



Library Indian Institute of Science Education and Research Mohali



DSpace@IISERMohali / Thesis & Dissertation / Master of Science / MS-19

Please use this identifier to cite or link to this item: <http://hdl.handle.net/123456789/5798>

Title:	To Investigate the cross-talk of Iron and Boron uptake pathway in Arabidopsis thaliana
Authors:	Kisan, Tikeswari
Keywords:	Nutrient Environmental factors
Issue Date:	May-2024
Publisher:	IISER Mohali
Abstract:	<p>Environmental factors that affect plants include salt, drought, high pH and temperature, nutritional deficiencies, infections, and more. Plants modify their transcriptional machinery in response to variations in the availability of nutrients. Plants use various cellular and developmental processes to adapt to their changing environment to cope with environmental stress caused by excess or deficit of nutrients. Seven key micronutrients are necessary for the proper growth and maintenance of plants. Among these, boron (B) and iron (Fe) are both vital micronutrients needed for plant development and growth. Lack of any one of these nutrients significantly inhibits plant growth. Abiotic stress is brought on by nutrient deficiencies, which can also interfere with plants' natural metabolism. Transcription regulations play a vital role in both the uptake of iron and boron, but when there is a combined deficiency of nutrients, plants are supposed to coordinate the crosstalk between two nutrient uptake pathways to preserve homeostasis. Since the iron-boron (Fe-B) cross-talk pathway is not well understood, we have performed a meta-analysis of publicly available RNA-seq datasets of treatments for iron and boron deficiencies using the Col-0 accession of Arabidopsis thaliana. Differentially expressed genes (DEGs) were extracted for each treatment. We observed that a large number of genes implicated in the Fe-B crosstalk, as well as the genes that are up-regulated under Fe deficiency, are down-regulated under B deficiency and vice-versa. Gene expression exhibits both antagonistic and synergistic subsets, and there is a notable overlap between the differentially expressed genes in response to combined nutrient deficiency. Our GO (Gene Ontology) analysis shows that DEGs are involved in many biological processes and those biological processes are affected by combined nutrient-deficiency conditions.</p>
URI:	http://hdl.handle.net/123456789/5798
Appears in Collections:	MS-19

Files in This Item:

File	Description	Size	Format	
embargo period.pdf		6.04 kB	Adobe PDF	View/Open

Show full item record



Items in DSpace are protected by copyright, with all rights reserved, unless otherwise indicated.