

Analysis of Differentially Expressed Genes of Korean Ginseng Grown under Ambient Heat

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[Introduction]

We analyzed leaf of Korean ginseng (*Panax ginseng*) to study the response of plants against ambient heat or heat stress.

[Materials and Methods]

We transplanted one-year ginseng plants to the field inside of temperature gradient greenhouse located in Eumsung, Chungbuk, Korea at 2014. The temperature gradient greenhouse facilities provide temperature gradient varies from outside natural condition to +6°C higher than outside temperature. We harvested leaf sample for RNA sequencing analysis every year from 2015 to 2017 once in a month from May to August and stored in -70°C until used. We analyzed mRNA and micro RNA (miRNA) sequences to find out differentially expressed transcripts. Based on differentially expressed genes (DEGs) we tried to find out the ambient heat or heat stress-related metabolic pathways. Overall, 1261 genes showed

[Results and Discussions]

tried to find out the ambient heat or heat stress-related metabolic pathways. Overall, 1261 genes showed differences in quantitatively, among them 1033 genes showed an increasing pattern and 228 genes showed down-regulation. We found that structural constituent of ribosome, metal ion binding, ATP binding, translation, chloroplast thylakoid membrane, ribosome, lipid metabolic process, heme binding and plasma membrane are top 10 GO terms identified in AmiGO2. Additionally, we mapped DEGs on pathway database of Kyoto Encyclopedia of Genes and Genomes (KEGG). We found that significantly affected pathways are such as plant hormone signal transduction, ribosome, basal transcription factors, proteasome, spliceosome, nucleotide excision repair, mRNA surveillance, and protein export pathway, etc. Additionally, we found novel micro RNAs and analyzed their target genes. The analyses results of DEGs, miRNA, GO terms will be discussed.

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