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Differential gene expression of soybean genotypes to flooding stress and SNP identification

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Flooding is a frequent environmental stress that reduces soybean (*Glycine max*) growth and affects nutrient and water uptake, and grain yield of soybean in many producing regions in the world. Characterization of genomic regions underlying the flooding tolerance will facilitate development of soybean varieties with increased tolerance to this stress. The objectives of this research are to identify genes differently expressed under flooding stress in two soybean genotypes with contrasting flooding tolerance, and select and validate SNPs identified from these candidate genes. The experiment was carried out under outdoor conditions in Federal University of Rio Grande do Sul, Brazil. Two soybean genotypes with contrasting flooding tolerance phenotypes, Tecirga 6070RR (tolerant) and Fundacep 62RR (sensitive) were grown in concrete tanks filled with lowland gleysolic soil. Both genotypes were subjected to flooding stress at growth stage V6 for a period of 48 h. Leaf and root samples were collected at 24 and 48 h after flooding stress, and used for physiological evaluations and RNAseq analysis. Physiological traits including chlorophyll fluorescence, N uptake, APX activity and H_2O_2 content were collected. APX activity only raised in the sensitive genotype. After 48 h under flooding, the sensitive genotype showed an increase in H_2O_2, while the tolerant one showed a decrease. This results hinted that H_2O_2 may act as a signaling molecule in the tolerant genotypes. RNAseq data has identified 23 putative genes responsible for flooding tolerance. These candidate gene sequences were then aligned with *Glycine max* genome (Wm82.a2.v1). SNPs that were polymorphic between the tolerant and susceptible genotypes with functional annotation in abiotic stress response were selected. Finally, 23 SNPs from 17 candidate genes distributed across 12 chromosomes were selected for validation. Kompetitive Allele Specific PCR (KASP) assays are designed from these SNPs and used to validate with a panel of soybean genotypes.