Genome wide analysis of root nodulation and root system architecture in soybean accessions

Ali Taheri[1], Korsi Dumenyo[1], Babu Valliyodan[2], Marc Libault[3], and Qijian Song[4]

[1]Tennessee State University
[2]Lincoln University,University of Missouri Columbia
[3]Lincoln University
[4]USDA-ARS Beltsville Agricultural Research Center

November 26, 2022

Abstract

Developing crops with better root system architecture and nitrogen use efficiency can lead to resilient crops capable of sustaining productivity in both optimum and stress environments. The increase in soybean global demand and its use in biodiesel and new soy-based products calls for new soybean cultivars that have higher yields, better nutritional values or desirable traits for specific use. The soybean germplasm collection at the USDA is a valuable resource in discovering novel allelic variations. This collection has not been screened extensively for the root nodule and root system architecture traits. We have already established root phenotyping platforms in our laboratory and we are proposing to screen a diverse pool of the USDA soybean collection for nodules and root system architecture traits. Availability of SNP data for this collection will let us run genome-wide analysis and identify QTLs responsible for different root traits. We will then use hairy root transformation to knockout/down some of the candidate genes in the loci identified in earlier reports and new QTLs identified in this project. This project will help us in deciphering the phenotypic variation in soybean root traits. Ultimately, better understanding of the regulatory mechanism controlling these traits can help us in developing resilient crops and a sustainable cropping system.

Hosted file

`essoar.10508704.1.docx` available at https://authorea.com/users/554496/articles/605640-genome-wide-analysis-of-root-nodulation-and-root-system-architecture-in-soybean-accessions

Title: Genome wide analysis of root nodulation and root system architecture in soybean accessions

Taheri, Ali[1], Korsi Dumenyo[1], Babu Valliyodan[2], Marc Libault[3], Qijian Song[4]

1. College of Agriculture, Tennessee State University, Nashville, TN

2. Lincoln University, Jefferson City, MU

3. University Of Nebraska, Lincoln, NB

4. USDA-ARS, Beltsville, MD

Developing crops with better root system architecture and nitrogen use efficiency can lead to resilient crops capable of sustaining productivity in both optimum and stress environments. The increase in soybean global demand and its use in biodiesel and new soy-based products calls for new soybean cultivars that have higher yields, better nutritional values or desirable traits for specific use. The soybean germplasm collection at the USDA is a valuable resource in discovering novel allelic variations. This collection has not been screened extensively for the root nodule and root system architecture traits. We have already established root phenotyping platforms in our laboratory and we are proposing to screen a diverse pool of the USDA soybean collection for nodules and root system architecture traits. Availability of SNP data for this collection will let us run genome-wide analysis and identify QTLs responsible for different root traits. We will then use hairy root transformation to knockout/down some of the candidate genes in the loci identified in earlier reports and new QTLs identified in this project. This project will help us in deciphering the phenotypic variation in soybean root traits. Ultimately, better understanding of the regulatory mechanism controlling these traits can help us in developing resilient crops and a sustainable cropping system.