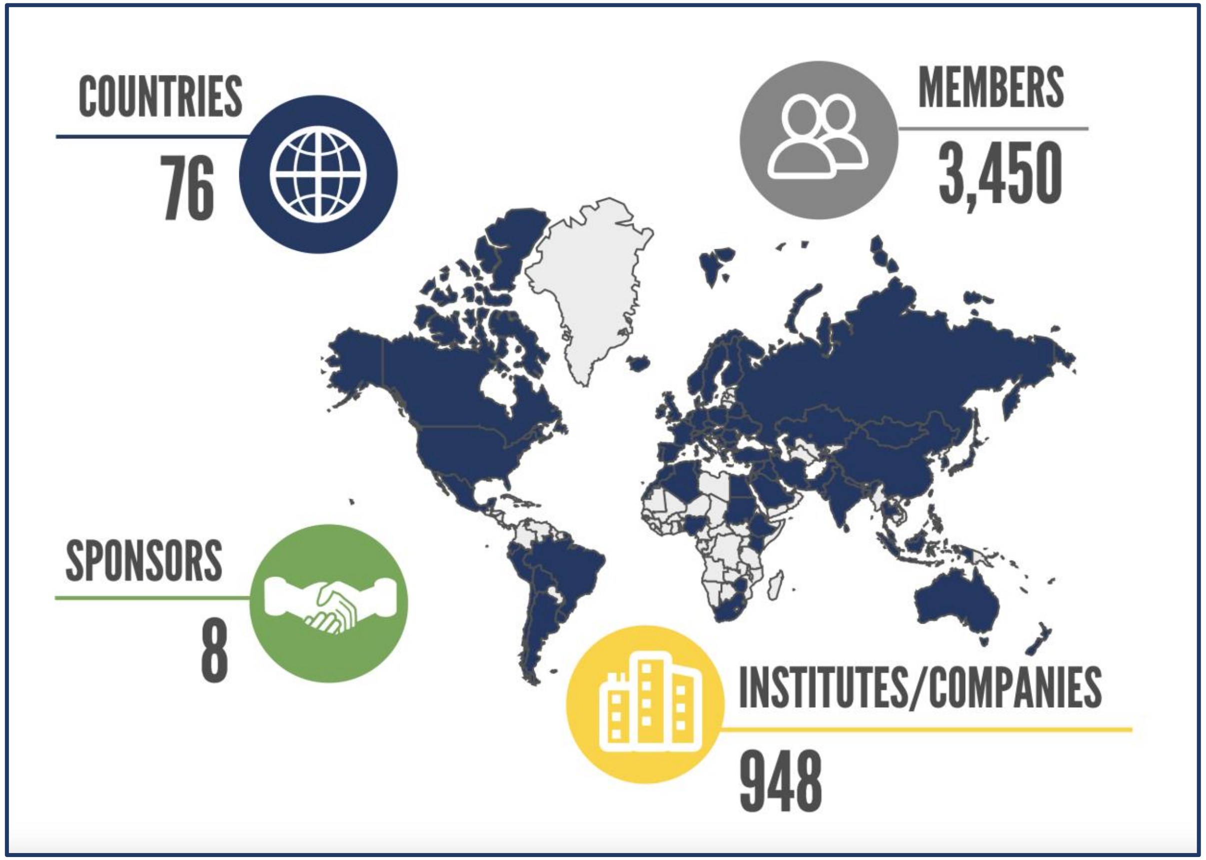
The International Wheat Genome Sequencing Consortium

Kellye Eversole
IWGSC Executive Director

14 March 2024

The International Wheat Genome Sequencing Consortium



- Established in 2005 by a group of wheat growers, plant scientists, and public and private breeders
- Goal: accelerate wheat improvement
- Generated the reference sequence of bread wheat (RefSeq) in 2017
- All data publicly available – Latest version of assembly and annotation is IWGSC RefSeq v2.1

DAICEL arbor biosciences

BASF We create chemistry

CIMMYT International Maize and Wheat Improvement Center

FLORIMOND DESPREZ

INRAE

KANSAS WHEAT

RAGT

syngenta

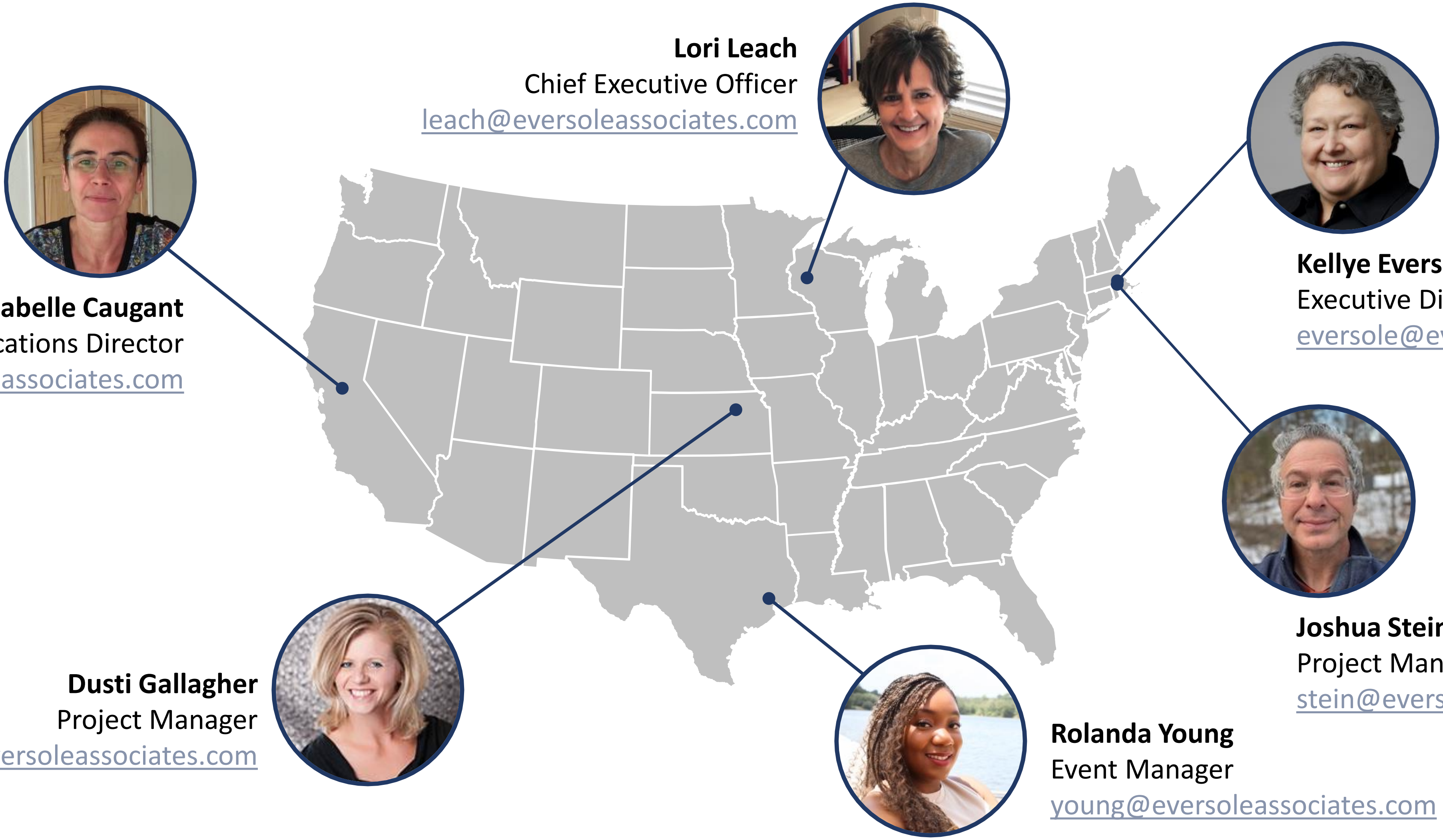
IWGSC 2.0 Vision

Enhance breeding through an increased understanding of the molecular basis of traits and their allelic diversity

IWGSC 2024 Activities

- IWGSC Wheat Diversity project – platinum quality sequences of 12 landraces representing breadth of wheat diversity, automated and manual annotation, and development of a Practical Haplotype Graph
- Continued collaborations with wheat genomic tool developers
- IWGSC Webinar series
- Participation in International Wheat Congress & PAG Australia
  - ✓ Stay tuned for the PAG Australia workshop – call for speakers
- Planning for 2025 workshops at PAG in San Diego
  - ✓ Stay tuned for the IWGSC PAG workshops – call for speakers & early career award

The IWGSC Team



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www.wheatgenome.org

international-wheat-genome-sequencing-consortium

@wheatgenome

Susanne Dreisigacker

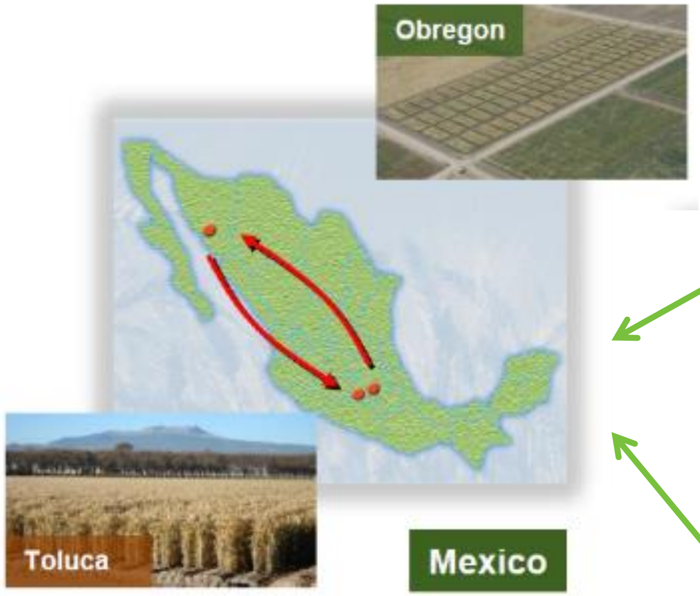
- Head of the Wheat Genetics and Molecular Breeding Laboratory, CIMMYT, Mexico
- Member of the IWGSC Board of Directors
- A champion in wheat genetics research
- Research interest: unravelling the genetic foundations of vital traits in wheat to advance genomics-assisted breeding strategies
- More than 300 published articles

Integration of the CGIAR consolidated genotyping services into the CIMMYT Global Wheat Program

Susanne Dreisigacker & the CIMMYT Global Wheat Program

Global Wheat Program – Heir of the Green Revolution

Wheat improvement programs



Mexico

- **Spring type wheat**
  - Bread wheat
  - Durum wheat
  - Triticale

Dr. Leo Crespo *Dr. Velu Govindan*

Bread Wheat Breeding

Dr. Karim Ammar

Durum Wheat & Triticale Breeding

- **Winter type wheat**
  - Bread wheat
  - CIMMYT-Turkey program

Winter Wheat Breeding Turkey

Dr. Behan Akin

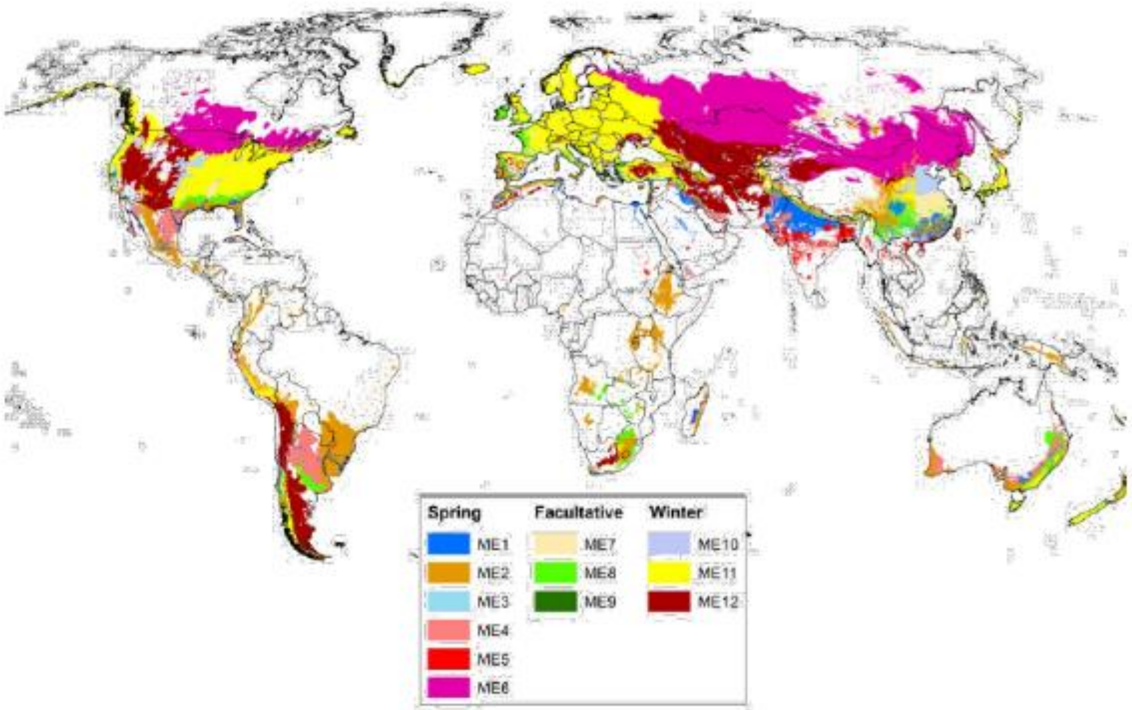
Turkey

CIMMYT Spring Bread Wheat Improvement Program

Targets ~65 million hectares

Target Environments

- **Irrigated: 25.8 million ha -** Northwestern Plain Zone of India, Central & Northwestern Pakistan, irrigated mid hills of Nepal, Ethiopia-irrigated mid-altitude/low land areas
- **High rainfall: 6.2 million ha -** Highlands of Ethiopia and Kenya
- **Drought stress: 20.1 million ha -** Central & Peninsular zone of India, Southern Punjab of Pakistan, hills of Nepal, Mediterranean region
- **Irrigated, heat stress: 10.3 million ha -** Northeastern Plain Zone of India, Sindh in Pakistan, Bangladesh, Terai of Nepal



- ➢ **2015-2021: 278 direct CIMMYT-derived varieties released in 26 countries; *~40 varieties/year***
- ➢ **Widely used as parents throughout the target regions and beyond**

GWP's Spring Bread Wheat Breeding pipelines

Pipeline 1
HW-OE-NM / HW-HT-NM

- Central Asia
- South Asia
- West Asia
- North Africa
- Sub-Saharan Africa
- Latin America

Pipeline 2
HW-HT-EM

- South Asia
- Latin America

Pipeline 3
HW-DT-NM

- Central Asia
- South Asia
- West Asia
- North Africa
- Sub-Saharan Africa
- Latin America

Pipeline 4
HW-DT-EM

- South Asia

Pipeline 5
HW-HiR-NM / HR-HiR-NM

- North Africa
- Sub-Saharan Africa

Dr. Sridhar Bhavani

Kenya

1. **H**ard **W**hite **O**ptimum **E**nvironment **N**ormal **M**aturity / **H**ard **W**hite **H**eat **T**olerance
2. **H**ard **W**hite **H**eat **T**olerance **E**arly **M**aturity
3. **H**ard **W**hite **D**rought **T**olerance **N**ormal **M**aturity
4. **H**ard **W**hite **D**rough **T**olerance **E**arly **M**aturity
5. **H**ard **W**hite/**R**ed **H**igh **R**ainfall **N**ormal **M**aturity

Selection traits in Spring Bread Wheat Product Profiles

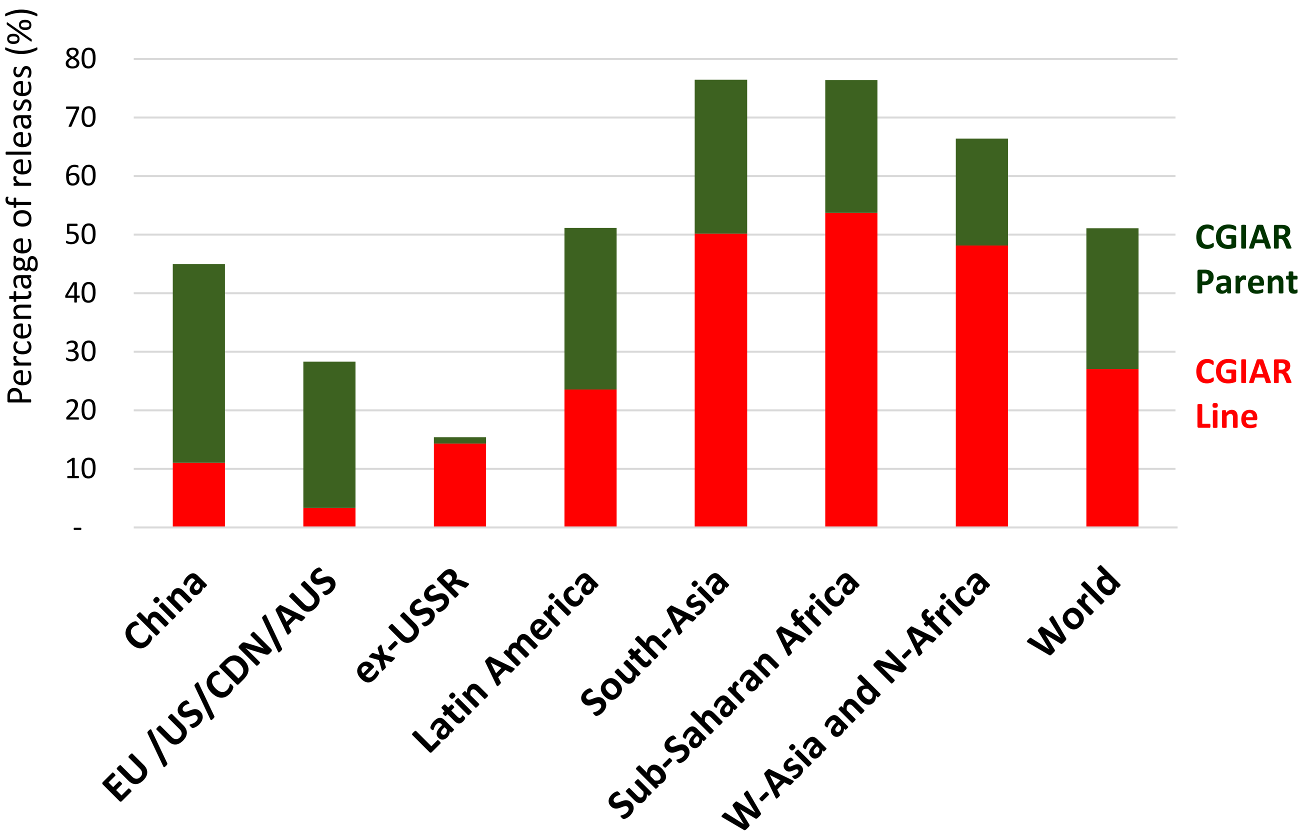
	24M ha	10M ha	7M ha	7M ha	2M ha
	Breeding Pipeline 1. Hard White-Optimum Environment- Normal Maturity	**Breeding Pipeline 2. Hard White- Heat Tolerant- Early Maturity**	**Breeding Pipeline 3. Hard White-Drought Tolerant- Normal Maturity**	**Breeding Pipeline 4. Hard White-Drought Tolerant- Early Maturity**	**Breeding Pipeline 5. Hard White- High Rainfall & Hard Red-High Rainfall- Normal Maturity**
	HW-OE-NM	**HW-HT-EM**	**HW-DT-NM**	**HW-DT-EM**	**HW-HiR-NM & HR-HiR-NM**
Key traits	**Size: 2x**	**Size: 2x**	**Size: 1x**	**Size: 1x**	**Size: 0.75x & 0.25x**
High and stable yield potential	XXX	XXX	XXX	XXX	XXX
Water use efficiency/Drought tolerance	X	X	XXX	XXX	XX
Heat tolerance	XX	XXX	XX	XXX	X
End-use quality (similar profiles)	XXX	XXX	XXX	XXX	XXX
Enhanced grain Zn (and Fe) content (new mainstreaming trait)	XXX	XXX	XXX	XXX	XXX
Stem rust (Ug99 & other)	XX	XX	XX	XXX	XXX
Stripe rust	XXX	XX	XXX	XX	XXX
Leaf rust	XXX	XXX	XXX	XXX	XX
Septoria tritici blotch	-	-	XXX	-	XXX
Spot blotch	X	XXX	-	X	-
Fusarium – head scab and myco-toxins	-	-	-	-	XX
Wheat blast- new threat in South Asia	X	XXX	X	X	X
Maturity	Normal-late	Early	Normal	Early	Normal

Importance: X= low, XX= moderate, XXX= high

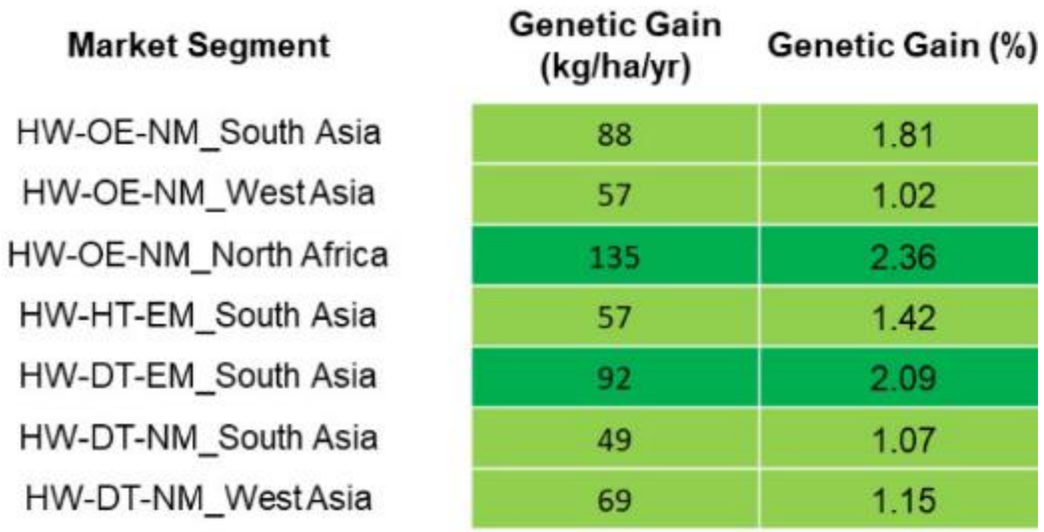
Common agronomic traits: *plant height, stem strength, leaf health, spike fertility, grain size & plumpness, etc.*

Impact of CGIAR Wheat Breeding Germplasm

Percent of spring bread wheat releases derived from CIMMYT and ICARDA by region and origin 1994-2014 (Lantican et al., 2016)

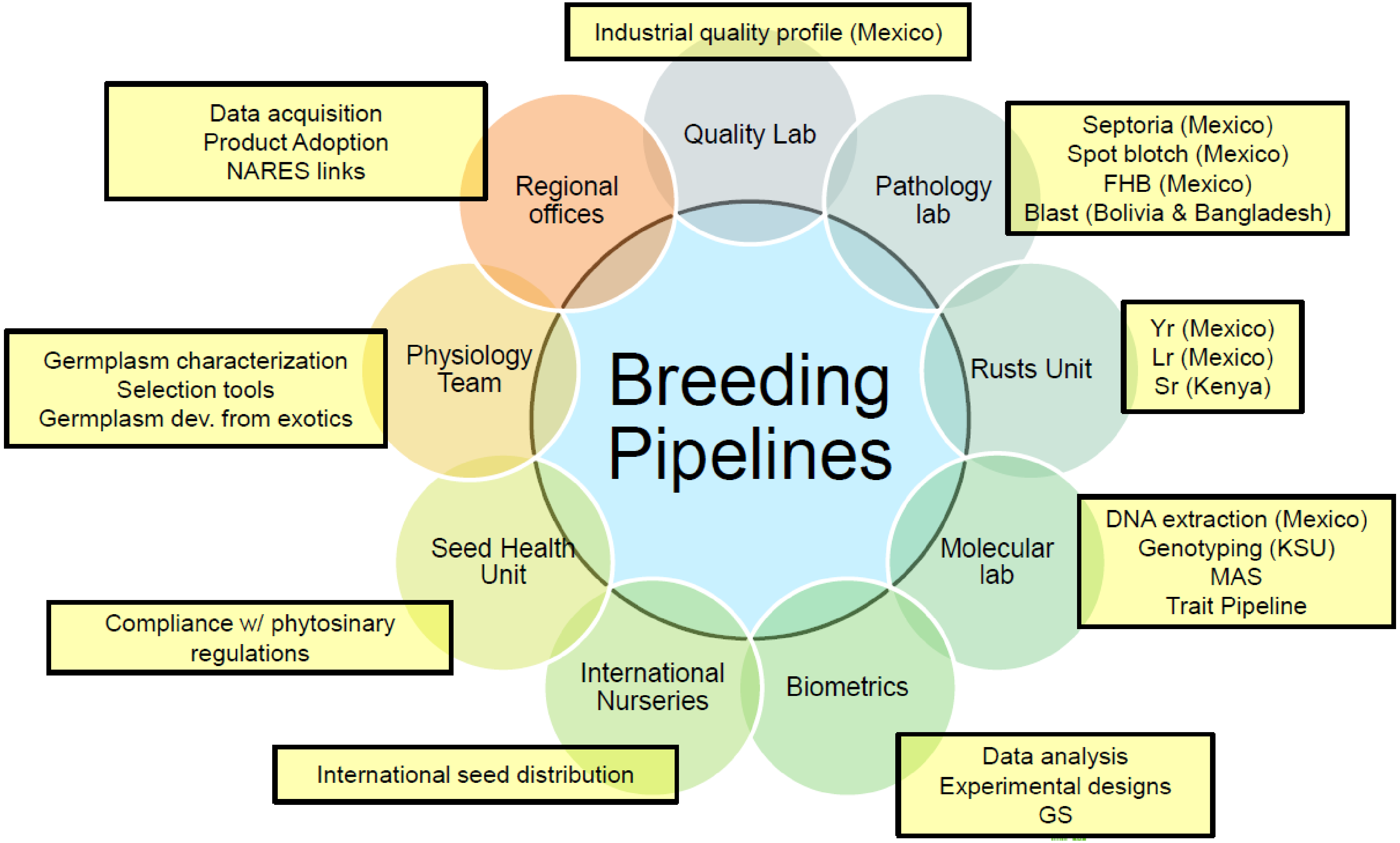


2022 GWP - Genetic Gain assessment



Market Segment	Genetic Gain (kg/ha/yr)	Genetic Gain (%)
HW-OE-NM_South Asia	88	1.81
HW-OE-NM_WestAsia	57	1.02
HW-OE-NM_North Africa	135	2.36
HW-HT-EM_South Asia	57	1.42
HW-DT-EM_South Asia	92	2.09
HW-DT-NM_South Asia	49	1.07
HW-DT-NM_WestAsia	69	1.15

Wheat Improvement team – Enabling Units



Industrial quality profile (Mexico)

Data acquisition
Product Adoption
NARES links

Septoria (Mexico)
Spot blotch (Mexico)
FHB (Mexico)
Blast (Bolivia & Bangladesh)

Yr (Mexico)
Lr (Mexico)
Sr (Kenya)

Germplasm characterization
Selection tools
Germplasm dev. from exotics

DNA extraction (Mexico)
Genotyping (KSU)
MAS
Trait Pipeline

Compliance w/ phytosinary regulations

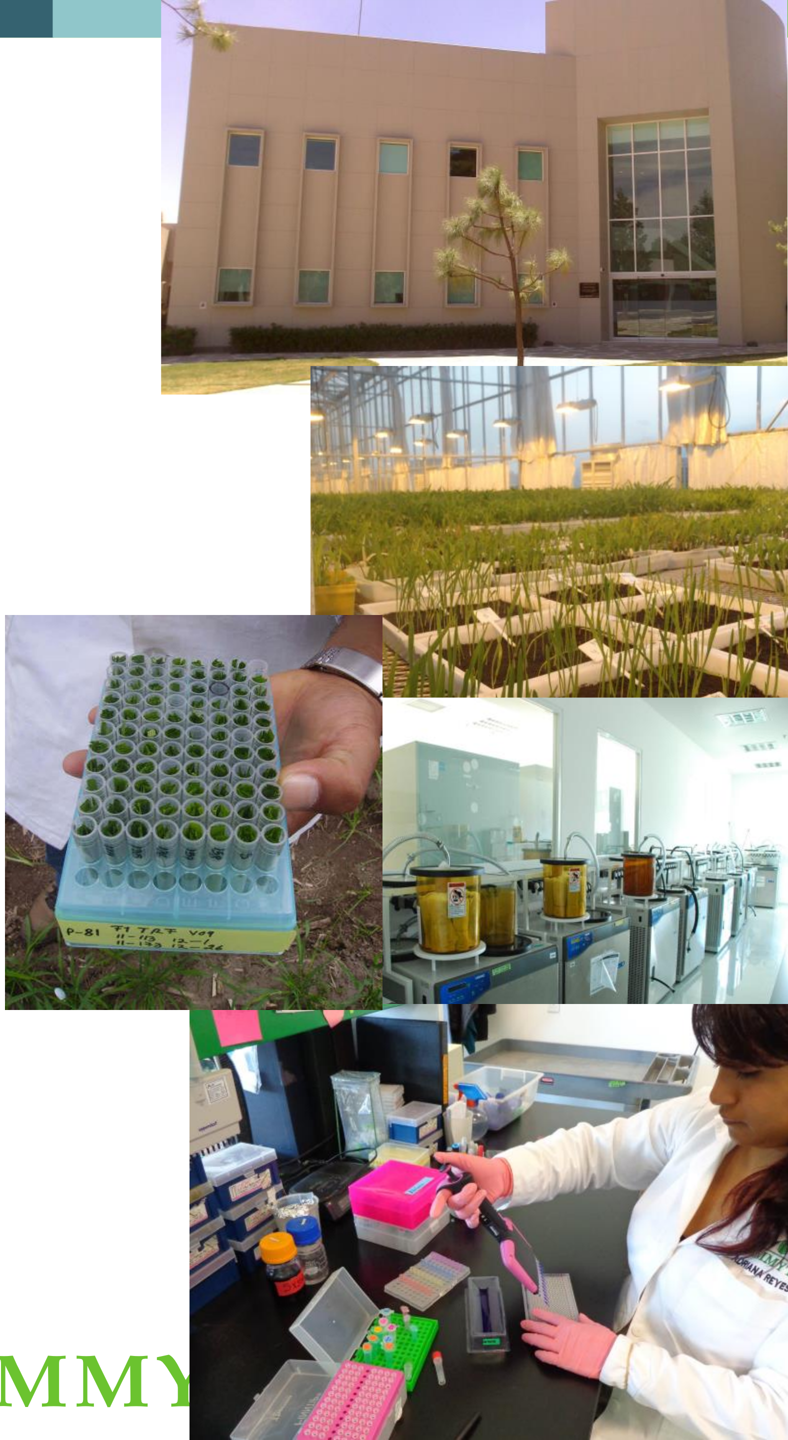
International seed distribution

Data analysis
Experimental designs
GS

Molecular lab activities

Support in trait discovery and deployment

- Genotyping support for trait discovery
- Trait-based marker design and marker validation
- Marker-assisted trait introgression and deployment
- Genotyping support applying genomic selection
- Integration of genomics tools, proof of concept of novel genomics-assisted breeding approaches and



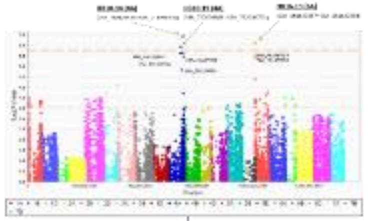
Integration of genomics tools in the CIMMYT GWP

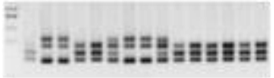
2001

Bi-parental mapping

2007

First GWAS study published

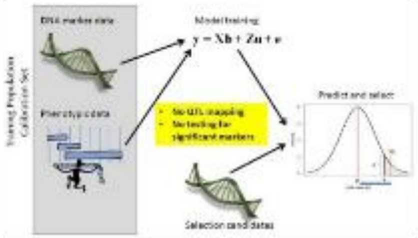




Marker-assisted selection (MAS) for few target genes via STS markers

2010

First Genomic Selection (GS) study published



2012

Switch to KASP SNP assays

2014

GS Phase I …going live

2016

CG consolidated genotyping services

Large scale parental development through MAS

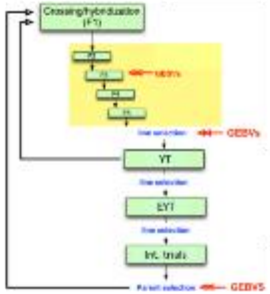
2018

GS Phase II, Sequencing of CIMMYT key parents

2020

Rapid generation advance facilities

Rapid bulk generation advancement and trait pipeline deployment



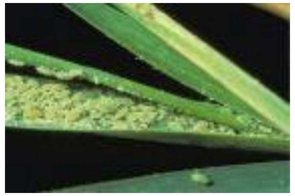
Current areas of trait discovery research

Enhanced nutritional value

- Dietary Fiber
- Mineral content
- Pre-harvest sprouting
- Whole grain quality characteristics

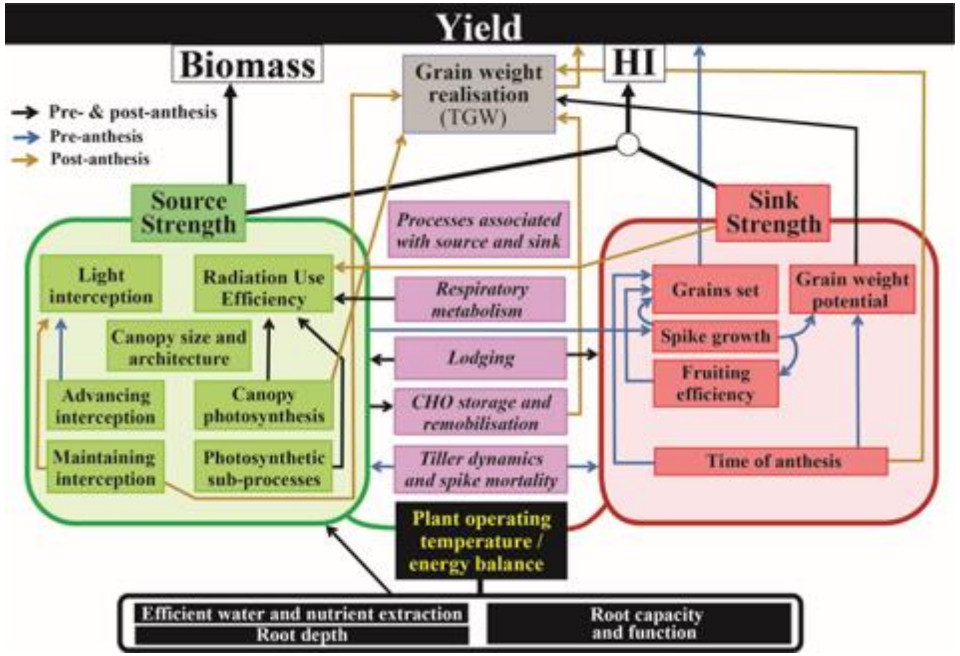
Biotic stress resilience

- Rust
- Wheat Blast
- Fusarium head blight
- Aphid resistance
- Kernel bunt

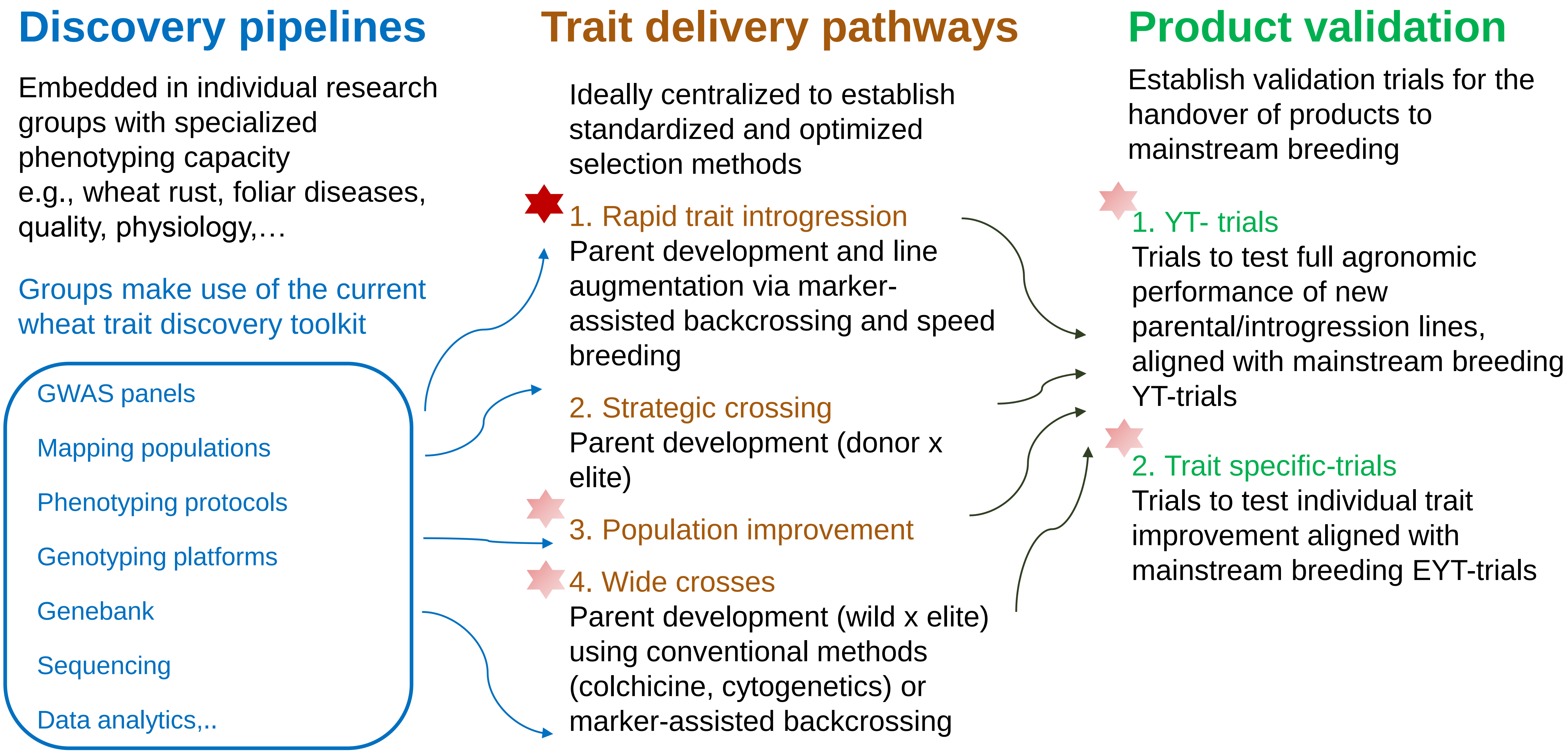


Adoption and climate resiliance

- Heat tolerance
- Drought tolerance
- Yield potential



Current GWP trait-introgression pathways



Discovery pipelines

Embedded in individual research groups with specialized phenotyping capacity
e.g., wheat rust, foliar diseases, quality, physiology,…

Groups make use of the current wheat trait discovery toolkit

- GWAS panels
- Mapping populations
- Phenotyping protocols
- Genotyping platforms
- Genebank
- Sequencing
- Data analytics,..

Trait delivery pathways

Ideally centralized to establish standardized and optimized selection methods

1. Rapid trait introgression
Parent development and line augmentation via marker-assisted backcrossing and speed breeding

2. Strategic crossing
Parent development (donor x elite)

3. Population improvement

4. Wide crosses
Parent development (wild x elite) using conventional methods (colchicine, cytogenetics) or marker-assisted backcrossing

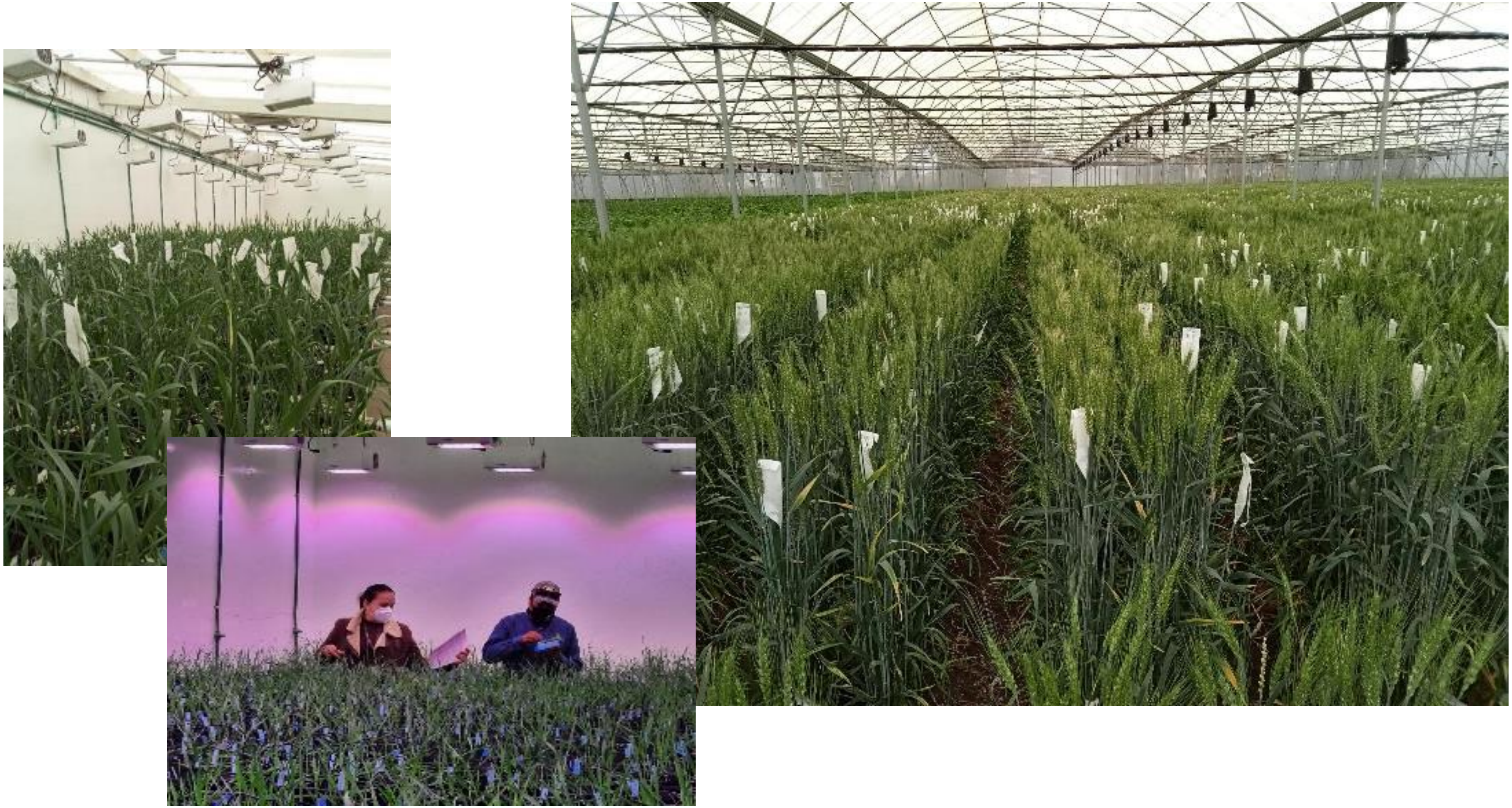
Product validation

Establish validation trials for the handover of products to mainstream breeding

1. YT- trials
Trials to test full agronomic performance of new parental/introgression lines, aligned with mainstream breeding YT-trials

2. Trait specific-trials
Trials to test individual trait improvement aligned with mainstream breeding EYT-trials

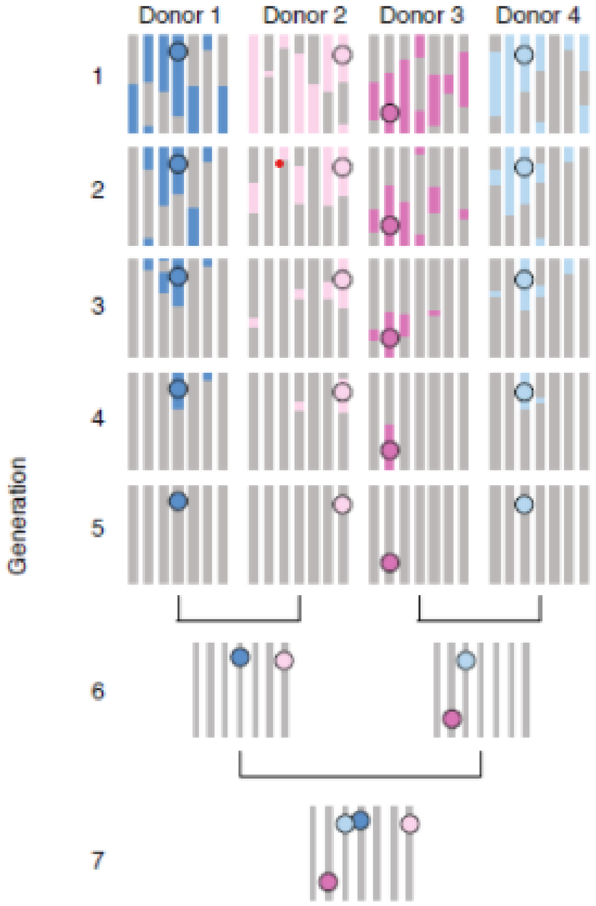
Rapid trait introgression of marker selectable genes /QTL



Centralized, marker-assisted trait introgression

Motivation

- Better coordination across breeding programs
- Clear alignment to established product profiles and market segments
- Transparency of trait advances (internal & external)
- Faster delivery improved native trait products to breeding programs and partners
- Streamline genotyping logistics and the use of shared genotyping services



Rapid introgression of marker selectable genes /QTL

Prioritization based on demand and value

- Demand of the associated trait in product profiles
- Evidence of QTL / gene value
- Lack of phenotypic variation of the trait
- Limited genetic diversity for the trait
- Selection efficiency
- Availability of sufficient accurate molecular markers and known purified donor parent
- Available funding

Rapid introgression of marker selectable genes / QTL, parental development and increased diversity

Disease resistance genes

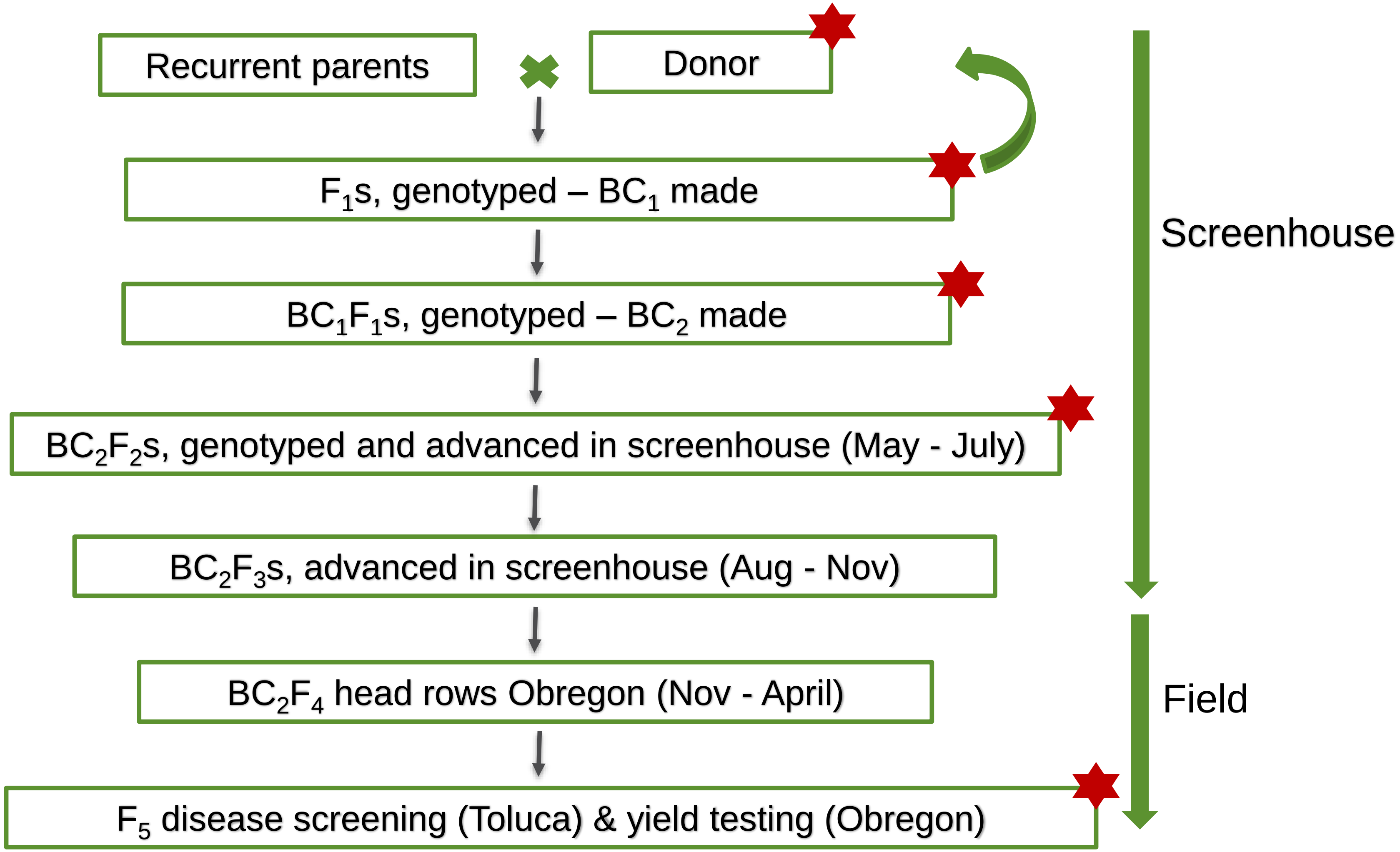
- Stem rust: *Sr13, Sr22, Sr25, Sr26, Sr50, Sr55/Yr46/Lr67*
- Yellow rust: *Yr5, Yr15, Yr51, Yr57, Yr59, YrSP*
- Fusarium head blight: *Sr2+Fhb1* and Q*Fhb.cim-2DLC*
- Septoria tritici blotch: *Stb6*, *Stb16*, *Qstb.cim-2BS.1/2*
- *Wheat Bast: 2NS translocation, Rmg7/8*

Novel diversity to enhance yield and climate resilience

- Heat/drought tolerance: *Qmst.cim-3B, 4B, 5B, 6D, 7D*
- TGW: *GL2, TaGW2 –mutants, Qgw-JIC-6A*
- Yield potential*: TaCol-B5*
- BNI

Rapid introgression of marker selectable genes /QTL

- Capacity of approximately 100 new crosses annually (Crossing block annually planted in May – June)
- Top crosses or F1 × F1 crosses being made for gene pyramiding
- Up to 10-15 recurrent parent used per selection target
- Two years to F_5 stage, trait and yield testing in mainstream breeding



Recurrent parents

Donor

F_1s, genotyped – BC_1 made

BC_1F_1s, genotyped – BC_2 made

BC_2F_2s, genotyped and advanced in screenhouse (May - July)

BC_2F_3s, advanced in screenhouse (Aug - Nov)

BC_2F_4 head rows Obregon (Nov - April)

F_5 disease screening (Toluca) & yield testing (Obregon)

Screenhouse

Field

Use of CG-shared genotyping services: LDSG

Excellence in Breeding Platform

EIB Low density genotyping services (LDSG)

- Optimized production markers
- Fast turn-around and low cost
- Multiples of 384 samples

International Maize and Wheat Improvement Center

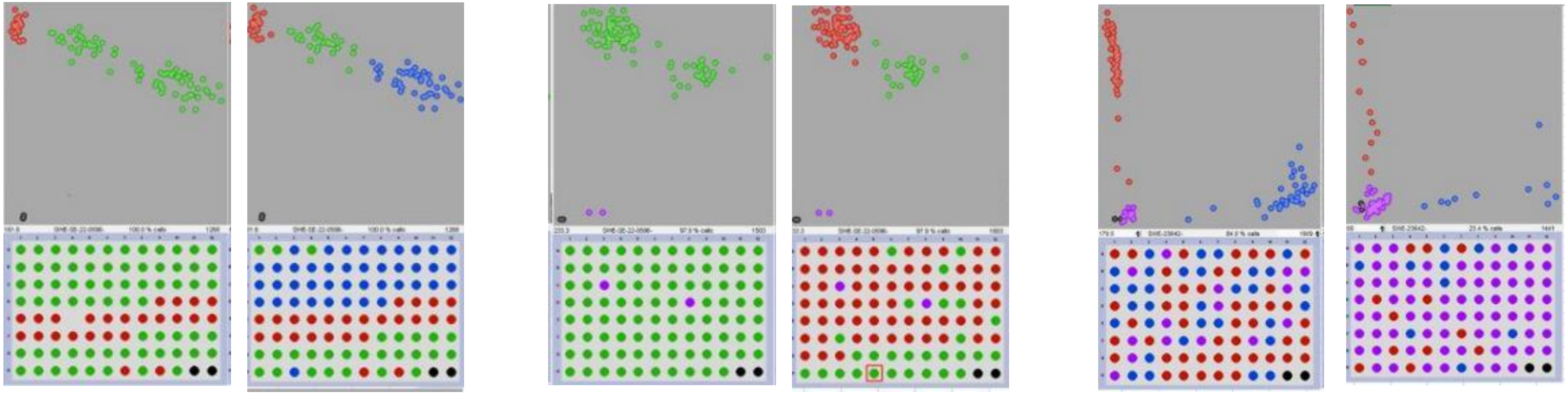
Wheat Molecular Breeding Lab (WMBL)

- Complex to run production markers (more flexible inhouse protocols)
- Gel-based / CAPS markers
- Small genotyping jobs (research based)
- New marker designs under validation

Use of CG-shared genotyping services: LDSG

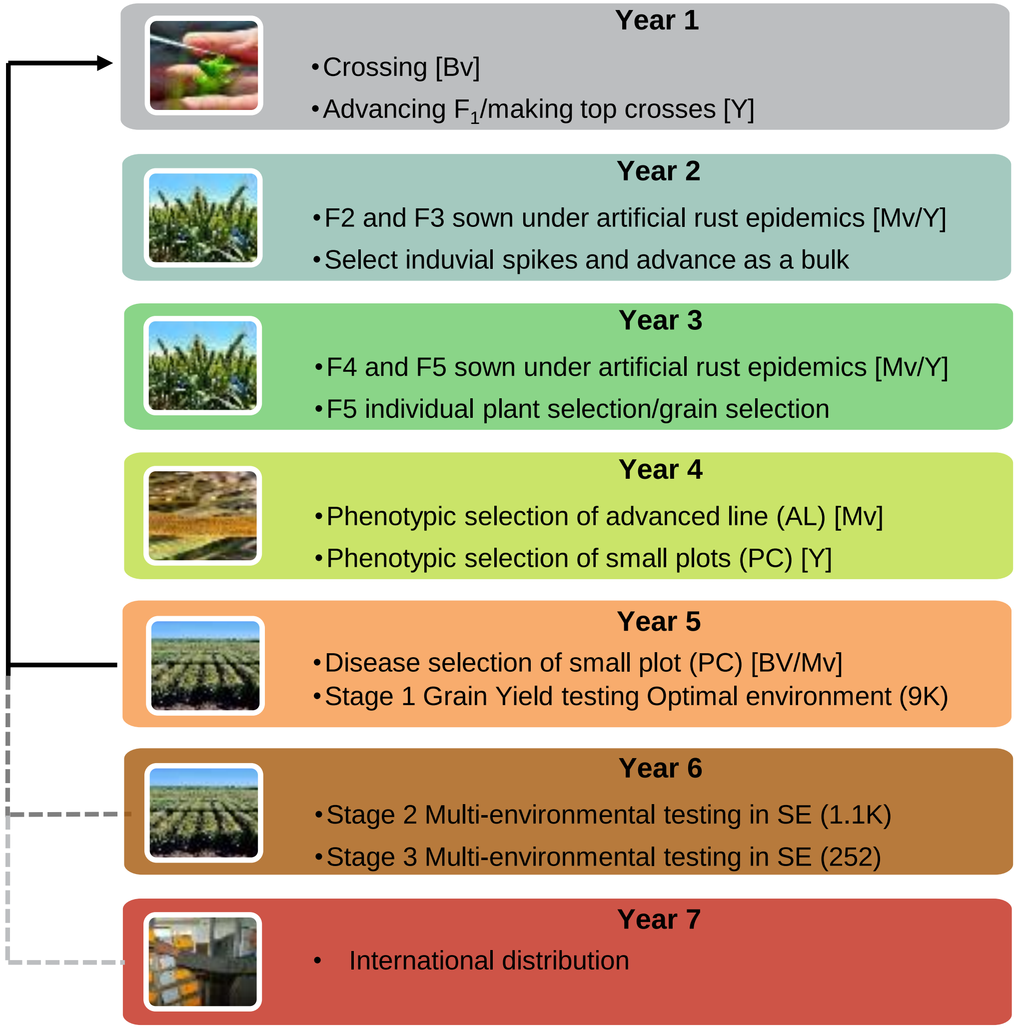
Challenges

- Automated calling of non-genome specific SNPs
- Variable proportions of missing data
- Scriptoria order submission not fully operational and link to EBS



Genomic selection (GS)

Selected Bulk Breeding Scheme – shuttle breeding



Year 1
- Crossing [Bv]
- Advancing F_1/making top crosses [Y]

Year 2
- F2 and F3 sown under artificial rust epidemics [Mv/Y]
- Select induvial spikes and advance as a bulk

Year 3
- F4 and F5 sown under artificial rust epidemics [Mv/Y]
- F5 individual plant selection/grain selection

Year 4
- Phenotypic selection of advanced line (AL) [Mv]
- Phenotypic selection of small plots (PC) [Y]

Year 5
- Disease selection of small plot (PC) [BV/Mv]
- Stage 1 Grain Yield testing Optimal environment (9K)

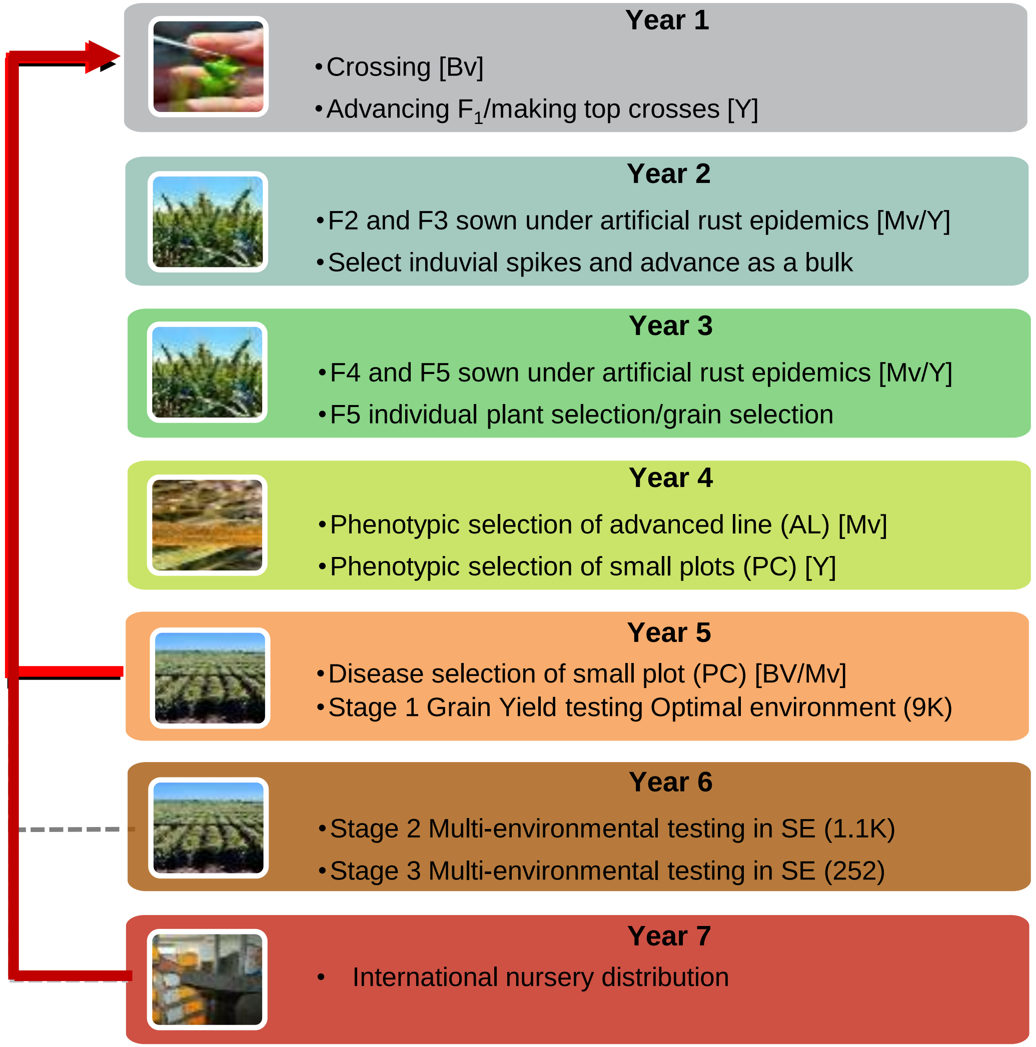
Year 6
- Stage 2 Multi-environmental testing in SE (1.1K)
- Stage 3 Multi-environmental testing in SE (252)

Year 7
- International distribution

- **Parents Recycling 5 years**
- **International distribution 7 years**

Slide: Guillermo Gerard

Rapid Bulk Generation Advancement Scheme



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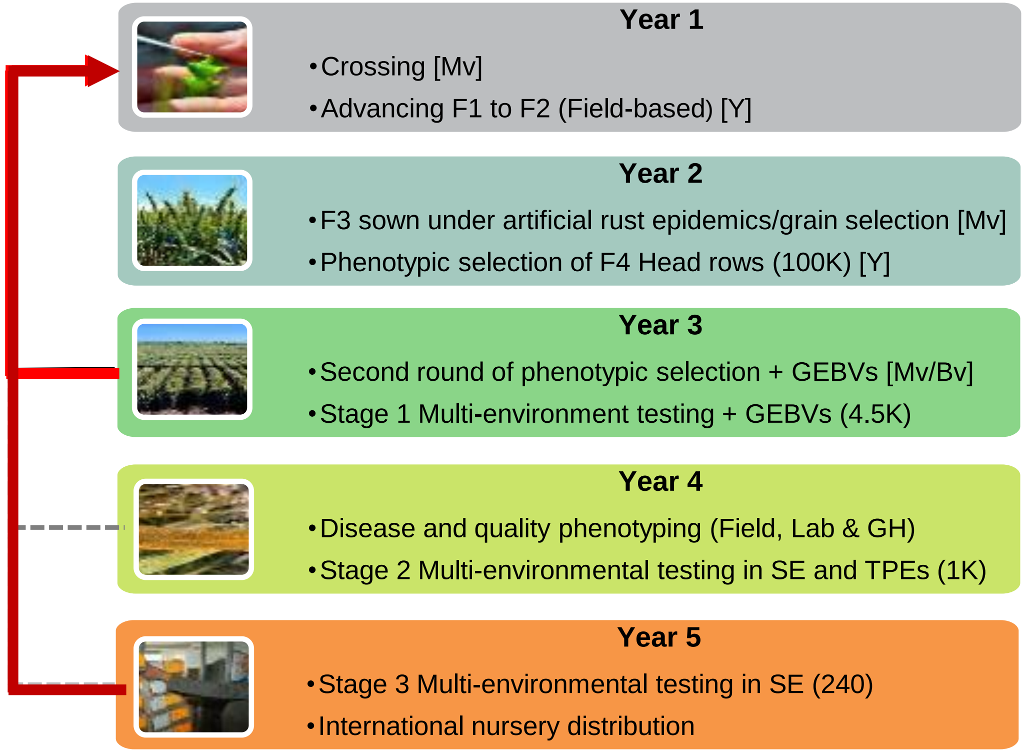
Year 6
- Stage 2 Multi-environmental testing in SE (1.1K)
- Stage 3 Multi-environmental testing in SE (252)

Year 7
- International nursery distribution



Year 1
- Crossing [Mv]
- Advancing F1 to F2 (Field-based) [Y]

Year 2
- F3 sown under artificial rust epidemics/grain selection [Mv]
- Phenotypic selection of F4 Head rows (100K) [Y]

Year 3
- Second round of phenotypic selection + GEBVs [Mv/Bv]
- Stage 1 Multi-environment testing + GEBVs (4.5K)

Year 4
- Disease and quality phenotyping (Field, Lab & GH)
- Stage 2 Multi-environmental testing in SE and TPEs (1K)

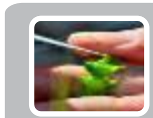
Year 5
- Stage 3 Multi-environmental testing in SE (240)
- International nursery distribution

Parents Recycling 3 vs 5 years
International distribution 5 vs 7 years

CIMMYT

Slide: Guillermo Gerard

Genotyping to apply GS at PCs "parcelas chicas"



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- Phenotypic selection of small plots (PC) [Y]

Year 5

- Disease selection of small plot (PC) + [BV/Mv]
- Stage 1 Grain Yield testing Optimal environment

genotyping

genotyping

Year 6

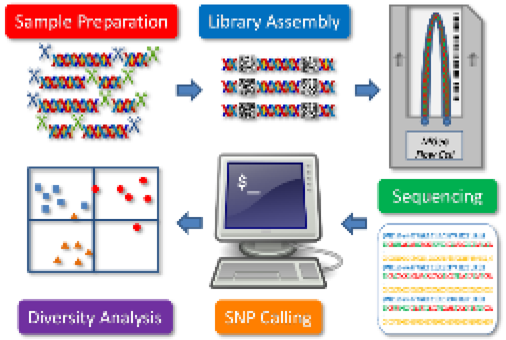
- Stage 2 Multi-environmental testing in SE (1.1K)
- Stage 3 Multi-environmental testing in SE (252)

Year 7

- International nursery distribution

2014 to 2019: Genomic selection in Stage 1 yield trials (n ≈ 9,000)

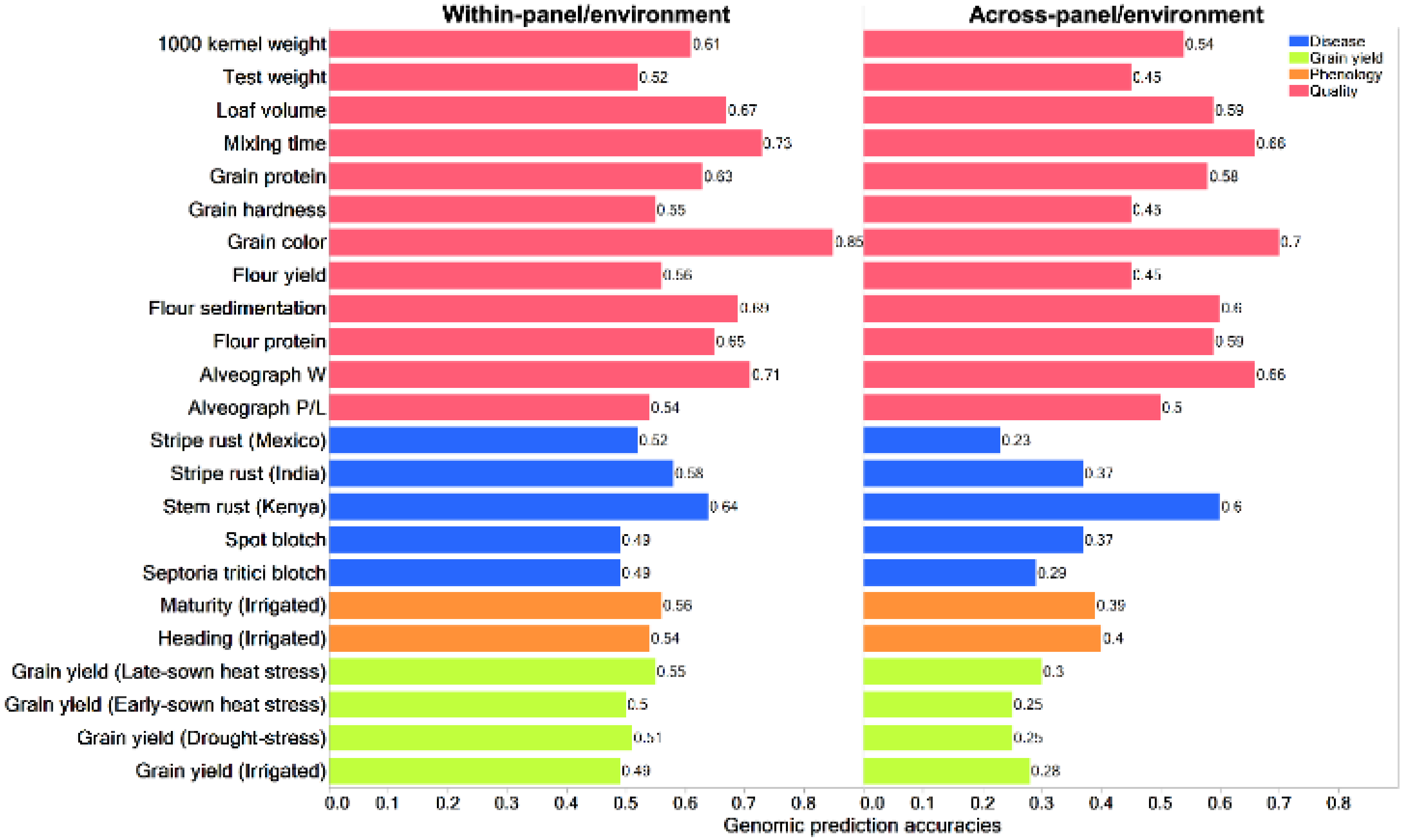
2020 to 2023: Genomic selection in pre - Stage 1 (n ≈ 13,000)



GBS, KSU
(Jul – Aug)

GS for advance to S1 yield trials and cross design

- ➢ Visual selection (disease, phenology and height)
- ➢ GEBVs, ABLUPs derived from historical data (>40 traits)
- ➢ Selection of 4.5K lines for S1
- ➢ Sparse testing in S1 in planning
- ➢ Marker-adjusted phenotypes for parental selection in NARES
- ➢ CIMMYT-NARS GS network in SA in panning



Source: P. Juliana

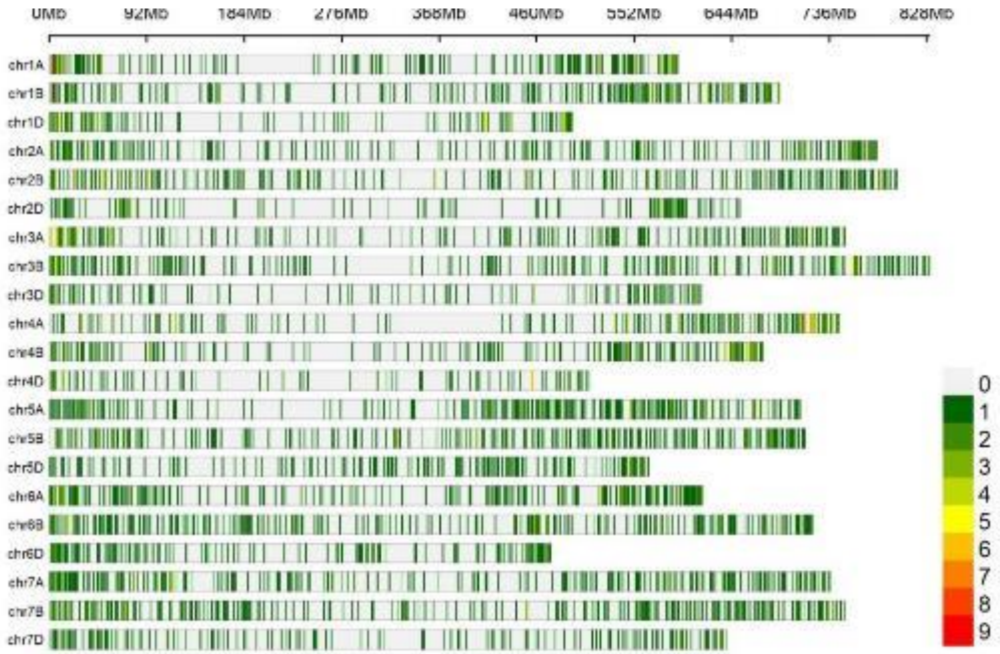
Mid-density genotyping service: MDSG

Intertek Agri-Services

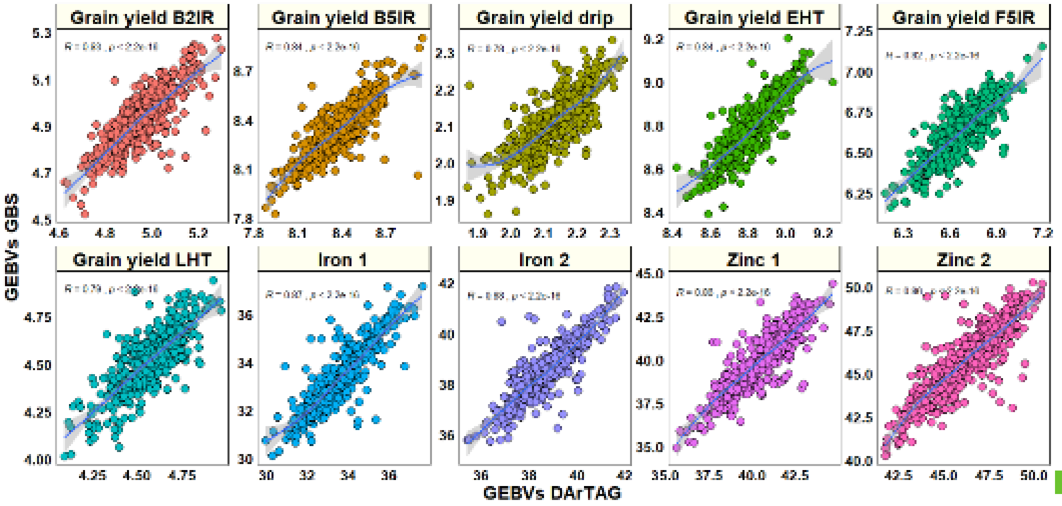
DArT diversity arrays technology

- TaDArTAG panel 2: 3900 genome-wide distributed SNPs including 156 gene-based markers and 312 QTL markers
- Results show similar and correlated GEBVs compared to GBS for >40 traits across years.
- USE: GS, variety identification, fingerprinting, MABC background selection

SNP distribution in the DArTAG panel 2



GEBVs GBS vs. DArTAG panel 2



MDSG: work in progress

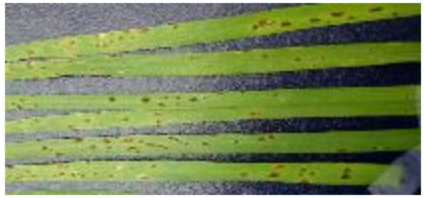
- TdDArTAG panel 1: ~3600 SNPs, in collaboration with CREA-Italy, ICARDA), update of TaDArTAG panel 2

- Mid- to higher density imputation of TaDArTAG panel 2 via:
  - the Practical Haplotype Graph (PHG, US-CIMMYT reference population) in collaboration with KSU (Kathie Jordan)
  - DEECA-imputation pipeline (Gabriel Keeble-Gagnere), DEECA – CIMMYT reference population (>800 genotypes)

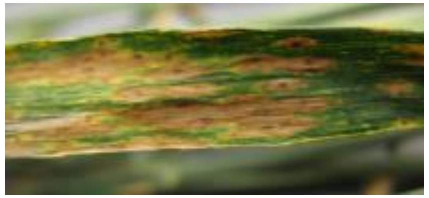
- Deploy something like "HaploCatcher" to postulate, report the presence of genes, haplotypes withing DARTAG panels.

- Deployment in pre-breeding (population improvement, recurrent rapid-cycle GS for two horizontal diseases)

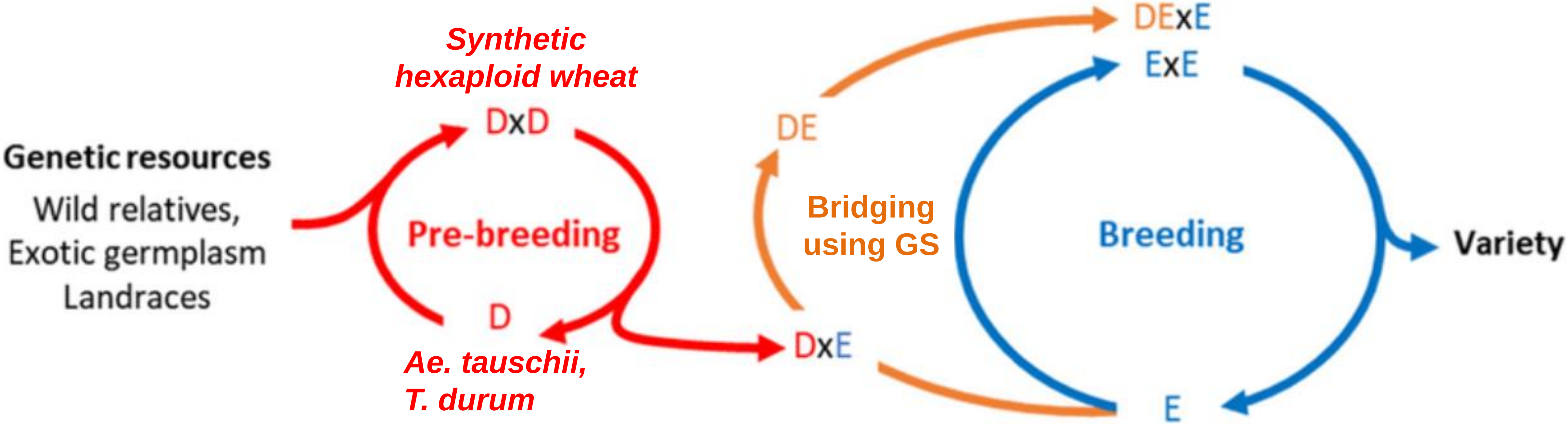
Recurrent selection to harness genetic resources and broaden the genetic base of elite pools



Spot blotch



Septoria tritici blotch



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