

# Identification of DArT-genomic regions associated with morpho-physiological traits in spring wheat seedlings under drought conditions

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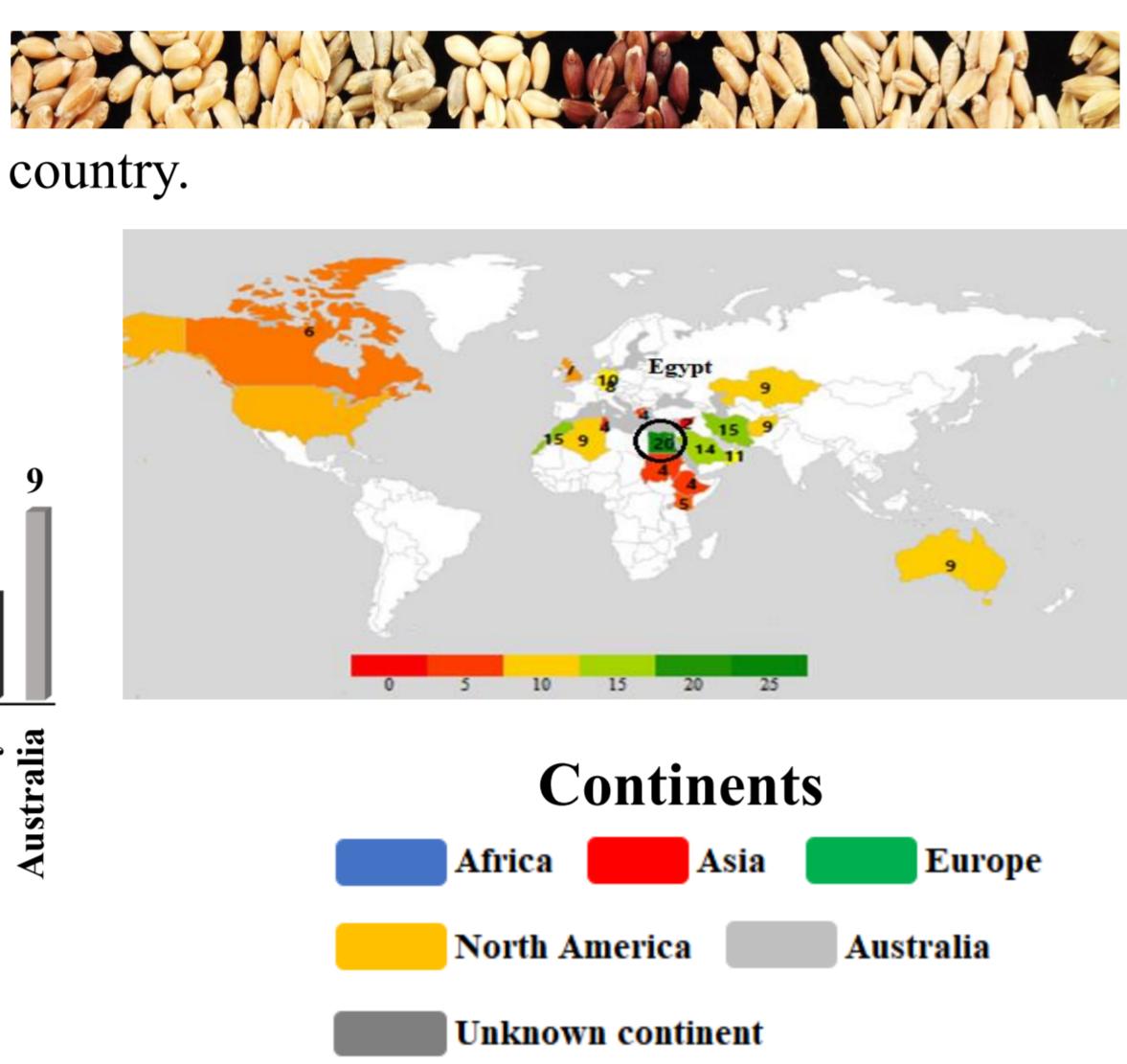
## Introduction

Wheat is one of the most important cereal crops worldwide due to its major role in food security. However, its growth and productivity are affected by various environmental factors, among which drought stress is one of the most significant factors negatively impacting wheat growth and yield at different growth stages. The seedling stage is a critical and highly sensitive stage to drought stress, as its effects extend to all subsequent growth stages. Genetic variation in drought tolerance at the seedling stage has not received much attention from researchers and plant breeders, especially in wheat. As a result, the genetic basis of drought tolerance at this stage is still poorly understood. Therefore, there is an urgent need to coordinate research efforts to explore genetic resources for drought tolerance at the seedling stage. **The objectives of this study were to 1) study the genetic variation in morphological and physiological traits in highly diverse wheat genotypes under drought stress conditions, 2) identify and validate DArT alleles associated with morphological and physiological traits under drought stress using genome-wide association study (GWAS), and 3) determine DArT markers with pleiotropic effects.**

## Material & Methods

### Plant materials

The plant material consisted of **172** diverse spring wheat genotypes. These genotypes were collected from 20 different countries across five continents, including 20 genotypes from **Egypt**.

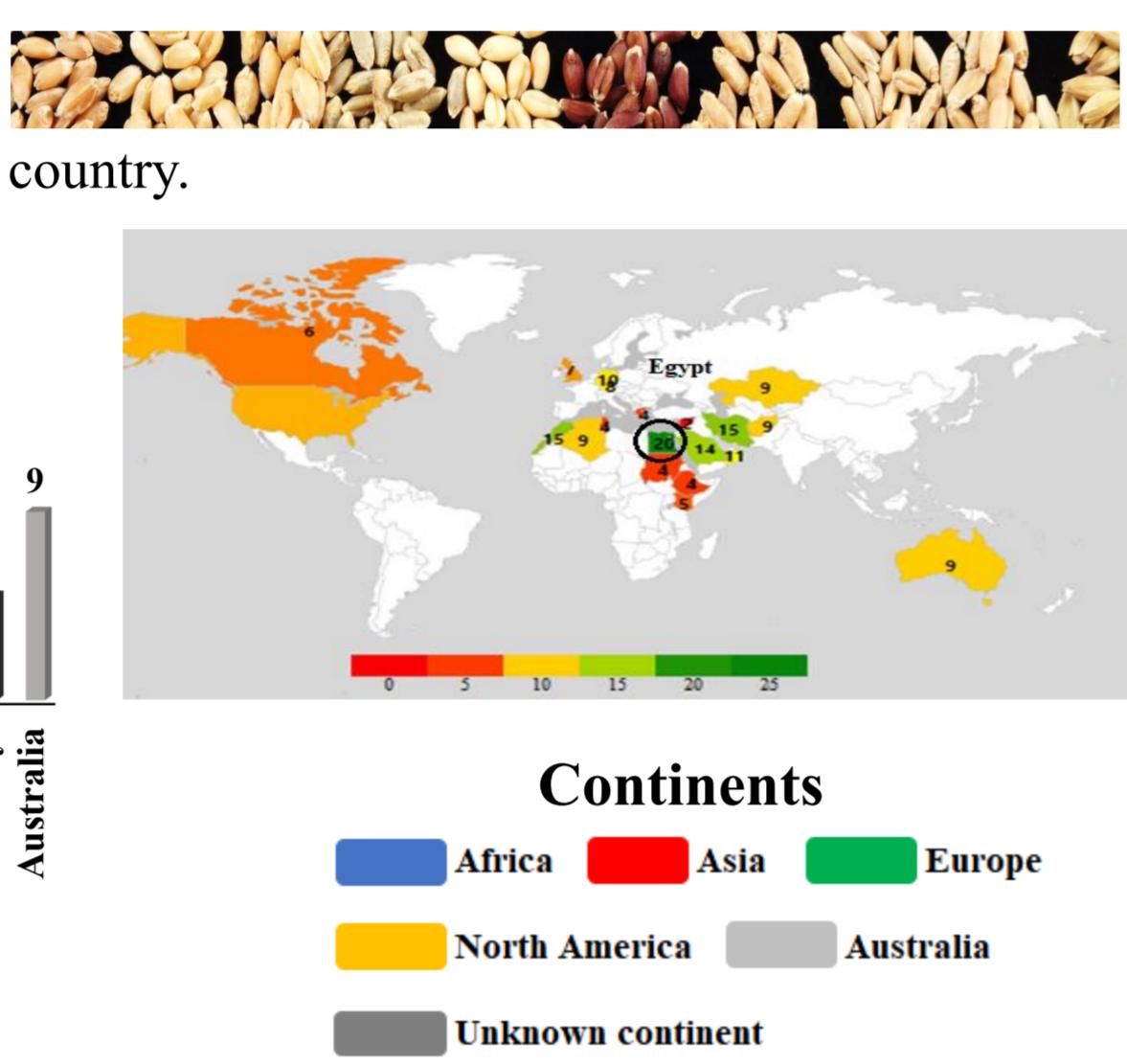


**Figure 1:** Number of genotypes used from each country.

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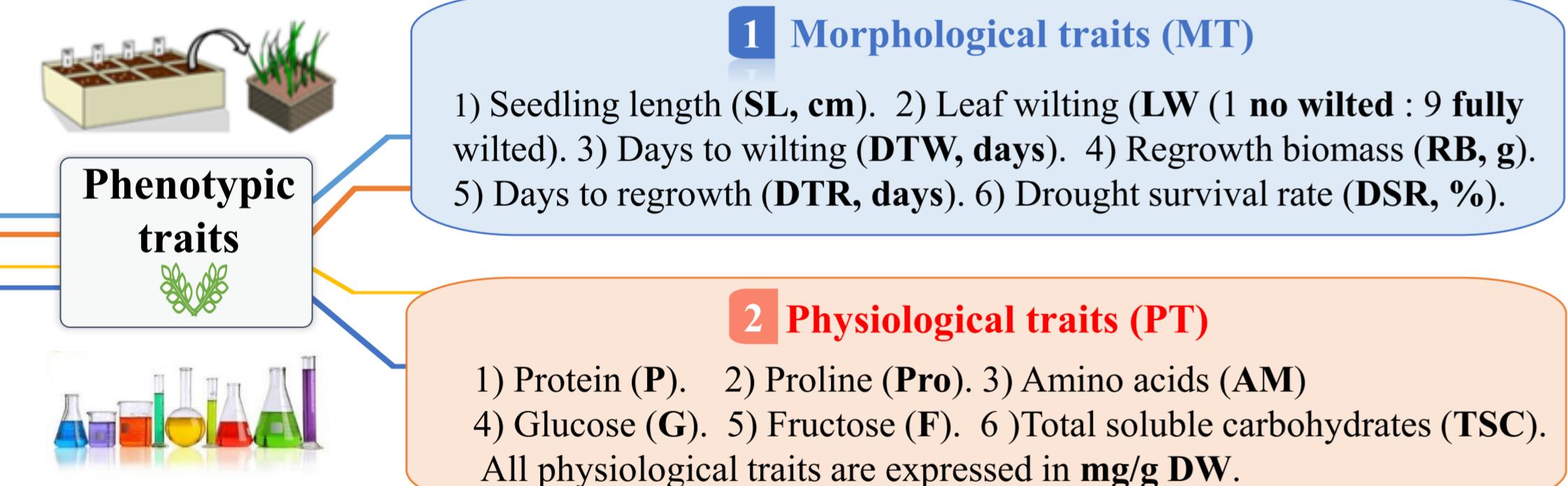
**Figure 1:** Number of genotypes used from each country.

### Experimental design and traits scoring

- The experiment was conducted in plant genetic Lab and physiological Lap at Assiut University, Egypt.
- All genotypes were tested under drought stress at the seedling stage.
- Randomized complete block design (RCBD) with seven replications (R=7)
- The genotypes were sown trays filled with sand soil (100%).
- Soil water capacity in the first irrigation **100% (16ml)** and **50% (8ml)** in the second irrigation. All tested plants were exposed to natural drought stress conditions by withholding irrigation for **13** days.

### Traits scoring

- Two types of traits were recorded on the leaves of all tested genotypes under drought stress.



- Leaf wilting trait was scored five times through visual scoring, and then all scores of leaf wilting were summed into one trait, called sum of leaf wilting (**S\_LW**).
- Drought tolerance index (**DTI**) at the seedling stage was previously developed and calculated by **Ahmed et al. (2022)**.
- All Phenotypic traits scored under drought stress were previously described in detail by **Ahmed et al. (2022)** and **Sallam et al. (2024)**.

### Statistical analyses of morpho-physiological traits

#### Phenotypic analyses

- Variance and covariance analyses for all traits scored were carried out using PLABSTAT and R software (**Utz, 1997**).

#### Genetic analyses

- A set of 407 DArT markers were collected from the U.S. National Plant Germplasm System database (<https://www.ars-grin.gov/>). These DArT markers were filtered and utilized in GWAS analysis.
- GWAS analysis was performed between DArT markers and all morphological and physiological traits using **rMVP** package with different statistical models.
- Significance of marker-trait associations (MTA) were identified at  $P\text{-value} \leq 0.001$ .

## Results & Discussion

### Phenotypic analyses

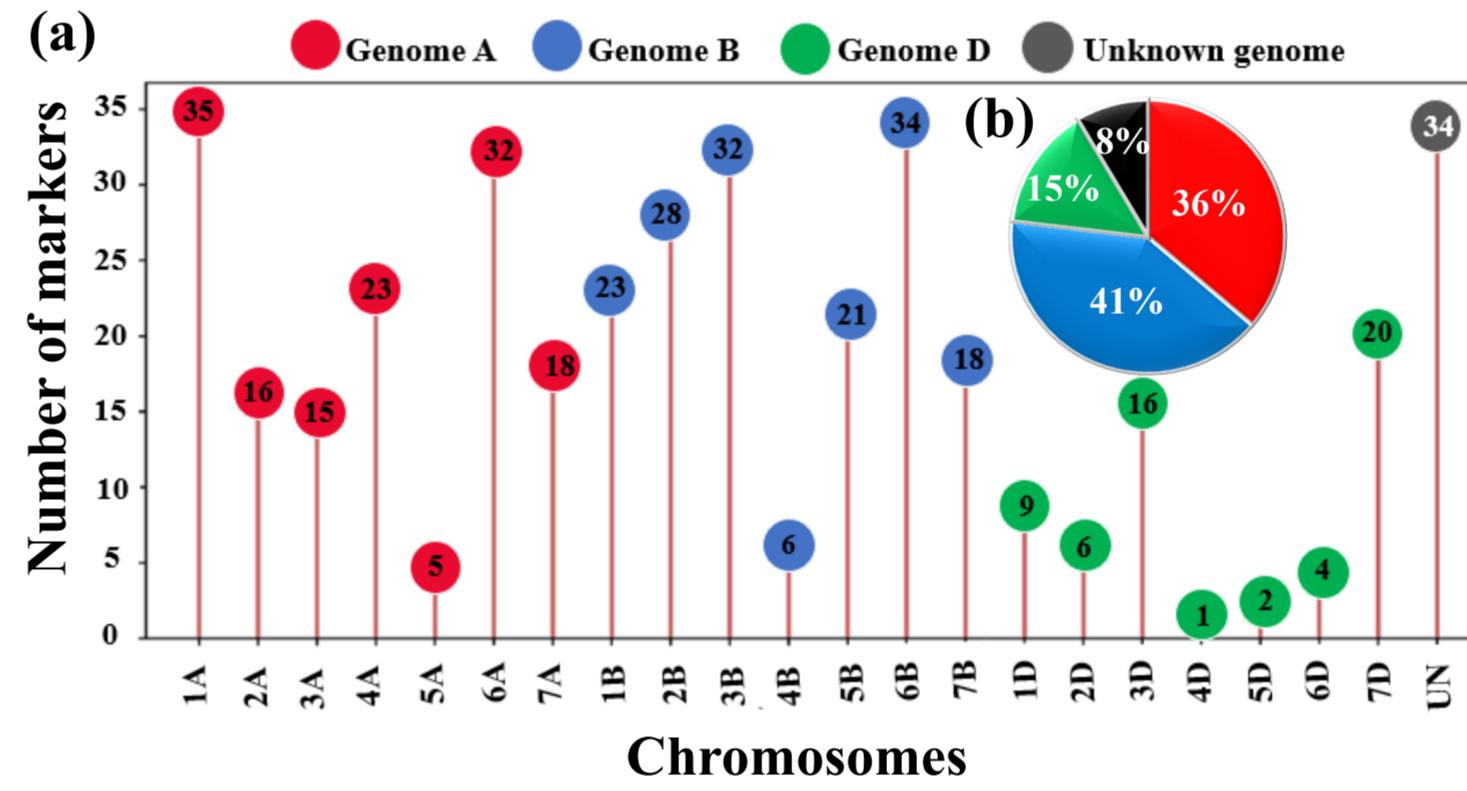
**Table 1:** Mean, *F*-value and heritability ( $H^2$ ) for all morphological and physiological traits under drought conditions.

Parameters	Morphological traits			Physiological traits			
	Mean	<i>F</i> -value	$H^2$	Parameters	Mean	<i>F</i> -value	$H^2$
SL	15.75	12.94**	92.27	P	127.74	34.87**	97.13
S_LW	20.53	6.64**	84.93	AM	9.09	89.41**	98.88
DTW	5.68	6.19**	83.85	Pro	2.45	871.59**	99.99
DTR	78.5	8.03**	87.55	G	85.47	342.77**	99.71
RB	11.94	11.52**	91.32	F	88.17	33.12**	96.98
DSR	19.6	6.24**	83.98	TSC	226.73	118.71**	99.19
DTI	5.62	10.76**	90.71				

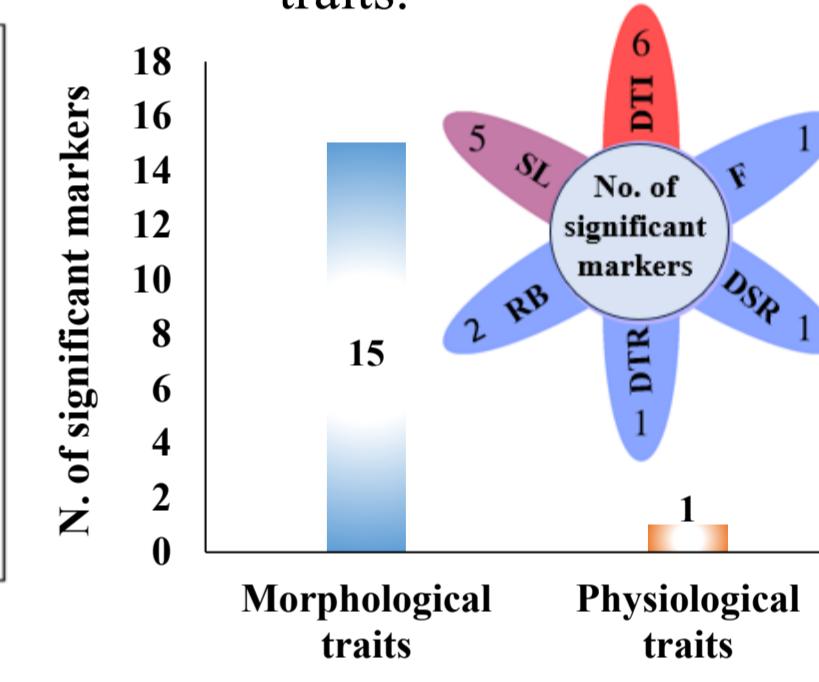
\*\* Significant at the 0.01 level of the probability.

### Genetic analyses

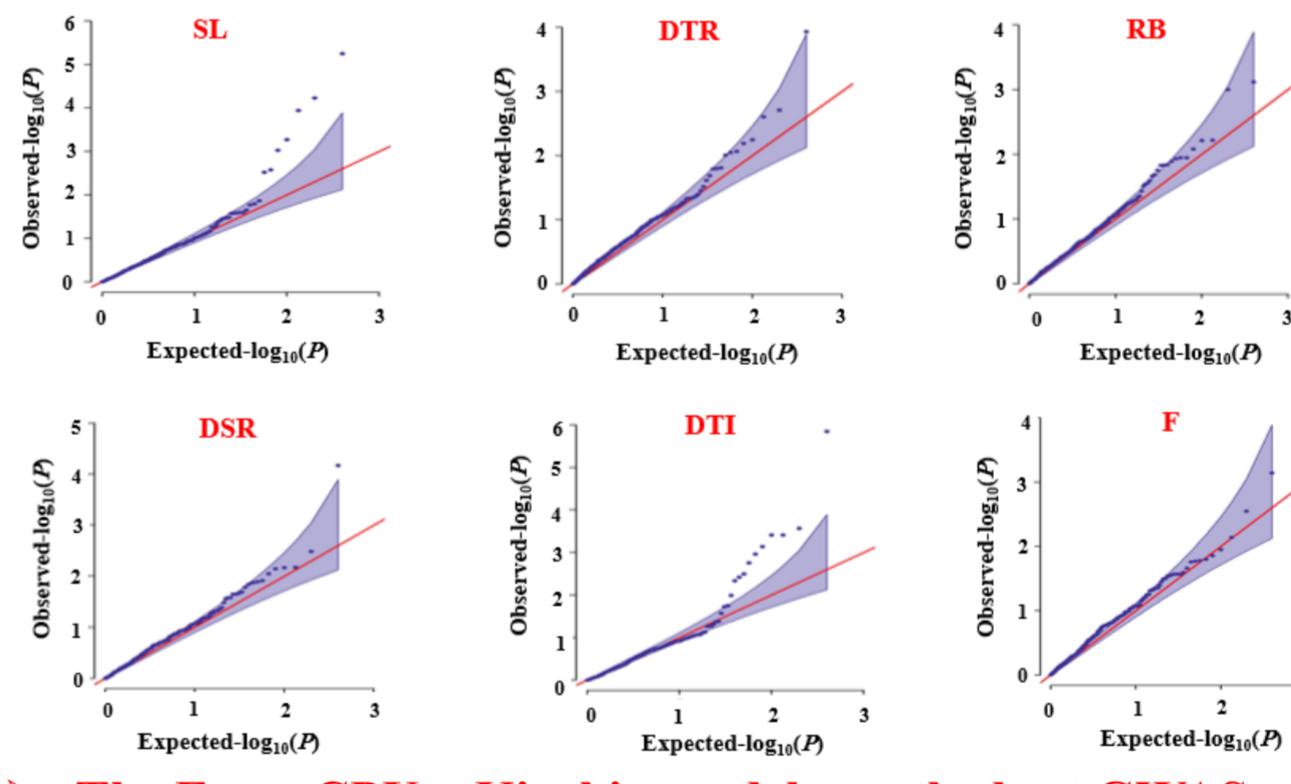
**Figure 2:** Distribution of DArT markers across different wheat (a) chromosomes and (b) genomes.



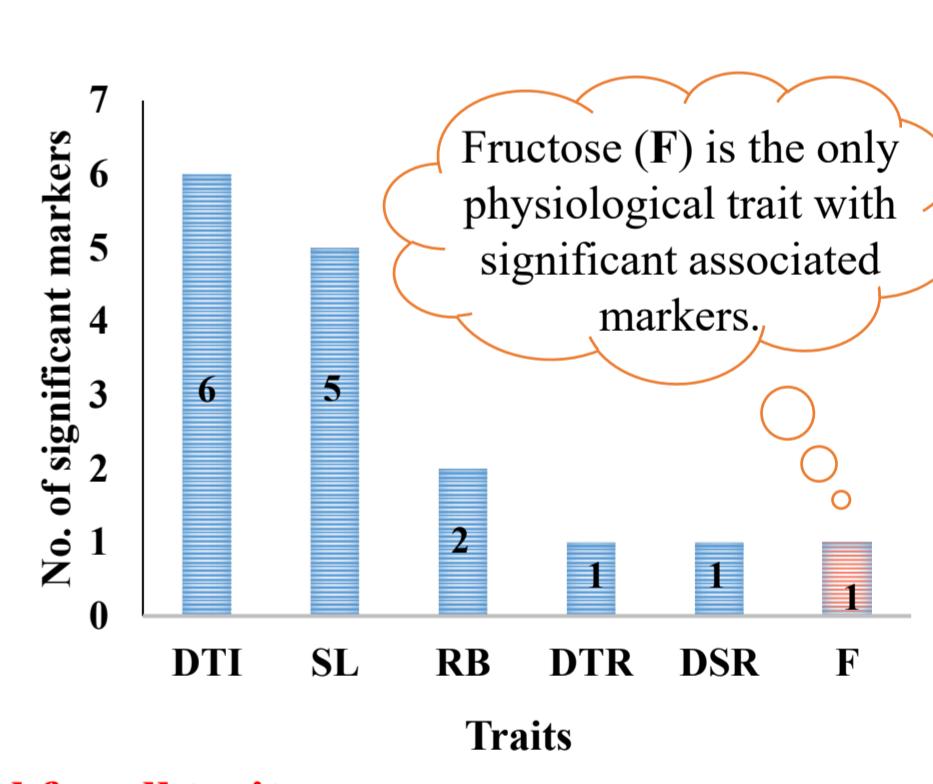
**Figure 3:** Number of significant markers associated with morpho-physiological traits.



**Figure 4:** Quantile-Quantile plot (Q-Q plot) for each traits detected by GWAS.

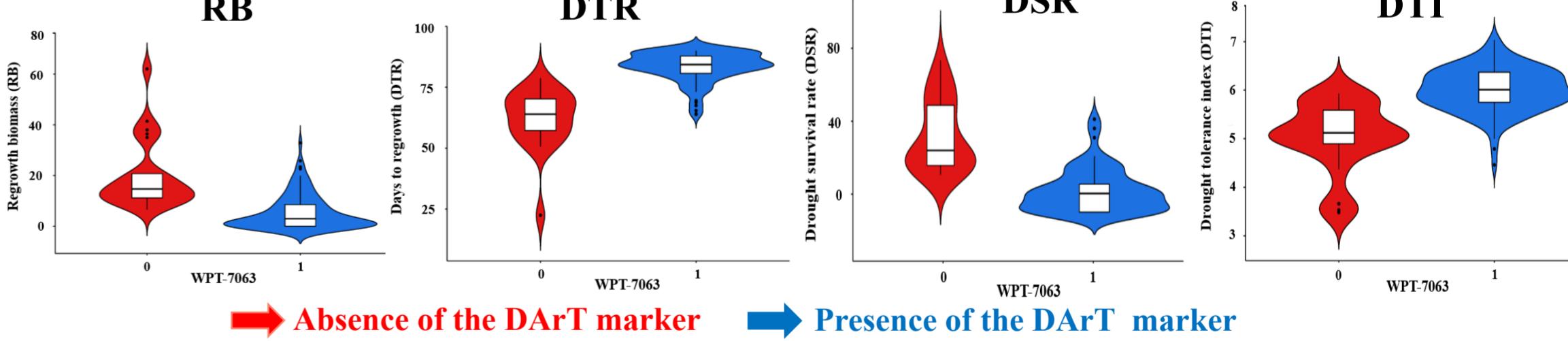


**Figure 5:** Number of DArT markers associated with each traits.



**The Farm CPU + Kinship model was the best GWAS model for all traits.**

**Figure 6:** The characterization of the common markers.



- The WPT-7063 marker 6A was common marker in four traits (DTR, RB, DSR, and DTI).
- This marker showed one trend in all associated traits as the visible allele of this marker decreased the drought tolerance (Susceptible).

**Table 2:** List of validated DArT markers associated with drought stress in wheat in earlier studies.

Trait	Chr.	Traits in this study	Traits in previous study	Characterization	References
WPT-7677	3B	DTI	GNPS, GYPS	Susceptible	Hashem et al. (2023).
RPT-7068	3B	DTI	GNPS, GYPS	Susceptible	
TPT-3689	6B	SL	PH	Susceptible	
WPT-664309	7D	SL	GNPS, GYPS	Tolerance	

Where; (Chr\*) refers to chromosome on which the marker was detected, grain number of spike (GNPS), grain yield per spike (GYPS), plant height (PH).

## Conclusion & Next Steps

- The four validated markers could be promising markers for marker-assisted selection(MAS) to accelerate genetic improvement for drought tolerance after validation in different genetic backgrounds. These markers could be converted to Kompetitive allele-specific PCR (KASP) used in the evaluation of other populations.
- More research efforts are needed to identify markers associated with physiological traits under drought stress in wheat seedlings.

## References

- 1) Ahmed AAM, Dawood MFA, Elfarash A, Mohamed EA, Hussein MY, Borner A, Sallam A (2022) Genetic and morpho-physiological analyses of the tolerance and recovery mechanisms in seedling stage spring wheat under drought stress. *Frontiers in Genetics*.
- 2) Sallam A, Dawood MFA, Jarquin D, Mohamed EA, Hussein MY, Borner A, Ahmed AAM (2024) Genome-wide scanning to identify and validate single nucleotide polymorphism markers associated with drought tolerance in spring wheat seedlings. *Plant Genome*.
- 3) Utz HF (1997) Plabstat: A computer program for statistical analysis of plant breeding experiments. Version 2N. *Institute of Plant Breeding*.
- 4) Hashem M, Sandhu KS, Ismail SM, Borner A, Sallam A (2023) Validation and marker-assisted selection of DArT-genomic regions associated with wheat yield-related traits under normal and drought conditions. *Frontiers in Genetics*.