Gene discovery of the regulatory factors for wood formation by gene co-expression network analysis

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Wood is mainly composed of cellulose, hemicellulose and lignin. Lignin is a phenolic polymer mainly derived from three monoligninols — coniferyl, sinapyl and 4-coumaryl alcohols. Monolignols are synthesized via the cinnamate/monolignol pathway (CMP), and finally polymerized by peroxidases. While many genes encoding CMP enzymes have been characterized until now, the regulatory mechanism of the gene expression by transcription factors is not well-known. To identify the function of the transcription factors involved in lignin biosynthesis, the gene co-expression network analysis by using microarray datasets of *Arabidopsis thaliana* is one of the prospective methods.

In this study, the author performed the gene co-expression network analysis with *A. thaliana* microarray datasets and narrowed down the candidate genes. Three candidate genes, which showed the expression pattern correlated with several CMP genes, *AtRING1*, *AtRING2* and *AtNAC1* were further characterized.

The author profiled the expression pattern of the genes involved in secondary cell-wall synthesis in each inflorescent stems of T-DNA insertion lines for *AtRING1*, *AtRING2* and *AtNAC1*. As a result, significant difference in the expression of the genes involved in cell-wall synthesis including CMP genes and *CesA* was found between T-DNA insertion and wild type lines.

We next measured the lignin content of T87 cells over-expressing *AtRING1* by acetyl bromide method. The lignin content was the same as the control. On the other hand, microarray analysis of T87 cells over-expressing *AtRING1* indicated that peroxidases were over-expressed in the cells. The above results suggested that up-regulation of *AtRING1* did not result in the change of lignin content, but resulted in the change of gene expression involved in cell-wall formation.