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Integration of mRNA-Seq analysis and QTL mapping provides promising candidate genes for cadmium tolerance in barley

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The high toxicity and ready uptake of cadmium (Cd) by plants has become a major agricultural problem. Our QTL analysis showed that the parents of the Oregon Wolfe Barley (OWB) mapping population have distinct responses to Cd toxicity. mRNA-Seq analysis of the parental seedlings after 2 h under 5 mM Cd stress identified 583 differentially expressed genes (DEGs) out of 42,860 genes in barley as candidate genes for Cd tolerance in Rec. Cd tolerant genotype Rec showed higher gene expression levels of proteins involved in signal transduction, transcription factors, chaperones, oxidative stress protection enzymes, cell wall metabolism, transporters and ion channels relative to cd susceptible genotype Dom. Furthermore, 157,179 moderate or high ranked single nucleotide polymorphisms (SNPs) were identified between genotypes using sufficient coverage with high quality sequence reads by sequence comparisons. These may affect gene expression, mRNA conformation (stability), and the subcellular localization of mRNAs and/or proteins in the two genotypes. We found that several Cd-responsive genes have SNPs, suggesting that they may participate in tolerance. Finally, the candidate genes were narrowed down by integrating the data from mRNA-Seq and the major QTL related to Cd tolerance. We indicated that integrating mRNA-Seq and QTL analyses is a useful method for providing insight into the mechanisms of response and tolerance to Cd stress in barley.
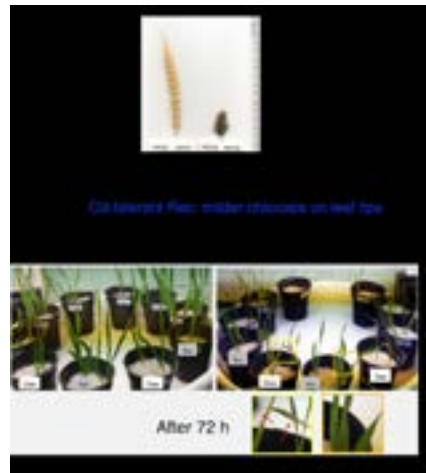
Biography

Behnam Derakhshani is currently a guest researcher at Institute of Crop Science, National Agriculture and Food Research Organization (NARO). He has completed his PhD at the University of Zanjan, Iran.

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