Iron Deficiency: Molecular Mechanisms for Sensing and Response in Plants

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Plants respond to iron deficiency with a number of physiological modifications that alter nutrient uptake, translocation, storage, and metabolism. Several transcriptomics and proteomics studies have begun to reveal how various constituents of a plant system coordinate these responses. However, the molecular mechanisms that trigger these dynamic changes await elucidation. Components of this mechanism have been described in the model plant Arabidopsis thaliana. Several bHLH transcriptional regulators, including FIT, bHLH38, bHLH39 and POPEYE (PYE) are involved in responding to low iron. PYE is encoded by a gene that is expressed primarily in the vasculature in response to low iron, while the protein appears to be localized in the nuclei of most root cells. Previously, we have shown that PYE interacts, in vitro, with close PYE homologs (PYHs) and that PYE directly and indirectly regulates the expression of genes that encode proteins involved in iron reduction, storage and translocation. The formation of mobile PYE/PYH heterodimers could play an important role in these regulatory processes. Interplay between PYE and its homologs appears to be controlled at the post-translational level by interaction with a third protein, BRUTUS, which may bind iron and, thus, sense iron content within roots. Using a number of molecular and biochemical approaches we are determining how and where these proteins interact in planta, and how iron availability triggers this interaction to facilitate response to low iron.