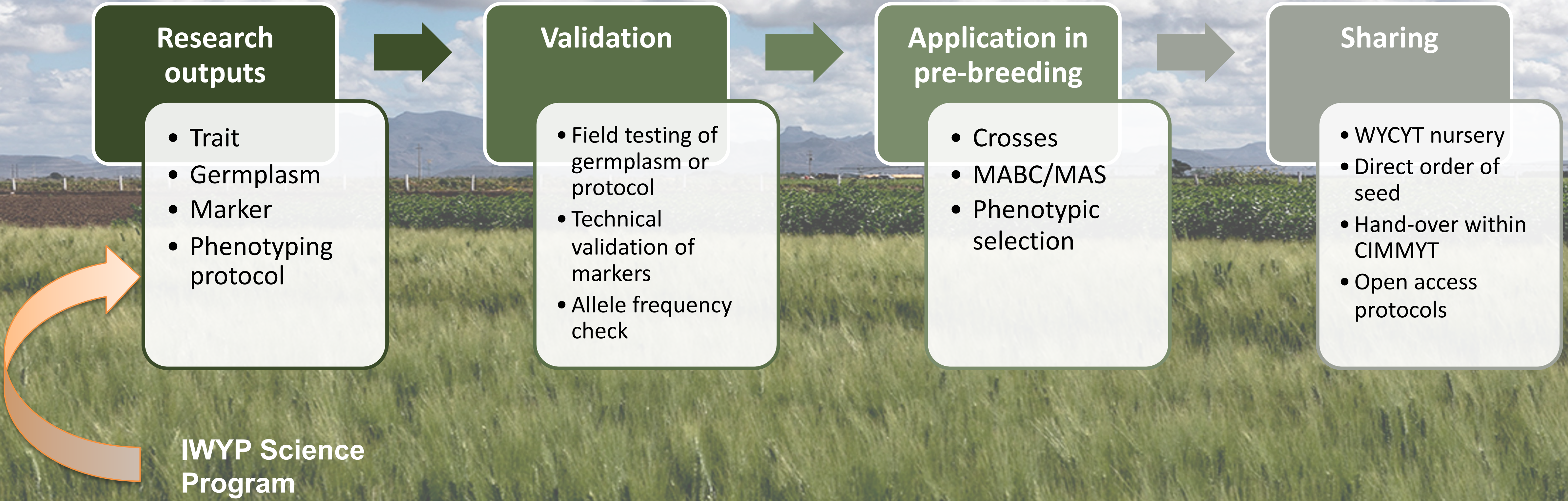
Past projects – what's in the CIMMYT pipeline. A translation story so far.

Carolina Rivera, Matthew Reynolds, Jacinta Gimeno, Susanne Dreisigacker, Guillermo Gerard

IWYP Conference, 10 & 12 September 2025

General pipeline of integration of research outputs in the IWYP Hub at CIMMYT



Research outputs

- Trait
- Germplasm
- Marker
- Phenotyping protocol

Validation

- Field testing of germplasm or protocol
- Technical validation of markers
- Allele frequency check

Application in pre-breeding

- Crosses
- MABC/MAS
- Phenotypic selection

Sharing

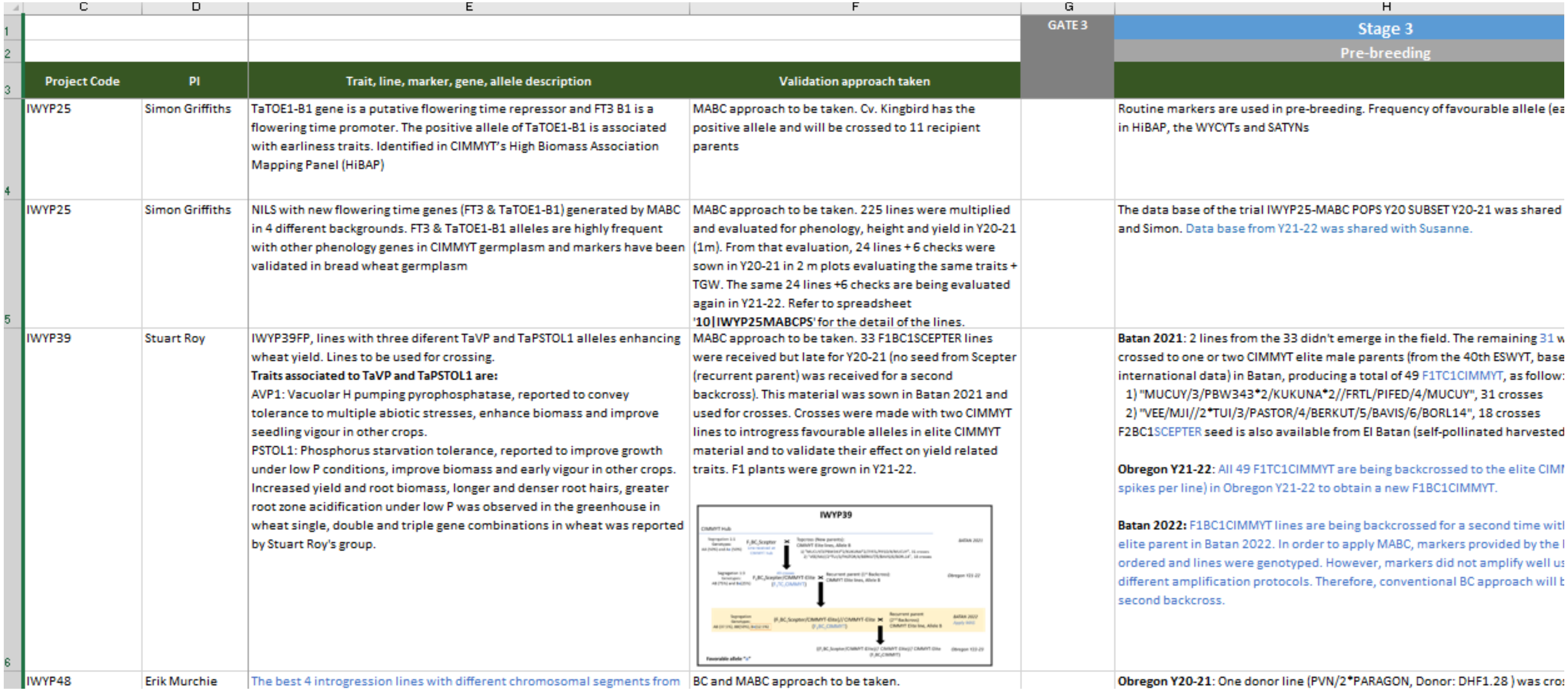
- WYCYT nursery
- Direct order of seed
- Hand-over within CIMMYT
- Open access protocols

IWYP Science Program

Types of research outputs tested in the IWYP Hub at CIMMYT

- **Trait discovery research: source and sink related traits** (e.g. spike hormones and fertility, canopy architecture, chlorophyll fluorescence kinetics in spikes, trehalose 6-phosphate, internode length).
- **Methodology validation research** (characterizing germplasm, screening parents, segregants and advanced lines).
- **Novel germplasm and alleles** (e.g. introgression of wild relatives with increased photosynthetic efficiency)
- **KASP markers designed for MTAs** (e.g. identified by Molero et al. 2019 and Joynson et al. 2021).
- **Deployment of IWYP derived molecular markers** (trait introgression, QTL profiling).

Documentation of research outputs entering the pre-breeding pipeline



	C	D	E	F	G	H
1					GATE 3	Stage 3
2						Pre-breeding
3	**Project Code**	**PI**	**Trait, line, marker, gene, allele description**	**Validation approach taken**		
4	IWYP25	Simon Griffiths	TaTOE1-B1 gene is a putative flowering time repressor and FT3 B1 is a flowering time promoter. The positive allele of TaTOE1-B1 is associated with earliness traits. Identified in CIMMYT's High Biomass Association Mapping Panel (HiBAP)	MABC approach to be taken. Cv. Kingbird has the positive allele and will be crossed to 11 recipient parents		Routine markers are used in pre-breeding. Frequency of favourable allele (ea in HiBAP, the WYCYTs and SATYNs
5	IWYP25	Simon Griffiths	NILS with new flowering time genes (FT3 & TaTOE1-B1) generated by MABC in 4 different backgrounds. FT3 & TaTOE1-B1 alleles are highly frequent with other phenology genes in CIMMYT germplasm and markers have been validated in bread wheat germplasm	MABC approach to be taken. 225 lines were multiplied and evaluated for phenology, height and yield in Y20-21 (1m). From that evaluation, 24 lines + 6 checks were sown in Y20-21 in 2 m plots evaluating the same traits + TGW. The same 24 lines +6 checks are being evaluated again in Y21-22. Refer to spreadsheet '10|**IWYP25MABCPS**' for the detail of the lines.		The data base of the trial IWYP25-MABC POPS Y20 SUBSET Y20-21 was shared and Simon. Data base from Y21-22 was shared with Susanne.
6	IWYP39	Stuart Roy	IWYP39FP, lines with three diferent TaVP and TaPSTOL1 alleles enhancing wheat yield. Lines to be used for crossing. **Traits associated to TaVP and TaPSTOL1 are:** AVP1: Vacuolar H pumping pyrophosphatase, reported to convey tolerance to multiple abiotic stresses, enhance biomass and improve seedling vigour in other crops. PSTOL1: Phosphorus starvation tolerance, reported to improve growth under low P conditions, improve biomass and early vigour in other crops. Increased yield and root biomass, longer and denser root hairs, greater root zone acidification under low P was observed in the greenhouse in wheat single, double and triple gene combinations in wheat was reported by Stuart Roy's group.	MABC approach to be taken. 33 F1BC1SCEPTER lines were received but late for Y20-21 (no seed from Scepter (recurrent parent) was received for a second backcross). This material was sown in Batan 2021 and used for crosses. Crosses were made with two CIMMYT lines to introgress favourable alleles in elite CIMMYT material and to validate their effect on yield related traits. F1 plants were grown in Y21-22.		**Batan 2021**: 2 lines from the 33 didn't emerge in the field. The remaining 31 w crossed to one or two CIMMYT elite male parents (from the 40th ESWYT, base international data) in Batan, producing a total of 49 F1TC1CIMMYT, as follow: 1) "MUCUY/3/PBW343*2/KUKUNA*2//FRTL/PIFED/4/MUCUY", 31 crosses 2) "VEE/MJI//2*TUI/3/PASTOR/4/BERKUT/5/BAVIS/6/BORL14", 18 crosses F2BC1SCEPTER seed is also available from El Batan (self-pollinated harvested **Obregon Y21-22**: All 49 F1TC1CIMMYT are being backcrossed to the elite CIM spikes per line) in Obregon Y21-22 to obtain a new F1BC1CIMMYT. **Batan 2022:** F1BC1CIMMYT lines are being backcrossed for a second time wit elite parent in Batan 2022. In order to apply MABC, markers provided by the ordered and lines were genotyped. However, markers did not amplify well us different amplification protocols. Therefore, conventional BC approach will second backcross.
	IWYP48	Erik Murchie	The best 4 introgression lines with different chromosomal segments from	BC and MABC approach to be taken.		**Obregon Y20-21**: One donor line (PVN/2*PARAGON, Donor: DHF1.28) was cro

Trait discovery research, past projects

CIMMYT Aligned projects, 'Low hanging fruits'

EXPLORING GENETIC DIVERSITY FOR BIOMASS AND TRAITS RELATED TO CANOPY PHOTOSYNTHESIS

EXPLORING GENETIC DIVERSITY FOR HARVEST INDEX AND IDENTIFYING IMPROVED SELECTION APPROACHES

DEVELOPING A HIGH THROUGHPUT SCREEN FOR SOURCE:SINK BALANCE TO TAP PHOTOSYNTHETIC POTENTIAL

Matthew Reynolds, Gemma Molero, Francisco Pinto, Carolina Rivera, Jacinta Gimeno, Francisco Pinera, Carlos Robles (CIMMYT)

Canopy architecture

Partitioning traits

HI-BM trade-offs

Fruiting efficiency

Spike and leaf photosynthesis

Lodging resistance

Validation of phenology genes

Germplasm characterization, methodology research, paths to yield, genetic dissection

Strong methodology research in the IWYP Hub at CIMMYT

HTP

Jiemeng Xu

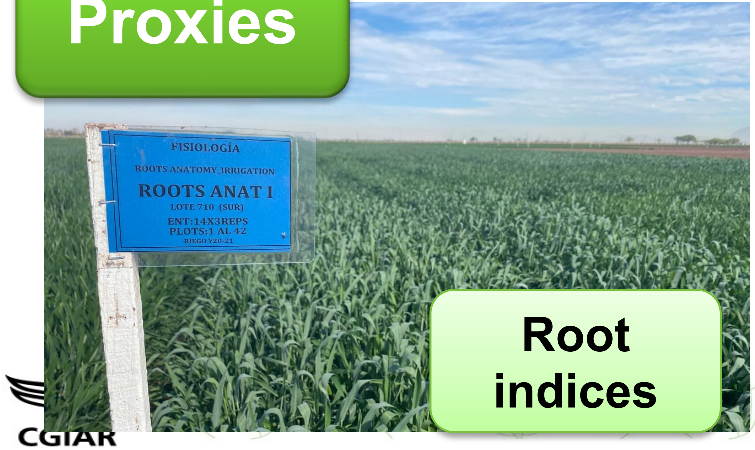
Phenocart

Francisco Pinto

UAVs

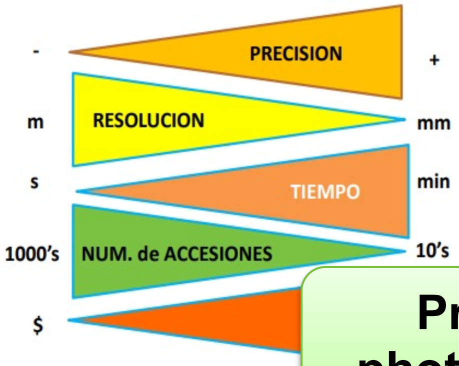
Proxies

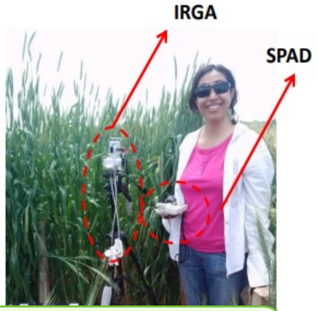
Lucia Nevescanin



Root indices

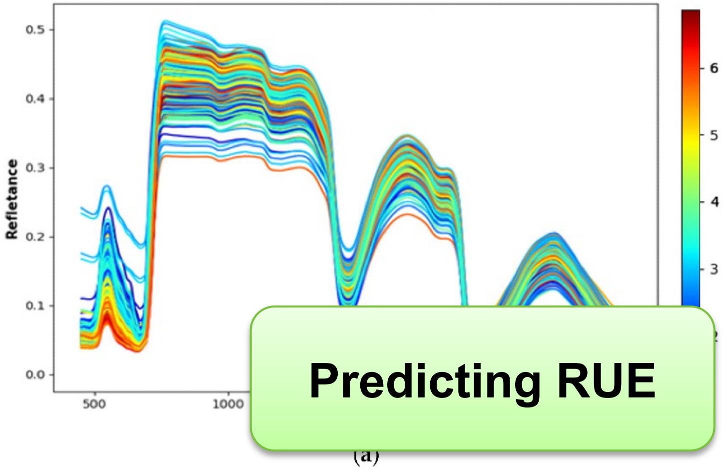
Viridiana Silva





Predicting photosynthesis

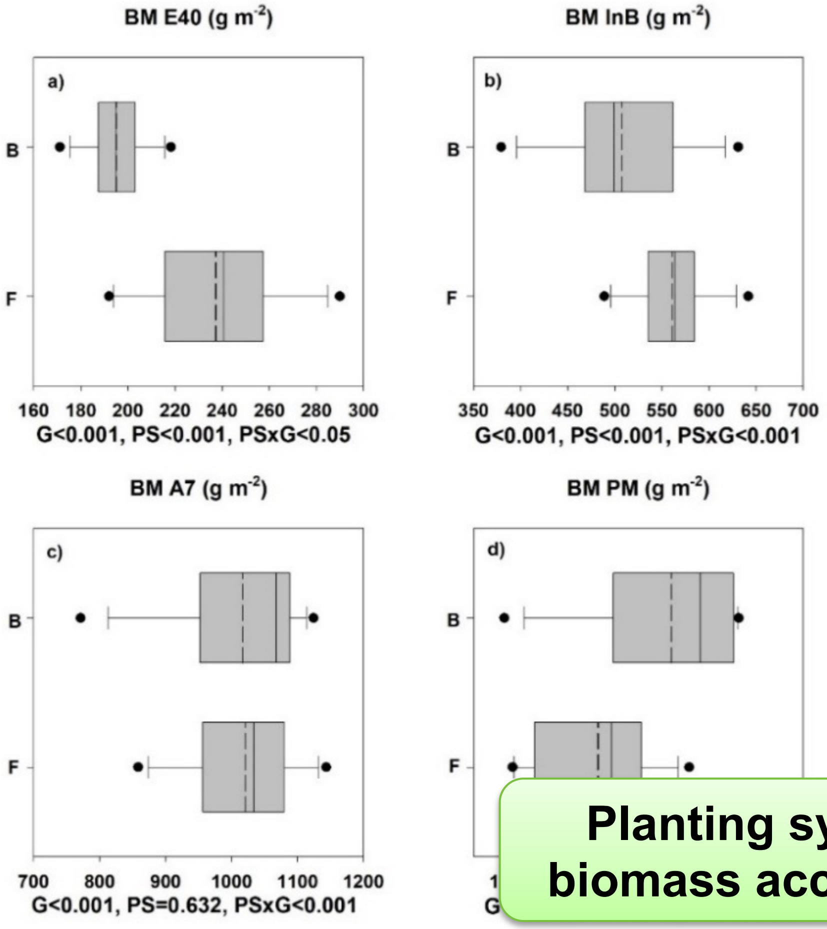
Carlos Robles



Predicting RUE

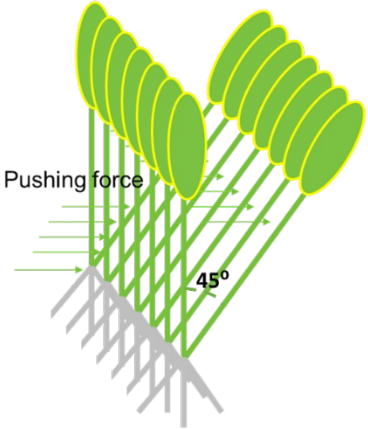
Strong methodology research in the IWYP Hub at CIMMYT

Planting systems, lodging resistance methods



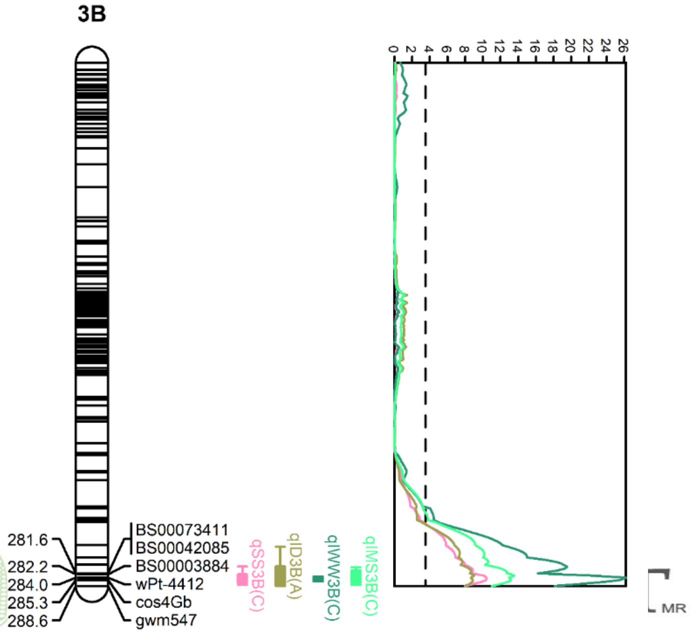
Marcela
Moroyoqui

Planting system on biomass accumulation



Francisco
Pinera

Lodging resistance methods and QTLs



CGIAR

Trait discovery research, past projects

Aligned and funded projects, external

ALTERING CANOPY ARCHITECTURE TO INCREASE CROP PHOTOSYNTHESIS AND YIELD

Richard Richards
Chief Research Scientist, Plant Industry, CSIRO

Rooty: A Root Ideotype Toolbox to Support Improved Wheat Yields

Project Lead – Eric Ober, National Institute for Agricultural Botany (NIAB) (GBR)
Principal partners
(GBR); University
Forschungszentru

Speeding the Adjustment of Photosynthesis to Shade-Sun Transitions to Increase Yield Potential in the Field

Project Lead – Elizabete Carmo-Silva, Lancaster University (GBR)
Principal partners – CIMMYT (MEX);

More

Improving Wheat Yield by Optimizing Energy Use Efficiency

Project Lead – Barry Pogson, Australian National University (AUS)
Principal partners – University of Western Australia (AUS); CIMMYT (MEX); University of Adelaide (AUS)

More

Using Next Generation Genetic Approaches to Exploit Phenotypic Variation in Photosynthetic Efficiency to Increase Wheat Yield

arlham Institute (GBR)
University (GBR); CIMMYT (MEX);
(AUS)

aximize Harvest Index by Controlling the Duration of Developmental Phases

Project Lead – Simon Griffiths, John Innes Center (GBR)
Principal partners – University of Bristol (GBR); University of Buenos Aires (ARG); CSIRO (AUS); CIMMYT (MEX); ICREA (ESP)

More

Wider and Faster: High-Throughput Phenotypic Exploration of Novel Genetic Variation for Breeding High Biomass and Yield in Wheat

Project Lead – Erik Murchie, University of Nottingham (GBR)
Principal partners – University of Bristol (GBR); Lancaster University (GBR); University of Essex (GBR)

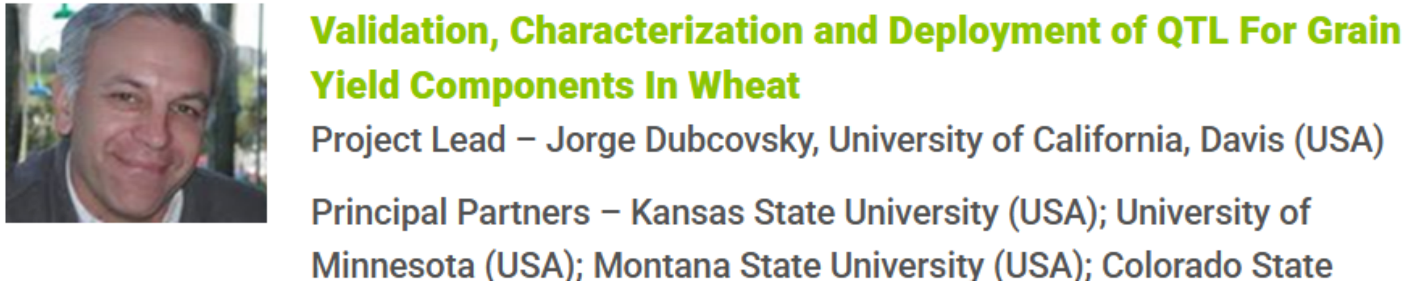
Germplasm characterization, methodology research, paths to yield, genetic dissection, marker development

CGIAR

CIMMYT MR

Trait discovery research, past projects

NIFA-IWYP projects



Validation, Characterization and Deployment of QTL For Grain Yield Components In Wheat

Project Lead – Jorge Dubcovsky, University of California, Davis (USA)

Principal Partners – Kansas State University (USA); University of Minnesota (USA); Montana State University (USA); Colorado State

Advancing Harvest Index In Wheat Through Genomic Enabled Physiological Breeding

Project Lead – Md Ali Babar, University of Florida (USA)

Principal Partners – University of Nottingham (GBR); CIMMYT (MEX); USDA-ARS Manhattan (USA)

QTL validation, genetic dissection, marker development

Collaboration with academic institutes

CANADA:
National Research Council (NRC)
Agricultiral and Agri-Food Canada (AAFC)

UK:
Cambridge University
Earlham Institute
John Innes Center
Lancaster University
Lincoln University
National Institute of Agricultiral Botany (NIAB)
Nottingham University
Oxford University
Rothamsted Research
University of Bristol
University of Essex
University of Liverpool

GERMANY:
University of Hohenheim
Technische Universitat Munchen
IPK Gatersleben
Forschungszentrum Juelich GmbH
Julius Kühn-Institut

SWITZERLAND: University of Zurich

THE NEDERLANDS: Wageningen University and Research

France INRA

JAPAN: University of Agriculture and Technology, Tokyo

USA:
Penn State University
Purdue University
SALK Institute
National Science Foundation
Texas A&M University
Washington State University
Arizona State University
Kansas State University
UCDavis
University of Florida

ITA
Bo

ISRAEL: Agricultural Research Organization (ARO) Volvani Center

CHINA:
Chinese Academy of Agricultural Science (CAAS)
China Agricultural University (CAU)
Dazhou Academy of Agricultural Sciences
North Western University

AUSTRALIA:
Australian Research Council (ARC)
Australian National University (ANU)
CSIRO
University of Melbourne
University of Adelaide
University of Sydney
University of Western Australia

CHILE: Universidad Austral de Chile

ARGENTINA: Universidad Nacional del Sur

GWP Physiology team 2017-2024
>200 visitors, >25 countries, > 70 institutions/universities

- Undergrad students
- Master students
- PhD students
- Scientists

Jacinta Gimeno, IWYP Hub Coordinator

OTHER COUNTRIES:
Iran, Mexico, Rusia, Sudan, Turkey, Uzbekistan, Zimbabwe, India…..

Novel germplasm and alleles from IWYP projects

IWYP48, wild relatives introgression lines for increased photosynthetic efficiency

Erik Murchie, Julie King

Crosses Y21-22

Crosses Y22-23

Obregon Y24-25	Summer 2025
F4BC2IWYP48-AP09 216 lines	F5BC2IWYP48-AP09 107 Lines

Applied MAS WRC0957 marker

CANPBY26 ???

IWYP76, triple mutants on TGW, yield and spike yield components genes

Cristobal Uauy, James Simonds

Y23-24
2nd backcross
applied MABC

Obregon Y24-25	Summer 2025
F2BC2IWYP76 18 families	F3BC2IWYP76 280 lines (10 fam)

MAS Applied G2373A_TaGW2, GW2-B_C2557Tb / C504T SNP, G7139A SNP marker

Novel germplasm and alleles from IWYP projects

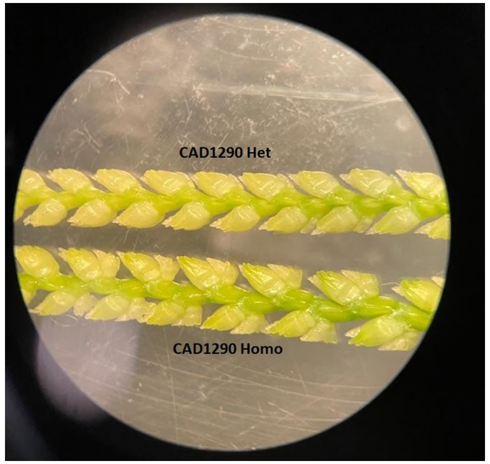
IWYP39, lines with TaVP and TaPSTOL1 alleles enhancing wheat yield

Stuart Roy

	Obregon Y24-25	Summer 2025	
Crosses Y21-22	CANPBY25 87 Lines	CANPBY25_SUBSET 65 Lines *Best performance in Y24-25	2025 13 WYCYT 11 Lines
Crosses Y22-23	F4PBSEL23 5 Families	PRECAN23 62 Lines	**CANPBY26 ???**

AP09, production of additional fertile spikelets and grain protein content

Scott Boden



	Obregon Y24-25	Summer 2025	
Crosses Y21-22	F4BC2IWYP48-AP09 21 lines	F5BC2IWYP48-AP09 10 Lines	**CANPBY26 ???**
	F2BC1IWYP-AP09_Y24-25 2 families	F1BC2IWYPAP09_BV25 21 crosses in head rows	

MAS Applied
HB-D2_5, HB-D2_1

Summary of projects, trials & traits involved in **crosses** over 10 years of IWYP

- Database of historical crosses was generated, including parental selection criteria (traits), project, origin trial and crossing strategy

Summary of projects, trials & traits transferred to candidate lines and nurseries over 10 years

- Database of historical candidate lines was generated, including parental selection criteria (traits), project, origin trial and crossing strategy, lines selected for international nurseries

IWYP outputs are reflected in the 12th WYCYT nursery

GID	Cross name*	Traits with high expression**	Grain yield (g/m^2)	Predicted grain yield (g/m^2)
9100618	REEDLING-GL5A_1/QUAIU	GFR, GY/day	918	798
9100621	REEDLING-GL5A_1/QUAIU	BM (rank 1), BM/day (rank 1), Gm2, GFR	864	793
9101046	REEDLING-GL5A_1/QUAIU	HI (rank 2), GPS, GFR	851	794
9100616	REEDLING-GL5A_1/QUAIU	GFP, GY/day	828	775
9101044	REEDLING-GL5A_1/QUAIU		828	759
9101027	REEDLING-GL5A_2/QUAIU	TGW (rank 2), BM/day	826	758
9101024	REEDLING-GL5A_2/QUAIU	HI, GPS, GFP	815	747
9101055	REEDLING-GL5A_1/QUAIU	BM/day	805	794
9101035	REEDLING-GL5A_2/QUAIU	TGW, HI, GWPS	793	743
9100728	REEDLING-GL5A_2/6/BCN/WBLL1//ROLF07/5/UP2338*2/SHAMA/3/MILAN/KAUZ//CHIL/CHUM18/4/UP2338*2/SHAMA		772	729
9100636	REEDLING-GL5A_1/QUAIU	HI, GPS	764	756

11 lines carrying the 5A QTL for grain length are part of the latest WYCYT nursery, in elite and CIMMYT backgrounds (update)

‘Hand-over’ examples within CIMMYT

Crop	**Project Value**	**Product Profile**	**Trait**	**Genes**
BW	Improved and diversified rust resistance	HW-OE-NM, HW-HT-EM, HW-DT-NM, HW-DT-EM	Stem and yellow rust	*Sr22, Sr50, Sr2, Yr57, Yr59, Sr35, Yr15, Yr5, Sr47, Sr25, Sr13, YrSP*
BW	Enhanced Fhb resistance	HW-HiR_NM	Fusarium head blight	*Fhb1, Qfhb.cim-2DLc*
BW	Improved STB resistance	HW-HiR_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	Improved TKW	HW-OE-NM, HW-HT-EM, HW-DT-NM, HW-DT-EM	TKW	*TaGW2, QGW-jic-6A, QGL-jic-5A*
BW	Novel diversity for stress tolerance (heat drought)	HW-DT-EM, HW-DT-NM, HW-HT-EM	Heat/drought tolerance	*LTP-HB3B, LTP-HB4B, LTP-HB5B, LTP-HB6D, LTP-HB7D-1, LTP-HB7D-2*

- **Low allele frequency (abiotic stress tolerance) in CIMMYT elite material**
- **Favorable TGW alleles are fully absent in CIMMYT elite material**
- **Candidate 10 WYCYT lines are first CIMMYT lines carrying those alleles in higher frequency**
- **Lines handed over to the Bread Wheat program at CIMMYT**
- **Favorable haplotype in chromosome 6D (Molero et al. 2022) is also related to yield under optimal conditions**

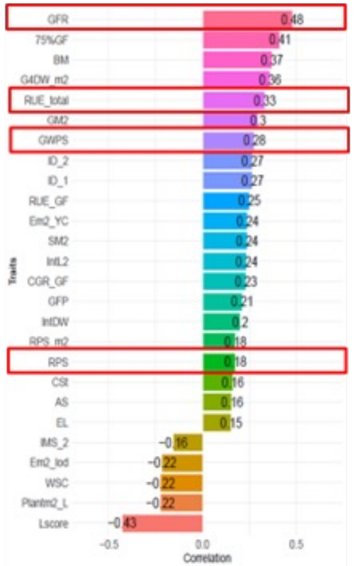
IWYP trait transfer to CIMMYT breeding program

Component I: germplasm characterization

1. Elite material to define current trait demand
2. Diverse sources of trait expression

***Component II:* trait prioritization**

Analysis of historical ESWYT data to select target IWYP traits in presence of feasible phenotyping methods

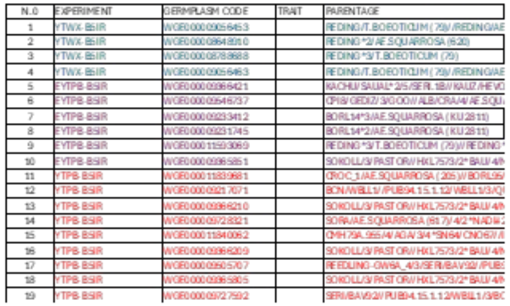


Component III: generation of PB material under latest elite background

Around 100 crosses done in 2023 and 100 in 2024 using IWYP derived material and the latest BW elite lines

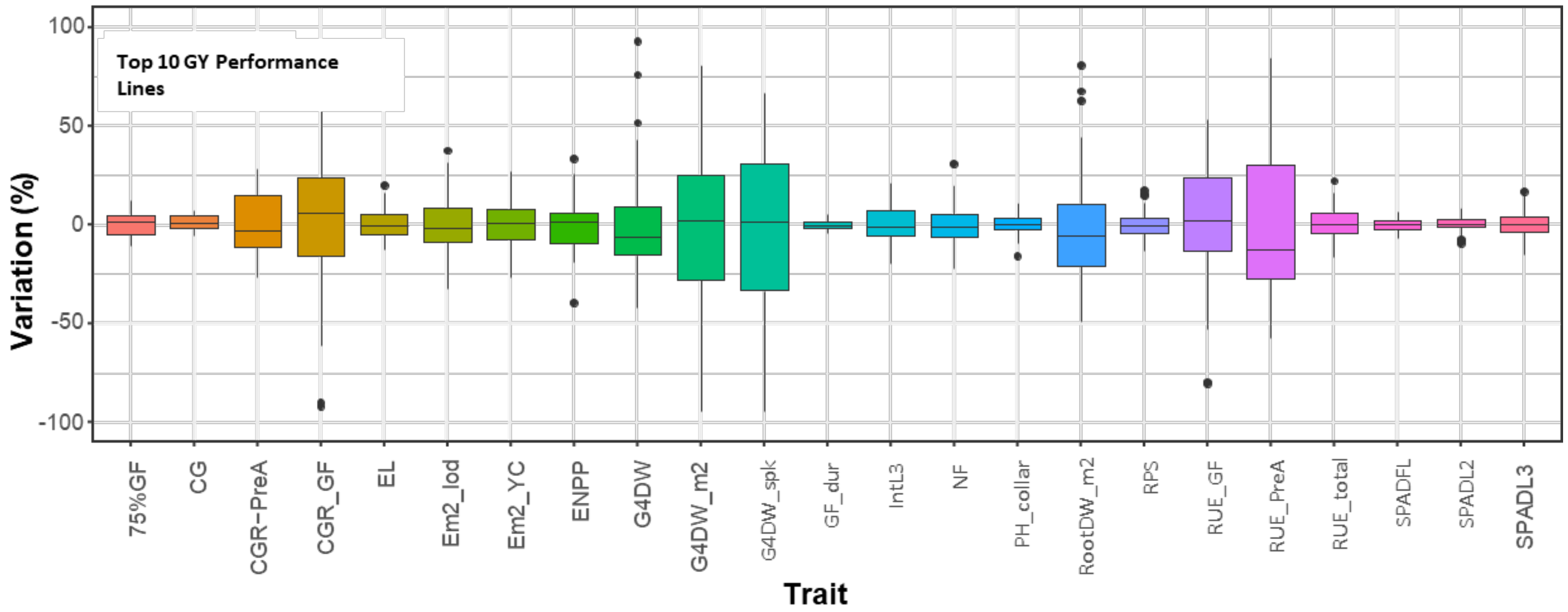
Component IV: transfer to breeding

Selected material to enter the BW CB (some material has entered already, see next slides)

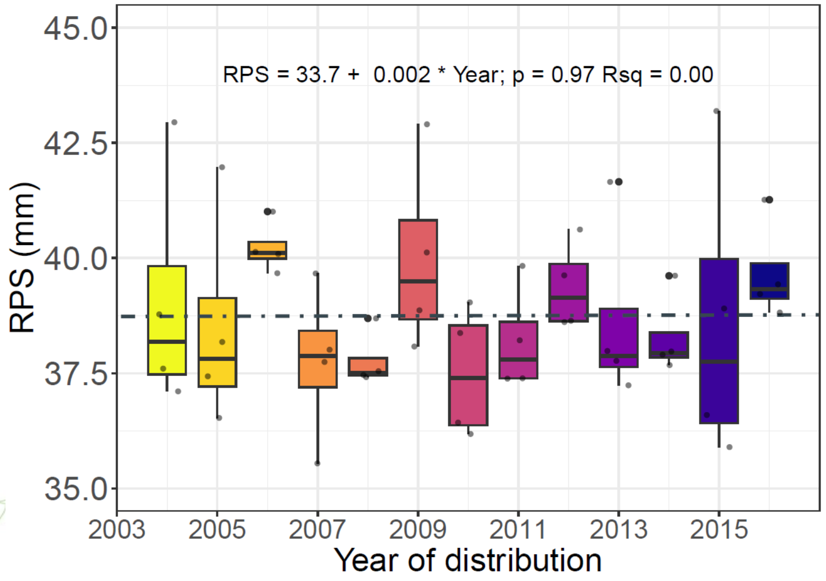


N.0	EXPERIMENT	GERMPLASM CODE	TRAIT	PARENTAGE
1	YTWX-BSIR	WGE000009056453		REDING/T.BOEOTICUM (79)//REDING/AE
2	YTWX-BSIR	WGE000008648010		REDING*2/AE.SQUARROSA (620)
3	YTWX-BSIR	WGE000008788688		REDING*3/T.BOEOTICUM (79)
4	YTWX-BSIR	WGE000009056463		REDING/T.BOEOTICUM (79)//REDING/AE
5	EYTPB-BSIR	WGE000009866421		KACHU//SAUAL*2/5/SERI.1B//KAUZ/HEVO
6	EYTPB-BSIR	WGE000009646737		CP18/GEDIZ/3/GOO//ALB/CRA/4/AE.SQU
7	EYTPB-BSIR	WGE000009233412		BORL14*3/AE.SQUARROSA (KU2811)
8	EYTPB-BSIR	WGE000009231745		BORL14*2/AE.SQUARROSA (KU2811)
9	EYTPB-BSIR	WGE000011593069		REDING*3/T.BOEOTICUM (79)//REDING*
10	EYTPB-BSIR	WGE000009865851		SOKOLL/3/PASTOR//HXL7573/2*BAU/4/
11	YTPB-BSIR	WGE000011839681		CROC_1/AE.SQUARROSA (205)//BORL95/
12	YTPB-BSIR	WGE000009217071		BCN/WBLL1//PUB94.15.1.12/WBLL1/3/
13	YTPB-BSIR	WGE000009866210		SOKOLL/3/PASTOR//HXL7573/2*BAU/4/
14	YTPB-BSIR	WGE000009728321		SORA/AE.SQUARROSA (817)/4/2*NADI/
15	YTPB-BSIR	WGE000011840062		CMH79A.955/4/AGA/3/4*SN64/CNO67//
16	YTPB-BSIR	WGE000009866209		SOKOLL/3/PASTOR//HXL7573/2*BAU/4/
17	YTPB-BSIR	WGE000009605707		REEDLING-GW6A_4/3/SERI/BAV92//PUB
18	YTPB-BSIR	WGE000009865805		SOKOLL/3/PASTOR//HXL7573/2*BAU/4/
19	YTPB-BSIR	WGE000009727592		SERI/BAV92//PUB94.15.1.12/WBLL1/3/BC

IWYP trait transfer to CIMMYT breeding program

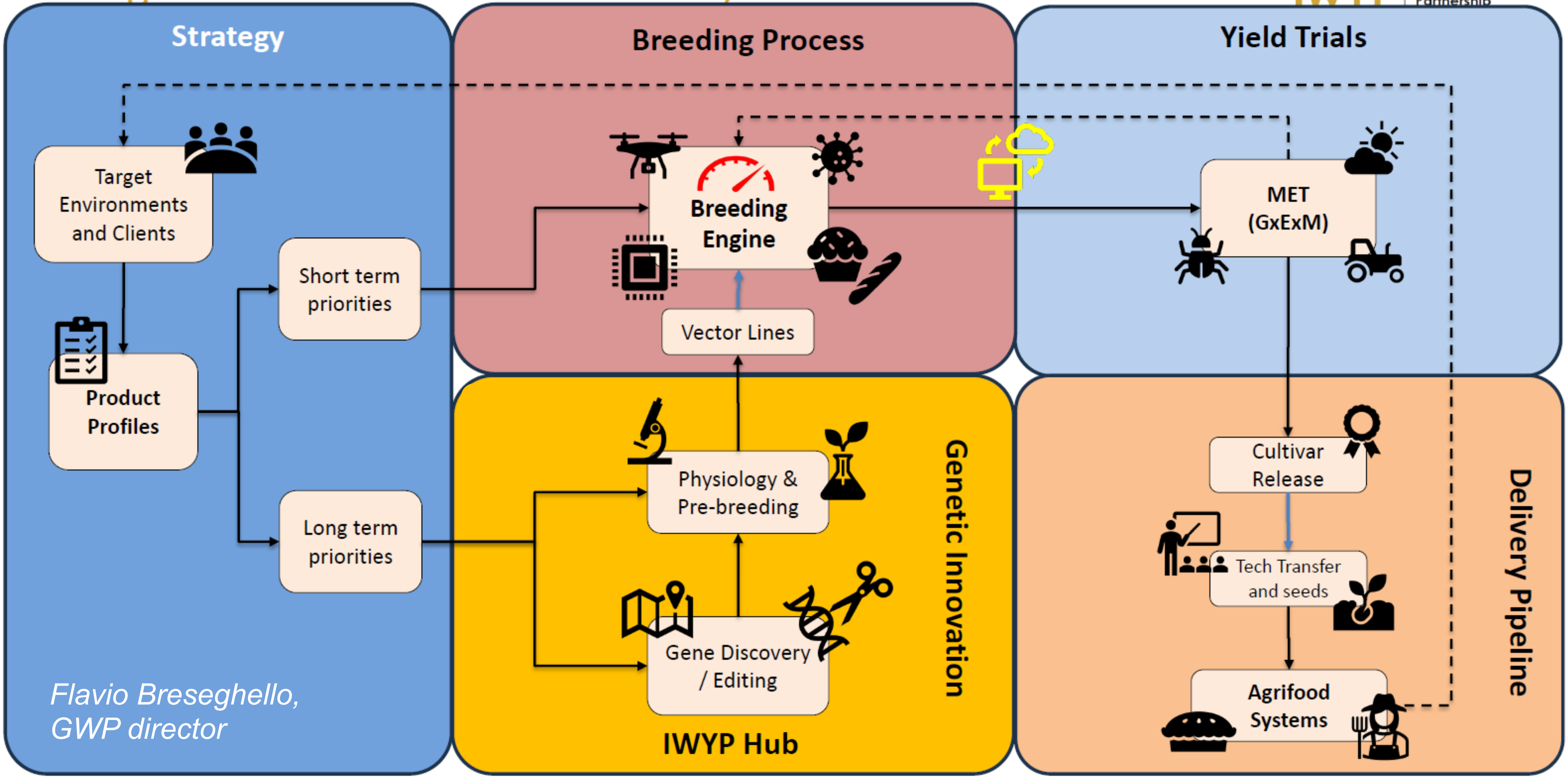


- **Low genetic variation in the breeding program**
- **Relationship with yield, biomass**
- **Null or low genetic gains**



CIMMYT Wheat Program (2025-2030) and IWYP Hub:
Integrated to Deliver Better Wheat; Now and in the Future

IWYP International Wheat Yield Partnership



Flavio Breseghello, GWP director

Stage gate process within the CIMMYT pre-breeding and breeding strategy

1

- Is the discovery of potentially important value?
- Does it contribute to current or likely future product profile(s)?

2

- Is the potential value of the new technology confirmed?
- Do data confirm that its potential benefit is sufficient to merit further investment?

3

- Do the (multi-location) data confirm the value of the trait for one or more prioritized product profiles?
- Is the trait absent, rare, or of substantially lesser value in the elite germplasm?
- Can we reliably select for the new trait?

4

- Is the new technology incorporated into germplasm that is sufficiently elite such that it can be used in mainstream breeding pipelines without unacceptable penalty to genetic gains?
- Is pre-breeding's work complete?
- If yes, handover to mainstream breeders at CIMMYT and through international nurseries; if no, decide whether and how to continue investing in the trait?

Take away points

- Hubs a unique model for research translation, allowing for testing material and protocols in multiple environments
- IWYP research outputs have been translated to ‘breeding ready’ products through the IWYP Hub al CIMMYT
- Investigate further what type of ‘useful’ genetic variation is missing in the breeding program to focus trait discovery and translation efforts
- Need to integrate a strategic incorporation of molecular and genomic tools in pre-breeding (stacking QTLs, GS based advancement, parental selection).
- Research outputs to follow a stage gate process before entering pre-breeding, defined by a multi disciplinary team.

Thank you for your interest!