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Molecular Responses to Waterlogging Stress in Sesame (*Sesamum indicum* L.) During Early Vegetative and Pre-flowering Stage Using RNA-seq

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[Introduction]

Recently, the demand for the cultivation area of the crops has been increasing in domestic paddy fields. At the same time, flooding in the rainy season are threatening with adverse weather. Waterlogging is a common abnormal environmental condition that limits plant growth and productivity. Waterlogging is thought to be one of the critical abiotic stresses leading to hinder crops yield including Sesame. This study was conducted to investigate RNA expression pattern of sesame leaves under waterlogging stress.

[Materials and Methods]

The seeds of sesame (*Sesamum indicum* L. var. Gunback) were collected from the RDA, Korea. Experiments were carried out in a greenhouse of paddy soil condition. The seedlings were exposed to waterlogging stress for 5 days at 2- and 10-leaf stage maintaining 2cm flooding above the soil surface. For transcriptomic studies, total RNA of leaves were extracted using RNeasy Plant mini Kit. RNA-seq was performed using the extracted RNA, and the differentially abundant transcripts were identified in response to waterlogging stress.

[Results and Discussion]

A total of 4455 genes from 2-leaf stage and 5153 genes from 10-leaf stage were revealed to be differentially expressed between normal and waterlogging conditions. Among them, top ranked differentially expressed genes from 2- and 10-leaf stage were mainly involved in energy and metabolism, stress and defense, and biological regulation. However, top five selected genes from both stage showed significantly differentiated expression between normal and waterlogging conditions. In the 2-leaf stage, genes of 105166101, 105161472, 105160297, 105175684 and 105177942 were selected whereas the LOC105166101 gene showed an increase in FPKM value from approximately 1855 to 3725 and induces cysteine proteinase expression. The LOC1051756 gene showed reduced FPKM values from 5828 to 1893. The expression of LHC was decreased by waterlogging stress, which is associated with the expression of chlorophyll a-b binding protein 21. In the 10-leaf stage, the genes of 105173924, 105166717, 105178780, 105178031 and 105177942 were selected. In addition, the LOC105166717 gene, which decreased FPKM value from 6593 to 1080, was associated with acidic endochitinase SE2-like, and it was thought that carbohydrate metabolism, amino sugar and nucleotide sugar metabolism were inhibited by waterlogging stress.

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