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Transcriptome Profiling in Sesame(Sesamum indicum L.) Leaves under Waterlogging Stress during Early Vegetative and Pre-Flowering Stage

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[Introduction]

Now a days, there is an increasing interest in the functionality and nutritional value of sesame seeds. In order to improve the utilization of arable land and increase income in Korea, field crops are introduced to paddy soils through paddy-upland rotation. As a result, the area of growing sesame seeds in paddy soil will increase. However, most of the field crops are sensitive to waterlogging stress when the crops are grown in paddy soil. Therefore, this study was conducted to find out the growth period of sesame that are most sensitive to waterlogging stress, and to determine the possible difference in their transcriptome profiles in response to waterlogging stress.

[Materials and Methods]

The seeds of Sesame were collected from the Rural Development Administration, Korea. To observe the morphological growth of sesame leaves, the present study was carried out in a glass greenhouse under paddy soil conditions. The seedlings were subjected to waterlogging in 2nd and 10th leaves maintaining 2 cm of soil surface, and treated for 5 days. Total RNA of the leaves was extracted using RNeasy Plant mini Kit. Through RNA sequencing, five genes from all differentially expressed genes to validate the reliability of the libraries that were highly related to waterlogging stress were selected.

[Results and Discussion]

In the 2-leaf stage, genes of 105166101, 105161472, 105160297, 105175684, and 105177942 were selected. The LOC105166101 gene was increased the FPKM value from about 1855 to 3725 that was known to induce cysteine proteinase expression. Cysteine proteinase has been implicated in plant responses to various biological and abiotic stresses and can play a decisive role in defense mechanisms. Sesame cysteine is believed to be degraded by de novo protease during seed germination to mitigate the inhibition of certain endogenous cysteine proteinases associated with specific physiological functions of seedling growth. LOC1051756 gene decreased FPKM value from about 5828 to 1893. It is associated with the expression of chlorophyll a-b binding protein 21. It is thought that the expression of light harvesting complex(LHC) is reduced by the waterlogging stress. LHC functions as a light receptor and captures and delivers energy to the photosystem to which it is bound. In the 10-leaf stage, 105173924, 105166717, 105178780, 105178031, and 105177942 genes were selected. The LOC105166717 gene, which has a reduced FPKM value from about 6593 to about 1080, is associated with acidic endochitinase SE2-like. In addition, the genes selected in the 2- and 10-leaf stage, LOC105177942, LOC105178780, and LOC105177942 were investigated as genes whose role is not clearly identified.

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