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Samar G. Thabet*, Yasser S. Moursi, Ahmed Sallam, Mohamed A. Karam,
and Ahmad M. Alqudah*

Abstract

Understanding the genetic basis of seed germination under salt stress as severe abiotic stress can help in improving barley plant growth performance, production, and productivity. Salt tolerance is complex trait that controlled by many genes and its genetic basis needs to be dissected. In the current study, 121 spring worldwide barley accessions were evaluated for salinity stress tolerance using 200 mM NaCl during seed germination and seedling developmental phase. Induced salt stress reduced the seed germination parameters and seedling related traits significantly. The genome-wide association scan (GWAS) was applied using 9K SNPs and revealed several interesting genomic regions including 80 significant SNPs associated with the studied traits. The genomic regions of these SNPs harbored around 1500 candidate genes within the linkage disequilibrium interval. Interestingly, many genes encoding potassium channel were mapped e.g. *AKT2* on chromosomes 1H. Genes identified in the current study were found to be linked to salinity stress tolerance during seedling developmental phase as a first time such as Squamosa promoter-binding-like protein 6 at chromosome 5H. Here, we demonstrated their putative role in salt tolerance at early developmental stages indicating that selection at early stages

would be reliable to improve salinity tolerance. Functional markers linked with the resistance loci would be useful for breeding to improve barley cultivars with enhanced tolerance to salt stress. Further genetic investigation on these loci and their linked genes would provide insight into understanding the molecular mechanisms of salt stress in barley.

Keywords: Barley, Candidate genes, GWAS, Salinity, Potassium channel.