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Physiological and molecular basis of flooding tolerance in soybean

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Flooding is an environmental stress that reduces soybean (*Glycine max*) growth, affects nutrient and water uptake, decreasing grain yield in many producing areas around the world. Characterization of physiological responses and the identification of genes underlying the flooding tolerance will facilitate the development of more tolerant varieties. The objectives of this project are to characterize the physiological and molecular responses of two soybean genotypes that present contrasting tolerance phenotypes when submitted to flooding stress. The experiment was carried out under outdoor conditions at UFRGS, Porto Alegre, Brazil. The indeterminate soybean genotypes (TECIRGA 6070RR – tolerant and FUNDACEP 62RR – sensitive) were grown in concrete tanks filled with lowland gleysolic soil. Treatments consisted of two water regimes (flooded and control = no flooded) imposed when plants were at V6 growth stage. Both genotypes were submitted to flooding during 48 hours using a water layer of approximately 5 cm. Control plants were maintained at 85% of field capacity. After the flooding period, tanks were drained. For physiological measurements and molecular analysis, leaves and roots were collected at 24 and 48 hours in flooding and 24 hours after the water was drained. Physiological traits including chlorophyll fluorescence, N uptake, APX activity and H_2O_2 content were recorded. Leaves collected at 24h after the beginning of water treatments, were used for RNAseq analysis. After 48h under flooding, the sensitive genotype showed an increase in H_2O_2 content, while the tolerant one showed a decrease. These results hinted that H_2O_2 may act as a signaling molecule in the tolerant genotype. According to RNAseq we have identified genes with expression levels that were altered by flooding stress. Comparing genotypes, TECIRGA presented 1,494 and 731 genes up-regulated and down-regulated, respectively, in the control condition. Regarding flooding treatment, 752 and 871 genes were respectively up- and down-regulated in this tolerant genotype.