

IOWA STATE UNIVERSITY
Digital Repository
Farm Progress Reports

2017 Report
Issue 1 2017 *Farm Progress Reports*

Number RFR-A1740

2018

Studies of Soybean Root System Architecture

Kevin Falk

Iowa State University, falk@iastate.edu

Asheesh Singh

Iowa State University, singhak@iastate.edu

Follow this and additional works at: <https://lib.dr.iastate.edu/farmprogressreports>



Part of the [Agriculture Commons](#), and the [Agronomy and Crop Sciences Commons](#)

Recommended Citation

Falk, Kevin and Singh, Asheesh (2018) "Studies of Soybean Root System Architecture," *Farm Progress Reports*: Vol. 2017 : Iss. 1 , Article 59.

Available at: <https://lib.dr.iastate.edu/farmprogressreports/vol2017/iss1/59>

This Horticulture Station is brought to you for free and open access by the Research and Demonstration Farms at Iowa State University Digital Repository. It has been accepted for inclusion in Farm Progress Reports by an authorized editor of Iowa State University Digital Repository. For more information, please contact digirep@iastate.edu.

Studies of Soybean Root System Architecture

RFR-A1740

Kevin Falk, graduate research assistant
Asheesh Singh, associate professor
Department of Agronomy

Introduction

Substantial phenotypic variation in root architecture systems between genotypes in soybean germplasm have been reported. Morphology parameters can be used to classify roots into different types and correlate root type to environmental advantages, such as nutrient acquisition and drought or flood tolerance. As plant genetic research continues to focus on above-ground traits, the difficulty in easily measuring below-ground traits restricts root studies. Because of this difficulty and root trait(s) genetic complexity, these generally are not used as breeding criterion. Soybean breeding has continued for a century with little focus on the root development, its architecture, structure, and function. Knowledge of the soybean root system and the genetic basis for these traits is essential to understanding how soybean roots drive yield, and to build more robust and resilient varieties.

Objectives with this study are to explore the root architecture diversity in soybean, create new protocols to identify diverse root traits, and to attempt to understand correlations between traits, both above and below ground, and relate these to yield. Understanding the diversity of root architecture can better help adapt the soybean genetic base for the climate of the future.

Materials and Methods

A subset panel of 300 genotypes of the soybean core collection ranges in geographical origins, maturity zones, and growth habit, along with varying other above-ground traits,

was planted in hill plots using two reps of a randomized complete block design. Two separate experiments of this configuration were conducted in 2017, one for plant extraction at the V1 (first trifoliolate leaf), and the other at the R8 (full maturity) growth stage, giving the entire field four complete sets of genotypes (two reps for V1 and two reps for R8). Border plots were planted around the perimeter of the experiment to minimize competition effects. Five seeds were planted by hand in each hill plot to a depth of 25 mm. The R8 experiment plants were reduced to a single plant at the V1 growth stage. Weeds were controlled manually using hoes. Water was applied as required. All five V1 plants were extracted from the soil together at 25 days after planting. The soil in this field at the Iowa State University Horticulture Research Station is high in sand content, creating an optimal media for manual extraction. Due to the amount of manual labor involved in these experiments that require careful handling of sample excavation and root-soil separation, eight to 10 people were required for the excavation process. Water was applied to the site prior to excavation to loosen the soil and reduce extraction damage.

Early season extraction. At 25 days after planting, V1 plants were extracted in a 25-cm diameter to a 30-cm depth using trenching spades (40 cm x 16 cm) to make multiple vertical incisions into the soil at a 12.5-cm radius and simultaneously lift the plants out of the ground. Roots then were rinsed and submerged in water until imaging. For imaging, three of five plants were selected per genotype and the root systems spread out with forceps on a tray of 5 mm of water. Images were taken from 50 cm above the tray with a Canon T5i digital camera. These 2D images were analyzed by ARIA 2.0 software developed by B. Ganapathysubramanian's

group at Iowa State University's Mechanical Engineering department.

Late season extraction. At maturity, plants were tagged and extracted in a 50-cm diameter to a 30-cm depth using four individuals with trenching spades (40 cm x 16 cm) to make multiple vertical incisions into the soil at a 25-cm radius and simultaneously lift the root out of the ground. The stem was cut at the soil line. The root and remaining attached soil was submerged into a 50 L plastic tote containing 25 L of water and soap. The soil was rinsed from the root taking caution to keep roots intact. The roots were labeled and submerged in water until imaging.

Stereo imaging platform. The imaging platform consists of a small booth measuring 2 meters wide by 1.5 meters tall and 1.5 meters deep. Two digital cameras controlled by a laptop computer, one below the root and one to the side, were pointed at the wall and ceiling to capture the root from multiple angles. Images from below and the side were taken before and after the root was rotated 180 degrees. Images were imported into ARIA 3D software, which allows for comprehensive evaluation of RSA of field grown plants.

Results and Discussion

Analysis is ongoing, however preliminary results suggest a strong evidence of immense genetic diversity among the tested genotypes. Root traits collected include number of root branches (V1, R8), volume of root tissue, length of root branches, surface area of the root system, secondary root branch angle from the primary root, and 3D structure and volume displaced by the root architecture (R8 extracted roots only). Efforts are ongoing to

learn relationships between root traits as well as above-ground characters. Using the phenotypic data and molecular data, genome-wide association studies will be done to identify novel genotypes with high genetic potential and important root trait genomic regions.

Acknowledgements

Primary funding for this work was provided by the Iowa Soybean Research Center. This project also was supported by the Iowa Soybean Association, Baker Center for Plant Breeding at ISU, USDA NIFA, Monsanto Chair in Soybean Breeding at ISU, and CRIS Project (IOW04314). Support from Nick Howell and other staff at the Horticulture Station is greatly appreciated. Technical support from Brian Scott, Jae Brungardt, Will Doepke, and other members of Singh Soybean group is appreciated.



Figure 1. Trenching spades are used to excavate soybean roots from the sandy soil.



Figure 2. Ten Iowa State University graduate and undergraduate students work to excavate 600 soybean roots at the ISU Horticulture Research Station.



Figure 3. Soybean roots are suspended in a photo booth with images taken using multiple cameras from multiple angles.