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**The Thesis Submitted for Ph.D Degree in the field of Plant breeding**  
**Association mapping of root architecture under salinity and**  
**drought stress in Iranian wheat indigenous populations**

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2022

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## Abstract

Wheat is one of the strategic and important crops in the world. Considering the role of roots and related traits in increasing water use efficiency and adaptation of plants to stress conditions and the quantitative nature of these traits, determining the genetics of the root system and how it relates to other agronomic traits is an important goal of breeding programs. Communication mapping is one of the methods that used to study genetics and determine the number of gene loci that control quantitative traits. Therefore, in this study, the correlation analysis of root traits in different wheat genotypes under salinity and drought stress conditions in Zabol University investigated. In this experiment, 240 bread wheat genotypes studied in terms of root length, stem length, number of capillary roots, number of main roots, root weight, stem weight, root dry weight, stem dry weight, leaf Chlorophyll content and Chlorophyll fluorescence characteristics evaluated. This study was conducted as a split plot in a completely randomized design with 2 replications in both salinity and drought stress conditions. In both salinity and drought stress conditions after 21 days of stress application, the studied traits were measured. In phenotypic evaluation, the results of analysis of variance showed that there was a significant difference in terms of all studied traits between wheat genotypes and two normal and stress environments. The results of correlation between traits also showed a significant relationship between most of the studied traits. Out of 3762 identified markers, 1890 SNP markers were obtained after filtering, which were used to study genetic diversity, population structure and relational mapping of traits. Based on the estimated value ( $K\Delta$ ), the genotypes divided into 3 subgroups. Indigenous wheat populations were also grouped into three subgroups based on cluster analysis by Ward minimum variance method. The results showed that the linkage imbalance along the chromosome varies from chromosome to chromosome and different genomes and decreases with increasing genetic distance, the linkage imbalance decreases. Significant marker-trait relationships investigated using mixed linear model (MLM). At salinity stress of 750 kW, significant associated with all traits in genomes A, B and D were identified. The 130 significant cytiols identified were related to 8 root traits. Under drought stress conditions, about 803 kT were identified, of which about 185 kT were related to root traits. Under normal conditions, 250 QT was identified, of which 90 qt was related to root traits. Most of the identified QTLs matched the reported genes and QTLs. The results of this study show that the ability of leading researchers to guide breeding programs to select suitable parents to prepare a compatible genotype as well as stable genotypes in terms of yield with changing environmental conditions in wheat is very efficient.

**Keywords: Environmental stress, Mapping association, Root architecture, Wheat.**