

B-132

Identification and characterization of fast neutron mutant soybean lines with altered seed composition for improvement of seed composition

*Elizabeth Prenger**, Institute of Plant Breeding, Genetics and Genomics, University of Georgia, Georgia, USA

Rouf Mian, Plant Physiology, USDA-ARS, North Carolina, USA

Robert Stupar, Department of Agronomy and Plant Genetics, University of Minnesota, Minnesota, USA

Zenglu Li, Institute of Plant Breeding, Genetics and Genomics, University of Georgia, Georgia, USA

Improved seed composition is one of the most important breeding goals in modern soybean breeding. Protein and oil concentration, amino acid profile, fatty acid content, and carbohydrate composition all play a vital role in the utility of soybean for food, feed, and fuel. A meal protein content of 48% or higher is desired for animal feed without sacrificing oil content. These criteria can be difficult for soybean breeders to meet due to a negative relationship between protein and oil contents, and between protein content and yield. Ideal soybean seed also contains high concentrations of essential amino acids such as Cysteine and Methionine; a healthier fatty acid profile with high oleic acid and low linolenic acid; and high levels of digestible sucrose with low raffinose and stachyose (RFOs). Fast neutron (FN) irradiation induces genomic deletions, duplications, and translocations in soybean resulting in mutant phenotypes. In this study, FN irradiation was used to develop two soybean mutant populations in elite backgrounds that were screened for altered seed composition phenotypes. Results from a total of five environments in two years and wet chemistry validation identified 40 stable mutant phenotypes for protein, oil, and sucrose contents. Twenty-three selected mutant lines have been entered into 2017 UGA Advanced Yield Trials to determine the impact of genomic changes on seed yield. Comparative genomic hybridizations (CGH) of four mutants are being performed to identify putative genomic regions responsible for the mutations, and bi-parental populations have been created to confirm these genomic regions. Identification of underlying genomic changes in seed composition mutants could enhance breeding efforts to improve soybean seed composition, and the mutants generated will provide useful breeding materials for improvement of seed composition characteristics in new soybean varieties.