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De novo transcriptomic analysis to identify differentially expressed genes during the process of aerenchyma formation in *Typha angustifolia* leaves

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Abstract: Lysigenous aerenchyma is formed through programmed cell death (PCD) in *Typha angustifolia* leaves. However, the genome and transcriptome data for this species are unknown. To further elucidate the molecular basis of PCD during aerenchyma formation in *T. angustifolia* leaves, transcriptomic analysis of *T. angustifolia* leaves was performed using Illumina sequencing technology, revealing 73,821 unigenes that were produced by assembly of the reads in T1, T2 and T3 samples. The important pathways, such as programmed cell death (PCD), aerenchyma formation, and ethylene responsiveness were regulated by these unigenes. *1-aminocyclopropane-1-carboxylate synthase* (*ACS*) and *1-aminocyclopropane-1-carboxylate oxidase* (*ACO*) were highly up-regulated as key enzymes for ethylene synthesis, along with *respiratory burst oxidase homolog* (*RBOH*), *metallothionein*, *calmodulin-like protein* (*CML*), and *polygalacturonase* (*PG*), may collectively explain the PCD involved in *T. angustifolia* aerenchyma formation. We hypothesize that fermentation, metabolism and glycolysis generate ATP for PCD. We searched the 73,821 unigenes against protein databases, and 24,712 were annotated. Based on sequence homology, 16,012 of the 73,821 annotated unigenes were assigned to one or more Gene Ontology (GO) terms. Meanwhile, a total of 9,537 unigenes were assigned to 126 pathways in the KEGG database. In summary, this investigation provides important