

Functional analysis of *Arabidopsis O-methyltransferase*

Kim Bong Gyu, Kim Jung Ho and Ahn Joong-Hoon

Department of Molecular Biotechnology, Bio/Molecular Informatics Center,
Konkuk University, Seoul, Korea;
TEL : +82-2-450-3764, FAX +82-2-446-9001

Abstract

Flavonoid compounds are of ubiquitous occurrence in plants, and display a wide range of functions that are essential for plant development and survival. O-methylation of flavonoids reduces the chemical reactivity of their phenolic hydroxyl groups and increase their lipophilicity.

A cDNA clone, ATOMT16, from *Arabidopsis thaliana* was isolated. The sequence analysis showed that it has a 842 bp ORF and high homology with O-methyltransferase. ATOMT16 was expressed in *Escherichia coli* as a glutathione S-transferase fusion protein and the expressed protein was purified with homogeneity.

To study the substrate of each product, several substrates including Quercetin, luteolin, naringenin, eriodictyol, kaempferol, catechin and caffeic acid were tested. Reaction products were analyzed by TLC and HPLC. AtOMT-16 converted Quercetin, luteolin and eriodictyol that have the hydroxyl group at the ortho position. In addition, AtOMT-16 could not convert 3'-hydroxy flavone, kaempferol, Naringenin that does not have the hydroxyl group at the ortho position. HPLC analysis of phenolic compounds with knock out mutant showed two difference peaks that were dramatically decreased.

References

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