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## Transcriptomic Profiling of Sorghum Leaves Responsive to Waterlogging Stress at the Vegetative Stage

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### [Introduction]

Sorghum (*Sorghum bicolor* L.), a widely grown staple food, feed, fodder and industrial crop, plays a critical role in supporting the growing world population. The production process of Sorghum is highly dependent on suitable environmental factors; however, frequent extreme weather can cause many different types of abiotic stresses, including waterlogging stress. To elucidate the molecular mechanisms of resistance to waterlogging stress in sorghum, RNA-seq was used for transcriptome profiling of sorghum leaves during vegetative stage exposed to waterlogging stress.

### [Materials and Methods]

The seeds of sorghum (*Sorghum bicolor* L. cv. Nampungchal) were collected from the Rural Development Administration, Korea, and the study was carried out at greenhouse in the Chungbuk National University. In the early stage of growth, the soil was saturated with water (up to 3 cm) from the feed port at the bottom of the pot for 10-days. After treatments, total RNA was extracted from the leaves and analyzed the samples using RNA-seq.

### [Results and Discussion]

Owing to the climate change impacts, waterlogging is one of the most hazardous abiotic stresses to crops, which also can result in a serious reduction in growth and development during the rainy season. A total of 2172 differentially expressed genes (DEGs) were detected from 3-leaf stage in comparisons between the control and stress condition. Of them, 971 genes were upregulated and 1201 genes were downregulated. However, in the case of 5-leaf stage, a total of 1691 genes were upregulated while 1863 were downregulated. Gene ontology analysis revealed that the most of the identified genes were involved in metabolism, stress and defense, and photosynthesis. In addition, we selected the top 5 genes that differ in the level of the volume that is more than twice as high as the fold change. LOC8056152, 8074608, 8084497, 8060298, 110436266 genes were selected in the comparative analysis of 3-leaf stage, and LOC8056151, 8062994, 8071524, 8060298, 8084497 genes were selected in the analysis of 5th leaf stage.

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