

**Studies of metabolic control of lignin biosynthesis by use of
Arabidopsis thaliana cultured cells**

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Lignin is one of the major components of wood, and changing lignin structures and concentrations strongly affect characteristic traits of wood. Therefore, to elucidate integrated mechanisms for lignin biosynthesis is important in cell-wall biotechnology.

Plant metabolisms including lignin biosynthesis are largely controlled by a variety of transcription factors. To identify the function of transcription factors involved in lignin biosynthesis, it is very useful to employ the newly developed gene co-expression network analysis by use of microarray data sets of *Arabidopsis thaliana*. By exploiting this strategy, in our laboratory, a transcription factor (referred to as transcription factor A in this study) was tentatively identified as a candidate, which controls syringyl lignin biosynthesis.

The aim of this study is to identify firmly the function of transcription factor A by characterizing lignins of transgenic *A. thaliana* T87 cells in which the expression of the gene encoding transcription factor A is upregulated. However, conventional methods for lignin analysis, which were optimized for secondary xylem tissues of wood, have not yet been optimized for plant cultured cells including the T87 cells. Hence, in this study, methods for analyzing lignin structures (thioacidolysis and nitrobenzene oxidation methods) and for determining lignin contents (acetyl bromide and Klason methods) were optimized for *A. thaliana* T87 cells. Then transgenic *A. thaliana* T87 cells were subjected to lignin analysis under the condition established above, and it was firmly confirmed that the transcription factor A can upregulate syringyl lignin biosynthesis.

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