Functional Expression and Chracterizationof an *Populus deltoides cDNA* Clone Encoding *O*-methyltransferase

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Abstract

Most of flavonoids found in plants were modified by methylation, hydroxylation and glycosylation. Among them, *O*-methyltransferases (OMT) are involved in secondary metabolism. These enzymes catalyze the transfer of a methyl group from *S*-adenosyl-L-methionine (SAM) to a hydroxyl or carboxyl group of the acceptor molecule to form methyl ether of methyl ester derivatives, respectively. Also, It have an effect on the solubility and thus on the antimicrobial activity of the flavonoid.

An methyltransferase, POMT-9, was cloned from *Populus deltoides* by RT-PCR method. POMT-9 consists of 1071 bp open reading frame which encodes a protein whose molecular weight is 38.9 kDa. Its predicted amino acid sequence shows homology with caffeic aicd *O*-methyltransferase from *Prunus dulcis*. In order to determine the substrate of POMT-9, POMT-9 was expressed in *Escherichia coli* BL21 as a glutathion *S*-transferase fusion protein. Several substrates including naringenin, qucertin, and kaempferol were tested. Reaction product was analyzed with thin layer chromatography and HPLC. POMT-9 converted Quercetin(3',4',5, 7-tetrahyroxyflavonol) into isorhamnetin (3'-methoxy-4',5, 7-trihydroxyflavanone) as well as luteolin and eriodictyol into the corresponding *O*-methylated compounds.

References

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