



شبكة المعلومات الجامعية
التوثيق الإلكتروني والميكروفيلم

بسم الله الرحمن الرحيم



HANAA ALY



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شبكة المعلومات الجامعية التوثيق الإلكتروني والميكروفيلم



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جامعة عين شمس التوثيق الإلكتروني والميكروفيلم

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**CONSTRUCTION OF HIGH DENSITY GENETIC
MAP FOR BREAD WHEAT THROUGH
GENOME WIDE ASSOCIATION
ANALYSIS**

By

ALSAMMAN MAHMOUD MOHAMMED ALI

B. Sc. Agric. Sc. (Biotechnology), AzharUniv. (2010)
M. Sc. Agric. Sc. (Genetics), Cairo Univ. (2017)

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Approval Sheet

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ABSTRACT

Alsamman Mahmoud Mohammed. Construction of High Density Genetic Map for Bread Wheat Through Genome Wide Association Analysis, Unpublished P.H.D. Thesis, Department of Genetics, Faculty of Agriculture, Ain- Shams University, 2021.

Wheat (*Triticum aestivum*) is an essential staple food in the developing world, where demand is projected to grow exponentially in the future; simultaneously, climate changes are projected to reduce supply in the near future. One of the main consequences of climate change is salinity, which negatively impacts the world's cultivated area and therefore affects the global wheat production. Our objectives are to study the population structure of several Egyptian and international wheat accessions to identify the genetic factors controlling the salinity stress response of bread wheat. In addition, genes that control some important agronomic parameters of wheat under salinity stress were identified. The wheat germplasm panel consisted of 70 accessions obtained from Egypt, Syria and Iran. The assessment of salinity tolerance was conducted over the years of 2018 and 2019 in the field and in the greenhouse. The genome association analysis (GWAS) and population structure analysis was conducted using six SCoT, five SSR and 93 SNP markers. Analysis of the population structure using allele frequency and phylogenetic analysis indicated that the studied wheat accessions were belong to four population groups. Where, for the most portion, Egyptian, Syrian and Iranian accessions were clustered depending on their country of origin. The GWAS analysis revealed 13 SNP markers that were significantly associated with morpho-agronomic wheat traits during salinity stress. These markers were closely related to genes that are known to have a direct link to wheat response to salinity stress such as *CYP709B2*, *MDIS2*, *STAY-GREEN*, *PIP5K9*, and *MSSP2* genes. This study revealed the genetic structure of adapted and imported wheat accessions, which could be used to select

potential wheat accessions for local breeding programs. In addition, the SNP genotyping assay is a very potential technique that could be efficiently applied to detect genes that control bread wheat response to salinity stress.

Key Words: Wheat, Salinity, SNP genotyping, SSR, SCoT, GWAS.

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