

M-114

GWAS and transcriptomic analysis reveals variation in the molecular basis of soybean tolerance to aluminum toxicity

*Yan Li**, National Center for Soybean Improvement, Nanjing Agricultural University, Jiangsu, China

Juge Li, National Center for Soybean Improvement, Nanjing Agricultural University, Jiangsu, China

Yang Li, National Center for Soybean Improvement, Nanjing Agricultural University, Jiangsu, China

Lijuan Zhou, National Center for Soybean Improvement, Nanjing Agricultural University, Jiangsu, China

Aluminum (Al) toxicity is a major factor limiting crop growth and production in acid soils. Soybean (*Glycine*) is an important legume grown on acidic soil and there is great variation in the Al tolerance among soybean germplasm. Therefore, a genome-wide association study (GWAS) of Al tolerance was carried out to understand the genetic variation in soybean tolerance to Al toxicity. The Al tolerance (relative root growth, RRG) of 512 soybean accessions, including 125 wild soybean (*G. soja*) and 378 cultivated soybean (*G. max*), was evaluated and analyzed together with 145,558 SNPs obtained by RAD-seq. Twenty-four loci were significantly associated with Al tolerance and five of them overlapped with previously mapped Al-tolerance QTL. The candidate genes within the Al-tolerance loci were selected and further investigated. Two pairs of soybean accessions differing in Al tolerance were subjected to physiological and transcriptomic analysis. The comparative analysis (by microarray) of KF-1 (Al-tolerant) and GF (Al-sensitive) revealed that the genes encoding antioxidant enzymes (mainly peroxidase, POD) were enriched in the Al-induced genes in KF-1 but not in GF, and the POD activities in the root tips of KF-1 increased to higher levels than GF after Al treatment. The results indicated that POD could scavenge the reactive oxygen species (ROS) in the root tips of KF-1 to contribute to its Al tolerance. The comparative analysis (by RNA-Seq) of another pair of soybean accessions, M90-24 (Al-tolerant) and Pella (Al-sensitive), revealed that genes involved in cellulose biosynthesis were enriched in Al-induced genes in M90-24 but not in Pella, and the RRG of M90-24 was further decreased after adding the inhibitor of cellulose synthase, which suggesting the potential role of cellulose synthase in the Al tolerance of M90-24. Our study suggests that there is great variation in the phenotypic, genetic, and molecular basis of soybean tolerance to Al toxicity.