

M-168

Dissection of genetic architectures of soybean seed protein, oil, and amino acids

*Sungwoo Lee**, Department of Plant Pathology, Chungnam National University, Daejeon, Republic of Korea

Kyujung Van, Department of Horticulture and Crop Science, The Ohio State University, Ohio, USA

Mikyung Sung, USDA-ARS, North Carolina State University, North Carolina, USA

Leah Mchale, Department of Horticulture and Crop Science, The Ohio State University, Ohio, USA

Soybean [*Glycine max* (L.) Merr.] is an economically important crop due to its various use in animal feeding, food, and industrial raw materials. To date, many genetic studies identified quantitative trait loci (QTL) controlling seed protein, oil, and amino acids via biparental QTL mapping. Genome-wide association mapping is another promising analytic approach to dissect complex traits by using historical recombinant events. The objective of this study was to evaluate selected 621 soybean accessions in maturity groups I to IV for protein, oil, and amino acid contents and to analyze statistical association between the trait values and genotypic data to identify useful alleles for the seed composition traits. All the soybean accessions with yellow seed coat, low seed shattering, low lodging, and low seed mottling were selected to avoid confounding effects on the traits of interest. During 2014 and 2015, the 621 accessions were grown in four locations in Ohio, North Carolina, and Illinois (total 5 environments), and seed composition data was obtained from the seeds harvested from each environment via near-infrared (NIR) spectrometer. Using the trait data and SoySNP50K data of the 621 accessions, genome-wide association analyses were conducted. This study detected 8 and 11 genomic regions significantly affecting protein and oil profiles. Two to five loci were identified for each amino acid. The most significant QTL for protein/oil was on Gm20, also reversely interacting with each other. Four QTL for protein had increased protein, while had little or no effects on oil. These QTL will be important to increase protein content without reduced oil content in soybean seed. The extent of individual allele effect was small for most of the SNP loci. Nine QTL for the amino acids are newly reported in this study, though individual QTL effect was small as in protein/oil contents.