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QTL for flooding tolerance and survival in a soybean RIL population

*Miles W. Ingwers**, Department of Crop and Soil Sciences, University of Georgia, Athens, USA

Chengjun Wu, Department of Crop, Soil, and Environmental Sciences, University of Arkansas, Arkansas, USA

Qijian Song, Soybean Genomics and Improvement Laboratory, USDA-ARS, Maryland, USA

Pengyin Chen, Fisher Delta Research Center, University of Missouri, Missouri, USA

Zenglu Li, Department of Crop and Soil Sciences, University of Georgia, Georgia, USA

Flooding stress deleteriously affects soybean (*Glycine max* L. Merr) growth, survival, and yield. Flooding, which is a major abiotic stress in the Mississippi Delta, causes oxygen deprivation (hypoxia) which damages roots and submerged tissues. We sought to identify flooding tolerance quantitative trait loci (QTLs) using 147 F₅ – derived recombinant inbred line (RIL) population from Benning × PI 416937. Parental lines Benning and PI416937, and RILs were grown over 2012, 2014, and 2015 and rated for both flooding tolerance, a visual determination of plant health, and percent survival in the field in Fayetteville, AR. Results indicated that Benning is tolerant and PI416937 is sensitive to the flooding stress. Analysis of variance indicated a significant genotype and genotype × year effect. The population was genotyped with an Infinium SoySNP6k BeadChip. QTL analysis employing composite interval mapping detected two significant QTLs (LOD>3) for flooding tolerance on chromosomes 12 and 19. The first QTL was only detected in 2012 while the second QTL was detected in both 2012 and 2015. Phenotypic variance explained by these QTLs ranged from 8.5 to 15.4 %. No significant QTLs were found for percent survival despite strong correlations between the flooding tolerance ratings and percent survival. Although large QTLs were not found for either of the two traits, the data does indicate specific lines tended to be the most, or the least, drought tolerant in each of the three years. Correlation among rank order for survival among years varied from 0.31 to 0.42, indicating a general consistency of rank order. The data collectively suggests that flooding tolerance and survival are complex traits, potentially controlled by numerous QTL and QTL × environment interactions. The consistency in rank order among years indicates that selection for specific genotypes using a phenotyping method is feasible and could help improve flooding tolerance and survival.