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Series - 023

Date & Time – October 24, 2017
Venue - Central 5-41; 2F (Conference Room # 1)
Speaker – Nobutaka Mitsuda
Title: **Comprehensive study of plant transcription factors --- Toward regulon biotechnology**
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Abstract

Transcription factor (TF) is a fascinating target of genetic manipulation to improve crop traits because TF regulates expression of many genes at once. We call this unit consisting of TF and its target genes as "regulon". Most TFs work as activator to activate gene expression like an accelerator of automobile. The model plant Arabidopsis thaliana has ca. 2,000 TFs, which regulate the expression of whole ca. 27,000 genes in the genome (regulonome). For functional analyses of plant TFs, we developed a gene-silencing technology CRES-T, the method to express repression-domain-fused TF in plant. This method changes most TFs to repressor (chimeric repressor) like a brake of automobile (Figure). We applied this method to almost all TFs in Arabidopsis and half of rice TFs and observed numerous aberrant phenotypes. We also prepared the pool of T2 seeds of CRES-T lines to find a particular phenotype of interest and have isolated many kinds of TFs which can confer stress tolerances. In addition to the model plants, we also applied CRES-T to various horticultural plants to modify their flower traits and constructed "FioreDB" database that stores phenotypic data and information regarding plant TFs. Furthermore, we prepared Gateway entry clones of almost all Arabidopsis TFs and more than 1,000 rice TFs and developed TF-only yeast-one/two-hybrid library. This library enabled us to isolate TF that interacts with specific DNA/protein efficiently. Using these tools, we are trying to establish the "regulon biotechnology" to create "tailor-made" plant which could meet various demands of farmers, companies, and consumers.