

# AVVERSITÀ FITOSANITARIE: LE SFIDE DI UNA GESTIONE ECOSOSTENIBILE



# 22 OPEN DISTAL 23

Moderatore: Paola Minardi



ALMA MATER STUDIORUM  
UNIVERSITÀ DI BOLOGNA  
DIPARTIMENTO DI  
SCIENZE E TECNOLOGIE AGRO-ALIMENTARI



**DISTAL**



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AGRO-ALIMENTARI

**22  
23  
'23** **OPEN  
DISTAL**

# Caratterizzazione delle risorse genetiche del patogeno e dell'ospite (frumento) per l'identificazione di fonti di resistenza e di fattori di avirulenza

**Thierry Marcel** - Biologie et Gestion du Risques (BIOGER), INRAE, Paris

**Marco Maccaferri, Matteo Bozzoli, J. Novi, F. De Sario, C. Liu, A. Prodi, R. Tuberosa** - DISTAL



**HORT@**  
— From research to field —



**WORKSHOP GTI "SALUTE DELLE PIANTE"**  
**AVVERSITÀ FITOSANITARIE: LE SFIDE DI UNA GESTIONE ECOSOSTENIBILE**

AULA 3, Viale Fanin 44, Bologna



# INRAE

National Research Institute for Agriculture, Food and Environment

- 18 Research Centres
- 14 Scientific Departments
- >200 Research Units
- >12,000 Employees



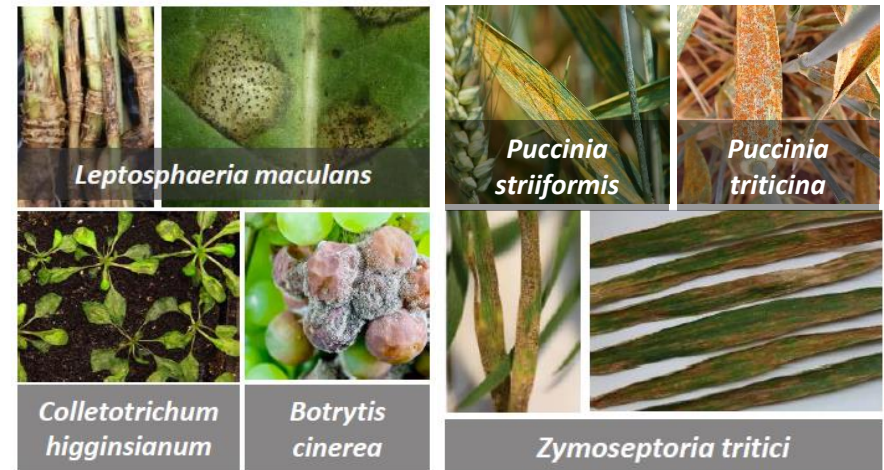
Our overarching goal is to address societal expectations for **sustainable and environmentally friendly strategies** in the fight against fungal diseases in major crop plants, and to **manage risks** associated with the dissemination and adaptive potential of phytopathogenic fungi.



## BIOGER Campus Agro Paris-Saclay

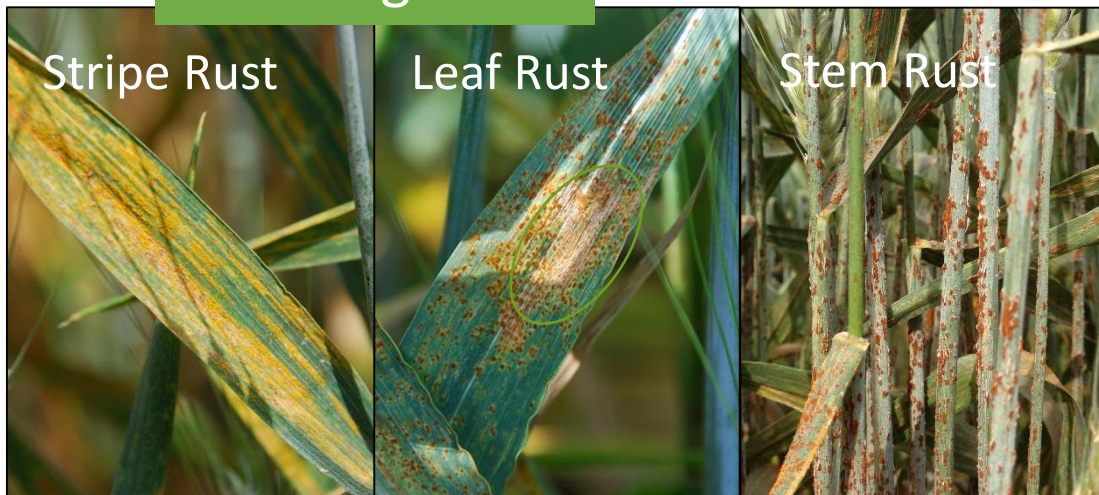


Reference research unit on fungal diseases of major European crops:



# INRAE BIOGER

Team “Epidemiology and evolution of fungal wheat pathogens”



## *Zymoseptoria tritici*

- Ascomycete (Dothideales)
- Heterothallic
- Latent necrotroph
- Dimorphic (yeast, mycelium)

## *Puccinia striiformis* f.sp. *tritici*

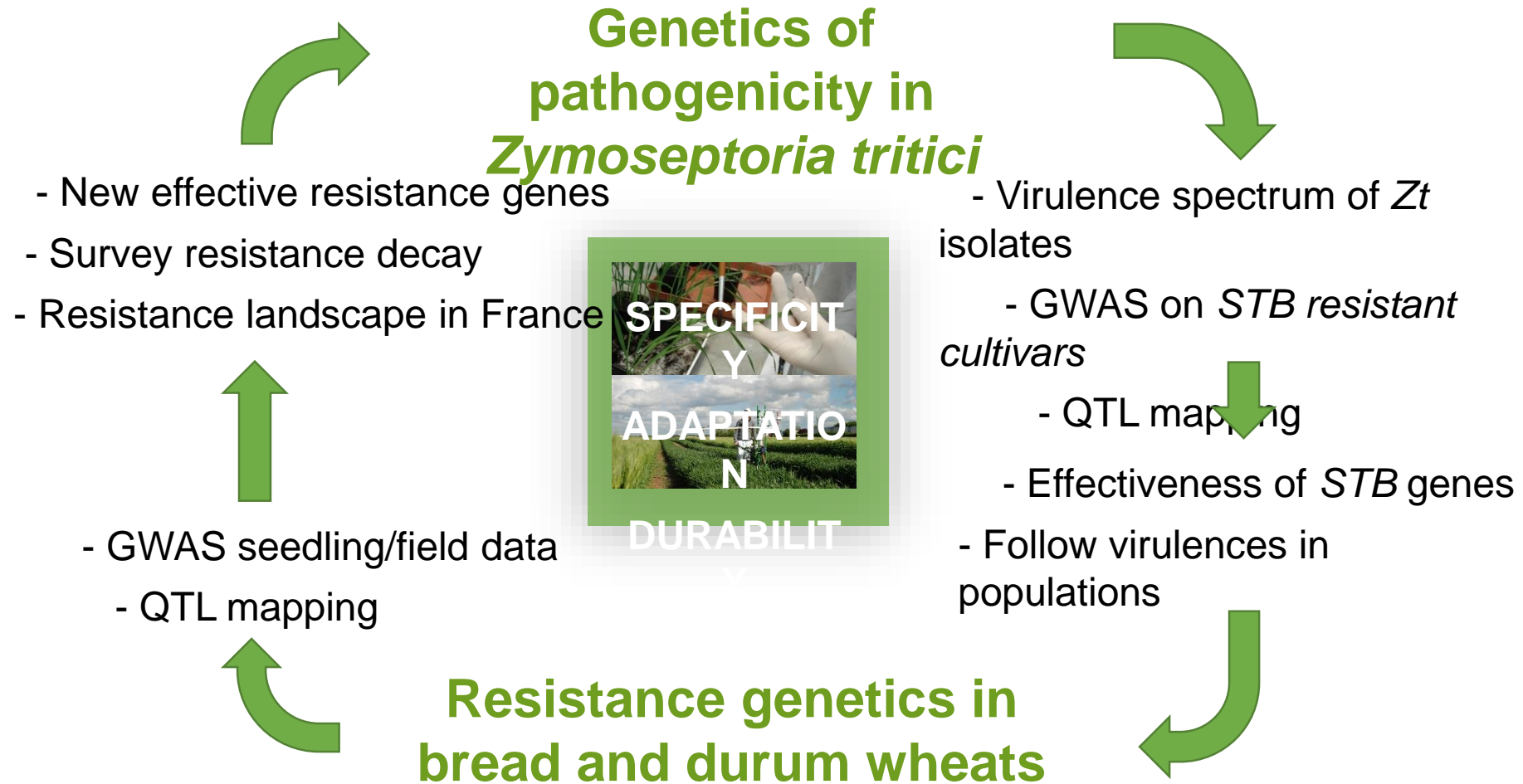
*P. triticina*

*P. graminis*

- Basidiomycetes (Uredinales)
- Heteroecious
- Obligate biotrophes

# INRAE BIOGER

Team “Epidemiology and evolution of fungal wheat pathogens”

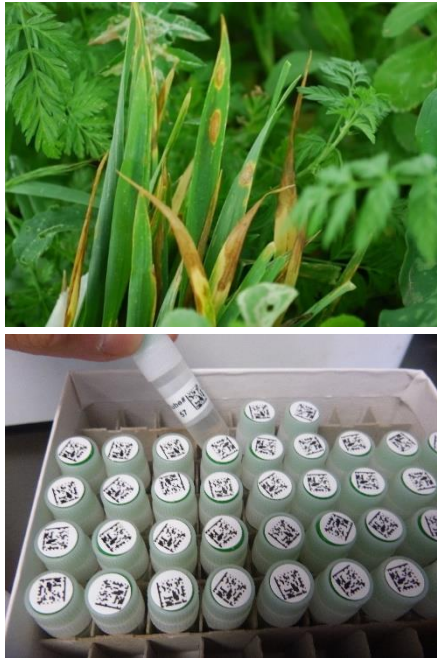




# Fungal genetics at the service of wheat breeders

## Collections and characterization of fungal isolates

COLLECTION of worldwide isolates



PATHOASSAYS under controlled conditions



surface sporulante (SPO)  
necrose (NEC)  
chlorose (CHL)  
surface verte (GRE)

Evaluation of VIRULENCE SPECTRA

ISOLATE	CULTIVAR	Tokuhung_29		Bulgaria_88		Veronopolis		Israel_493		Tadina		Symbtek_CS		Cadenza		Est. Federal		Synth. W7984		Solsonne		Newkuz_101500		TE-9111		Salmouni		Alina		Celia	
		STB1	STB6	STB2	STB6	STB3	STB6	STB4	STB6	STB5	STB6	STB7	STB8	STB9	STB6	STB7	STB8	STB9	STB6	STB7	STB10	STB11	STB12	STB13	STB14	STB15	STB16q				
INRA19-TM0074	Pakito	17	0	0	42	0	0	5	6	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		
INRA19-TM0079	Bermude	17	2	2	7	0	0	5	0	8	0	0	0	3	0	1	0	0	0	0	0	0	27	1	0	0	0	0	0		
INRA19-TM0044	Velasko	13	0	1	0	0	0	0	0	12	0	0	0	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
INRA19-TM0029	Rubisko	50	7	27	7	0	2	0	10	1	3	1	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0		
INRA19-TM0024	Rubisko	72	0	0	0	0	0	0	2	0	0	0	0	NaN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
INRA19-TM0059	Advisor	52	7	0	28	2	1	22	3	0	63	0	3	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0		
INRA19-TM0011	Ionesko	13	8	0	18	13	3	13	25	NaN	22	5	0	0	0	0	0	0	0	0	0	8	0	0	0	0	0	0	0		
INRA19-TM0064	Apache	70	0	0	0	0	0	0	15	0	33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
INRA19-TM0039	Bermude	65	0	2	1	0	0	30	3	0	3	0	8	0	0	0	0	0	0	0	0	48	0	0	0	0	0	0	0		
INRA19-TM0214	Pakito	45	0	0	0	0	0	70	43	0	57	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0		
INRA19-TM0124	Oregrain	10	0	0	0	0	0	70	29	0	83	0	5	0	0	0	0	0	0	0	0	67	0	0	0	0	0	0	0		
INRA19-TM0134	Oregrain	42	0	0	0	0	0	0	38	0	88	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
INRA19-TM0069	Bergamo	47	2	0	13	3	2	73	12	0	13	7	13	0	0	0	0	0	0	0	0	12	0	0	0	0	0	0	0		
INRA19-TM0006	Filon	92	0	0	0	0	0	0	25	0	27	0	0	0	0	0	0	0	0	0	0	23	0	0	0	0	0	0	0		
INRA19-TM0001	Filon	53	0	0	0	0	0	0	55	0	7	0	0	0	0	0	0	0	0	0	0	67	0	0	0	0	0	0	0		
INRA19-TM0034	Filon	35	5	0	0	0	0	0	72	0	8	0	0	0	0	0	0	0	0	0	0	47	0	0	0	0	0	0	0		
INRA19-TM0016	LG-Absalon	70	15	6	18	5	0	52	0	0	25	0	2	0	0	0	0	0	0	0	0	42	0	0	0	0	0	0	0		
INRA19-TM0154	Bermude	53	42	3	12	0	5	70	60	0	10	0	0	0	0	0	0	0	0	0	0	40	0	0	0	0	0	0	0		
INRA19-TM0179	Bermude	80	15	2	77	23	0	18	0	5	3	3	17	87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
INRA19-TM0054	Cellule	93	0	0	0	0	0	0	3	0	37	0	0	0	0	0	0	0	0	0	0	57	0	0	0	0	0	0	0		
INRA19-TM0144	Apache	100	37	0	7	0	3	25	80	0	87	0	0	0	0	0	0	0	0	0	0	2	73	0	0	0	0	0	0		
INRA19-TM0139	Arkass	50	5	15	3	0	7	48	35	0	100	9	0	NaN	83	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
INRA19-TM0104	LG-Absalon	100	3	0	0	0	0	0	100	0	60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
INRA19-TM0019	Rubisko	77	0	0	1	0	0	0	63	0	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
INRA19-TM0129	Advisor	68	13	0	2	2	3	2	70	0	77	0	0	0	0	0	0	0	0	0	0	11	18	0	0	0	0	0	0	0	
INRA19-TM0114	RGT-Velasko	17	7	2	50	18	0	100	65	0	25	0	0	0	0	0	0	0	0	0	0	3	60	0	0	0	0	0	0	0	
INRA19-TM0109	LG-Absalon	80	2	0	33	13	0	38	87	1	100	0	0	0	0	0	0	0	0	0	0	10	53	0	0	0	0	0	0	0	
INRA19-TM0169	Triomphe	60	3	0	8	77	0	92	80	0	100	0	0	0	0	0	0	0	0	0	0	7	13	0	0	0	0	0	0	0	
INRA19-TM0049	Terroir	67	67	7	7	37	3	67	75	1	100	10	0	3	27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
INRA19-TM0099	LG-Absalon	100	0	0	0	0	0	10	100	0	93	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
INRA19-TM0174	Terroir	100	100	2	45	0	0	17	87	0	68	0	0	0	0	0	0	0	0	0	0	30	33	0	0	0	0	0	0	0	
INRA19-TM0119	Rebelde	100	38	1	13	2	1	75	90	0	97	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
INRA19-TM0204	Advisor	42	0	25	32	NaN	58	62	33	25	20	8	27	20	63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
INRA19-TM0164	Trapeze	87	48	0	53	0	0	72	47	0	83	0	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	
INRA19-TM0149	Apache	100	10	0	2	0	3	100	87	0	100	0	1	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
INRA19-TM0089	RGT-Velasko	100	0	0	0	0	0	15	100	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
INRA19-TM0159	Apache	100	3	5	48	80	0	98	93	0	85	0	3	3	95	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
INRA19-TM0094	Alivan	100	92	33	23	57	7	100	100	0	55	0	0	0	37	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
INRA19-TM0209	Apache	100	12	0	30	78	0	100	97	0	97	0	0	0	47	100	2	0	0	0	0	0	0	0	0	0	0	0	0	0	
INRA19-TM0084	Bermude	100	12	0	92	60	13	100	87	0	100	0	0	70	100	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

[Maximum leaf sporulating area; FSOV 2018 S DivR]

Differential wheat cultivars carrying the different *Stb* resistance genes

Database with 193 BW isolates and 162 DW isolates characterized

# Fungal genetics at the service of wheat breeders

## Collections and characterization of fungal isolates

COLLECTION of worldwide isolates

PATHOASSAYS under controlled conditions

Evaluation of VIRULENCE SPECTRA

- Determine the effectiveness of *Stb* resistance genes against *Z. tritici*
- Selection of isolates to :
  - Evaluate breeding material and varieties
  - Screen for new sources of resistance
  - Postulate the presence of known *Stb* genes
  - Perform genetic studies of host resistance and/or fungal pathogenicity

LIMITATION: Important resource but not representative of the highly genetically diverse *Z. tritici* populations >> need for high-throughput tools to work at the population level

ISOLATE	CULTIVAR	Cultivar															
		Tokuhung_29	Bulgaria_88	Veronopolis	Israel_493	Tadina	Symbek_C5	Cadena	Est. Federal	Synth. W7984	Sobosno	Newkuz K1590	TE-9111	Sabouni	Alina	Celia	
INRA19-TM0074	Pakito	17	0	0	42	0	0	5	6	0	0	0	0	1	0	0	
INRA19-TM0079	Bermude	17	2	2	7	0	5	0	8	0	3	0	1	0	27	1	
INRA19-TM0044	Velasko	13	0	1	0	0	0	0	12	0	17	0	0	0	0	0	
INRA19-TM0029	Rubisko	50	7	27	7	0	2	0	10	1	3	1	3	0	1	0	
INRA19-TM0024	Rubisko	72	0	0	0	0	0	0	2	0	NaN	0	0	0	0	0	
INRA19-TM0059	Advisor	52	7	0	28	2	1	22	3	0	63	0	3	0	10	0	
INRA19-TM0011	Ionesko	13	8	0	18	13	3	13	25	NaN	22	5	0	0	8	0	
INRA19-TM0064	Apache	70	0	0	0	0	0	0	15	0	33	0	0	0	0	0	
INRA19-TM0039	Bermude	65	0	2	1	0	0	30	3	0	3	0	8	0	48	0	
INRA19-TM0214	Pakito	45	0	0	0	0	0	70	43	0	57	0	0	0	5	0	
INRA19-TM0124	Oregain	10	0	0	0	0	0	70	29	0	83	0	5	0	67	0	
INRA19-TM0134	Oregain	42	0	0	0	0	0	0	38	0	88	0	0	0	0	0	
INRA19-TM0069	Bergamo	47	2	0	13	3	2	73	12	0	13	7	13	0	12	0	
INRA19-TM0006	Filon	92	0	0	0	0	0	0	25	0	27	0	0	0	0	23	
INRA19-TM0001	Filon	53	0	0	0	0	0	0	55	0	7	0	0	0	0	67	
INRA19-TM0034	Filon	35	5	0	0	0	0	5	72	0	8	0	0	0	0	47	
INRA19-TM0016	LG-Absalon	70	15	6	18	5	0	52	0	0	25	0	2	0	42	0	
INRA19-TM0154	Bermude	53	42	3	12	0	5	70	60	0	10	0	0	0	40	0	
INRA19-TM0179	Bermude	80	15	2	77	23	0	0	18	0	5	3	3	17	87	0	
INRA19-TM0054	Cellule	93	0	0	0	0	0	0	3	0	37	0	0	0	0	57	
INRA19-TM0144	Apache	100	37	0	7	0	3	25	80	0	87	0	0	2	73	0	
INRA19-TM0139	Arkass	50	5	15	3	0	7	48	35	0	100	9	0	NaN	83	0	
INRA19-TM0104	LG-Absalon	100	3	0	0	0	0	0	100	0	60	0	0	0	0	0	
INRA19-TM0019	Rubisko	77	0	0	1	0	0	0	63	0	17	0	0	0	0	0	
INRA19-TM0129	Advisor	68	13	0	2	2	3	2	70	0	77	0	0	11	18	0	
INRA19-TM0114	RGT-Velasko	17	7	2	50	18	0	100	65	0	25	0	0	3	60	0	
INRA19-TM0109	LG-Absalon	80	2	0	33	13	0	38	87	1	100	0	0	10	53	0	
INRA19-TM0169	Triomphe	60	3	0	8	77	0	92	80	0	100	0	0	7	13	0	
INRA19-TM0049	Terroir	67	67	7	7	37	3	67	75	1	100	10	0	3	27	0	
INRA19-TM0099	LG-Absalon	100	0	0	0	0	0	10	100	0	93	0	0	0	0	0	
INRA19-TM0174	Terroir	100	100	2	45	0	0	17	87	0	68	0	0	30	33	0	
INRA19-TM0119	Rebelde	100	38	1	13	2	1	75	90	0	97	0	0	0	0	60	
INRA19-TM0204	Advisor	42	0	25	32	NaN	58	62	33	25	20	8	27	20	63	0	
INRA19-TM0164	Trapeze	87	48	0	53	0	0	72	47	0	83	0	0	0	100	0	
INRA19-TM0149	Apache	100	10	0	2	0	3	100	87	0	100	0	1	0	100	0	
INRA19-TM0089	RGT-Velasko	100	0	0	0	0	0	15	100	0	100	0	0	0	0	100	
INRA19-TM0159	Apache	100	3	5	48	80	0	98	93	0	85	0	3	3	95	0	
INRA19-TM0094	Alivan	100	92	33	23	57	7	100	100	0	55	0	0	37	100	0	
INRA19-TM0209	Apache	100	12	0	30	78	0	100	97	0	97	0	0	47	100	2	
INRA19-TM0084	Bermude	100	12	0	92	60	13	100	87	0	100	0	0	70	100	2	

[Maximum leaf sporulating area; FSOV 2018 S DivR]

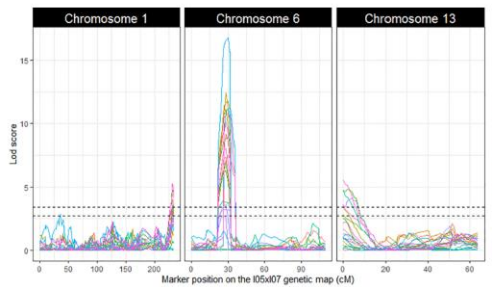
Differential wheat cultivars carrying the different *Stb* resistance genes

Database with 193 BW isolates and 162 DW isolates characterized

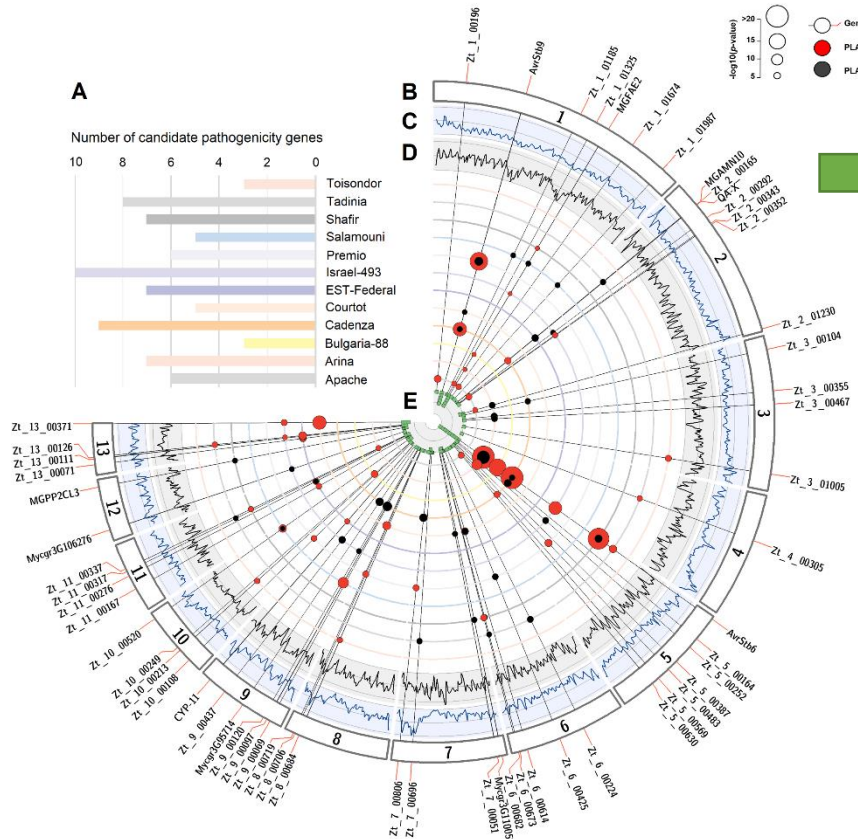
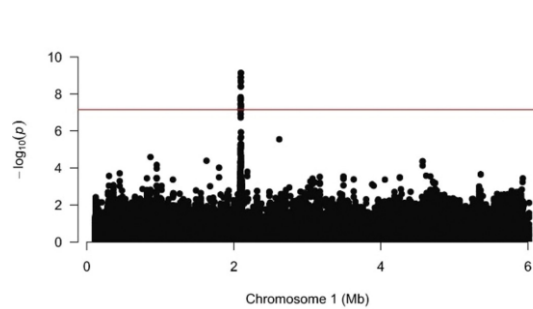
# Fungal genetics at the service of wheat breeders

## Identification of avirulence genes in the fungus

### QTL mapping (*AvrStb20q*)



### GWAS (*AvrStb9*)



- AvrStb6*
  - AvrStb20q*
  - AvrStb15?*
- } Small secreted proteins
- AvrStb9* – Secreted protease-like protein
  - AvrStb?* – Methyltransferase

- Pathogenicity has a complex polygenic architecture and is predominantly quantitative.
- Virulence-associated genes are mostly host specific.
- Help to fine-map and clone the corresponding *Stb* resistance genes in wheat.

Zhong *et al.* (2017), *New Phytol*  
 Amezrou *et al.* (2022) *bioRxiv*  
 Amezrou *et al.* (2023), *PLOS Pathog*  
 Langlands-Perry *et al.* (2023), *Front Plant Sci*

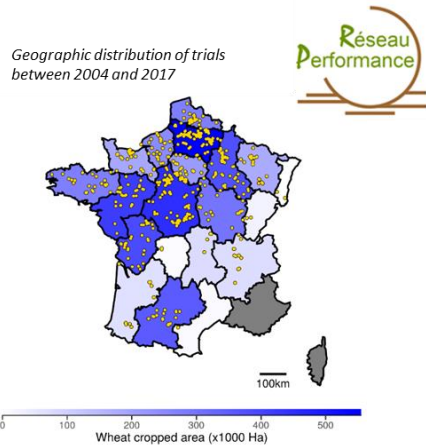


# Fungal genetics at the service of wheat breeders

## Surveying the evolution of virulences in fungal populations

Targeted amplicon sequencing in “population DNA” of *Z. tritici*

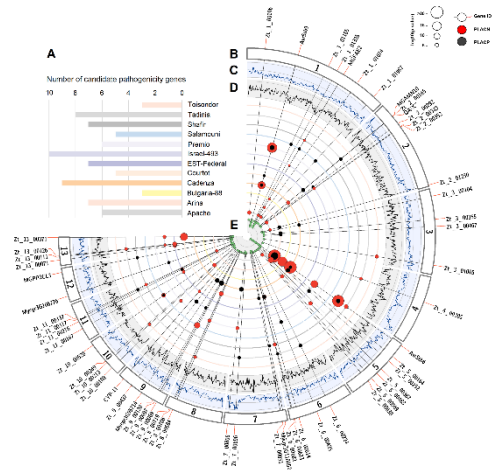
### SAMPLING



1 field = 50 leaves  
with lesions grinded  
together and used  
for DNA extraction

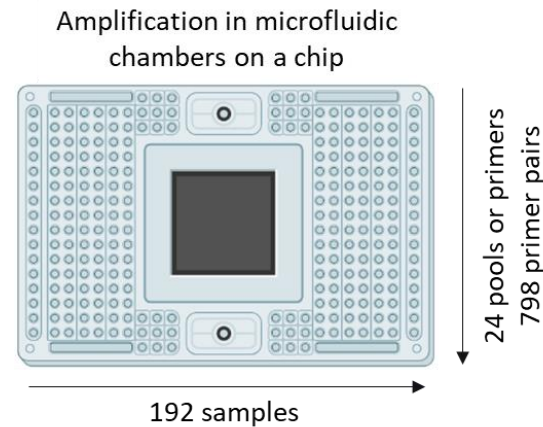
Bellah *et al.* (2023), PLOS ONE

### PRIMER DESIGN



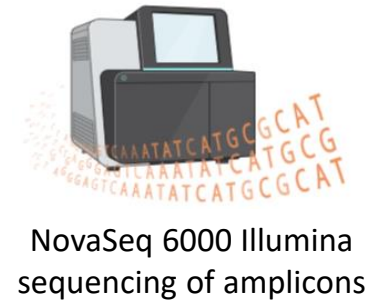
Specific, conserved  
and diagnostic

### HIGH-PLEX PCR



192 samples \* 798  
primer pairs

### SEQUENCING



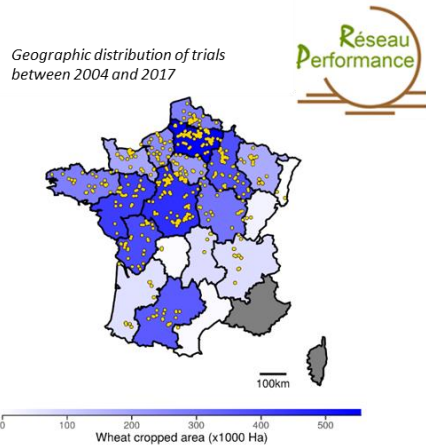
Identification of  
sequence variants  
and their frequency  
in each sample

# Fungal genetics at the service of wheat breeders

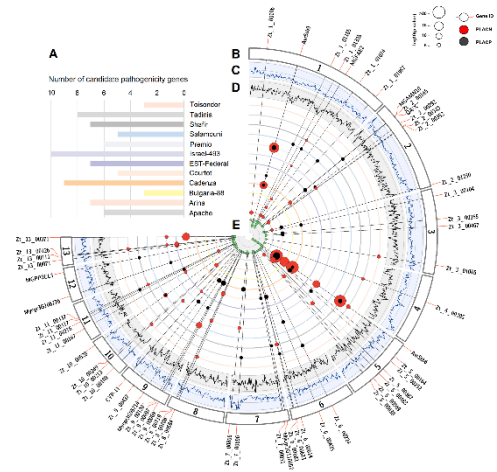
## Surveying the evolution of virulences in fungal populations

Targeted amplicon sequencing in “population DNA” of *Z. tritici*

### SAMPLING

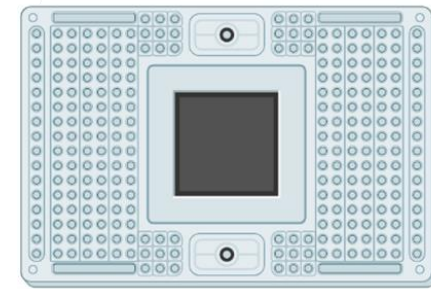


### PRIMER DESIGN



### HIGH-PLEX PCR

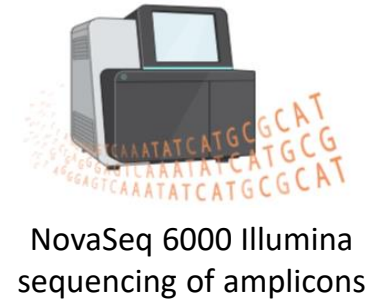
Amplification in microfluidic chambers on a chip



24 pools or primers  
798 primer pairs

192 samples

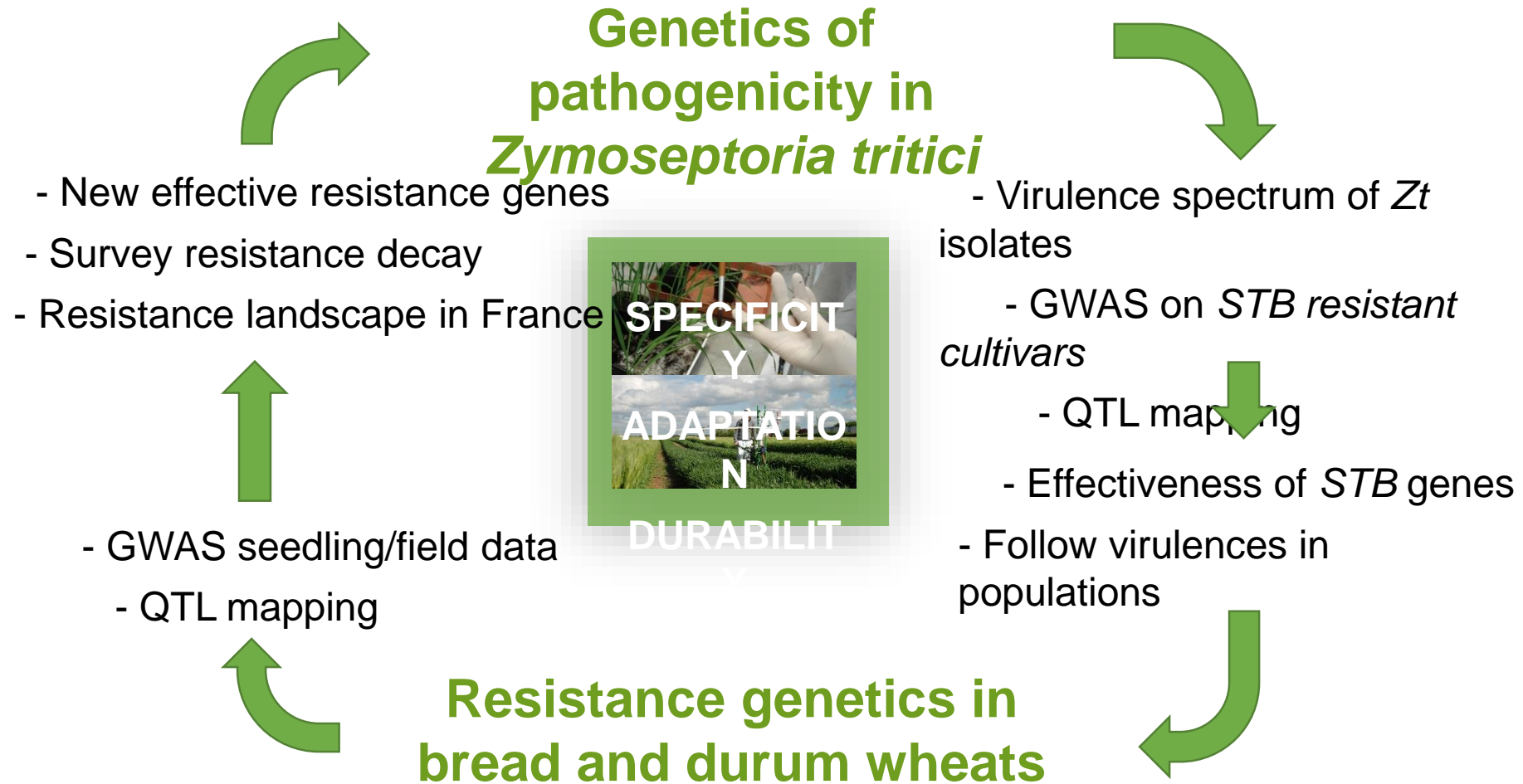
### SEQUENCING



- Overcome the limits and complementary to the characterization of single isolates :
  - Geographic distribution of variants: knowledge on the effectiveness of *Stb* resistance genes
  - Frequency of virulence on sampled cultivars: following the overcoming of *Stb* resistance genes

# INRAE BIOGER

Team “Epidemiology and evolution of fungal wheat pathogens”



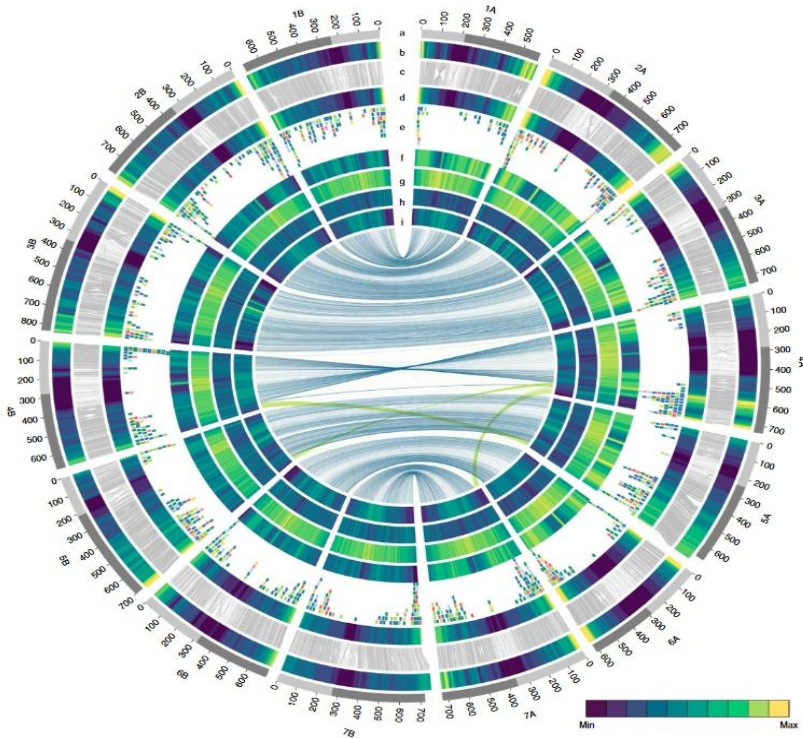


# The Need for the Durum reference Genome

- «Svevo» Gold-standard Reference genome assembly of *Triticum spp durum* (Maccaferri et al., 2019)



Durum wheat genome highlights past domestication signatures and future improvement targets



Golden quality

Assembly size	10.5 Gb
Gaps size	149.1 Mb
Gaps	1.42%
L50 (length)	5.97 Mb
L90 (length)	1.09 Mb
High confidence genes	66,559
Low confidence genes	303,404

The genomic sequence is instrumental for:

- Investigating the useful genetic diversity in worldwide germplasm collections
- retrieving novel loci and alleles for agronomic traits of interest, previously lost due to genetic erosion





# The Global Durum Genomic Resource

Four collaborative panels for germplasm characterization have been developed

## 1) GLOBAL TETRAPLOID wheat COLLECTION (GTC):

Developed by Svevo genome consortium

GERMPLASM BANKS → To sample the diversity in tetraploids

- 806 durum wheat landraces (DWL)
- 144 durum-related subspecies (DWL)
- 364 domesticated emmer wheat (DEW)
- 115 wild emmer wheat (WEW)

## 2) GLOBAL DURUM PANEL (GDP):

A breeding dedicated tool, (modern varieties and landraces)

BREEDERS → EWG-DWGB, ICARDA-CIMMYT

- 500 modern durum wheat (DWC)
- 200 durum wheat landraces (DWL)

1. Genotyping  
(Illumina 90K SNP array)
2. Genome-Wide  
Association Mapping
3. Allele mining

## 3) INNOVAR DURUM PANEL

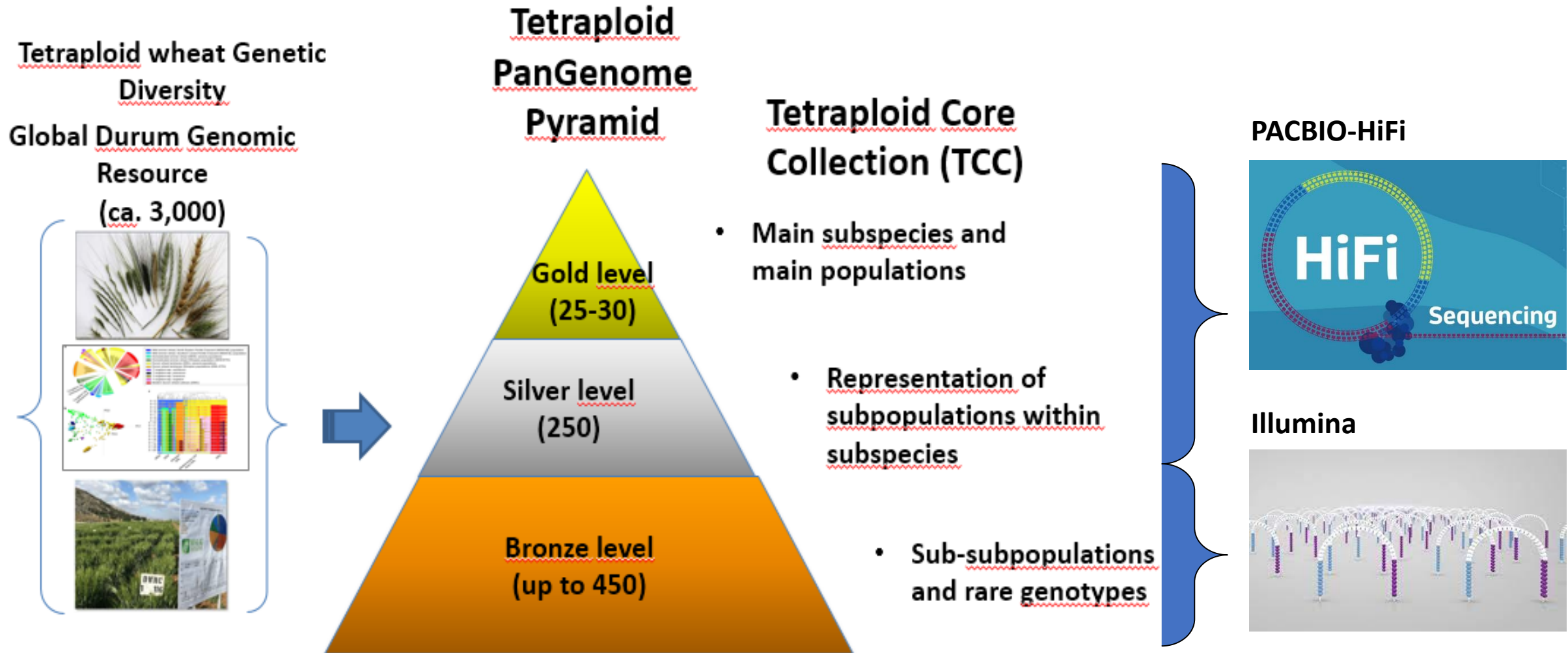
(250 European varieties)

## 4) TETRAPLOID CORE COLLECTION (TCC)

(250 accessions)



# Finally, The **Tetraploid Core Collection (TCC)** has been sourced from **GDP + TGC** (haplotype-based population analysis).





# Identification of novel materials and loci to increase the varietal resistant response to Septoria Tritici Blotch and Yellow Rust

- ❑ The identification of materials provided with resistance (possibly 'durable' and 'broad spectrum') in the wheat germplasm, and especially in durum Mediterranean germplasm, is critical to breed for sustainability and to reduce the use of chemicals
  - ✓ **Yellow Rust (YR), is a pathogen of worldwide impact.**
    - In Italy and the whole Mediterranean region new YR races with novel mutations and increased aggressiveness spread and cause recurrent yield loss and high pesticide use.
    - This is exacerbated by the climate change effects.
  - ✓ **Septoria Tritici Blotch, is the pathogen that causes the majority of the pesticides use in Europe**
    - The cultivated Mediterranean durum materials are mostly depleted of resistance genes.
    - STB is becoming a major disease for mediterranean durums.



# Identification of novel materials and loci to increase the varietal resistant response to Septoria Tritici Blotch and Yellow Rust

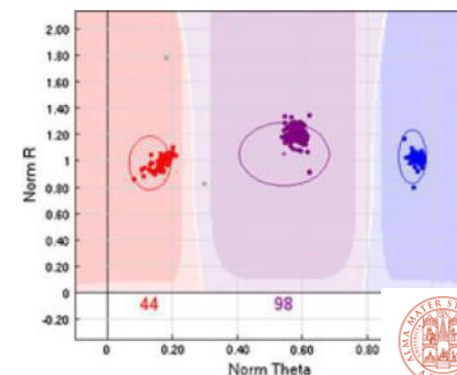
## GDP, TGC and INNOVAR panels

Field and growth  
Chamber  
phenotyping



Illumina Infinium 90K SNP chip array  
+ Haploview analysis

## Haplotype GWAS



# Steps in the Genome-Wide Association Mapping

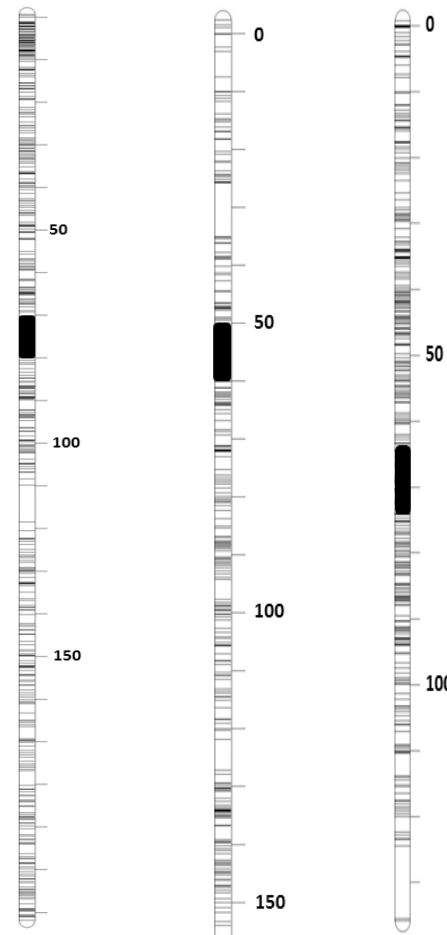
**A e B**

Costituzione di un panel di genotipi e valutazione fenotipica delle accessioni



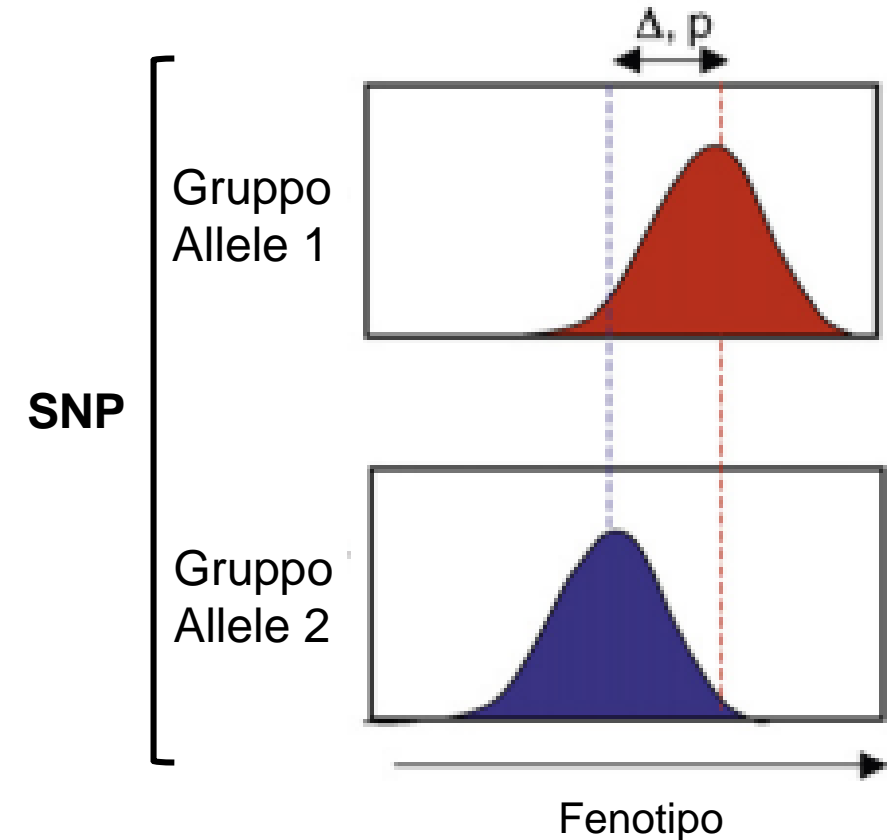
**C**

Genotipizzazione delle accessioni: quali alleli ai loci marcatori?



**D**

Applicazione di modelli statistici marcatore per marcatore



Adattato da Rafalski, 2010



# Wheat Phenotyping at UNIBO

PHENOTYPING DURUM WHEAT FOR FUSARIUM HEAD BLIGHT AND SEPTORIA TRITICI BLOTCH AT UNIBO



**Mist irrigation-assisted nursery for reliable FHB and STB phenotyping under artificial inoculation in Cadriano experimental station**



**Fusarium head blight (FHB)**



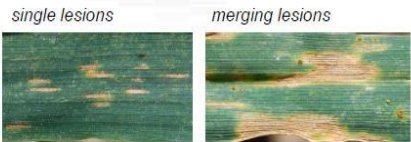
**Septoria tritici blotch (STB)**

# Durum wheat landraces Diversity panel evaluated for STB in Cadriano field in 2022 (background data)

☐ 600 durum and other *Triticum turgidum* landraces

☐ Partially replicated and Modified augmented design with repeated checks and blocks

## Notation scale



- 0: immune
- 1: one single sporulating lesion
- 2: two to five single sporulating lesions
- 3: more than five sporulating lesions
- 4: mix of single and merging lesions
- 5: only merging sporulating lesions
- 6: 10% to 25% sporulating leaf area
- 7: 25% to 50% sporulating leaf area
- 8: 50% to 75% sporulating leaf area
- 9: over 75% sporulating leaf area

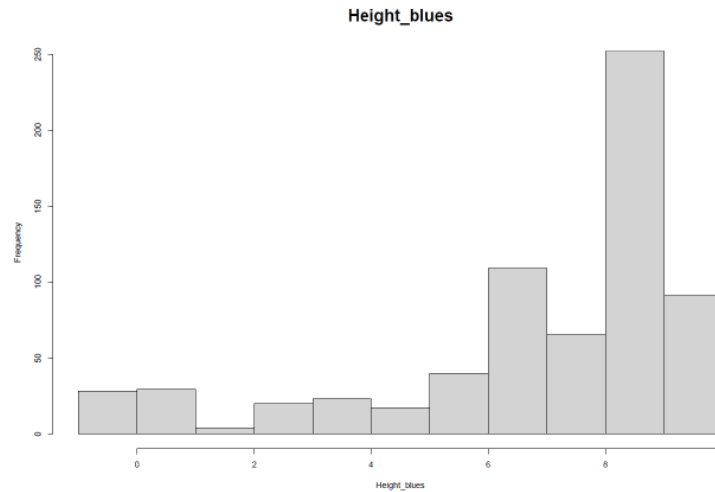


FIGURE 41: DISTRIBUTION HISTOGRAMS FOR BLUES VALUES RELATED TO INFECTION HEIGHT

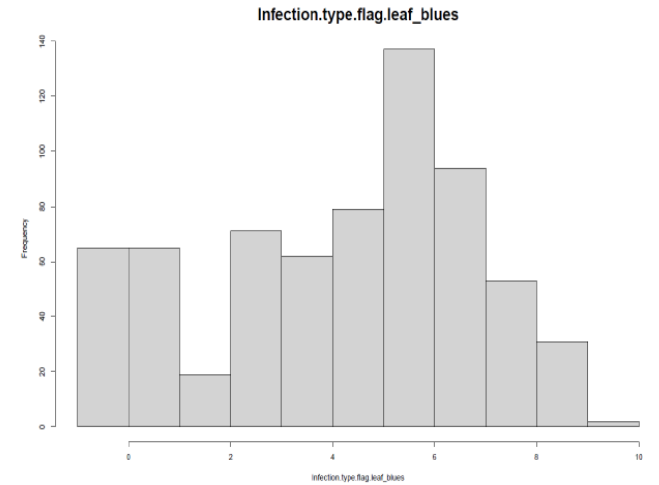
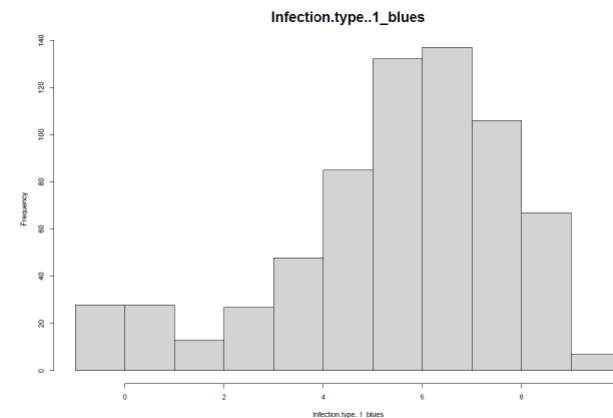


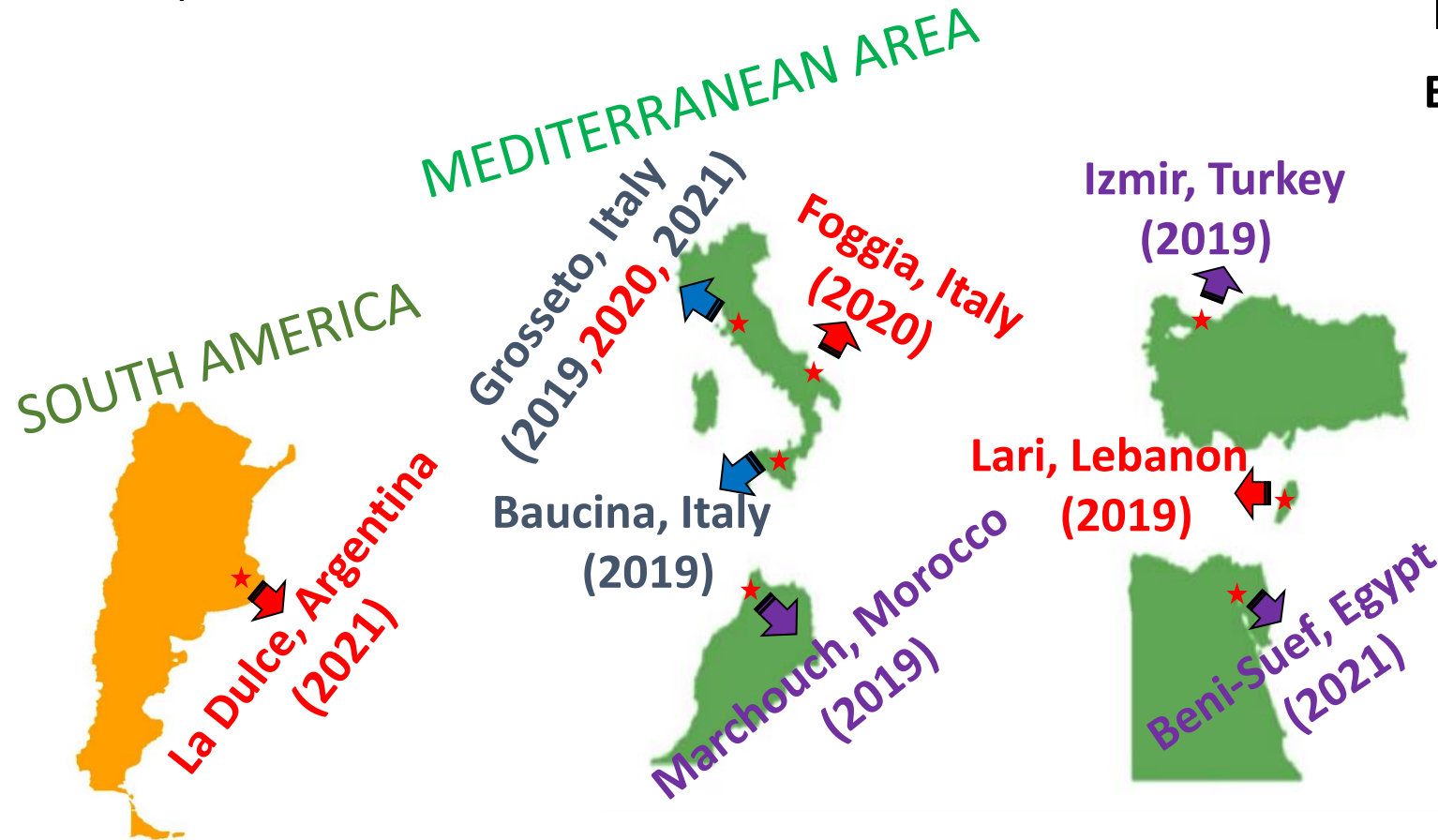
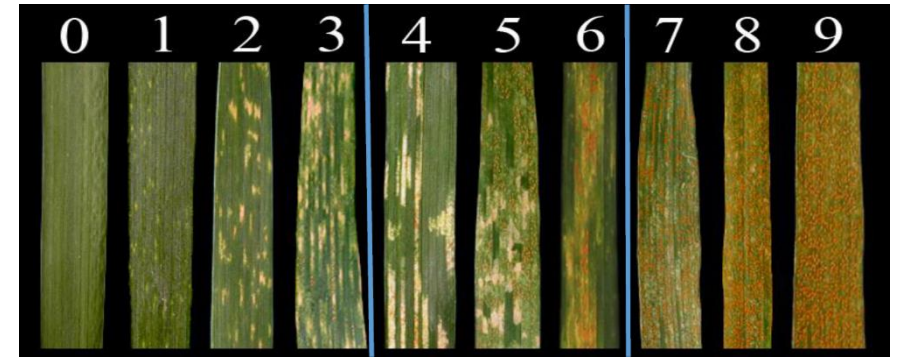
FIGURE 42: DISTRIBUTION HISTOGRAMS FOR BLUES VALUES RELATED TO FLAG LEAF INFECTION



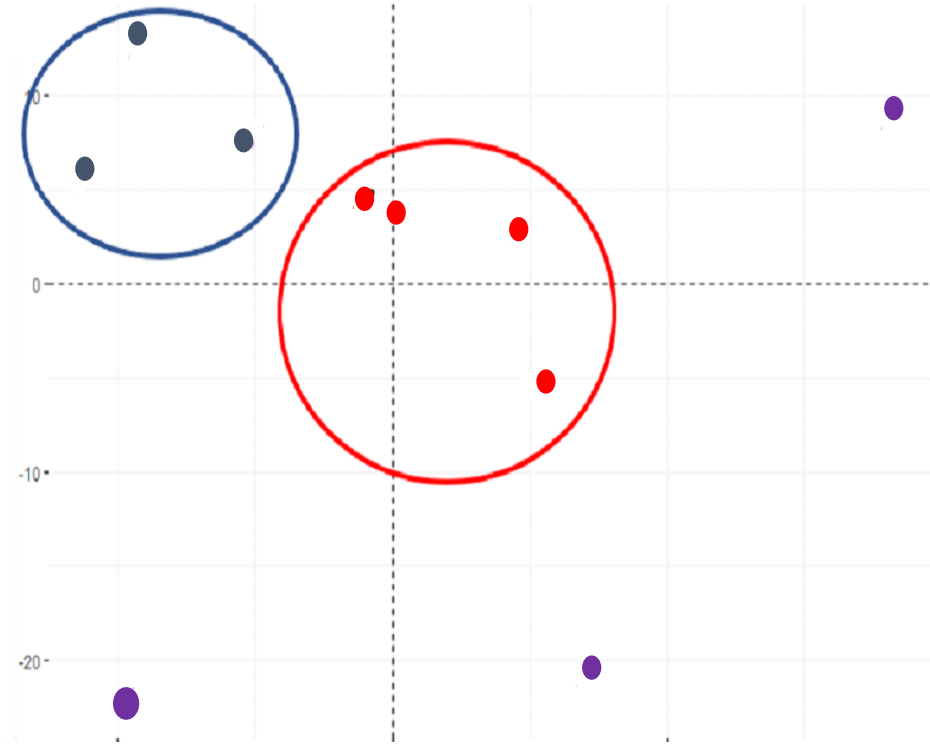


# GWAS for Yellow Rust Resistances

- A Multi-environmental / Multi-year survey and Association study was conducted
- Infection Type (IT) and Disease Severity (DS) were recorded
- GDP panel was used



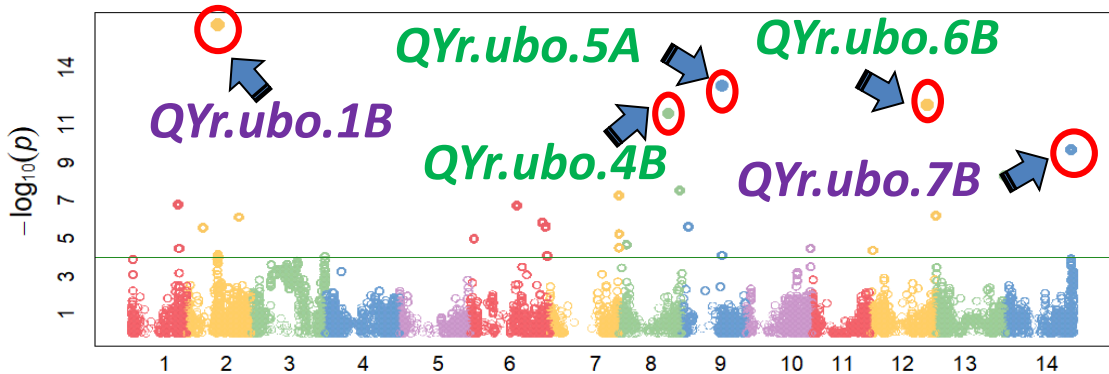
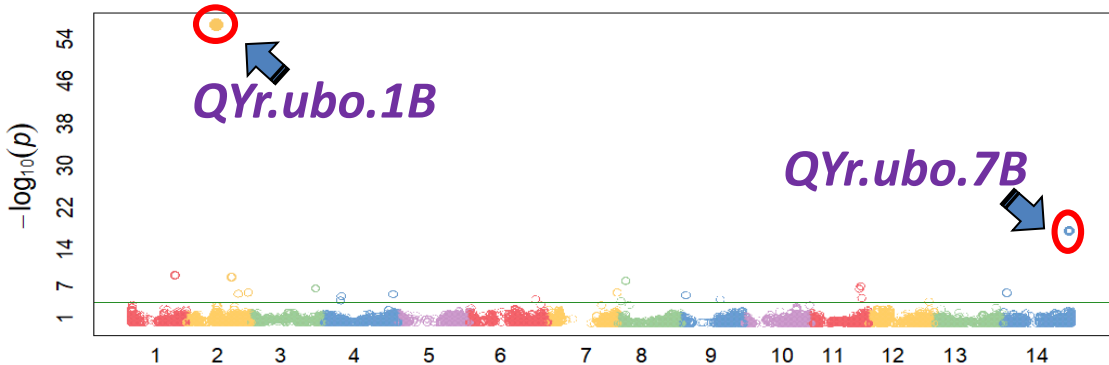
## ENVIRONMENTAL CLUSTERING DETECTION



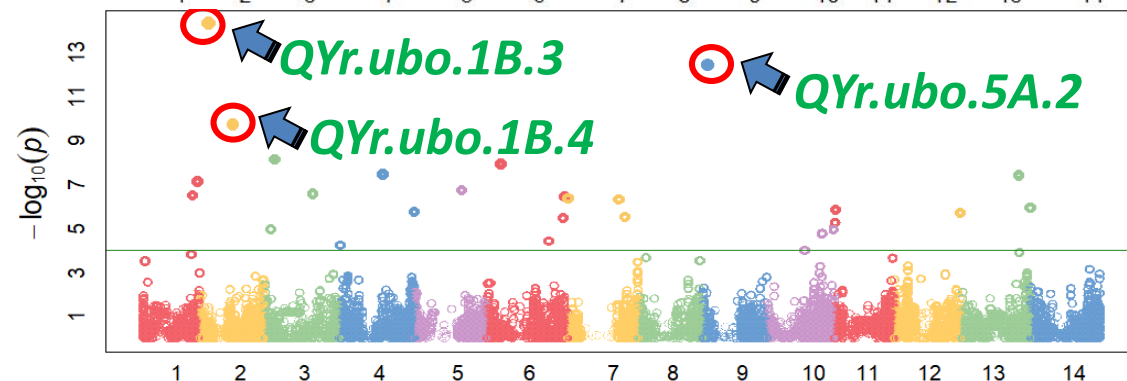
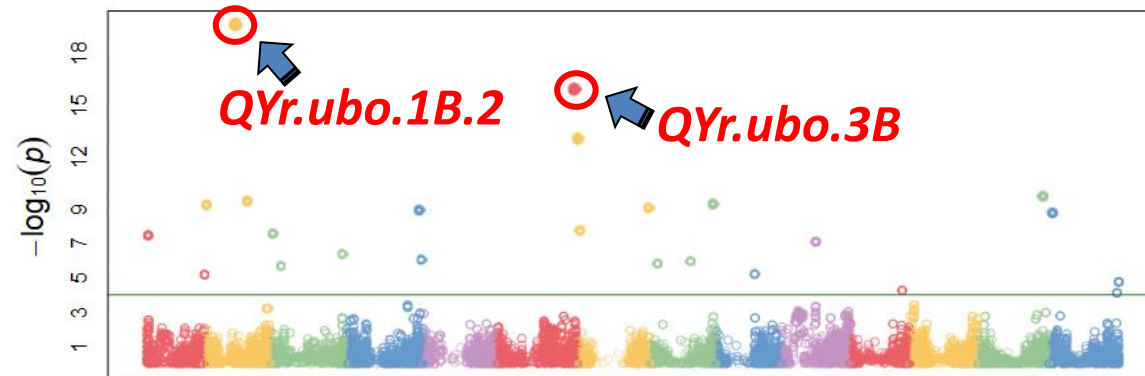


# GWAS RESULTS

## 1<sup>st</sup> ENVIRONMENTAL CLUSTER

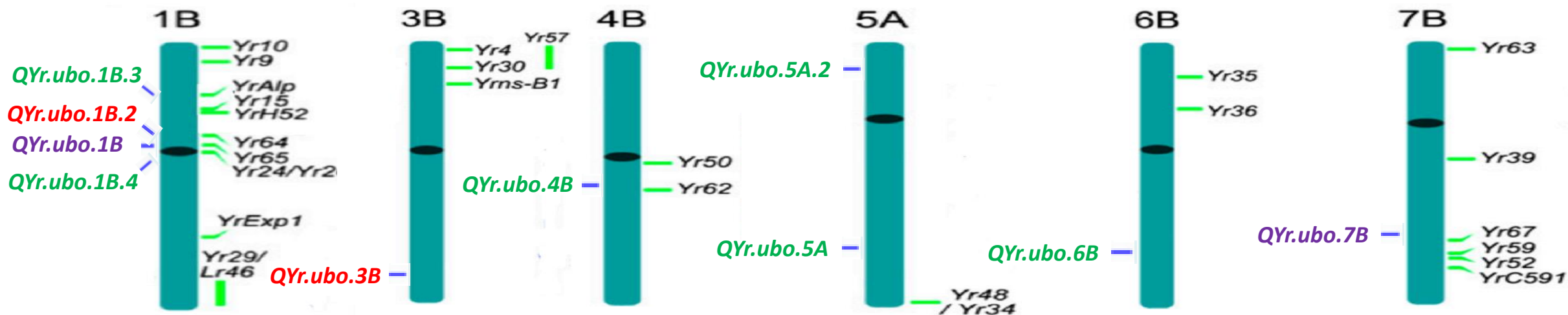


## 2<sup>nd</sup> ENVIRONMENTAL CLUSTER



INFECTION TYPE  
(IT)

DISEASE SEVERITY  
(DS)





**SusCrop – ERA-NET**

Cofund on Sustainable Crop Production

FACCEJPI

**Objective: Rapid integration of novel valuable loci/alleles into cultivated germplasm.**

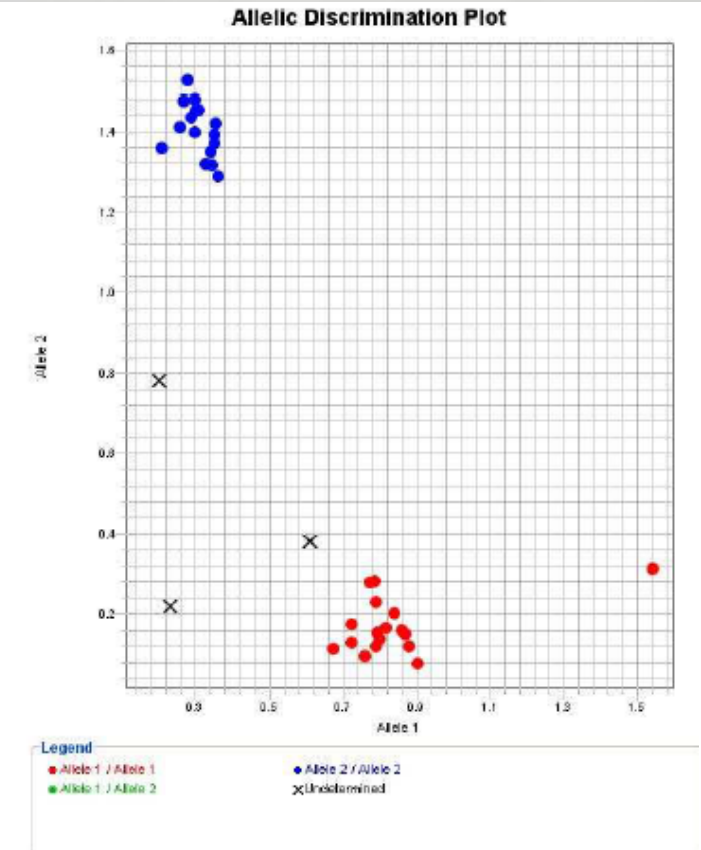
P involved: UNIBO, CREA, UCD, INRAE-G, KWS, SEC.

Donors from WP1/WP2 known to carry novel valuable loci/alleles for **adaptation, root architecture, STB and FHB response** will enter a marker-assisted backcross scheme (UNIBO, CREA, KWS)

**Previous mapping and marker-trait association results (WP1) will be deployed to develop Diagnostic molecular markers based on KASP® fluorescent technology.**

UNIBO has developed a **primer design pipeline** for difficult polyploid wheat.

Novel markers/genetic stocks **will be deposited to public germplasm bank institutions**, protocols will be reported in MASWHEAT ([//maswheat.ucdavis.edu/](http://maswheat.ucdavis.edu/)).





**HORT@**  
— From research to field —



# GRAZIE A TUTTI PER L'ATTENZIONE!

Thierry Marcel - BIOGER, INRAE

Marco Maccaferri, Matteo Bozzoli, J. Novi, F. De Sario, C.

Liu, A. Prodi e R. Tuberosa - DISTAL

**22**  
**OPEN**  
**'23**  
**DISTAL**

WORKSHOP GTI "SALUTE DELLE PIANTE"  
AVVERSITÀ FITOSANITARIE: LE SFIDE DI UNA GESTIONE  
ECOSOSTENIBILE



# AVVERSITÀ FITOSANITARIE: LE SFIDE DI UNA GESTIONE ECOSOSTENIBILE



22 OPEN  
DISTAL  
23

GRAZIE A TUTTI!



ALMA MATER STUDIORUM  
UNIVERSITÀ DI BOLOGNA  
DIPARTIMENTO DI  
SCIENZE E TECNOLOGIE AGRO-ALIMENTARI