

PB-44

Transcriptome Profiling Identifies Genes of Waterlogging-Tolerant and -Sensitive Rapeseeds Differentially Respond to Waterlogging Stress at the Flowering Stage

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[Abstract]

Rapeseed is a crop that is waterlogging sensitive, and it is necessary to breed waterlogging tolerance varieties. Our study presents the comparative transcriptome changes in two rapeseed lines, i.e., waterlogging-tolerant ('J8634-B-30') and -sensitive ('EMS26') lines under control and waterlogging stress treatments at the flowering stage. RNA-sequencing analysis revealed 13,279 differentially expressed genes (DEGs) for 'J8634-B-30' and 8,682 DEGs for 'EMS26' under waterlogging stress condition compared to control. Among DEGs of 'J8634-B-30', 6,818 were up-regulated and 6,461 were down-regulated. On the other hand, among the DEGs of 'EMS26', the number of down-regulated genes (5,240) were higher than that of up-regulated genes (3,442). Gene ontology enrichment analysis showed that DEGs related to glucan metabolic, cell wall, and oxidoreductase activity were significantly changed in 'J8634-B-30'. Kyoto Encyclopedia of Genes and Genomes (KEGG)-based analysis in 'J8634-B-30' identified up-regulated DEGs being involved in MAPK signaling pathways. In addition, the DEGs belonging to mechanisms responding to waterlogging stress, i.e., plant hormones, carbon metabolism, Reactive oxygen species (ROS), Nitric oxide (NO) etc. were compared in rapeseed lines. Several DEGs including ethylene-responsive transcription factor (*ERF*), constitutive triple response (*CTR*) (in ethylene signaling pathway), monodehydroascorbate Reductase (*MDAR*), NADPH oxidase (in ROS pathway), cytochrome c oxidase assembly protein (*COX*) (in NO pathway) up-regulated in 'J8634-B-30'. These outcomes provided the valuable information for further exploring the genetic mechanism of waterlogging tolerance in rapeseed.

[Acknowledgement]

This work was conducted with the support of the Cooperative Research Program for Agriculture Science and Technology Development (Project No. 01433202).

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