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Understanding and improving flooding tolerance in soybean using genetic and genomic tools

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Continuous climate change causes severe soil flooding (waterlogging) with a predicted 30% increase in heavy precipitations by 2030. Waterlogging is also confounded by the irrigation timing and management. Our research group focuses on understanding the molecular mechanism and genetic improvement of waterlogging tolerance in soybean. Screening of a core set of USDA germplasm including the wild species identified several waterlogging tolerant lines that were then used to develop mapping populations. Four quantitative trait loci (QTL) were mapped from two mapping populations, and the favorable alleles of two major QTL are identified from exotic parents. Waterlogging-tolerant germplasm lines were developed by marker-assisted selection to incorporate the tolerant alleles to elite backgrounds. The improved germplasm lines have comparable yield potential to commercial checks under non-stress condition and outperform the commercial checks by 30-40% under flooding condition. Fine-mapping of a major QTL delimited the QTL into a genomic region containing a putative gene. The tolerant allele was found to have an insertion of 11-bp poly-A in the 5'-untranslated-region, which suppresses its own translation and promotes root growth under both non-stress and stressed conditions. The naturally-occurring variations between the two alleles in root growth and waterlogging tolerance were confirmed by studies using soybean transgenic roots and composite transgenic plants. Phylogenetic analysis revealed that the tolerant allele is a recent mutation and has not been introduced into current U.S. elite germplasms. By comparing field performance of the near-isogenic-lines, the tolerant allele was observed to improve yield by 16-40% under non-stress conditions possibly due to better root system. Preliminary experiments also indicated that the improved root traits by the tolerant allele also had potential to improve drought tolerance in soybean. These findings provided genetic/genomic resources to protect yield in soybean and revealed the importance of roots in crop improvement.