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Abstract

Soil salinity stress causes osmotic/ionic imbalances and induces oxidative stress that causes cellular structure damage, perturbs metabolism, antioxidant system (comprising enzymatic and non-enzymatic components) and hence inhibits plant growth performance. In this study, we used genome-wide association scan (GWAS) in 174 diverse spring barley accessions which were exposed to salt stress under field conditions at the vegetative stage to uncover the genetic basis of antioxidant components and agronomic traits. High activities of enzymatic and content of non-enzymatic antioxidants were observed under salt stress compared to control conditions. Under salt stress, all the agronomic and yield-related traits were significantly reduced. Six genomic regions were associated with antioxidants and agronomic traits under salt stress conditions which were found to be linked with candidate genes. Several significant associations were

physically located inside or near genes which are potentially involved in antioxidants. Two candidate genes at 2H (40,659,364 bp) and 7H (416,743,127

bp) were found to be involved in Dihydroflavonol 4-reductase/flavanone protein and Glyceraldehyde-3-phosphate dehydrogenase, respectively. The allelic variation at SNP of BK_07 at 7H inside the GAPDH gene demonstrates a negative selection of accessions carrying A allele. This allele appears in cultivars with lower activity of enzymatic antioxidants e.g. superoxide dismutase and catalases under salt stress conditions. These accessions are predominantly two-rowed, cultivars, originated from Europe, and carrying photoperiod sensitive alleles. The detected associated molecular markers in this work are considered as an important source for selection of increased amount of antioxidant compounds in barley under stress conditions.

Keywords: Antioxidant, barley, Genome-wide association, Grain yield, Marker-trait association, Salinity tolerance.