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

Roots are the "hidden half" of the plants and play an essential role in plant development by absorbing water and nutrients from the soil and providing anchorage. Global warming alters soil properties that limit root development and cause drought-like conditions that reduce water and nutrient uptake by the roots, ultimately affecting plant growth. It is, therefore, necessary to study Root System Architecture (RSA) traits and breed plants with better root architecture that can resist these conditions. RSA comprises various root traits, including total root length, root angle, the number of lateral roots, and many other traits. However, the challenges in phenotyping these traits have resulted in a lack of research in this area. In this project, we are studying RSA traits in 500 late-maturity soybean accessions by germinating seeds on germination papers, transferring them to blue blotting papers, and imaging the roots 21 days after transfer. Image analysis for 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 the Genome Association and Prediction Integrated Tool (GAPIT) package in R to identify genomic loci associated with each trait. The results from this study will aid in the discovery of new genes that play a key role in root system architecture and help in breeding novel cultivars that are resistance to changing climates.