

Transcriptome analysis of internal and external stress mechanisms in *Aster spathulifolius* Maxim.

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ABSTRACT

Aster spathulifolius Maxim. belongs to the Asteraceae family which is distributed only in Korea and Japan. It is recognized as a traditionally medicinal plant and economically valuable in ornamental field. However, among the Asteraceae family, the *Aster* genus, which lacks genomic resources and information of molecular function. Therefore, we used high throughput RNA-sequencing transcriptome data of the *A. spathulifolius* to know molecular level function. DeNovo assembly produced 98,660 unigenes with N50 value 1126 bp. Unigenes were analyzed for functional annotation against NCBI database like plant database of nucleotide (Nt) and non-redundant protein (Nr), Pfam, Uniprot, KEGG and Transcriptional factor (TF). In addition, Distribution of SSR markers also analyzed for future perspectives. Further, Comparing with other two Asteraceae family species like, *Karelinia caspica* and *Chrysanthemum morifolium* to the *A. spathulifolius* shows the number of genes that regulated in internal and external stress respectively salt-tolerant and heat and drought stress to understand the molecular basis related to the different environments stress.

Keywords: *Aster spathulifolius*, RNA-Seq, functional annotation, SSR, Stress gene