

## Research Progress

### Objectives 1 and 2:

#### Highlights:

- The Chile nurseries were successful, and seed was received in time for normal planting in Iowa.
- New sources of resistance for disease resistance (including, soybean cyst nematode) and abiotic stresses were identified and used as parents in the 2017 crossing nurseries.
- Single plant selections were made in the breeding populations.
- Single plot selections were made in the short row plots for incorporation in yield tests.
- Yield trials (small plot and regular yield plot) were grown, and selections will be made in Fall 2017.
- At the time of reporting, combine harvest is continuing but near completion; single plant pulls and pod picks have been completed.
- F1 seed of new populations, developed to meet our objectives, has been sent to Puerto Rico and Chile.

Thirty-nine populations were created in the 2016-2017 winter nursery. Over the 2017 season, sixty-seven populations will be created in the 2017 summer and winter crossing blocks at Ames, IA, Juana Diaz, PR, and Rancagua, Chile.

In addition to high yield, parents in crossing blocks were selected for yield protection traits (tolerance/resistance to biotic and abiotic stresses), genetic diversity, abiotic stress tolerance, and seed compositional traits.

Bulk populations and short-row plots were grown in Chile winter nurseries (2016-2017). Visual selection was made among short-row progeny rows in off-season nurseries, and these selections were grown in multi-location yield tests in Iowa in 2017. Pod picks and individual plant pulls were made in Chile, and the seed returned was planted either in bulk populations or progeny rows for selection and continued yield testing. One-hundred twenty-five populations were planted in Ames, IA: thirty-nine were from winter nursery in Puerto Rico; seventy-nine were from winter nurseries in Chile; and seven were early generation diversity populations (courtesy: Dr. Randy Nelson). Pod picks or single plant pulls were done on 124 populations in Fall 2017.

In 2017, 7620 small yield plots were planted at Ames, IA. The entries (6511), from 2016 bulk populations, winter nursery populations, and single plants from yield trials, were from 51 populations with yield protection traits (aphid tolerance, disease resistance), genetic diversity, and compositional traits. After selection for desirable agronomic traits, these will be grown in regular yield plots in 2018.

Selections from 2016 short-row yield trials and Chile progeny rows were advanced to long-row yield trials and planted in the US in multiple locations in 2017. The total number of entries was 1835 from 48 populations, and the total plot number was 8020. Traits in these populations were high yield, genetic diversity, aphid tolerance, quality traits, and disease resistance/tolerance.

Thirteen entries from 2016 first-year, long-row yield trials were selected and planted in an advanced long-row yield test at multiple locations throughout Iowa in 2017.

Eight populations created with stacked aphid resistance were grown in Chile in 2016-2017. Single plants were pulled, threshed, and planted in two-row, short-row yield tests in Iowa in 2017. Selections will be advanced to long-row yield trials at multi-locations in the US in 2018.

### Objectives 3 and 4:

PDF Susan Xu has been hired for molecular marker assisted selection breeding system and repository. Marker protocols for SCN, disease resistance and compositional traits are being standardized. These will be screened on selections from 1835 multi-location entries tested in 2017 season. This will be accomplished in 2017 fall/ 2018 spring as harvested was on-going at the time of reporting.

Seed density study has been completed and Race Higgins, PhD student, is not completing data analysis and writing the manuscript so results can be shared with the farmer and researcher communities. The residue traits studies to look at maximizing profitability in corn-soybean rotation. Race is scheduled to defend in spring 2018. Row width study has also been completed and PhD student, Kyle Parmley, is working on data analysis and manuscript writing. These results have been shared through presentation already (see section below on presentation).

Peer reviewed paper published acknowledging ISA support (Oct'16 – Mar'17):

1. Naik HS, Zhang J, Lofquist A, Assefa T, Sarkar S, et al. (2017) A real-time phenotyping framework using machine learning for plant stress severity rating in soybean. *Plant Methods* 13: 23.
2. Zhang J, Naik HS, Assefa T, Sarkar S, Reddy RVC, et al. (2017) Computer vision and machine learning for robust phenotyping in genome-wide studies. *Scientific Reports* 7: 44048.
3. Jubery TZ, Shook J, Parmley K, Zhang J, Naik HS, et al. (2016) Deploying Fourier Coefficients to Unravel Soybean Canopy Diversity. *Frontiers in Plant Science* 7: 2066.
4. Moellers TC (#), A Singh, J Zhang, J Brungardt, M Kabbage, DS Mueller, CR Grau, A Ranjan, DL Smith, RV Chowda-Reddy, AK Singh\* (2017). Main and epistatic loci studies in soybean for *Sclerotinia sclerotiorum* resistance reveal multiple modes of resistance in multi-environments. *Scientific Reports*. 7, Article number: 3554.
5. de Azevedo Peixoto L, Moellers TC, Zhang J, Lorenz AJ, Bhering LL, Beavis WD, et al. (2017) Leveraging genomic prediction to scan germplasm collection for crop improvement. *PLoS ONE* 12(6): e0179191.

Student presentations in conferences/ significant meetings acknowledging ISA support (Oct'16 – Sept'17):

1. Higgins, RH and Singh, AK. "Can high-throughput phenotyping help predict soybean yield in contrasting environments?" (Dec. 2016) 4<sup>th</sup> International Plant Phenotyping Symposium - CIMMYT. El Batan, Mexico & (Feb. 2017) Soybean Breeder's Workshop. St. Louis, MO & (March 2017) ISU Plant Breeding Symposium. Ames, IA.
2. Higgins, RH "Uncovering biomass partitioning and residue quality traits for soybean improvement" (March 2017) United Soybean Board High Protein Project Meeting. Chesterfield, MO.
3. Higgins, RH "G x M – leveraging phenomic tools to understand yield drivers" (August 2017) Visiting Monsanto breeder group. Ames, IA
4. Ibore M et al. Characterization of the Molecular Basis of Resistance to Soybean Aphids (*Aphis glycines* Matsumura). The Stupka Symposium. ISU, Ames, IA.
5. Falk K et al. Studies of Root System Architecture in Soybean using Computer Vision and Stereo Imaging. March 2017 RF Baker Plant Breeding Symposium
6. Falk K et al. Studies of Root System Architecture in Soybean using Computer Vision and Machine Learning. Dec. 2016 - IPPS - CIMMYT Mexico.

7. Falk K et al. Studies of Root System Architecture in Soybean using Computer Vision. Purdue Plant Science Symposium, Aug 3, 2017, and in Iowa State University Mini Soybean Symposium, Sept 13, 2017.
8. Parmley, K., et al. Customizing soybean cultivar development through aerial and ground phenotyping. Purdue Plant Science Symposium. West Lafayette, IN, 2017.
9. Parmley, K. et al. Customizing soybean cultivar development through aerial and ground phenotyping. 4th International Plant Breeding Symposium. CIMMYT, Mexico, 2016.
10. Jubery T, J Shook, et al (2017) Deploying Fourier coefficients to unravel soybean canopy diversity. Colorado State University- NSF-NRT meeting.
11. Zhang J., Naik H.S., Assefa T., Sarkar S., Reddy R.V., Singh A., Ganapathysubramanian B. and Singh A.K. Image-based phenotyping and machine learning to advance genome-wide association and prediction analysis in soybean. CIMMYT 4th International Plant Phenotyping Symposium, 2016, Texcoco, Mexico.

## Talks

1. Singh AK (2017). “Phenomics: another hype or something more?”, Soybean Breeder’s Workshop. Feb 14, 2017.
2. Singh AK and KG Falk (2017). “How Can We Use Genetic Diversity to Improve Soybean Production: Tapping the Hidden Potential Through Roots”, Iowa Soybean Association Research Conference. Feb 8, 2017.
3. Singh AK (2016). “Soybean Breeding Program at ISU”, RF Baker Center for Plant Breeding. Ames, November 2, 2016.
4. Singh AK (2016). “The role of soybean breeding program at ISU for interdisciplinary research”, RF Baker Center for Plant Breeding. Ames, November 2, 2016.
5. Higgins, RH “Uncovering biomass partitioning and residue quality traits for soybean improvement” (March 2017) United Soybean Board annual meeting. Chesterfield, MO.
6. Singh AK and K Falk. How can we use Genetic Diversity to Improve Soybean Production: Tapping the Hidden Potential Through Roots. February 2017 Iowa Soybean Association Research Conference
7. Singh AK, K Falk. How can We Use Genetic Diversity to Improve Soybean Production: Tapping the Hidden Potential Through Roots ISA Research Conference 2017 (Singh and Falk) (Feb 8, 2017)
8. Falk K, AK Singh. Leveraging Advanced Technologies to Learn about Soybean Root Systems. IA Soybean Research Center Annual Meeting (Sept 8, 2017).
9. Parmley, K. “Management Driven Breeding.” Singh soybean breeding group host of Japanese visitors. Ames, IA 2017
10. Parmley, K., Falk, K. “Drivers of Yield: What We Know.” Muscatine Island Research and Demonstration Farm Field Day. Muscatine, OK, 2017
11. Parmley, K. “The Yield Puzzle.” Singh soybean breeding group Monsanto breeding lead visit. Ames, IA, 201
12. Parmley, K., Higgins, RH. “Seed composition traits in three studies.” United Soybean Board High Protein Project Meeting. Chesterfield, MO, 2016.

## Awards

1. Race Higgins 4<sup>th</sup> Graduate & Professional Student Research Conference Contest. 3-Minute Thesis - 3<sup>rd</sup> place \$250 award - “Uncovering biomass partitioning and residue quality traits for soybean improvement” (April 2017)

2. Falk K. NSF World Soybean Research Conference Travel Award (2017)
3. Falk K. Purdue University Graduate Student Scholarship Travel Award (2017)
4. Falk K. Monsanto Travel Award (2016)
5. Parmley K. Travel award recipient, Purdue Plant Science Symposium. West Lafayette, IN, 2017.