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Title:	Meta- analysis of iron- and boron deficiency transcriptomes of arabidopsis thaliana
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Abstract:	<p>Iron (Fe) and Boron (B) are essential micronutrients critical for plant growth and development. Plant growth is severely inhibited under the deficiency of either of these nutrients. Nutrient deficiency can disturb the normal metabolism in plants, causes abiotic stress and force the plants to adapt to induce changes in their mineral uptake pathways. Both Fe and B uptake are controlled by regulation of transcription, and during combined nutrient deficiencies, plants are likely to co-ordinate crosstalk between the two nutrient uptake pathways. Only a few details of Fe-B crosstalk are known; therefore, to investigate the interactions between the two nutrient deficiency response plant adaptations to them, we performed a meta-analysis of publicly available RNA-seq datasets of iron and boron deficiency treatments using Col-0 accession of Arabidopsis thaliana. Differentially expressed genes were extracted for both the treatments, and the gene expression changes in the treatment subsets were visualised for analysis. On cataloguing the lists of candidate genes with filtering, it was observed that many of the genes involved in the Fe-B crosstalk already play an important role in Fe and B homeostasis. Many of the DEGs were not directly regulated by Fe or B uptake genes, which shows regulation occurring at other levels as well. Functional annotation of the DEG subsets revealed those multiple biological processes are affected by the nutrient deficiency stress, which is likely due to changes in metabolism caused by Fe or B deficiency. The GO analysis shows that genes involved in multiple abiotic and biotic stress responses are differentially expressed and have critical implications for plant growth and survival. Overall, this study presents new information about Fe-B crosstalk and its implications for plant stress tolerance.</p>
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