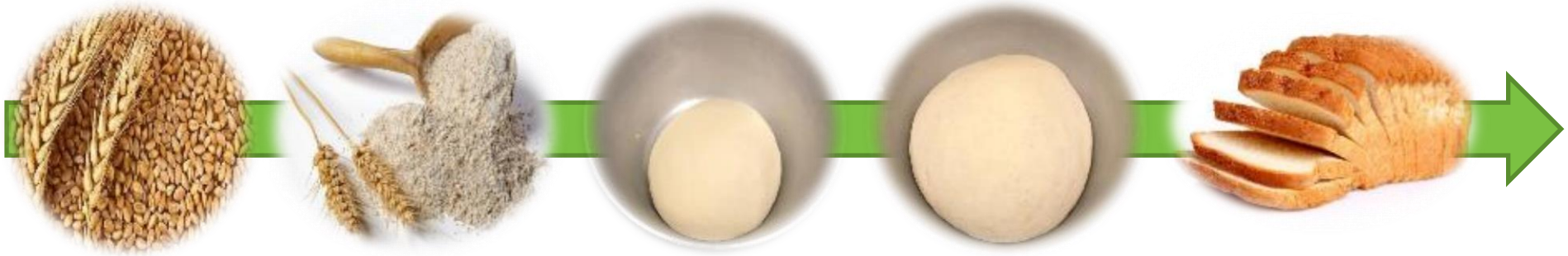
Effect of the bread production process on micronutrient retention using biofortified wheat



On-going study

Fundamental to understand efficacy of biofortification and impact of wheat processing on nutritional value

Zn processing studies led by Maria Itria Ibba

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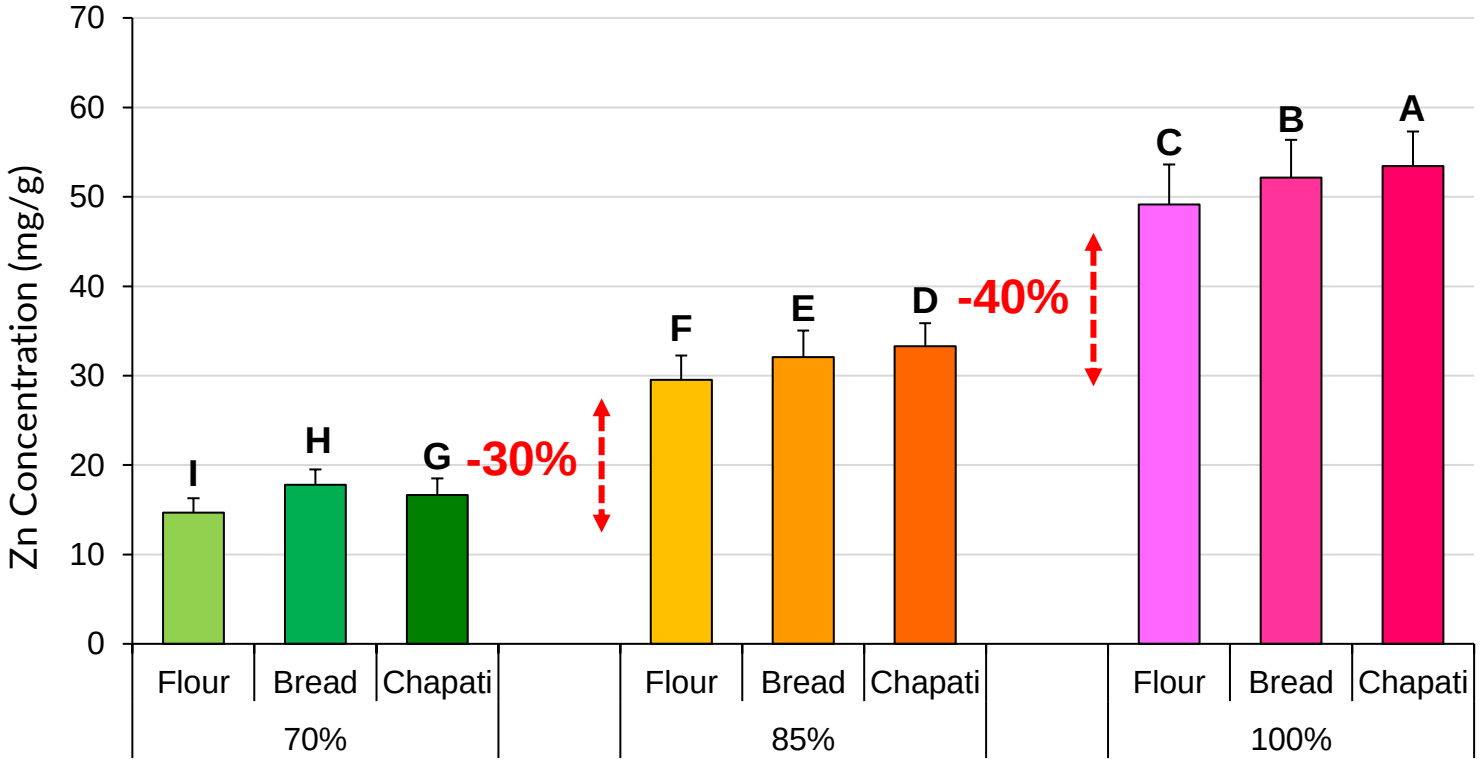
Grain and flour processing & Zn concentration



- Significant reduction starting from 85% extraction rate
- Bread or chapati production does NOT negatively affect Zn concentration

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Improvement of wheat grain fiber (Arabinoxylan) content

Current research focused on:

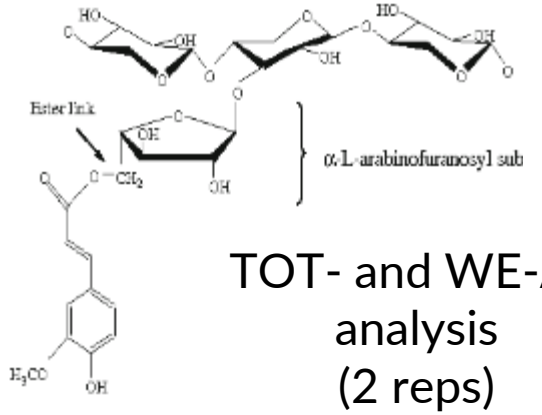
1. Identification of germplasm associated with improved grain fiber content
2. Development of tools to facilitate the selection of high-fiber wheat lines
3. Understanding the environmental effect on grain fiber content variation
4. Understanding the effect of the arabinoxylan content variation on wheat quality

Results of these studies could potentially lead to an increased daily consumption of dietary fibers

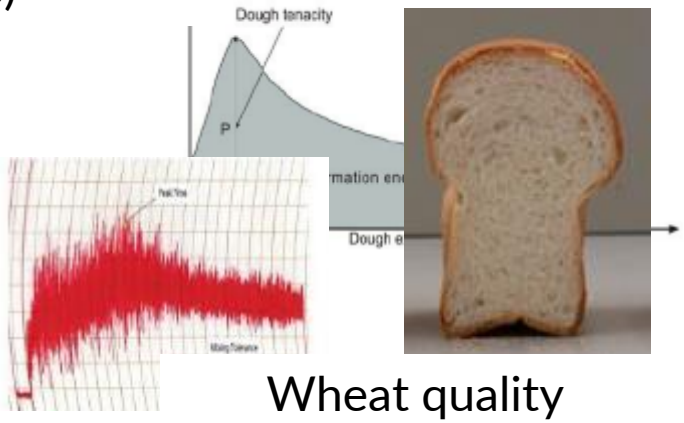
Arabinoxylan studies led by Maria Itria Ibba

Hernandez-Espinosa et al., 2020. https://doi.org/10.1016/j.jcs.2020.103062; Ibba et al., 2021. https://doi.org/10.1016/j.jcs.2021.103166

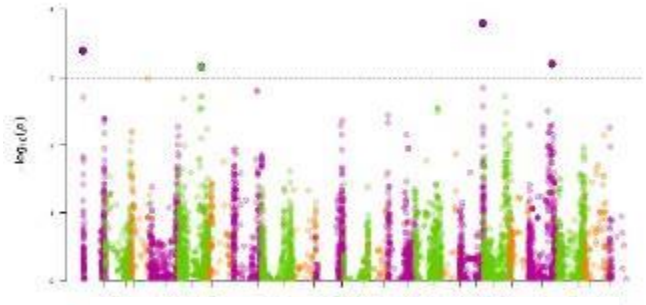
~ 190 hard spring common wheat lines (2018/2019)



TOT- and WE-AX analysis (2 reps)



Wheat quality analysis



GWAS

Arabinoxylan studies led by Maria Itria Ibba

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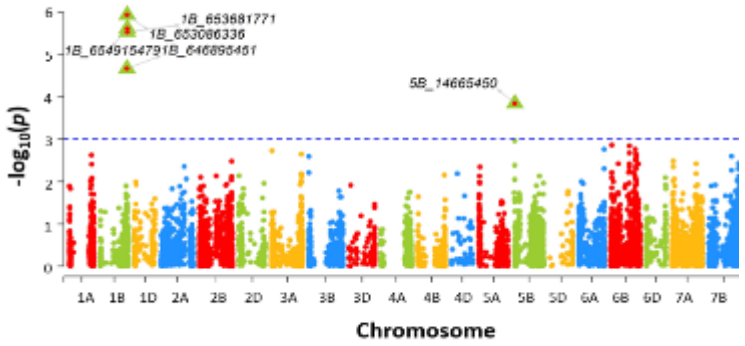
Increasing dietary fiber

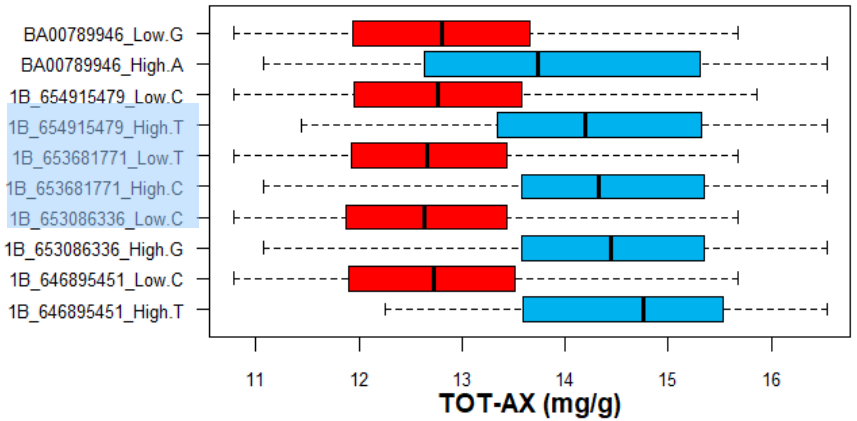
From discovery to breeding application: CIMMYT has identified genetic regions increasing dietary fiber

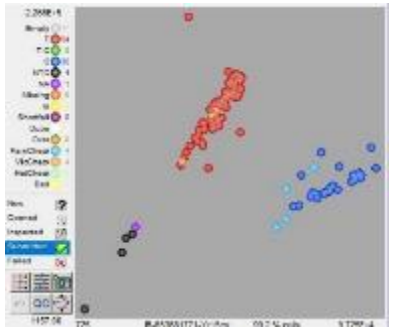
Discovery: a large effect genetic region was identified that enhanced arabinoxylan content

Validation: the identified region clearly distinguishes elite lines showing low or high contents.

Use in breeding: reliable molecular markers developed and are being applied to evaluate CIMMYT breeding lines.







Arabinoxylan studies led by Maria Itria Ibba

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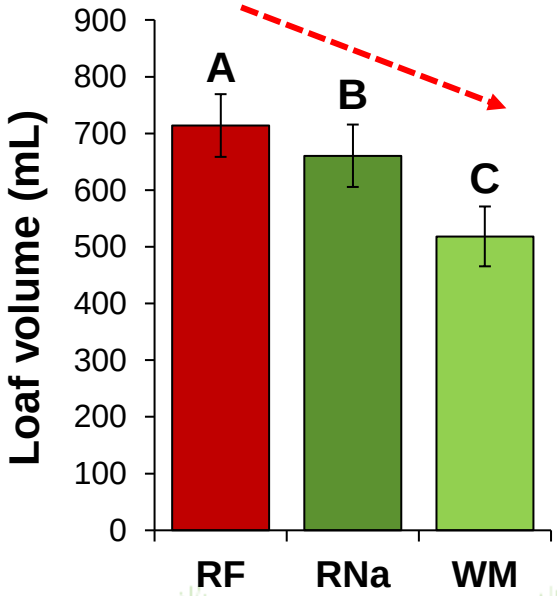
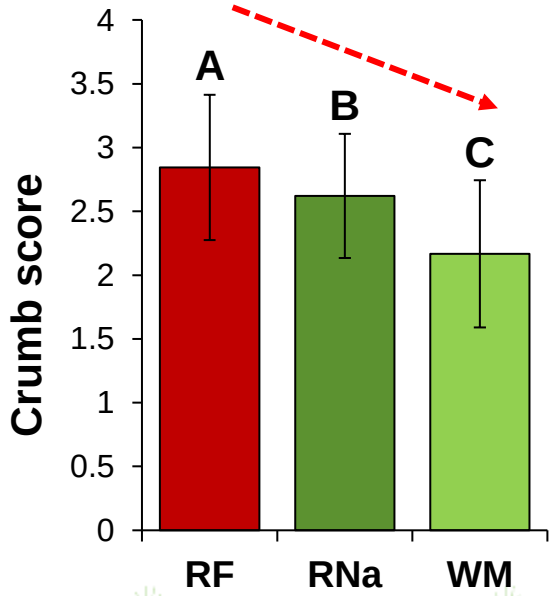
Selection for wholemeal bread quality

Are we using the best methods to predict lines with high “healthy” breakmaking potential?

Experiments conducted using full quality characterization and using three bread making procedures:

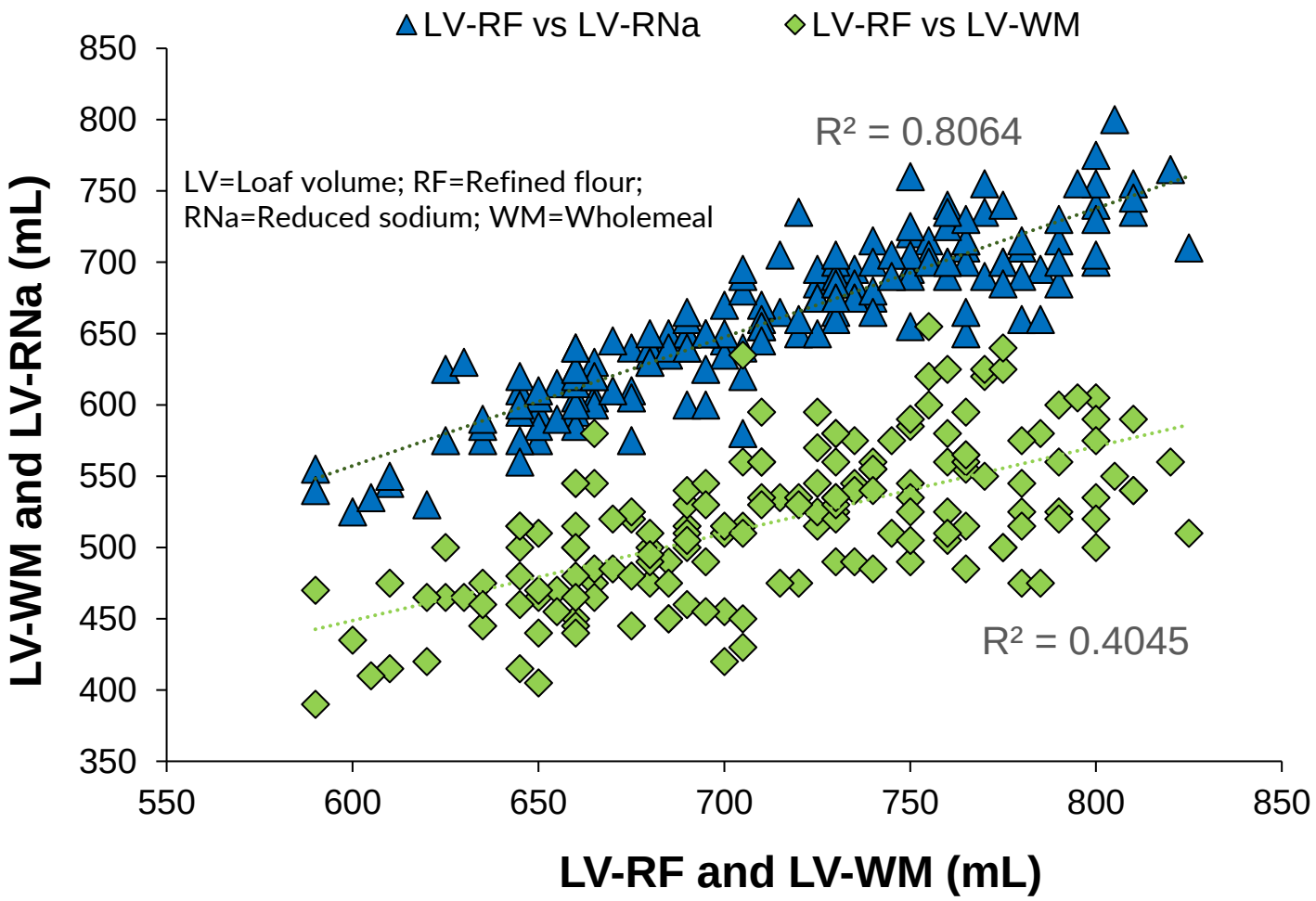
- Classic (refined flour and 1g NaCl)
- Low sodium (refined flour and no added salt)
- Wholemeal (Reconstituted flour and 1g NaCl)





Hernández-Espinosa *et al.* (2021) https://doi.org/10.1002/cche.10457

Comparing bread loaf volumes



Main findings:

- Current standard protocols can be used effectively to select high-quality low-sodium breads
- Current standard protocols can be used to estimate the wholemeal breadmaking quality

Hernández-Espinosa *et al.* (2021)
https://doi.org/10.1002/cche.10457

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Genetic resources

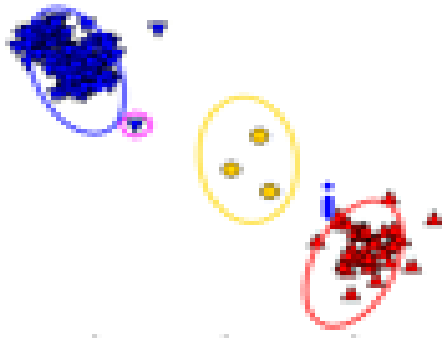
Elite germplasm

Multi-environments

Phenotyping methods

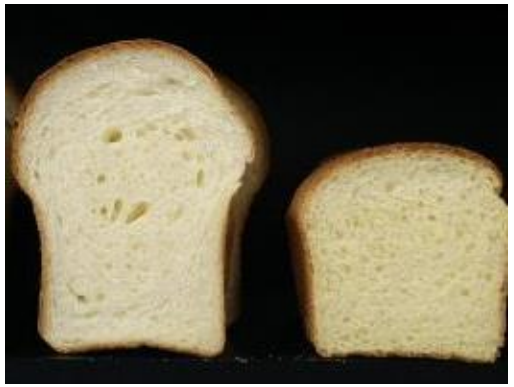
Remote sensing

Equitably deploying breeding tools & resources



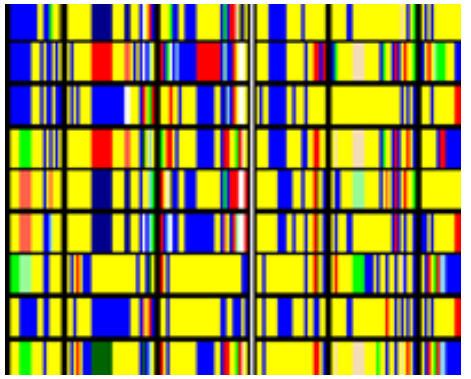
Marker-assisted selection

Pan-genomes



Quality traits

Biotechnology



Genomic selection

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Find out more about the CIMMYT Global Wheat Program and our donors & partners:
https://www.cimmyt.org/work/wheat-research/
https://wheat.org/








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