



ALMA MATER STUDIORUM  
UNIVERSITÀ DI BOLOGNA

# Migliorare il frumento duro per resistenza alle principali patologie fungine e virali: un obiettivo comune di APSOV e di UNIBO

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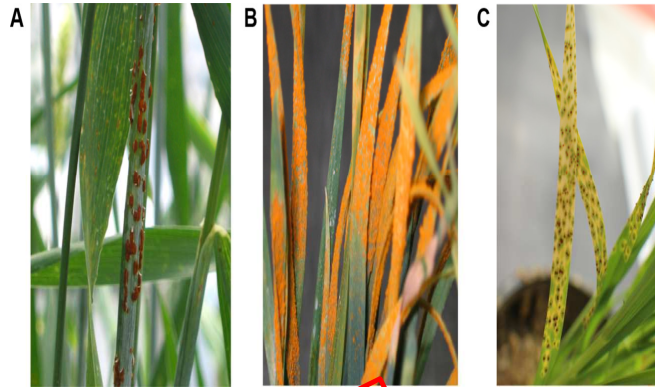
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24

OPENDISTAL  
20 SETTEMBRE

# Durum wheat (AABB) and main fungal diseases



## Wheat Rusts

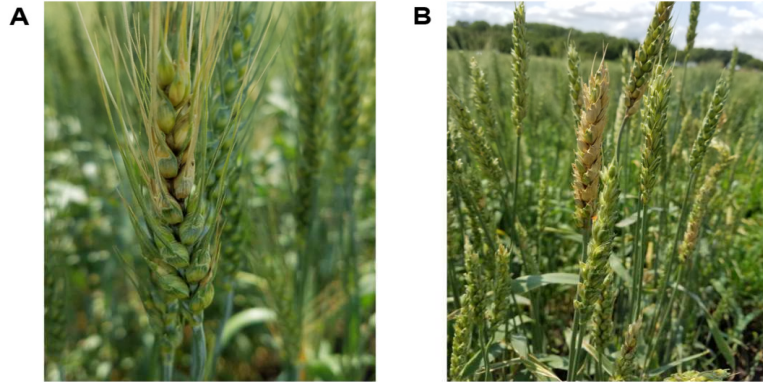


Leaf Rust

Yellow Rust

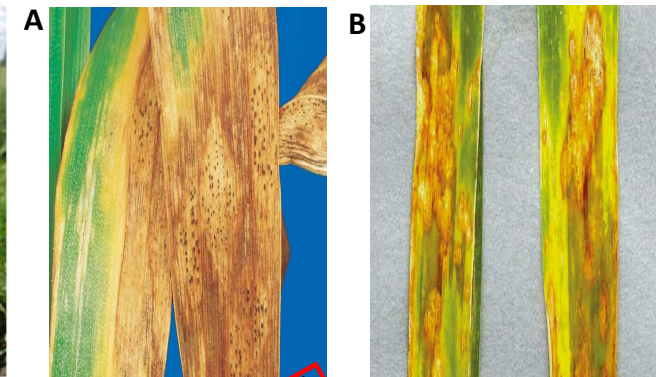
Stem Rust

## Scab Disease



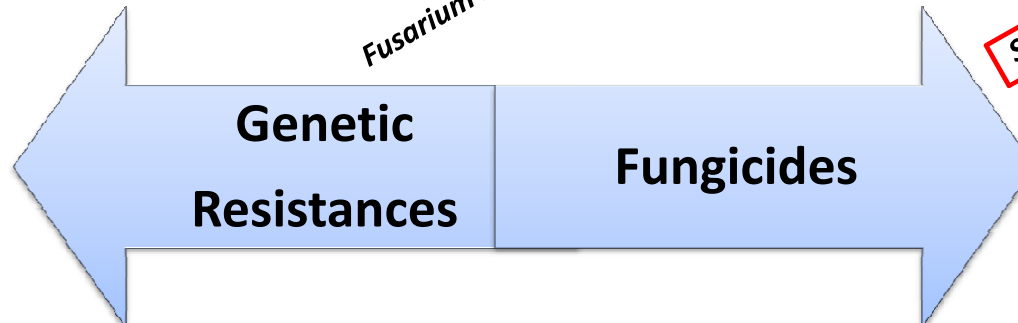
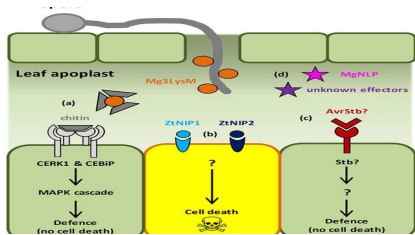
Fusarium Head Blight

## Blotch Diseases



Septoria tritici blotch

Septoria nodorum blotch



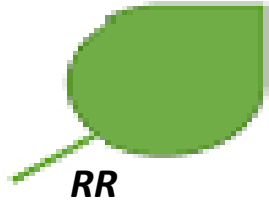
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# Wheat Disease Resistances

Two main classes of resistance (R) genes:

- All Stage Resistance (ASF)

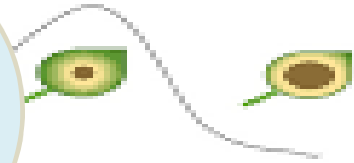
Qualitative Resistance



**Need for exploring novel sources of genetic diversity and characterizing the ones present in the Elite breeding material**

Resistance (APR)

Quantitative Resistance



Disease Severity

- *Puccinia striiformis*, the causative agent of Yellow rust (Yr)

- 86 Yr loci mapped
- Only 4 mapped in durum wheat
- Limited number of QTLs mapping study conducted in durum wheat



- *Puccinia striiformis*, the causative agent of Yellow rust (Yr)

- 23 Stb loci mapped
- No Stb gene mapped in durum wheat
- Limited number of QTLs mapping study conducted in durum wheat





# The Global Durum Genomic Resources

Two collaborative panels for germplasm characterization have been developed

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

Developed by Svevo genome consortium

GERMPLASM BANKS  To sample the diversity in tetraploids

- 1574 durum wheat landraces (DWL) and durum-related subspecies
- 364 domesticated emmer wheat (DEW)
- 115 wild emmer wheat (WEW)

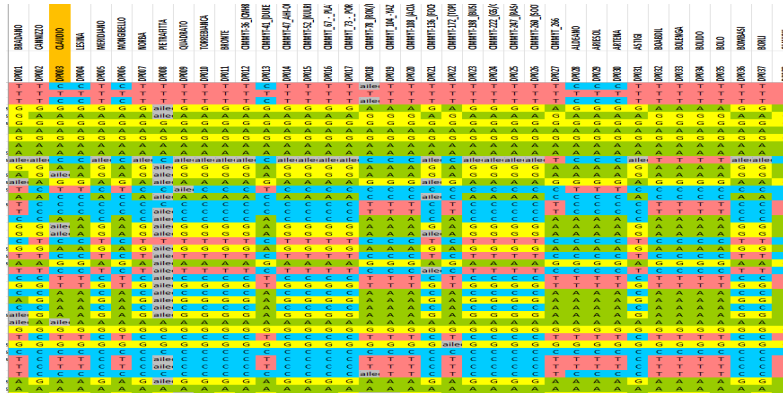
## 2) GLOBAL DURUM PANEL (GDP):

A breeding dedicated tool, (modern varieties and landraces)

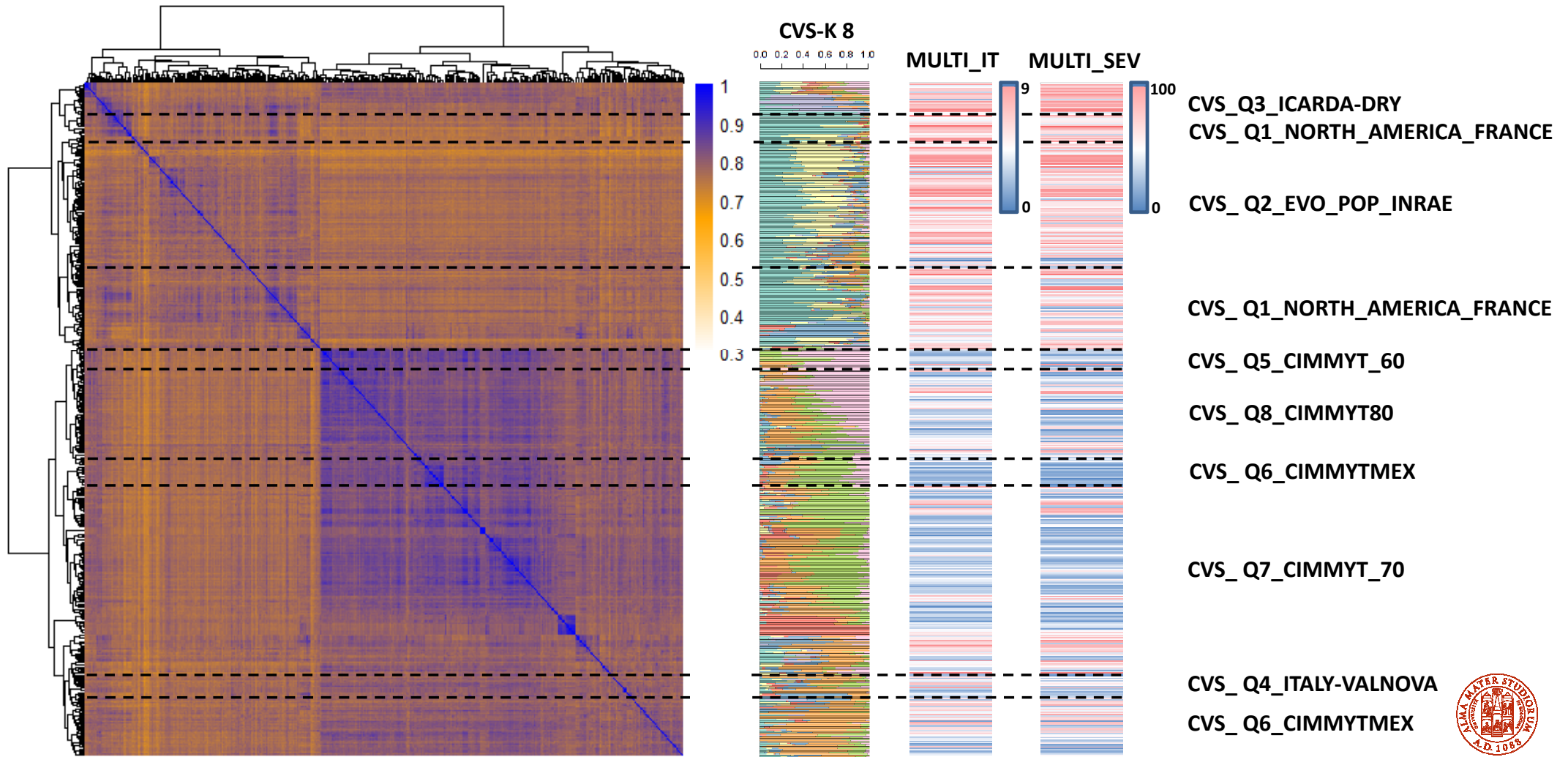
BREEDERS  EWG-DWGB, ICARDA-CIMMYT

- 800 modern durum wheat (DWC)
- 350 durum wheat landraces (DWL)

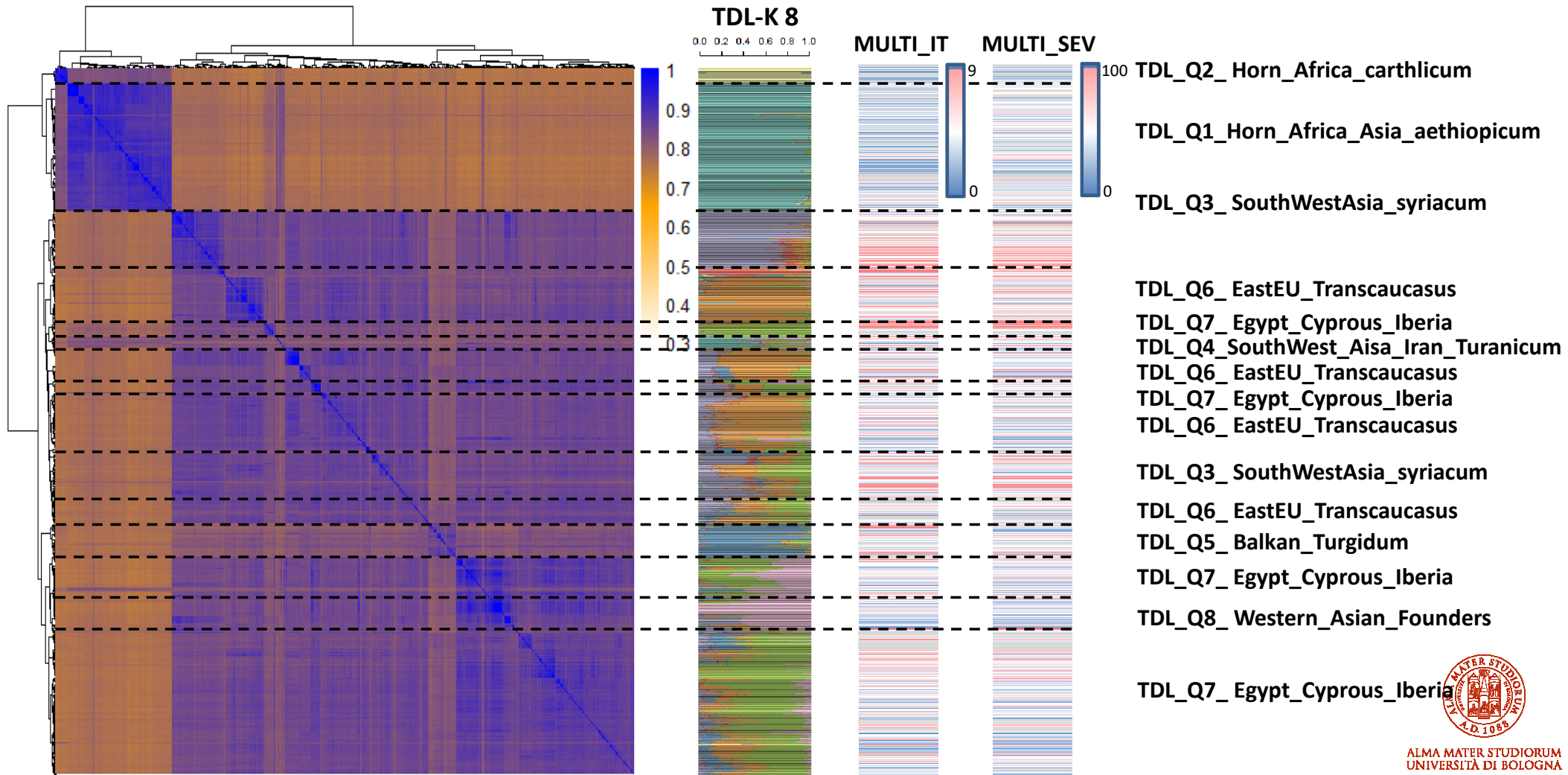
Illumina 90K wheat SNP array 3,142 genotype  
Global Hapmap generated



# population structure of cultivars (CVS)



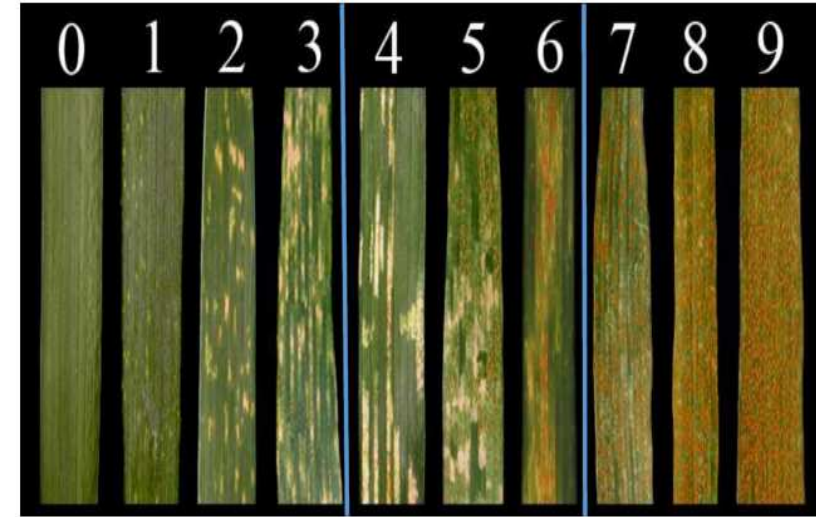
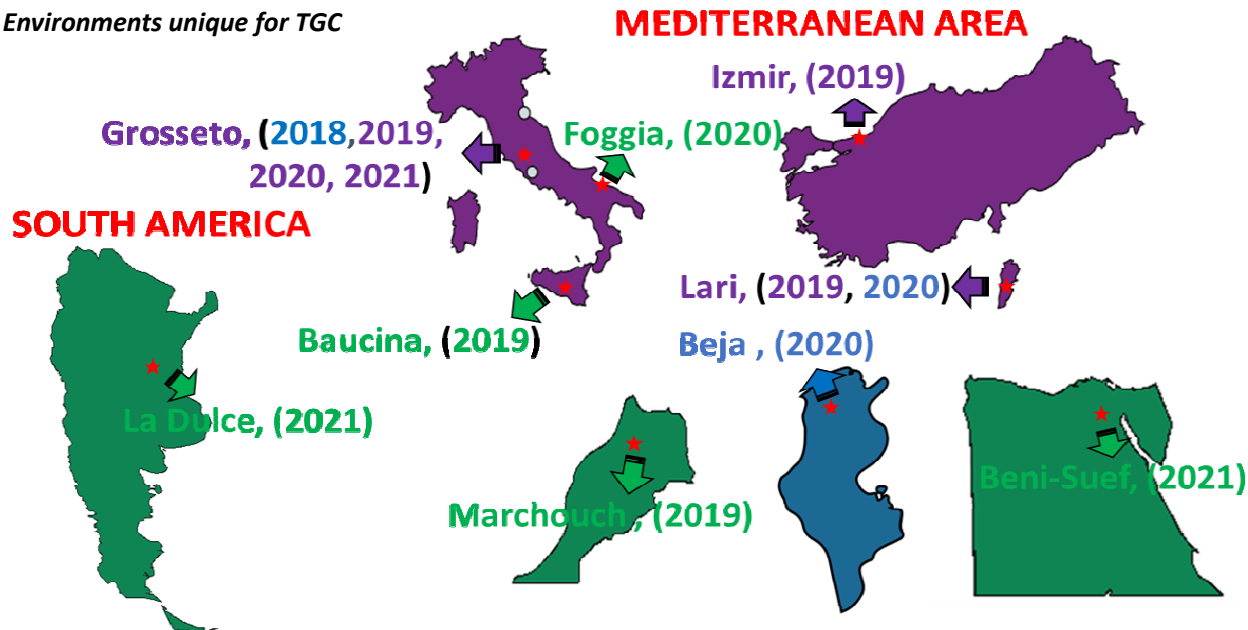
# population structure of *Triticum turgidum* landraces (TDL)



# Yr-Multi-environmental / Multi-year field survey

- GDP and TGC panels
- A Multi-environmental / Multi-year field survey and GWAS
- Infection Type (IT) and Disease Severity (DS)

- Environments in common between GDP and GTC
- Environments unique for GDP
- Environments unique for TGC



0-3\_ resistant

4-6\_ partially resistant

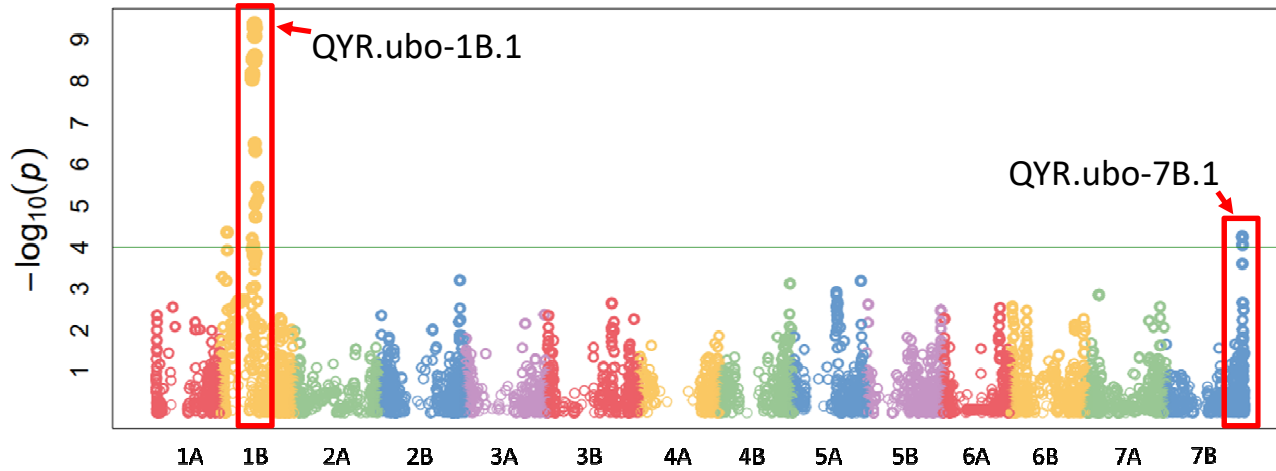
7-9\_ susceptible



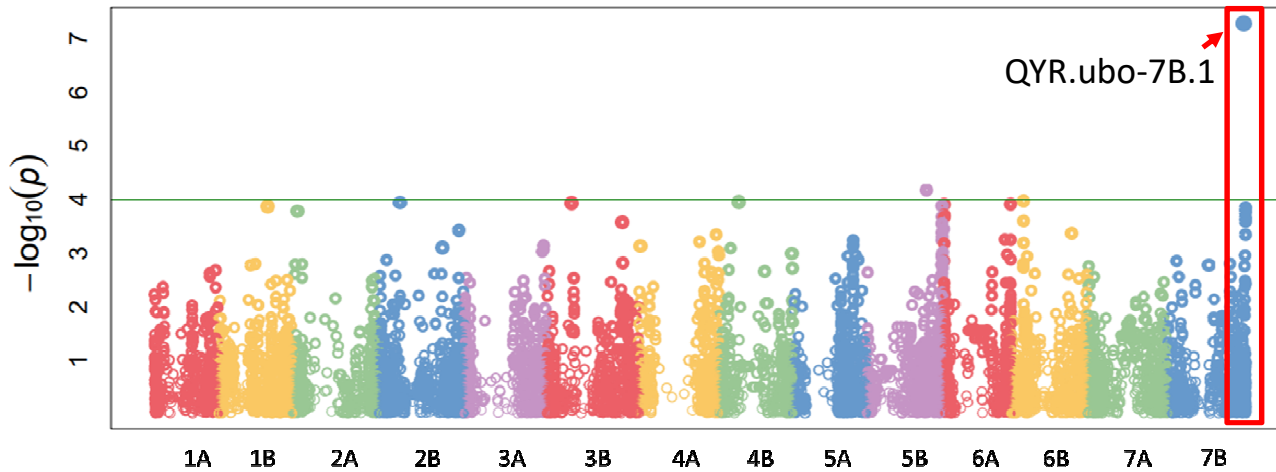
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# Genome Wide Association Study (GWAS) for Yr QTLs in CVS and TDL

CVS



TDL

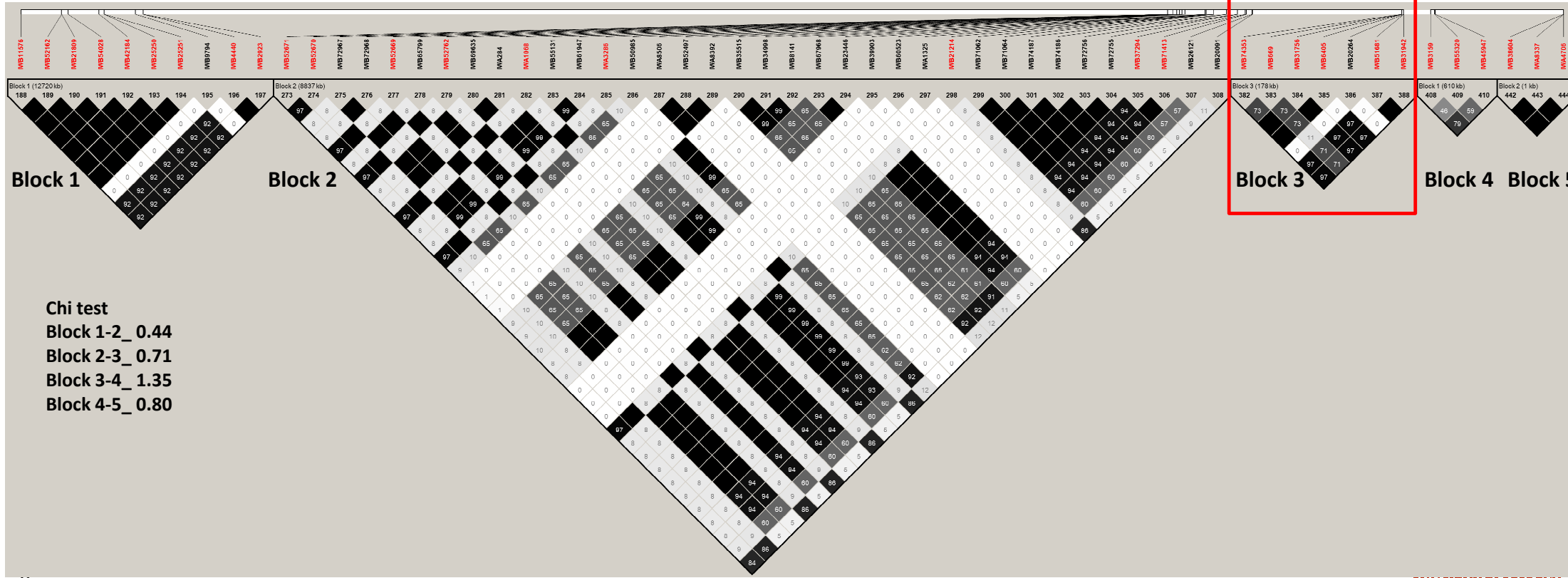
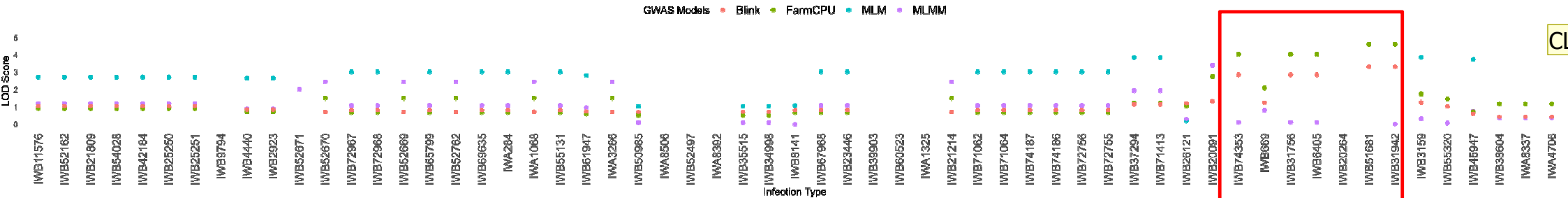


Type	QTL	significant	R <sup>2</sup>
CVS	QYr.ubo-1B.1	****	13.9%
TDL	QYr.ubo-1B.1	*	2.67%
CVS	QYr.ubo-7B.1	***	4.21%
TDL	QYr.ubo-7B.1	****	6.41%





# QYr.ubo-1B.1 in cultivars



Chi test  
 Block 1-2\_ 0.44  
 Block 2-3\_ 0.71  
 Block 3-4\_ 1.35  
 Block 4-5\_ 0.80

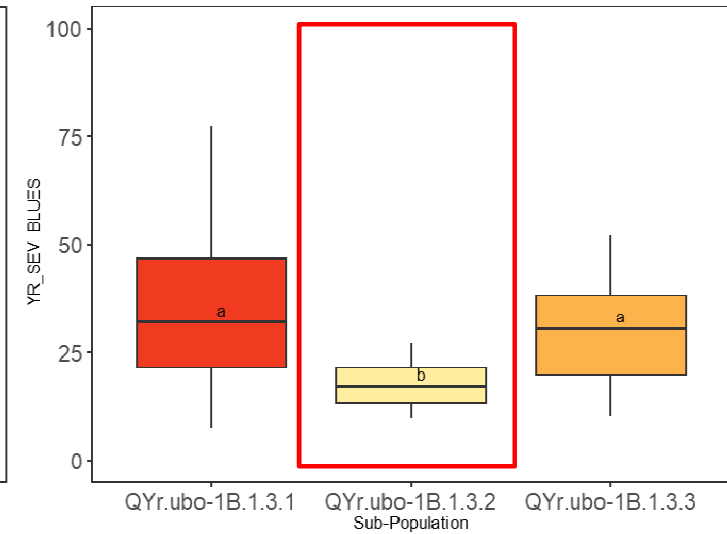
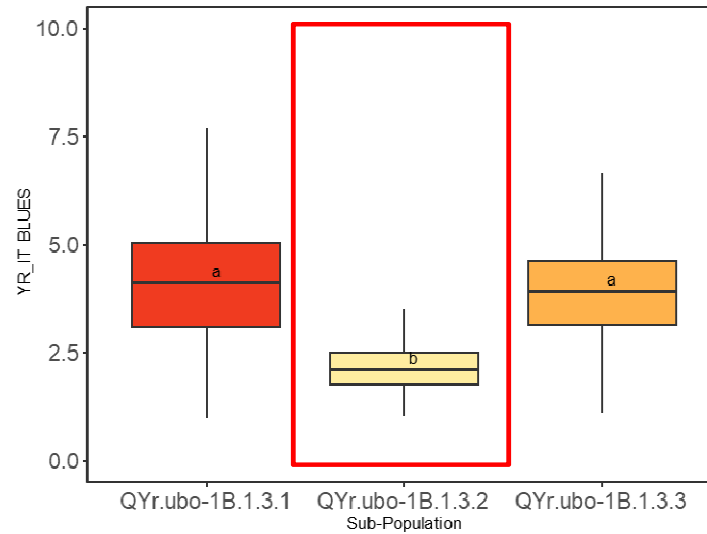
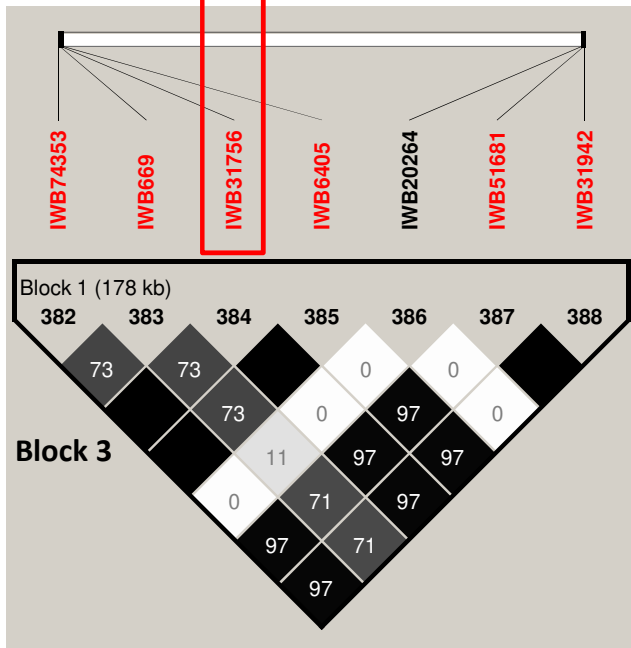
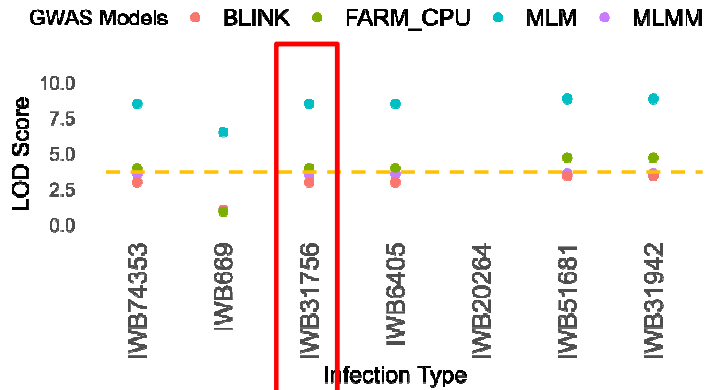
## Diapositiva 9

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**CL1**

Chunyi Liu; 17/09/2024

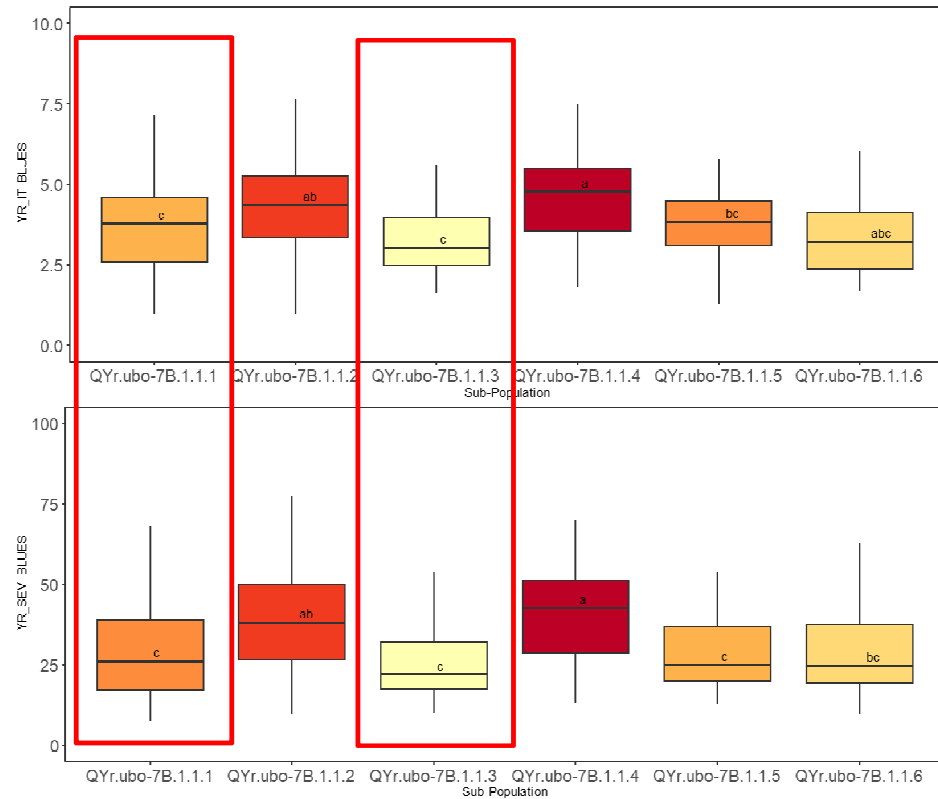
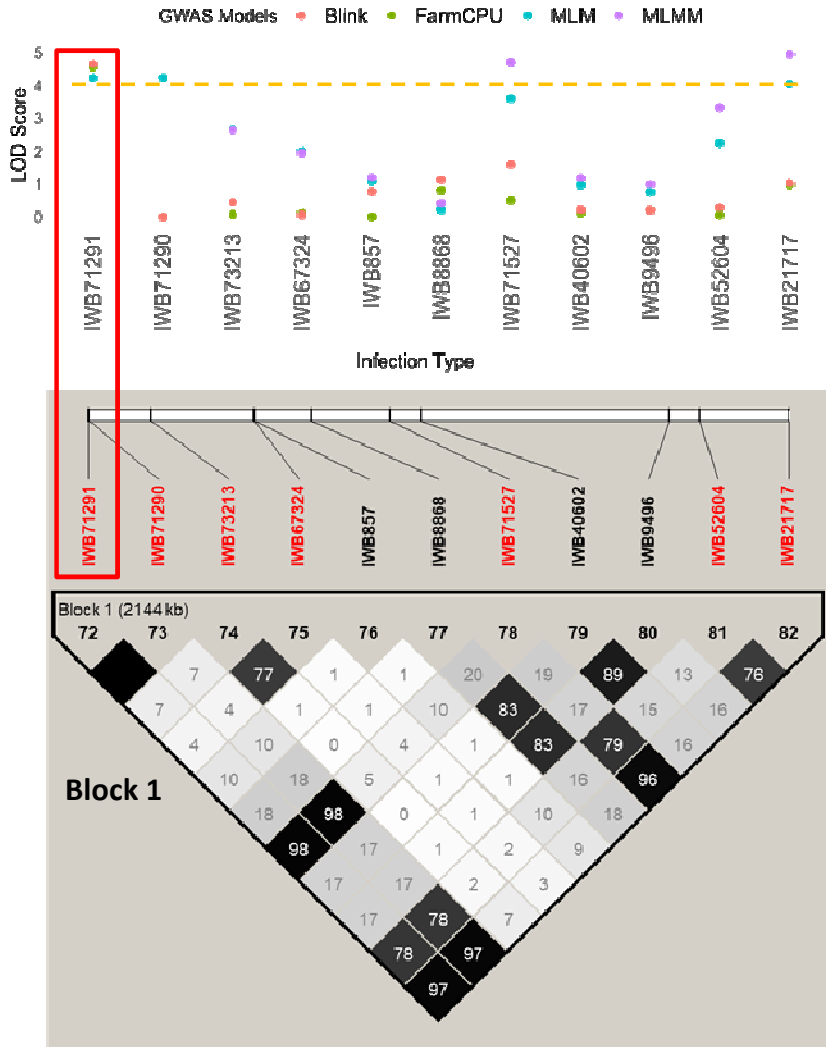
# QYr.ubo-1B.1.3 in cultivars



QTL	haplotype	IT/SEV	average blues	cultivars average	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	global count
QYr.ubo-1B.1.3.2	CATTGCG	IT	2.26	3.98	0	1	1	3	0	20	1	1	27
		SEV	18.4	33.1									
QYr.ubo-1B.1.3.1	AGGCGTA	IT	4.14	3.98	60	28	9	13	19	64	78	36	307
		SEV	34.4	33.1									



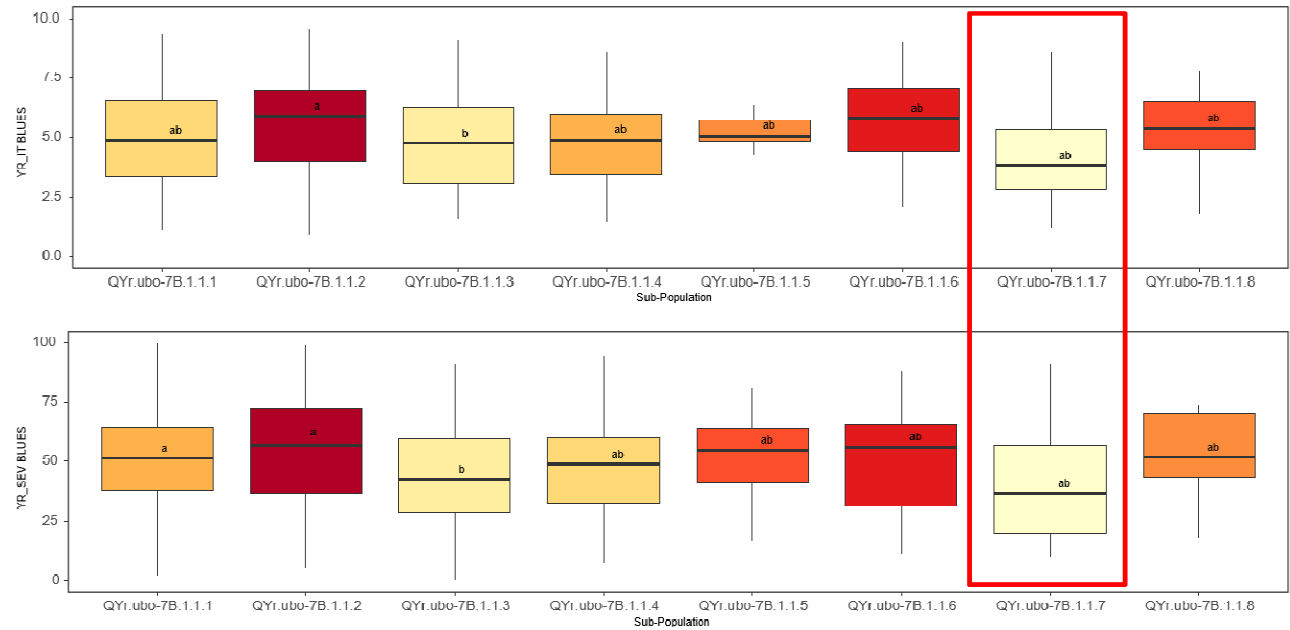
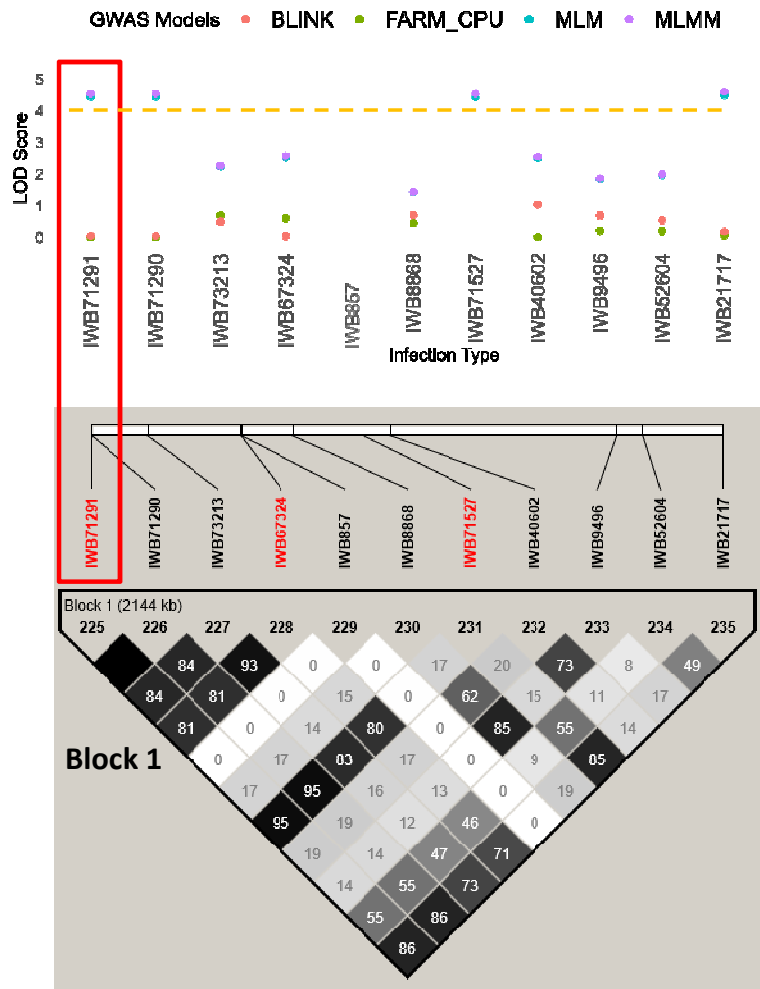
# QYr.ubo-7B.1 in cultivars



QTL	haplotype	IT/SEV	average blues	cultivars average	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	global count
QYr.ubo-7B.1.1.3	TTAGGGTCATT	IT	3.28	3.98	3	0	0	0	0	8	24	8	43
		SEV	25.8	33.1									
QYr.ubo-7B.1.1.1	TTAGAGTCATT	IT	3.71	3.98	30	8	1	1	0	23	31	31	118
		SEV	29.8	33.1									
QYr.ubo-7B.1.1.4	CGAGAACTCCC	IT	4.64	3.98	5	1	9	0	13	8	1	0	37
		SEV	40.8	33.1									



# QYr.ubo-7B.1 in landraces

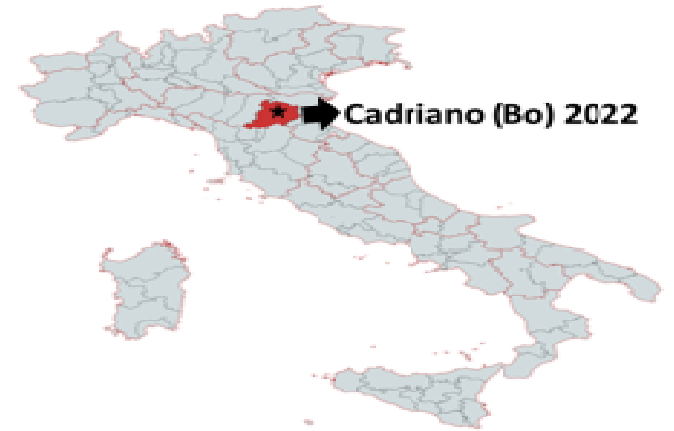


QTL	haplotype	IT/SEV	average blues	landraces average	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	global count
QYr.ubo-7B.1.1.7	TTAGAGTCATT	IT	4.43	5.06	0	0	2	1	3	2	2	5	15
		SEV	40.6	50.35									
QYr.ubo-7B.1.1.2	CGAGAACTCCC	IT	5.53	5.06	34	10	28	0	6	12	67	159	
		SEV	55.3	50.35									

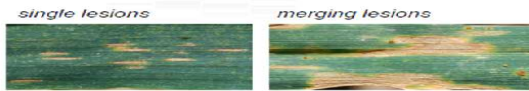


# Explorative GWAS for Resistance to *Septoria tritici* blotch

- 501 accessions belonging to the TGC panel
- Infection Type in the flag leaf (IT\_FL) and in the canopy (IT\_CANOPY):



### 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



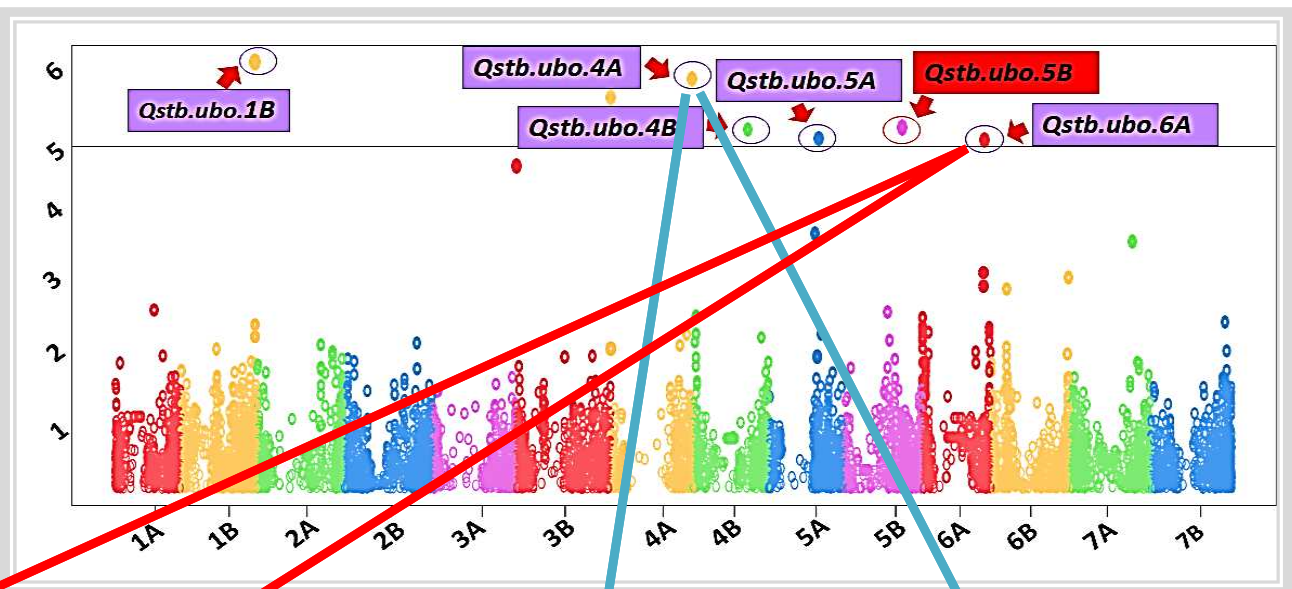
Resistant Parent: \_  
Susceptible Parent: (S)

## QTLs Linkage Mapping Study

Populations	RILs	Genotyping chip
<u>CEEDUR</u> (Q4) X WID (S)	295	TaBW35K SNP
<u>TRINAKRIA</u> (Q8) X S9R (S)	203	TaBW35K SNP
<u>RUSSELLO</u> (Q6) X SVEVO (S)	207	iSelect90K SNP
<u>KYPEROUNDA</u> (Q7) X MERIDIANO (S)	295	TaBW35K SNP



# Overlapping GWAS and Linkage Mapping regions



- QTLs\_GTC\_Cadriano\_2022
- QTLs\_Meridiano x Kyperounda
- QTLs\_Russello x Svevo

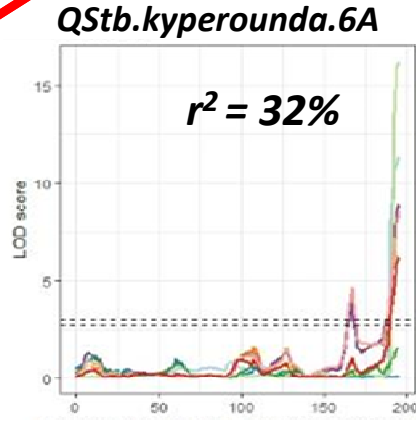
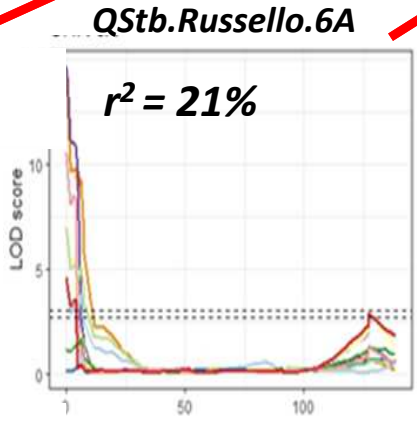
$r^2 = 21-32\%$

Qstb. ubo.6A

Qstb. Russello.6A

Qstb. Kyperounda.6A

Chr 6A



Chr 4A

Qstb. ubo. 4A

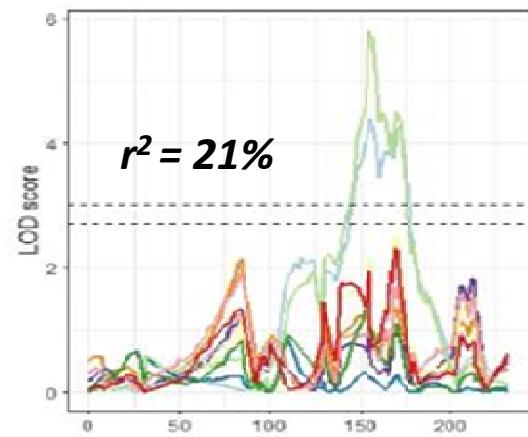
Qstb. Kyperounda.4A

FL-4A

Stb7

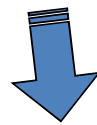
Stb12

$r^2 = 21\%$

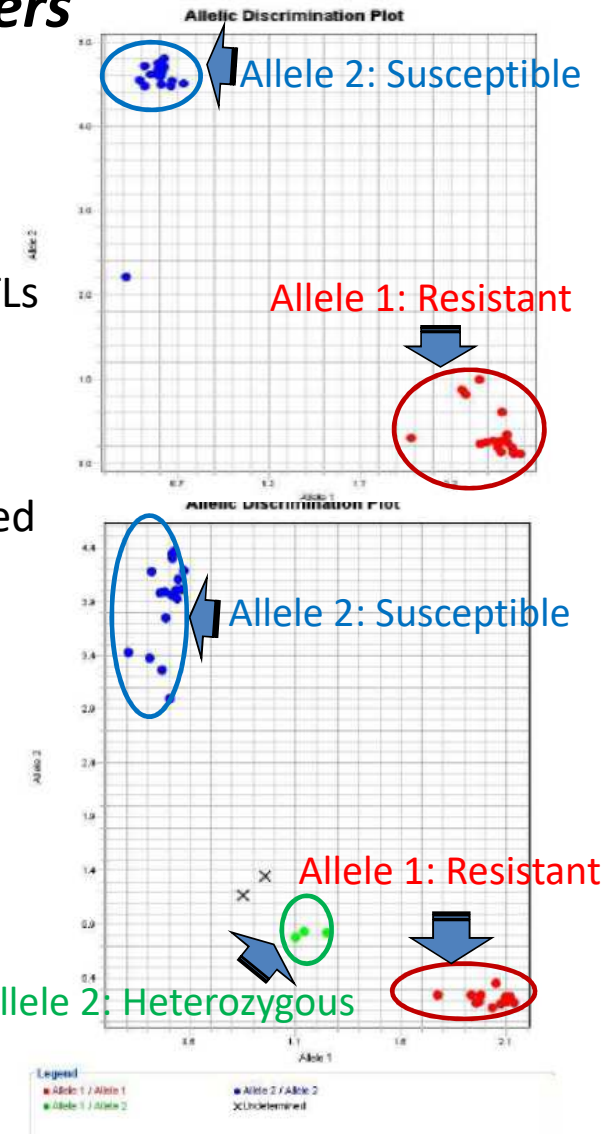


# Kompetitive Allele Specific PCR (KASP): Diagnostic Markers

- For ***QYr.ubo-1B.1.3*** in Yr, two set of diagnostic KASP markers have been designed from the corresponding SNPs to observe the effect and validate the QTLs
- KASP genotyping was performed on GDP panel
- New diagnostic markers are ready to be designed and tested for the new detected QTLs for both Yr and Stb



Developing a series of ready-to-use diagnostic markers, closely linked to candidate genes, to use for breeding



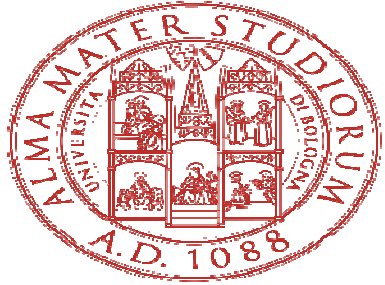


## ***Take-home messages***

- ❑ ***Two strong Yr loci, effective in Mediterranean environments***, have been identified in the GDP and GTC panel:
  1. ***QTL*** mapped on ***Chr.1B*** showed very high LODs and a clear **resistant haplotype** was detected for this QTL
  2. ***QTL*** mapped on ***Chr.7B*** was detected in both GDP and GTC but not a clear distinction among resistant and susceptible haplotypes was observed.
  
- ❑ **Several regions underlying *Stb* resistances loci**, effective in Mediterranean environments, have been identified in the GTC panel
  
- ❑ **Linkage Mapping Populations**, deriving from a cross between *Triticum durum* landraces carrying ***Stb* resistances** and elite durum wheat cultivars were used to map QTLs with high R<sup>2</sup>.
  
- ❑ **Diagnostic KASP markers** are going to be designed and tested on the detected QTLs, with the **potentiality of being used for breeding purposes**



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CIMMYT  
International Maize and Wheat  
Improvement Center



ICARDA

Karim Ammar

Filippo Bassi



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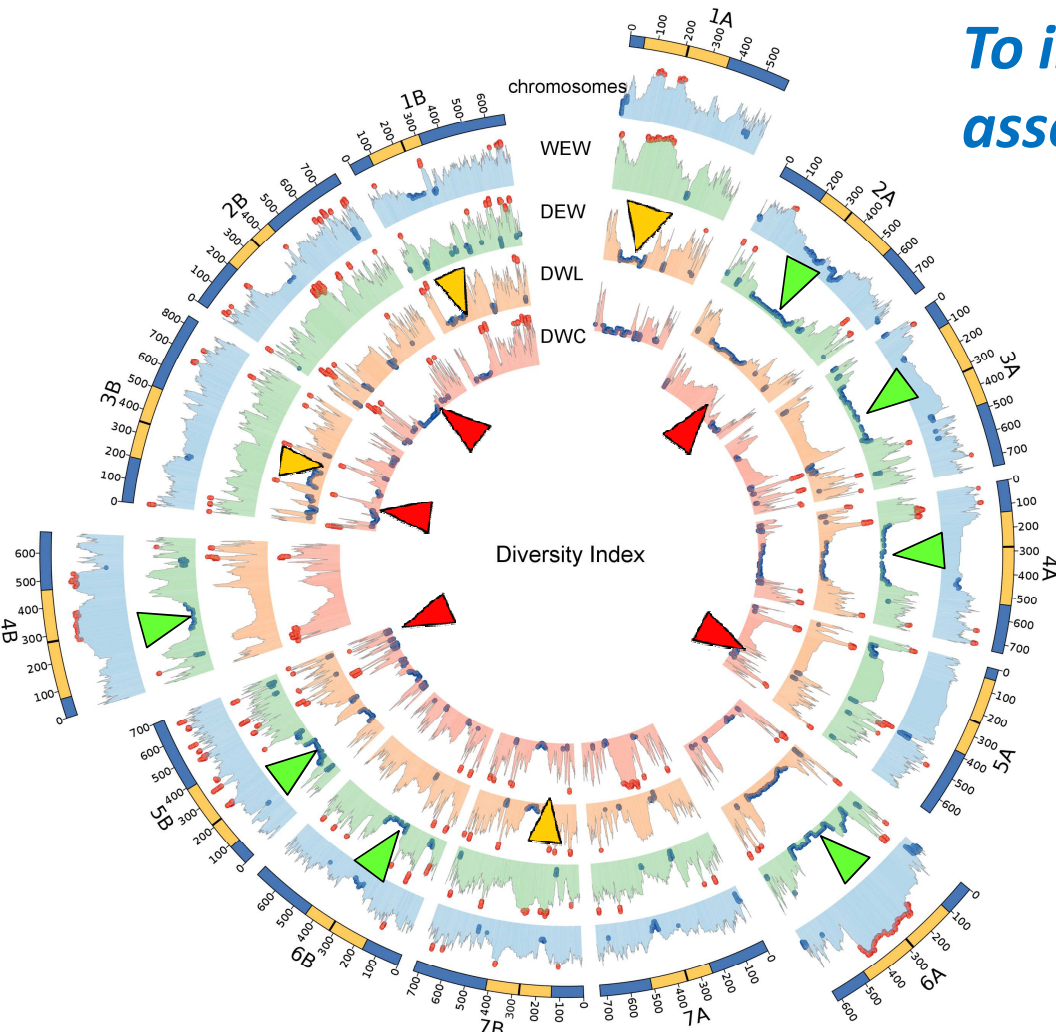


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# Genome view of SNP-based genetic diversity, based on Svevo genome as framework

*To investigate the diversity erosion associated to domestication and breeding*



▶ **WEW-DEW HAD THE LARGEST IMPACT IN DIVERSITY DROP (30% of the genome affected)**

▶ **DEW-DWL ADDITIONAL DIVERSITY DROPS ARE EVIDENT (Chr. 1A)**

▶ **DWL-DWC: SPECIFIC DROPS FOR BREEDING NUMEROUS REGIONS SHOWING NEAR-FIXATION OF ALLELIC DIVERSITY**





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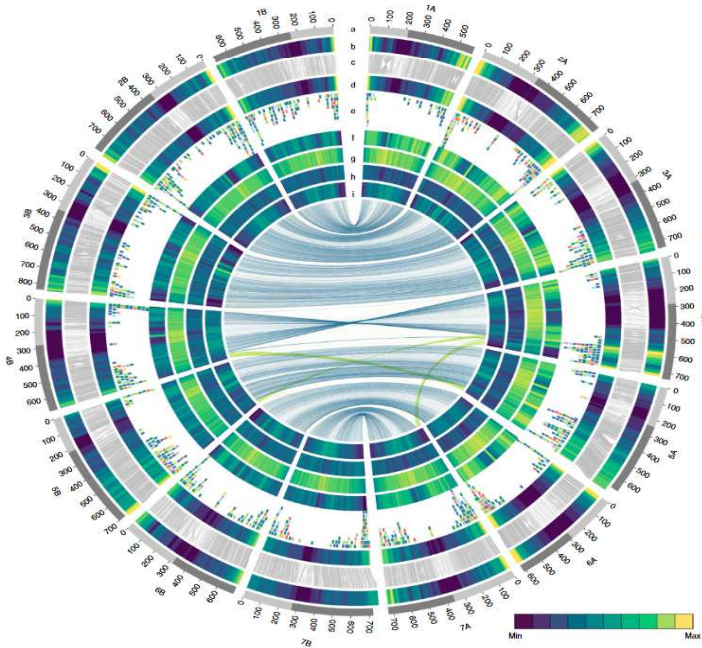
- «Svevo» Gold-standard Reference genome assembly of *Triticum spp durum* (Maccaferri et al., 2019)

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



Durum wheat genome highlights past domestication signatures and future improvement targets



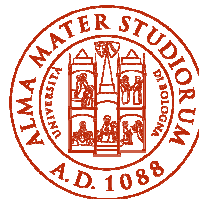
The genomic sequence is instrumental for:

- 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









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