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Characterizing the arabidopsis frd3 mutant through an activation tagging screen

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Iron is an essential element present in many common proteins, and is crucial in a number of metabolic pathways. This role is evident in the multiple disorders due to iron deficiency. Anemia, caused by iron deficiency, is the most common nutritional disorder affecting the world's population. As most people throughout the world depend primarily on plants for their nutritional needs, one way of reducing this problem will be to enhance the bioavailable iron content of plants. A better understanding of how plants acquire, transport and store iron is needed before this goal can be achieved. The Arabidopsis *frd3* mutant constitutively activates its iron uptake mechanisms, resulting in an over accumulation of iron and other metals. This iron is however mislocalized and never enters leaf cells where it is ultimately required. Recent work has suggested that the FRD3 protein transports citrate into the root vasculature which is necessary for the correct localization of iron throughout the plant. One way to learn more about the FRD3 protein, and about iron homeostasis in plants, is through an activation tagging screen looking for suppressors of the *frd3* phenotype. Briefly, the activation tagging construct has been transformed into *frd3* plants using the established agrobacterium floral dip method. Suppressor mutants have been selected using a ferric chelate reductase assay. Putative mutants have been transferred to soil, and are currently growing to produce seed in order to re-analyze the next generation. After mutant confirmation, TAIL-PCR will be used to identify the activated gene. Additional mutant characterization will also be carried out at this stage. At least three classes of genes could be identified through this screen: (1) other citrate effluxers that will perform the same function as FRD3, (2) repressors of FRO2, the root ferric chelate reductase or (3) transporters that would facilitate movement of iron into leaf cells. The discovery and further characterization of these genes would greatly facilitate our understanding of iron nutrition in plants.