

Development of transcriptome database of Korean ginseng to study physiological responses to ambient heat

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[Introduction]

Medicinal plant ginseng (*Panax ginseng*) is a perennial long-day plant and adaptive to low light and favor to relatively lower temperature conditions. Korean ginseng is one of the typical plants have been threatened by current climate change particularly heat stress during the early summer season of the Korean peninsula. Plants are grown under constitutive changing of environmental conditions and response to external conditions at both protein and transcription level. The effects of heat on plant growth are broad and influence the yield directly. Heat stresses could be classified depending on intensity and duration. Fundamental changes of growth condition by climate change maybe or maybe not classified as a stress on plant growth. The effects of a short and unanticipated impact of elevated heat on the plant could be different with those of under longer extension of ambient heat.

[Materials and Methods]

To examine differently expressed gene sets by ambient heat stress of ginseng, we grow the ginseng plants for four years in normal and ambient higher temperatures year-round using fan-ventilated temperature-gradient greenhouse facilities located in Eumsung, Chungbuk, Korea. We harvested the ginseng leaves at various time point for three consecutive years from 2015 to 2017. Among them, we used ginseng leaf sample collected on August 30, 2015, and May 4, 25 and June 22, 2017, grown under two different temperature G3 and G5 which defined as normal and +3°C ambient condition, respectively. We sequenced mRNAs and micro RNAs of these eight ginseng leaf samples using NGS technology carried by Macrogen® (Seoul, Korea).

[Results and Discussions]

Due to the lack of genome sequencing data of ginseng, to overcome mapping difficulties of short mRNA sequences, we made contigs through transcripts assembly with already reported ginseng transcriptome data and used these contigs like pseudomolecules. Here, we report the first ginseng leaf transcriptome database which has assembled transcripts contigs, heat related DEGs and pathway mapping data which affected by heat. These ginseng transcriptome database geared up with BLAST search functions and users can download search outputs. We analyzed the ginseng transcriptome data and revealed various known and unknown genes and novel miRNAs which response to the heat. We will discuss the academic importance of this transcriptome database.

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