

# Genome-Wide Association study for root system architecture traits in field Soybean [*Glycine max* (L.) Merr.]

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**NAPPN Annual Conference Abstract: Genome-Wide Association study for root system architecture traits in field Soybean [*Glycine max* (L.) Merr.]**

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Roots are the “hidden half” of the plants, which play an essential role in plant development by drawing water and nutrients from the soil and providing anchorage to the plants. Global warming alters soil properties that limit root development and produces drought-like conditions that reduce water and nutrient uptake by the plant roots, ultimately affecting plant growth. It is, therefore, necessary to study Root System Architecture (RSA) traits and breed plants with better root architecture capable of resisting these conditions. RSA comprises various root traits including total root length, root angle, number of lateral roots, and many other traits. Due to the challenges in phenotyping these traits, the research on RSA is lacking behind. In this project, we are studying RSA traits in 500 late-maturity soybean accessions based on germinating the seeds on germination papers, transferring them to blue blotting papers, and imaging the roots 21 days after transfer. Image analysis for the root traits will be carried out using RootNav2.0 software. These phenotypic data and SNPs selected from Illumina Infinium SoySNP50K iselect SNP Beadchip will be used to perform Genome-wide Association Studies (GWAS) using Genome Association and Prediction Integrated Tool (GAPIT) package in R to identify genomic loci associated with each trait. The results from this study will help in discovery of new QTLs or genes that play a key role in root system architecture and help in breeding novel cultivars that are resistance to changing climate.