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Soybean Proteomics to reveal the tolerant mechanism at initial-flooding stress

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Soybean is sensitive to flooding stress, which markedly reduces its growth. To identify the mechanism of flooding tolerance at initial stage in early-stage soybean, proteomic technique was used. Flooding tolerant mutant line and abscisic acid (ABA)-treated soybean, which exhibited flooding tolerant phenotype, were used as materials. Two-day-old soybeans were flooded for 3 h as initial flooding stress and roots were collected for proteomic as well as metabolomics and transcriptomic analyses. Commonly changed metabolites, proteins, and genes between mutant and ABA-treated soybeans were considered as flooding-tolerance related candidate factors. Finally, omics results were integrated to analyze the flooding tolerant mechanism in soybean. These results suggest that flooding tolerance at initial stage in early-stage soybean might be through protecting newly synthesized proteins and enhancing activities of antioxidative enzymes to remove reactive oxygen species. Furthermore, regulation of energy metabolism is crucial step for flooding tolerance and inhibition of cell wall loosening might contribute to flooding tolerance in soybean.