Characterization of *O*-methyltransferases involved in lignin and lignan biosynthesis

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An *Arabidopsis thaliana* gene, At5g54160, was annotated as a caffeic acid *O*-methyltransferase CAOMT (= 5-hydroxyconiferaldehyde OMT, CAldOMT) (AtOMT1) gene based on its high sequence homology to *Populus tremuloides* CAOMT. However, Muzac et al. reported that a recombinant AtOMT1 did not methylate caffeic acid, whereas the protein methylated efficiently a flavonoid, quercetin [1]. Later, Goujon et al. reported that an At5g54160-knockout *Arabidopsis* mutant lacks syringyl unit in the lignin, again suggesting that the gene is involved in syringyl lignin biosynthesis [2]. In this study, the author identified firmly the *bona fide* function of At5g54160 gene as *AtCAldOMT* based on biochemical characterization of the recombinant protein and lignin analysis of an At5g54160-knockout T-DNA tag line mutant

Sakakibara et al. established a pathway from matairesinol to yatein which is a typical heartwood lignan and a key precursor to the antitumor lignan, podophyllotoxin in *Anthriscus sylvestris* [3]. The conversion involves four reactions steps, two of which is methylation of phenolic hydroxyl groups of lignans, probably catalyzed by lignan OMT(s). Umezawa et al. has reported the first molecular cloning of the gene encoding lignan OMT from *Carthamus tinctrius* maturing seeds [4], which catalyzes regioselective methylation of matairesinol to give rise to arctigenin, but not isoarctigenin. Taking advantage of this gene sequence, the author tried to isolate OMT genes in biosynthesis of podophyllotoxin and yatein in *Podophyllum peltatum* and *Anthriscus sylvestris*.

References

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