M-134

Identifying genes important for determining lateral branch angle in soybean

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Canopy architecture of plants is an important determinant of light interception and consequently photosynthesis, and ultimately yield in crop species. We have explored the variation in canopy architecture in a fast neutron (FN) mutagenized population of soybean as well as in a set of diverse lines from the USDA Soybean Germplasm Collection. We have observed variation in both populations for several traits, such as lateral branch angle, branching density, branch orientation and overall plant shape. Changes in shoot architecture and particularly those that display differences in the angle of lateral branch are of particular interest. In the FN collection, we have identified mutants that were altered in branch angle. Our aim is to identify, map and clone the loci responsible for determining branch angle in soybeans. We are using a complementary approach of bulk segregate whole genome sequencing and array Comparative Genomics Hybridization to map regions of the genome controlling the phenotype. Using this approach, we have identified candidate genes in the mapped regions that may be important for controlling lateral branch angle. Experiments are underway to functionally characterize the candidate genes as well as to determine the effect of lateral branch angle on overall yield of soybean. Additionally, association mapping with the USDA Soybean Germplasm Collection has identified regions with significant associations with the branch angle phenotype.