

**PB-69**

## Application of Pac-Bio Sequencing, Trinity, and rnaSPAdes Assembly for Transcriptome Analysis in Medicinal Crop *Astragalus membranaceus*

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### [Abstract]

*Astragalus membranaceus* (*A. membranaceus*) has traditionally been used as a medicinal plant in East Asia for the treatment of various diseases. *A. membranaceus* belongs to the legume family and is known to be rich in substances such as flavonoids and saponins. Recent pharmacological studies of *A. membranaceus* have shown that the plant has immunomodulatory, anti-oxidant, anti-cancer, and anti-inflammatory effects. However, knowledge of major biosynthetic pathways in *A. membranaceus* is still lacking. Recently developed sequencing techniques enable high-quality transcriptome analysis in plants, which is recognized as an important part in elucidating the regulatory mechanisms of many plant secondary metabolic pathways. However, it is difficult to predict the number of transcripts because plant transcripts contain a large number of isoforms due to alternative splicing events, which can vary depending on the assembly platform used. In this study, we constructed three unigene sets using Pac-Bio isoform sequencing, Trinity and rnaSPAdes assembly for detailed transcriptome analysis in *A. membranaceus*. Furthermore, all genes involved in the flavonoid biosynthetic pathway were searched from three unigene sets, and structural comparisons and expression profiles between these genes were analyzed. The isoflavone synthesis was active in most tissues. Flavonol synthesis was mainly active in leaves and flowers, and anthocyanin synthesis was specific in flowers. Gene structural analysis revealed structural differences in the flavonoid-related genes derived from the three unigene sets. This study suggests the need for the application of multiple unigene sets for the analysis of key biosynthetic pathways in plants.

### [Acknowledgement]

This research was supported by “National Institute of Agricultural Sciences” (Project No. PJ015035), Rural Development Administration, Republic of Korea

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