# Molecular characterization of bread wheat under saline conditions

Presented by

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A Thesis Submitted

to

**Faculty of Science**

**In Partial Fulfillment of the**

**Requirements for**

**the Degree of**

**PhD**

**(Agricultural Biotechnology)**

**(Biotechnology / Biomolecular Chemistry)**

**Chemistry Department**

**Faculty of Science**

**Cairo University**

**(2021)**

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# Abstract

In many parts of the world including Egypt, salinity significantly restricts the growth of wheat. Phenotyping elite bread wheat germplasm has high importance for its effective utilization in breeding programs. The objectives of this study were to screen elite bread wheat genotypes versus egyptian checks, under saline soil conditions and assessing interrelationships between grain yield and yield-related traits in El-Arish, Egypt. In addition, marker trait associations and genome wide association mapping were performed for quantitative trait loci detection for different agronomic traits. One experiment was conducted in two seasons; under saline soil conditions of El-Arish, Sinai, where soil ECe was 8.68 and 9.31 dSm-1 in the first and second season, respectively. A simple lattice design (13x13) with two replications was used. Data for the the thousand-grain weight , highest plant survival rate, plant height, number of seeds/spike, number of spikes/plant and seeds/spike, spike length, spike weight and grain yield were collected in the field. Principle component analysis (PCA), Genotype by Trait (GT) Biplot technique and Pearson's correlation were performed. We detected genomic loci associated with salt tolerance using over, 24145 single nucleotide polymorphism for the ten phenotypic traits studied in this experiment. In addition, characterizing candidate genes neighboring the associated SNPs was done. Another experiment was performed to compare the performance of the 159 elite genotypes versus the 15 Egyptian checks, in alpha lattice design at saline field of EC 10 ds/m. Data for the the thousand-grain weight , highest plant survival rate, plant height, number of seeds/spike, number of spikes/plant and seeds/spike, spike length and spike weight were collected in the field. Bread wheat genotypes recorded significant differences ($p<0.01$) for all studied traits under a saline environment. The promising genotype(s) were identified (No. 129 and No. 148) which had the highest grain yield. Results of Pearson's correlation indicated that the traits, spikes/plant (0.77) and tillers/plant (0.73) were strongly and positively correlated with grain yield/plant (GY). The identified promising genotypes and secondary traits could be offered to bread wheat breeders for use in future breeding programs to improve salinity tolerance. The results of the genome wide association mapping showed that ten trait-marker associations were detected on the 1D, 3A, and 6B chromosomes of bread wheat. For spikes/plant and tillers/plant, seven common SNPs (SNP- BobWhite_c8340_511, SNP- BobWhite_rep_c49102_169, SNP- BS00068520_51, SNP- IAAV3900, SNP-

Kukri_c34195_357, SNP- Kukri_c80104_809 and SNP- wsnp_RFL_Contig429_4978628) were identified on chromosome 3A. For plant height, SNP- Excalibur_c91980_139 was identified on chromosome 6B in the two seasons and for spike length, SNP- D_GA8KES401EYUM8_190 was identified on chromsome 1D. SNP BobWhite_rep_c49102_169 was previously reported to be linked to germination under salt stress. BS00068520_51 was found to be associated to thousand kernel weight while the SNPs Kukri_c34195_357 and Kukri_c80104_809 were associated with flour colour related traits, under non saline conditions. These SNPs were associated with spikes and tillers/plant in the present study. The other six SNPs are novel to be found to salinity tolerance related traits. The results of the comparison between the performance of the elite genotypes and the Egyptian cultivars suggested that the elite wheat genotypes had maximum values for the traits under study except for seeds/spike, spike length and spike weight. Thus, it is recommended to cross the superior Egyptian cultivars for the seeds/spike, spike length and spike weight with the elite genotypes to improve their performance in these traits.