

S-14

Utilizing multi-spectral readings to differentiate genotypes in two soybean NAM populations

*William Schapaugh**, Department of Agronomy, Kansas State University, Kansas, USA

Brent Christenson, Kansas State University, Kansas, USA

Over the past decade, plant breeding has experienced tremendous growth in the utilization of high-throughput genomic techniques but the same advancements have not been observed in phenotyping. Spectral reflectance data from the plant canopy may represent a technique to improve efficiency in phenotyping breeding populations. The objective of this study was to use handheld spectral reflectance data to characterize populations from the Soybean Nested Association Mapping Population (SOYNAM) for yield and maturity. The study was conducted on SOYNAM populations NAM10 (IA3023 x LD00-3309) and what was initially identified as NAM46 (IA3023 x PI 507681) at eight locations in Kansas from 2013 to 2015. Spectral reflectance data were collected during reproductive growth in both irrigated and rain fed conditions. Multiple linear regression was used to create models for each environment and population as well as combined models for yield and maturity. Environments and entries differed in yield, maturity and spectral reflectance with significant genotype by environment interactions for all phenotypic traits. The genotype by environment interaction was a larger portion of the phenotypic variance in the NAM10 population than for the NAM46 population. Spectral reflectance bands in the blue, green, red, and near-infrared regions of the spectra explained a significant amount of phenotypic variation among genotypes in both SOYNAM populations. Modeling significance varied among environments with spectral models explaining as much as 85% of the phenotypic variation among entries in yield or maturity in a population. However, in some environments the ability of spectral data to characterize phenotypic differences among entries was limited. This study found that spectral reflectance data can distinguish high yielding genotypes within diverse populations and can be used to separate relative maturity of genotypes, but modification in methodology to capture reflectance data may be necessary to provide a desirable level of consistency in phenotypic predictions.