Loci controlling moisture conversion of durum wheat (*Triticum turgidum* sp. *durum*) productivity

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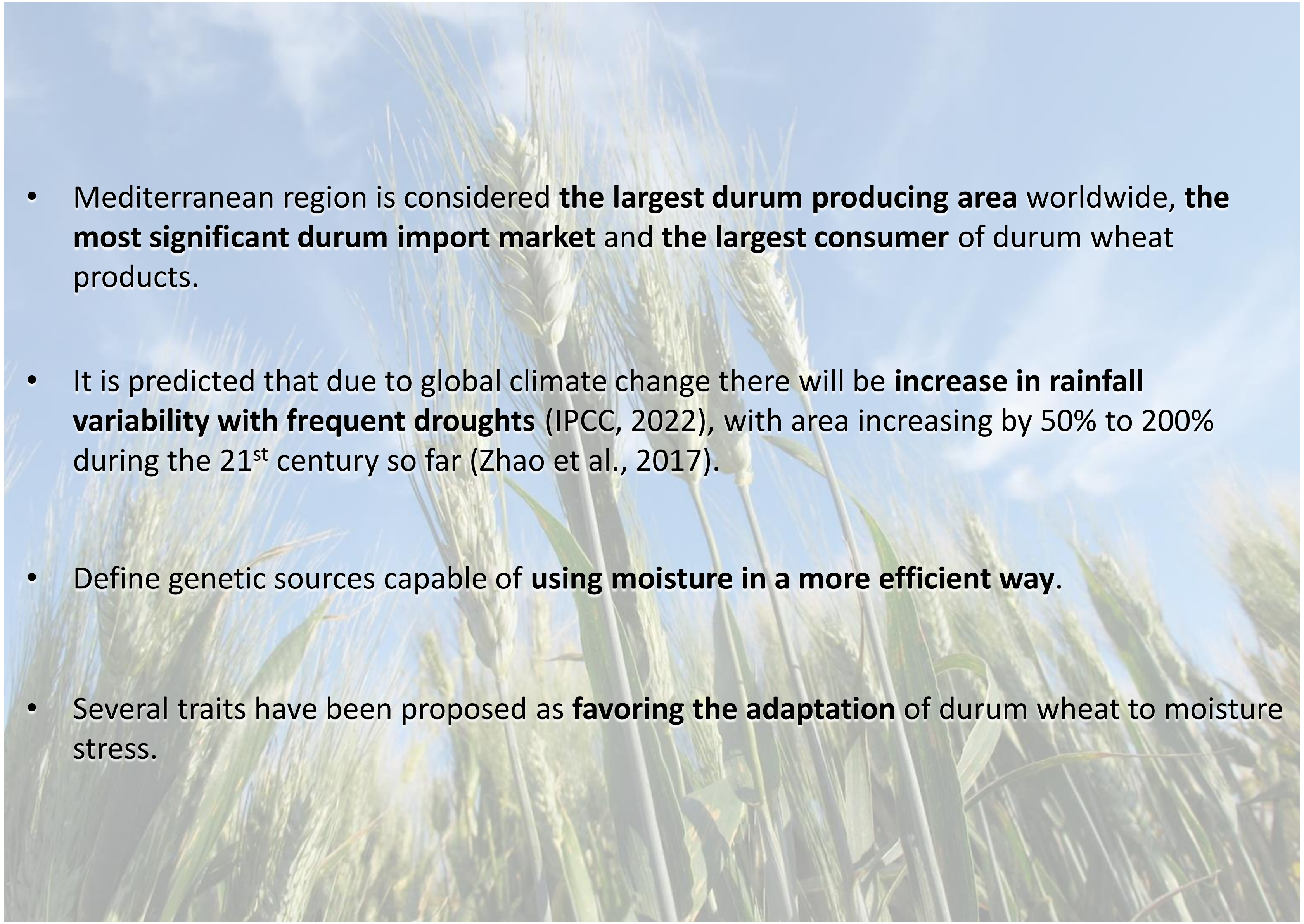
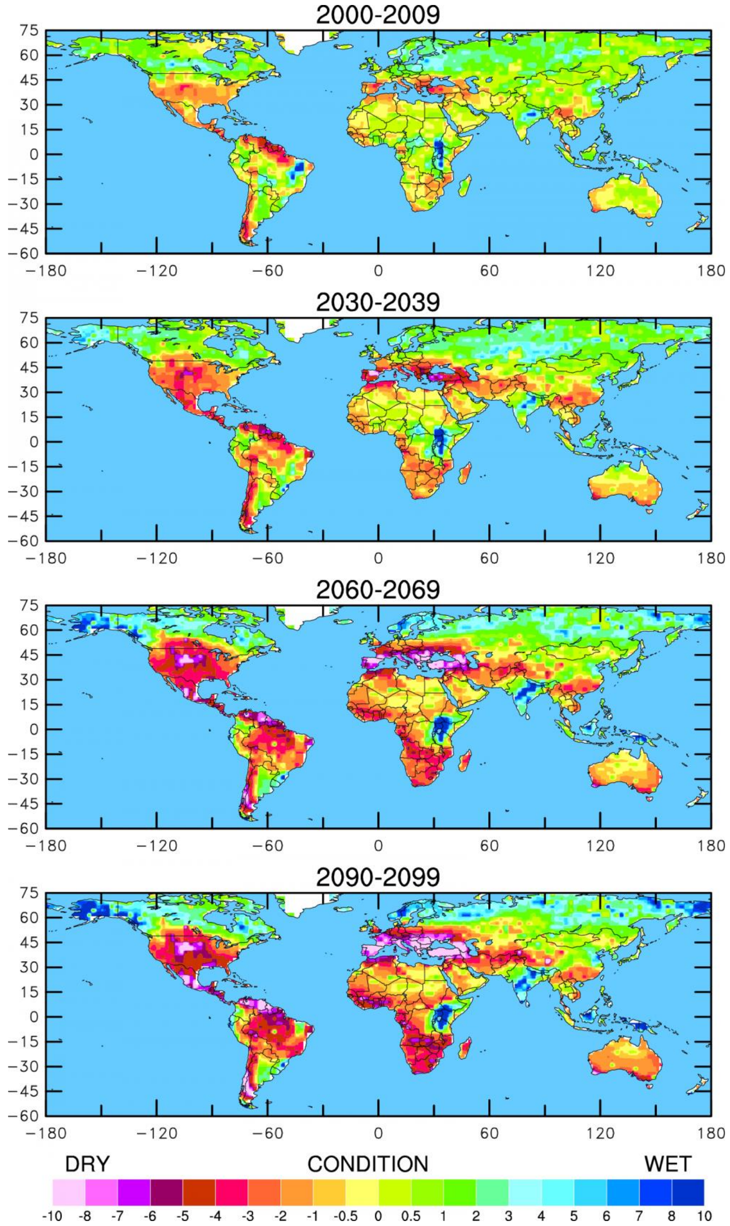
INTRODUCTION



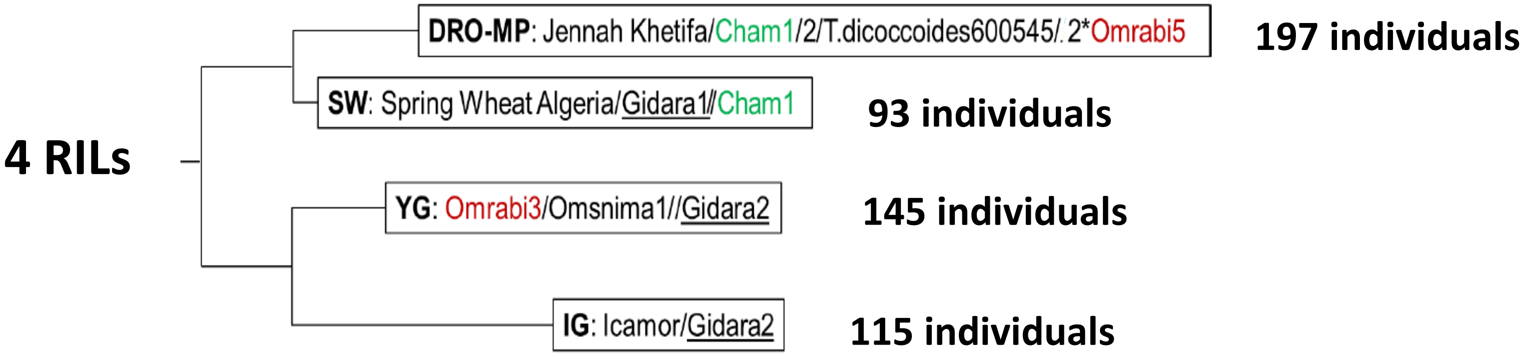
- Mediterranean region is considered **the largest durum producing area** worldwide, **the most significant durum import market** and **the largest consumer** of durum wheat products.
- It is predicted that due to global climate change there will be **increase in rainfall variability with frequent droughts** (IPCC, 2022), with area increasing by 50% to 200% during the 21st century so far (Zhao et al., 2017).
- Define genetic sources capable of **using moisture in a more efficient way**.
- Several traits have been proposed as **favoring the adaptation** of durum wheat to moisture stress.



Publication: Wiley Interdisciplinary Reviews: Climate Change

QTL analysis for drought tolerance

Field experiment, phenotyping and genotyping



4 RILs

DRO-MP: Jennah Khetifa/Cham1/2/T.dicoccoides600545/.2*Omrabi5 — **197 individuals**

SW: Spring Wheat Algeria/Gidara1//Cham1 — **93 individuals**

YG: Omrabi3/Omsnima1//Gidara2 — **145 individuals**

IG: Icamor/Gidara2 — **115 individuals**

Terbol, 1 year

Marchouch, 2 years

Sidi el Aidi, 1 year

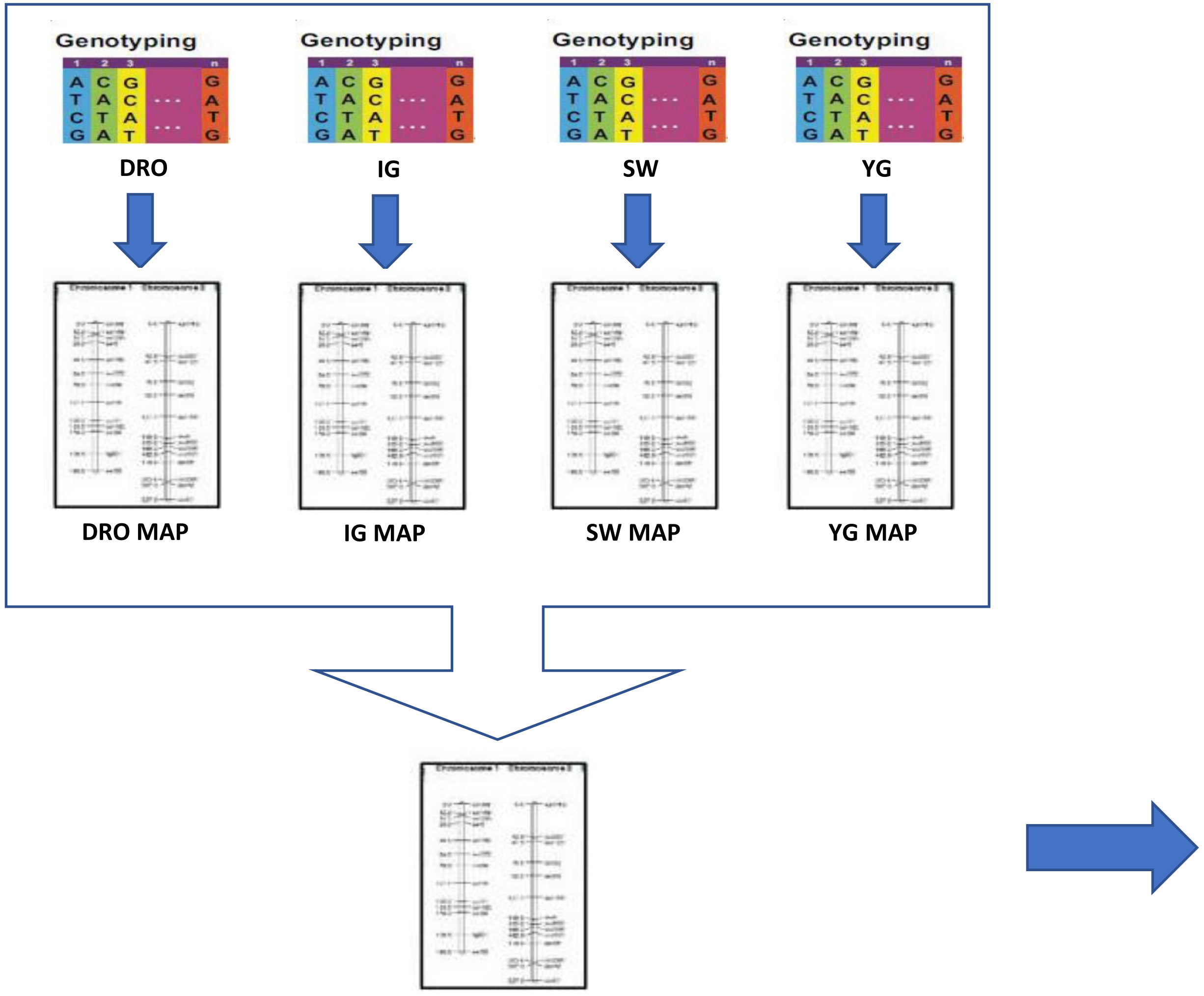
Jemaa Shaim, 1 year

SEVERITY OF DROUGHT STRESS

- ➢ 550 individuals , were genotyped using genotyping by sequencing (GBS) → **4909 SNPs**

Zaïm M, Kabbaj H, Kehel Z, Gorjanc G, Filali-Maltouf A, Belkadi B, Nachit MM, Bassi FM. **2020**. Combining QTL Analysis and Genomic Predictions for Four Durum Wheat Populations Under Drought Conditions. **Frontiers in Genetics** 11, 316.

Methodology



DRO

IG

SW

YG

DRO MAP

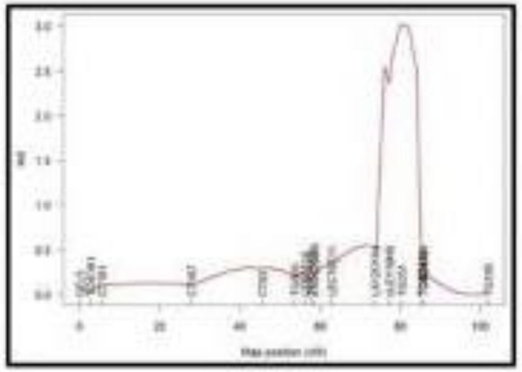
IG MAP

SW MAP

YG MAP

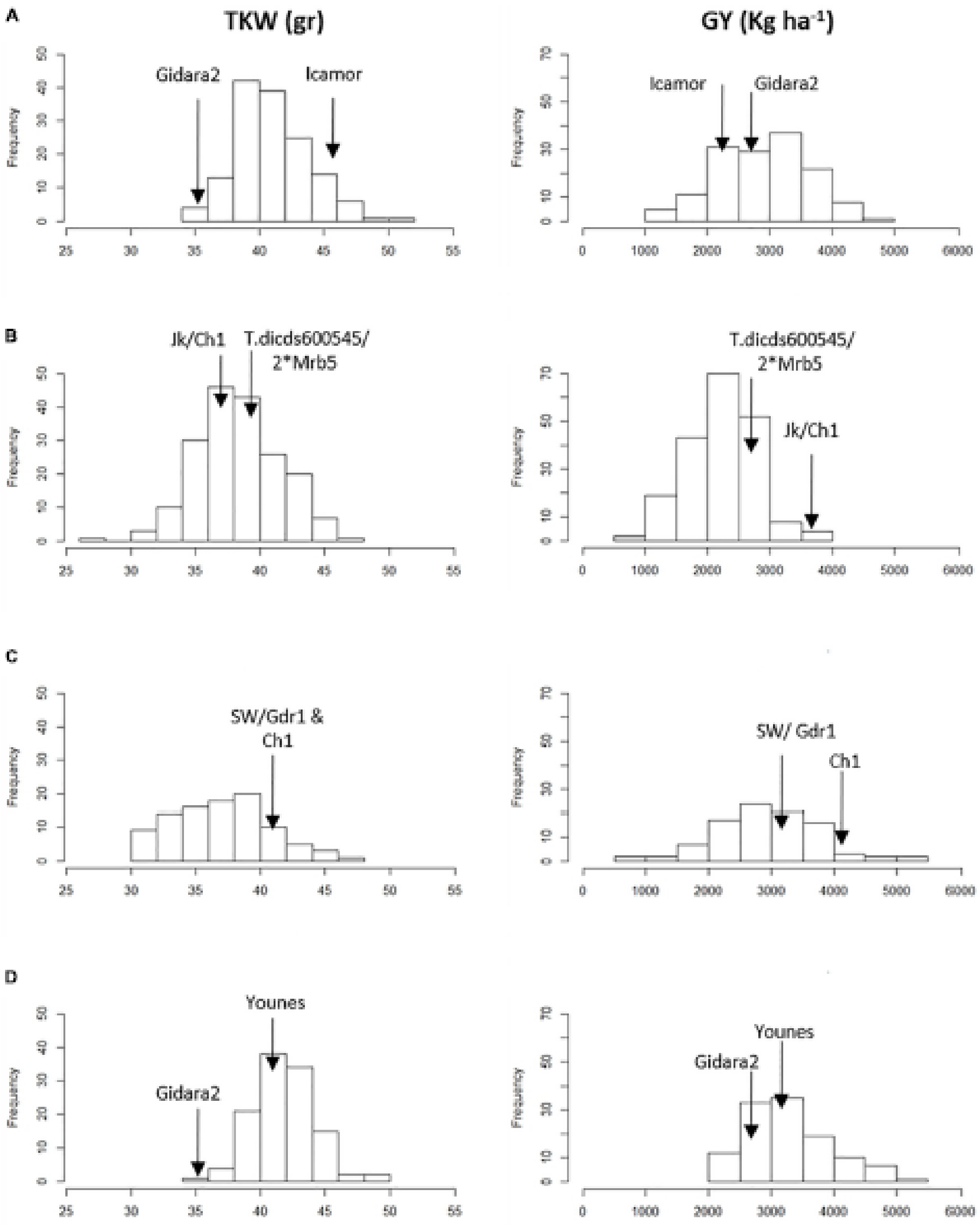
Consensus Map

Field phenotyping



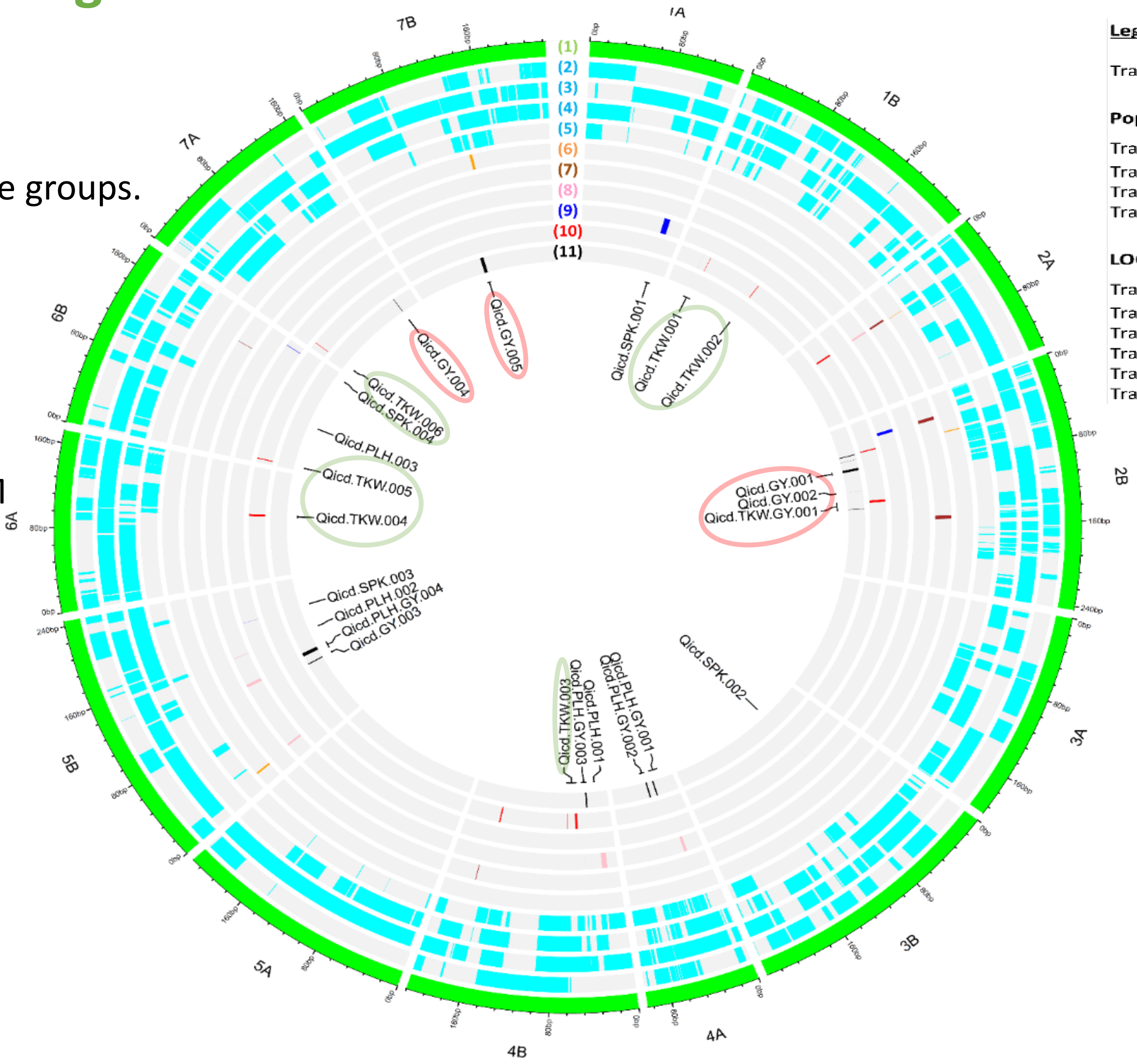
QTL analysis

Phenotypic evaluation of the RILs populations



QTL analysis for drought tolerance

- ✓ 3,200 markers assigned to 14 linkage groups.
- ✓ Total genetic distance of 2,700 cM
- ✓ Density of one marker each 0.85 cM



Legend

Track (1): Consensus map

Populaions Maps

Track (2): IC
Track (3): DRO
Track (4): SW
Track (5): YG

LOCI

Track (6): DTH
Track (7): DTM
Track (8): PLH
Track (9): SPK
Track (10): TKW
Track (11): GY

Genome wide association mapping for moisture stress conditions

Plant material and Field experiment across 18 environments

Discovery panel (Core collection)

2015-2016: 384 entries, Augmented design

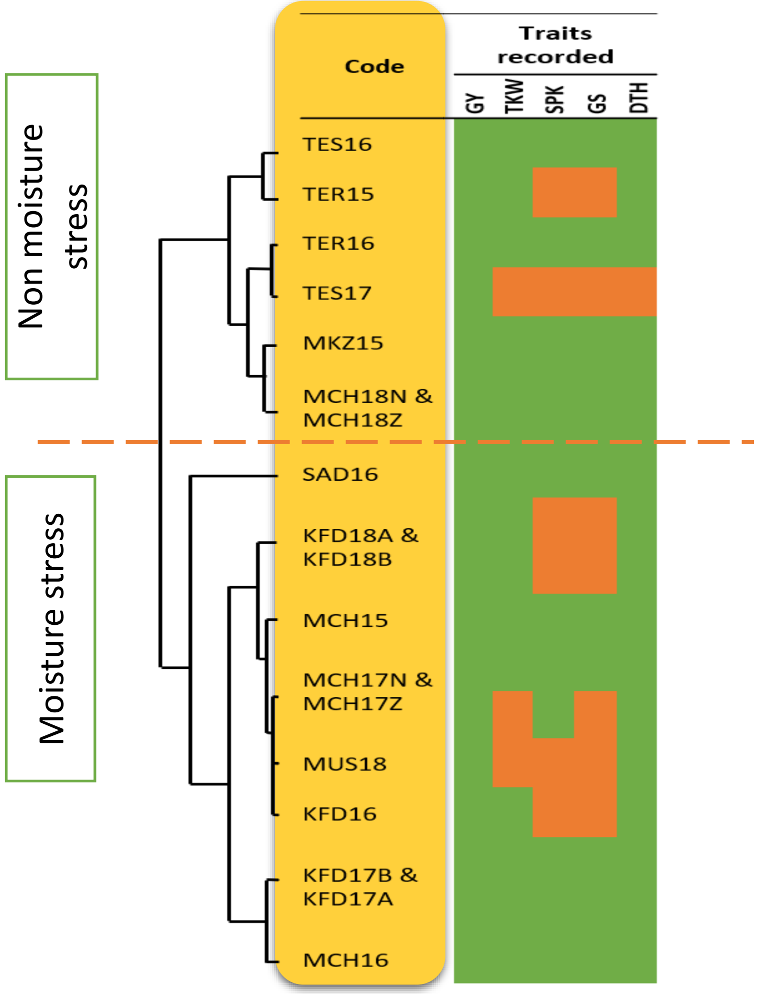
2017-2018: 144 entries, Alpha lattice design

confirmation panel (IDON-42)

2019: 94 entries, Augmented design

Validation panel (IDON-43)

2020: 94 entries, Augmented design




TES16-17 (Core collection)

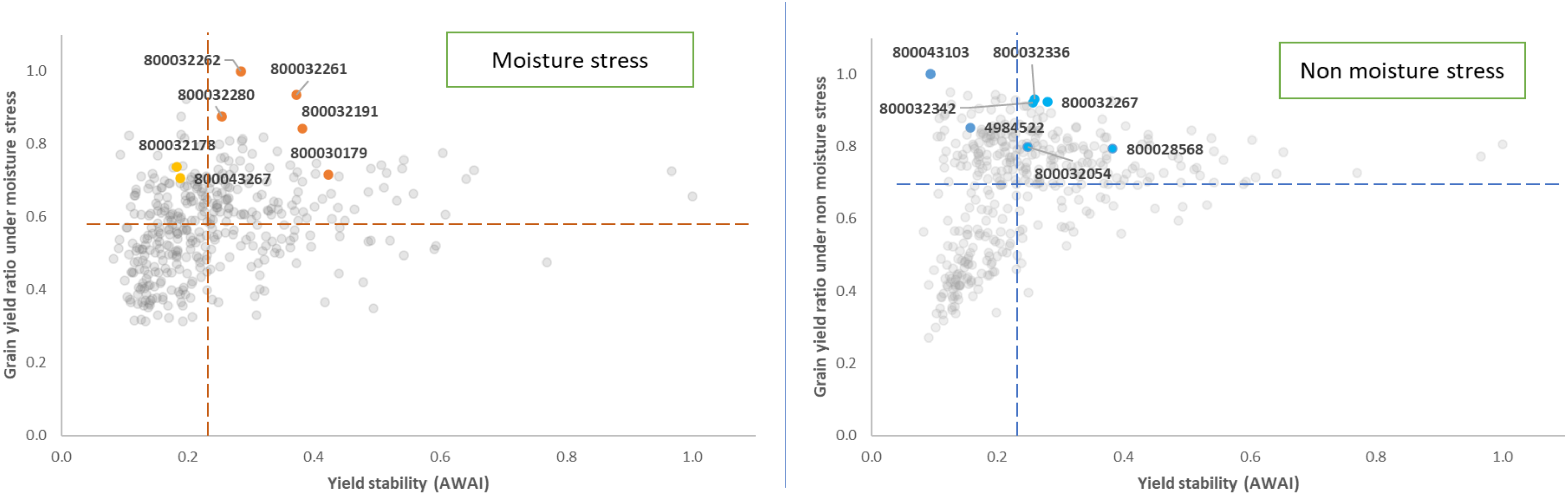

MKZ15 (Core collection)


TER15-16 (Core collection)


MCH15-18 (Core collection)

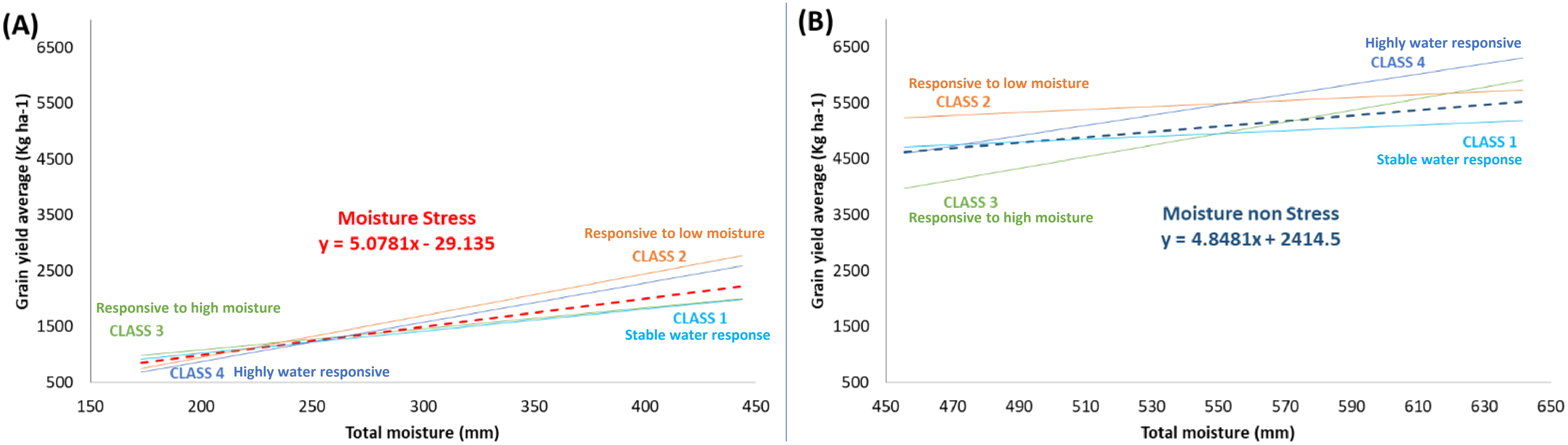

SAD16 (Core collection)
SAD19 (IDON42)
SAD20 (IDON43)

Discovery panel performance and yield stability

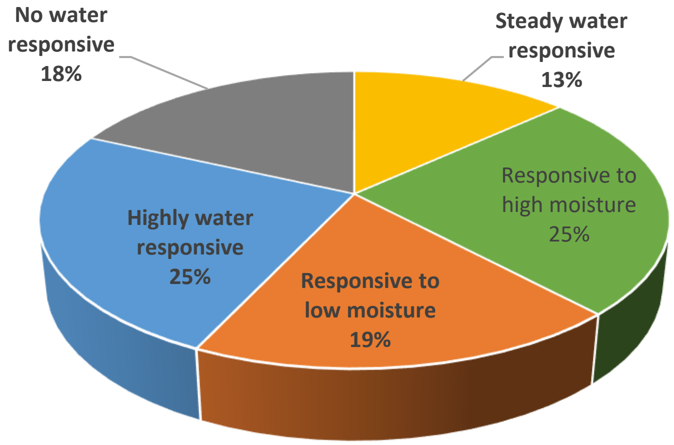


Biplot between the genetic component of yield and the GxE interaction component used to determine the best genotypes combining both G and GxE for grain yield across 11 moisture stressed (right) and 7 no-stressed (left) environments. Dashed lines trace the average for each axis.

Relationship between grain yield and moisture



Classes	Definition	r2 (GY vs moisture)	b_i (moisture stress)	b_i (non-moisture
1	Stable water response	**	$b_i < 5.08$	$b_i < 4.85$
2	Responsive to low moisture	**	$b_i > 5.08$	$b_i < 4.85$
3	Responsive to high moisture	**	$b_i < 5.08$	$b_i > 4.85$
4	Highly water responsive	**	$b_i > 5.08$	$b_i > 4.85$
5	No water response	Ns	$b_i < 0$	$b_i < 0$

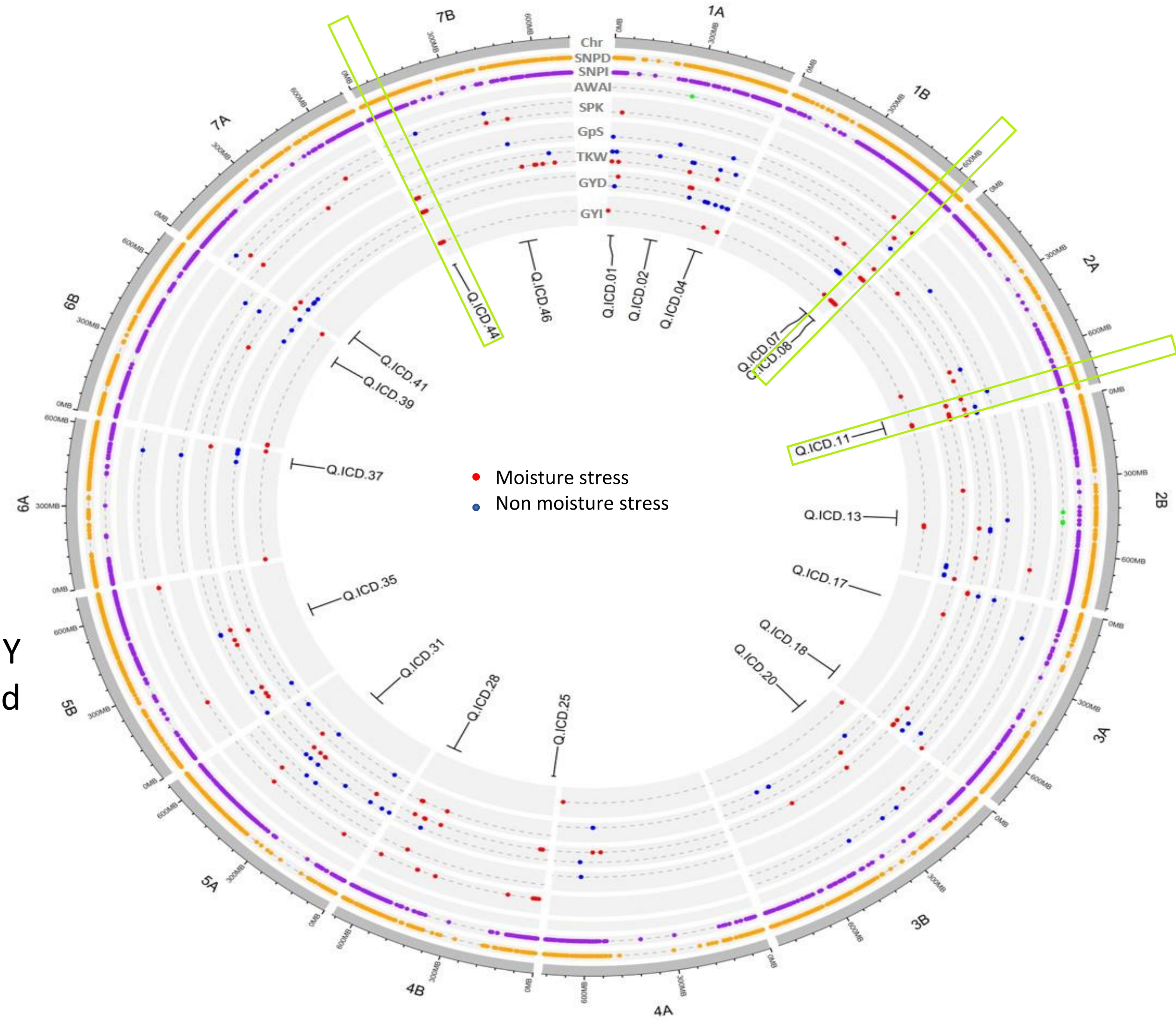


Genome wide association mapping for moisture stress conditions

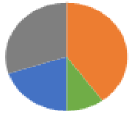
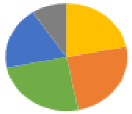
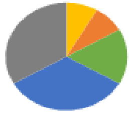
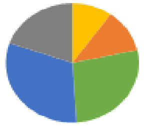
280 significant MTAs, distributed across 46 QTLs.

Consistent QTL for GY and yield component traits using discovery and confirmation panels

Q.ICD.08, Q.ICD.11 and Q.ICD.44 were linked to GY under moisture stress in both the discovery panel, and the confirmation panel, when tested at Sidi al Aydi.



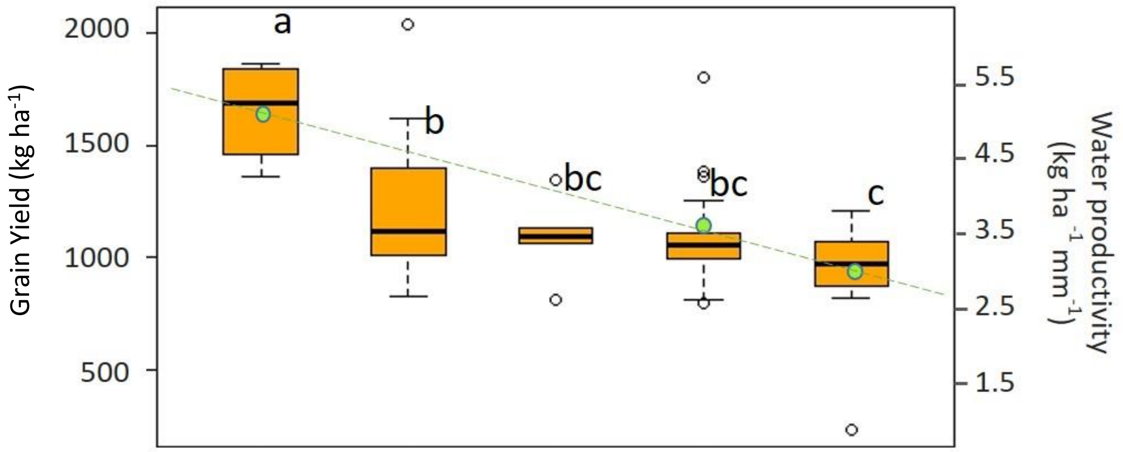
Effect of different allele combination on water productivity classes

Haplotypes	WP (kg ha^{-1} mm^{-1})	QTL.ICD.08	QTL.ICD.11	QTL.ICD.44	Classes frequencies
Hap 1	**6.5**	+	+	+	
Hap 2	**5.4**	-	+	-	
Hap 4	**5.3**	+	-	-	
Hap 5	**5**	-	-	-	

🟨 Steady Water Responsive (16)
🟧 Responsive to Low Moisture (22)
🟩 Responsive to High Moisture (30)
🟦 Highly Water Responsive (30)
⬛ No Water Responsive (22)

Haplotype 1 with favorable alleles at all loci reached the highest average WP , with 40% of the genotypes belonging to class 2. Interestingly, the same allelic combination is responsible for high grain yield under moisture stress.

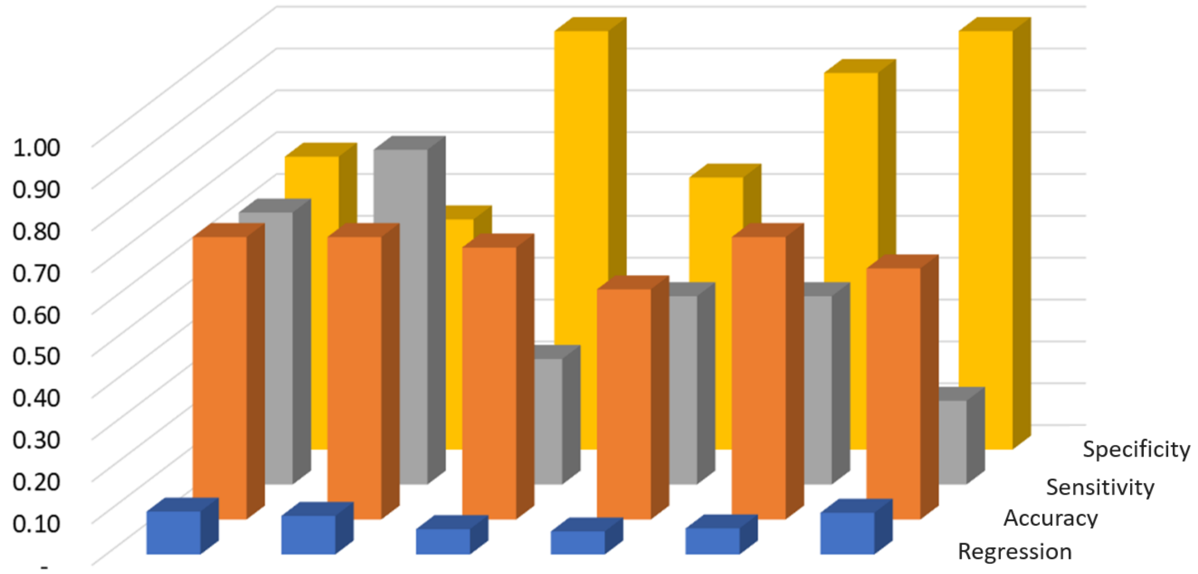
Allelic effect for the combination of 3 loci associated with GY on the “confirmation panel” under moisture stress



	Hap 1	Hap 2	Hap 3	Hap 4	Hap 5
Q.ICD.08	+	+	-	+	-
Q.ICD.11	+	-	-	-	-
Q.ICD.44	+	+	+	-	-

Haplotype 1 carrying only favorable alleles at all QTLs showed a GY advantage of more 700 kg ha^{-1} compared with haplotype 7 with no positive alleles at the three loci and a consequent higher water productivity of 2.2 kg ha^{-1} mm^{-1}.

KASP markers validation on an independent set of 94 elite lines of ICARDA tested under severe drought



ID	**AX-95631864**	**AX-94507963**	**AX-94549122**	**AX-94910470**	**AX-95191125**	**Combined**
Chr	1B	1B	1B	2A	7B	1B + 2A + 7B
QTL	Q.ICD.08	Q.ICD.08	Q.ICD.08	Q.ICD.11	Q.ICD.44	3 QTL
Allele 2	G:G	G:G	A:A	C:C	G:G	-
Allele 1	A:A	A:A	G:G	G:G	A:A	-
MAF	48%	36%	91%	43%	33%	5%

The combination of the 5 markers resulted in increasing the precision, with only top performing lines being selected

CONCLUSION

Three QTLs were associated with GY under drought, some of them were linked with yield components.

Allelic haplotype diversity using the three most promising QTLs, causes water productivity of up to +2.2 kg ha^{-1} mm^{-1} and grain yield of up to +700 kg ha^{-1} across moisture stressed conditions.

The three QTLs were validated into KASP markers and can further be utilized in marker assisted selection.

S E B
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RESEARCH PAPER

Genomic regions of durum wheat involved in water productivity

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GRDC
GRAINS RESEARCH & DEVELOPMENT CORPORATION

Thank you!