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Leveraging genomic tools to dissect iron deficiency tolerance in soybean

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Iron Deficiency Chlorosis (IDC) is an important problem for soybeans grown in the upper Midwestern United States. We are leveraging genomic resources to characterize soybean's iron deficiency response. Transcriptomic studies of roots and leaves at 30, 60 and 120 minutes after iron stress have identified thousands of differentially expressed genes. While there is little overlap in individual gene expression between time points and tissue types, we observe the same biological pathways being affected after both short and long term iron stress exposure. These studies reveal the unique aspects of IDC responses in soybean. At the same, we have used a genome wide association study to characterize IDC responses in 460 diverse soybean PI lines from 25 different countries. This approach identified significant markers, genomic regions, and novel genes associated with iron deficiency tolerance. Cluster analysis of significant SNPs in the major iron quantitative trait locus (QTL) on chromosome 03 (Gm03) allowed us to deconstruct this historically prominent QTL into multiple candidate iron tolerance genes. These studies highlight differences between crops and model species and demonstrate the importance of leveraging cutting edge genomic approaches in crops for crop improvement.