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Abstract

Salinity stress is one of the abiotic stresses that influence the morpho-physiological, antioxidants, and yield-related traits in crop plants. The plants of a core set of 138 diverse barley accessions were analyzed after exposure to salt stress under field conditions during the reproductive phase. A genome-wide association scan (GWAS) was then conducted using 19,276 single nucleotide polymorphisms (SNPs) to uncover the genetic basis of morpho-physiological and grain-related traits. A wide range of responses to salt stress by the accessions was explored in the current study. GWAS detected 263 significantly associated SNPs with the antioxidants, K^+/Na^+ content ratio, and agronomic traits. Five genomic regions harbored interesting putative candidate genes within $LD \pm 1.2$ Mbp. Chromosome 2H harbored many candidate genes associated with the antioxidants ascorbic acid (AsA) and glutathione (GSH), such as superoxide dismutase (SOD), ascorbate peroxidase (APX), and glutathione reductase (GR), under salt stress. Markedly, an A:C SNP at 153,773,211 bp on chromosome 7H is located inside the gene

HORVU.MOREX.r3.7HG0676830 (153,772,300–153,774,057 bp) that was annotated as l-gulonolactone oxidase, regulating the natural variation of SOD_S and APX_S. The allelic variation at this SNP reveals a negative selection of accessions carrying the C allele, predominantly found in six-rowed spring landraces originating from Far-, Near-East, and central Asia carrying photoperiod sensitive alleles having lower activity of enzymatic antioxidants. The SNP-trait associations detected in the current study constitute a benchmark for developing molecular selection tools for antioxidant compound selection in barley.

Keywords: Barley · Multi-locus GWAS · Antioxidants · Ionic balance · K^+/Na^+ content · Salt stress