

GENOME-WIDE ASSOCIATION STUDY OF ELITE SPRING BREAD WHEAT (*TRITICUM AESTIVUM* L.) GENOTYPES UNDER DROUGHT CONDITIONS ACROSS DIFFERENT LOCATIONS

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ABSTRACT

Drought, is the main abiotic stressor that significantly reduces bread wheat's grain yield and related-traits. A genome-wide association study was conducted using the 10K wheat SNP markers for grain yield and related traits of 246 spring bread wheat genotypes from ICARDA to identify the genomic regions and marker-trait associations (MTAs) responsible for drought tolerance. Grain yield (GY), days to heading (DHE), days to maturity (DMA), plant height (PLH), and thousand kernel weight (TKW), were evaluated at Merchouch station (Morocco); in the other hand only grain yield that was considered for the rest of the environments; Terbol (Lebanon), Kheferdan (Sudan), and ARC (Egypt), as well as Tassaout, and Sidi El Aidi (Morocco); spanning two years 2015-2016 and 2016-2017, as per variance analysis. Grain yield and related-traits showed a considerable variation among genotypes. Moreover, GWAS using a mixed linear model (MLM), revealed 53 MTAs across the six environments on 14 chromosomes. With an average r^2 value of 0.26, Genome D has the highest linkage, followed by Genomes B and A with r^2 values of 0.22 and 0.21, respectively. GY had the highest MTA rating (35), followed by TKW (9) and 3 for each of the other agronomic traits (DHE, DMA, PLH) at Merchouch station. "CAP8_c1393_327" was the most significant associated marker correlated with grain yield located on chromosome 3A across Sid El Aidi station. Additionally, the SNP markers "wsnp_Ra_c26091_35652620" displayed extremely significant and stable MTA for TKW on chromosome 5B at Merchouch station. The markers and candidate genes reported throughout this study have the potential to be used in marker-assisted selection to enhance wheat genotypes in terms of yield and resistance to drought limitations.

INTRODUCTION

Wheat, one of the world's most widely cultivated cereal crops, faces significant challenges due to the increasing prevalence of drought conditions in many regions. Drought, characterized by extended periods of water scarcity, can have detrimental effects on wheat production, leading to reduced yields and compromised crop quality [1-2]. In response to these challenges, researchers and breeders are actively working to develop drought-tolerant wheat varieties [3].

Nonetheless, the process of breeding for drought tolerance encounters challenges primarily due to the extensive variation in drought conditions, in alignment with the genetic complexity of drought tolerance and the accompanying mechanisms of plant response.

In the current work, a panel of 246 different bread wheat lines from ICARDA germplasm was phenotyped and sequenced using 10k SNP markers obtained from 90k Illumina iSelect arrays [4].

The vast variety of both the genetic panel and SNP markers, according to our hypothesis, should uncover intriguing connections with drought-related phenotypes under Multiple locations. This research has three main objectives: (i) to pinpoint the most effective combination of secondary traits for screening drought tolerance, (ii) to uncover significant marker-trait associations (MTAs) linked to these traits, and (iii) to choose the top-performing genotypes that exhibit both high yield and drought tolerance.

METHODOLOGY (continued)

Genotyping

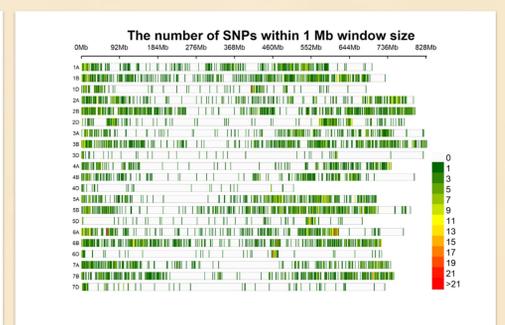
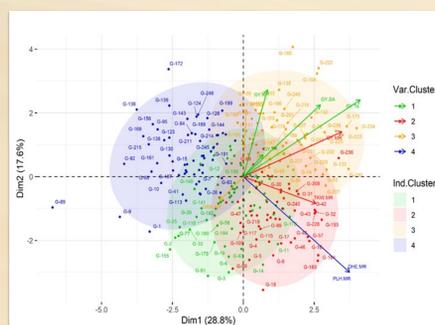
The lines were genotyped using 10K single nucleotide polymorphism (SNP) markers.

Association Mapping

The GAPIT program was used to identify the best model and find marker trait associations (MTAs) for each trait.

All the detected MTAs at a critical p-value were considered as a significant association and the Manhattan plots were generated using GAPIT under R software.

RESULTS



Principal component bi-plot of 246 bread wheat genotypes grown during two seasons (2016-2017) under drought conditions at Merchouch, Sidi El AYDI, Tassaout, Terbol, ARC, and Kheferdan stations.

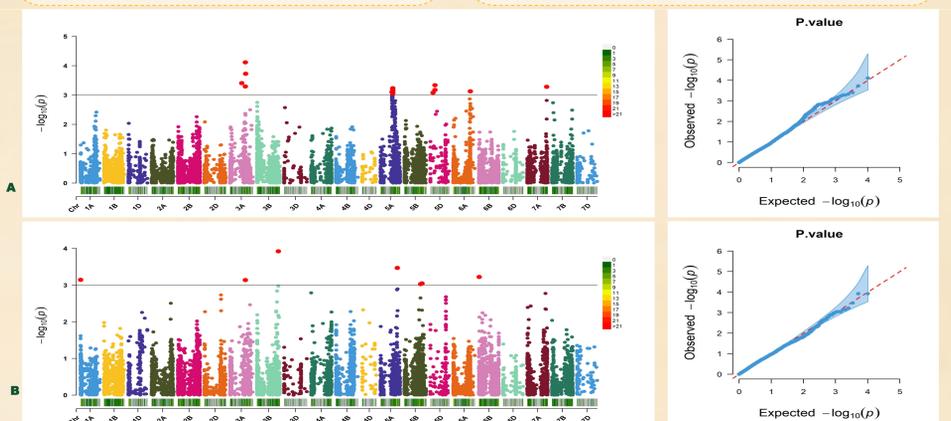
Marker density on each bread wheat chromosome of 246 bread wheat genotypes.



Plots of susceptible and drought tolerant genotypes in the field.



Drought tolerant wheat genotypes Morocco, Merchouch, ICARDA



Manhattan plots and the QQ plots of 246 bread wheat genotypes for grain yield at Sidi El AYDI (A) and ARC (B) stations during 2016 and 2017 crop seasons. The horizontal line shows the $-\log_{10}(p)=3$ threshold.

METHODOLOGY

Mapping Population

A set of 246 spring bread wheat (*Triticum aestivum* L.) genotypes, sourced from the spring bread wheat breeding program at the International Center for Agricultural Research in Dry Areas (ICARDA), was examined to pinpoint associated markers for grain yield and a range of agronomic traits related to drought tolerance.

Phenotyping

The mapping population was evaluated under contrasting field conditions at Merchouch, Tassaout, and Sidi El Aidi station (Morocco); Terbol (Lebanon), Kheferdan (Sudan), and ARC (Egypt); spanning two years 2015-2016 and 2016-2017. Following an alpha lattice design.

The lines were phenotyped for Grain Yield, Days to Heading, Days to Maturity, Plant Height, and Thousand Kernel Weight.

CONCLUSION

In light of these results, the markers and candidate genes identified have the capacity to be employed in marker-assisted selection, aiming to improve wheat genotypes with regard to both yield and their ability to withstand drought-related challenges. Further investigations should be carried out to validate the efficiency of these markers in the selection for drought tolerance under various environments and genetic backgrounds.

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