

## البحث الأول

((البحث غير مستخلص من رسالة علمية))

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#### Abstract

Plant biologists aim for the genetic improvement of barley adaptation to salinity stress. This study was designed to explore the natural variation of responsive physiological and agronomic traits in a diverse spring barley panel under salt-affected soil and the application of selenium nanoparticles (Se-NP) during the vegetative phase. Significant phenotypic variation was detected among the accessions in response to salt stress. Application of 1 mM Se-NP enhanced thousand-kernel weight (TKW) by 28% while decreasing the Na<sup>+</sup> contents in the flag leaves by 53%. The genomic analysis lead to having in total, of 146 associated SNPs with salt-responsive traits using 19 K SNPs in a genome-wide association study analysis. High significant SNPs were located within or near candidate genes which are potentially involved in the stress tolerance mechanism via enhancing the expression of Na<sup>+</sup>/H<sup>+</sup> antiporters and tonoplast H<sup>+</sup>-ATPase. The candidate genes include *HORVU.MOREX.r3.2HG0184880* and *HORVU.MOREX.r3.2HG0199370* that encodes sulfite reductase and

anthocyanidin reductase, respectively, confirming the crucial role of Se-NP in improving barley salt tolerance. We further showed the allelic variation inside

the genes associated with traits under Se-NP leads to enhancing the accumulation of N, P, K<sup>+</sup>, ion homeostasis, antioxidant metabolism, nitrogen uptake, and ultimately grain yield. This study provides desirable alleles for salt tolerance in barley breeding strategies.

**Keywords:** Barley, GWAS, Ion homeostasis, LD, Selenium, Soil salinity.