Pintersity of Tsukuba **Diversity** of Tsukuba **Plant Transgenic Design Initiative** 48th PTraD Research Seminar **T-PIRC Research Seminar**

Date and Time: 2019/9/3 (Thu) 13:30 –14:15 Place: Gene Research Center, Seminar Room (211)

Identification of Small RNAs and Target Genes in Ethylene

Signal Transduction in Oncidesa 'Gower Ramsey'

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Oncidesa is a popular orchid with high economic value in cut-flower markets around the world. Either exogenous and endogenous ethylene induces petal senescence of Oncidesa. The shelf-life of Oncidesa had been prolonged when ETHYLENE INSENSITIVE3 (EIN3), the key transcription factor in ethylene signal transduction, was knocked down by gene silencing. Transcriptome of OgEIL1-RNA interfering transgenic and non-transgenic plants were analyzed to understand the gene expression and regulation of mRNAs and small RNAs (sRNAs) and we tried to construct the OgEIL1 regulatory network in Oncidesa. After high-throughput sequencing and de novo assembling, we got 587,771 transcripts in Oncidesa transcriptome. Among the sRNA sequences of Oncidesa, a total of 177 and 31 known miRNAs were annotated in leaf and flower, respectively. Eight and twenty putative novel miRNAs were identified in leaf and flower, respectively, after prediction by software. There are more differentially expressed transcripts and sRNAs between organs than those between transgenic and non-transgenic plants. According to gene ontology enrichment test of differentially expressed transcripts in OgEIL1-RNA interfering plant, many enriched GO terms were related to sulfur metabolic process. The gene expression levels of miR164 family which are negatively regulated by EIN3 were up-regulated in the OgEIL1-RNA interfering transgenic plant. The target transcripts of differentially expressed miRNAs were identified and some of them are transcription factors involving in ethylene response, such as AR2, bHLH, EIL, and NAC. These results indicate that EIN3 may not only directly regulate the expression of ethylene-related genes, but also control the miRNAs to manipulate the Oncidesa gene network delicately.

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