## PB-57

## Constructing Reference Transcriptome Sets of *Codonopsis lanceolata*(Deodeok) and *Ixeridium dentatum*

Tae-Ho Lee<sup>1</sup>\*, Yun-Ho Oh<sup>1</sup>

<sup>1</sup>Genomics Division, National Institute of Agricultural Sciences, Jeonju 54874, Republic of Korea

## [Abstract]

As the aging population increases and interest in well-being increases, the importance of developing special crops increases. Natural medicine based on the special crops has been mainly used as an adjunct therapy for many diseases and symptoms based on culture, traditional medicine, and experience. In particular, it is attracting attention as a new resource to develop new drugs such as Artemisinin, a treatment for malaria. In order to efficiently use crops, it is essential to establish omics data such as genomes, transcriptomes, and metabolites of special-purpose crops. However, many special-purpose crops have large, heterogeneous and polyploid genomes that require high cost and long time to reference genome sequencing. Therefore, we built an inexpensive, fast, but very useful reference transcriptome as the first step. We constructed high-quality reference transcriptom sets of *Codonopsis lanceolata* and *Ixeridium dentatum* with PacBio data. Our team will continue to construct reference transcriptoms of more special-purpose crops, and the data will be released by the National Agricultural Biotechnology Information Center (NABIC) in order to be widely used in agricultural as well as medical R&D.

## [Acknowledgement]

This work was carried out with the support of "Cooperative Research Program for Agriculture Science and Technology Development (Project No. PJ01503502)" Rural Development Administration, Republic of Korea

\*Corresponding author: E-mail. thlee0@korea.kr Tel. +82-63-238-4558