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Title: Genetic basis of drought tolerance during seed germination in barley

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Abstract

Drought is one of the harshest abiotic stresses hindering seed germination, plant growth, and crop productivity. A high rate and uniformity of germination under stressful conditions are vital for crop establishment and growth; thus, for productivity. A better understanding of the genetic architecture of seed germination under drought stress is a prerequisite for further increasing yield potential. Barley is considered one of the most abiotic stresses-tolerant cereals. Elucidating the drought tolerance of barley during seed germination would indeed pave the way towards improving the performance of all cereals. However, we still know relatively little about the genetic control of drought tolerance during the seed germination phase. In our study, 218 worldwide spring barley accessions were subjected to PEG-induced drought during seed germination. Induced drought stress "20% PEG" significantly reduced the seed germination parameters and seedling related traits. A genome-wide association scan (GWAS) was used to identify genomic regions associated with our trait of interest. In total, 338 single nucleotide polymorphisms (SNPs) were found to be associated with several traits distributed across seven barley chromosomes, of which 26 genomic regions were associated with candidate genes. The current study found some of the quantitative trait loci (QTL) that have previously been reported to be linked to seed germination-related traits under drought conditions, as well as some new associations. Noteworthy, the identified QTL colocalized with a number of genes (within interval ± 0.5 Mbp) that are exclusively distributed on chromosomes 1H, 2H, and 5H. The annotation of these genes in barley shows their roles in drought tolerance through encoding different transcription factors. The function of the identified genes during seed germination was also confirmed by the annotation of their counterparts in Arabidopsis. The current analyses show the power of the GWAS both for identifying putative candidate genes and for improving plant adaptive traits in barley.

Keywords: Drought; barley; GWAS; seed germination; candidate gene