

A-152

Leveraging phenomics to predict soybean yield in contrasting environments

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Improving seed yield is the most important objective in soybean [*Glycine max* L. (Merr.)] breeding programs. The objective of this study is to find the physio-genetic parameters that drive soybean yield through a critical assessment of physiological traits at multiple crop growth stages. This study included thirty-two genotypes from the soybean nested association mapping (SoyNAM) panel consisting of maturity groups II and III, indeterminate and semi-determinate growth habits, and with ancestries ranging from Plant Introduction accessions to modern elite cultivars. Three contrasting treatments of planting density (50K, 140K, 230K per acre) were treated as a fixed factor to study the physio-genetics of yield in differing crop management conditions. Experiments were grown in replicated tests at five environments in Central Iowa. Physiological parameters collected included leaf area index (LAI), intercepted photosynthetically active radiation (iPAR), canopy temperature, SPAD chlorophyll content, and multiple hyperspectral remote sensing vegetation indices through a spectroradiometer via ground truthing. Physiological traits were collected over multiple reproductive growth stages throughout the growing season and seed yield was collected per yield plot. Yield prediction equations were built using adaptive elastic net, and several physiological traits were identified as best predictors of yield in different environments and/or density treatments at different crop growth stages. On-going research is attempting to determine the genetic factors related to spectral indices using SoyNAM mapping population sub-set through spectroradiometer and aerial multi-spectral cameras based phenotyping.