

## *Arabidopsis* O-methyltransferase (OMT) Family

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### Abstract

O-methylation that is mediated by O-methyltransferases (OMTs) is a common modification in natural product biosynthesis and contributes to diversity of secondary metabolites. OMTs use phenylpropanoids, flavonoids, other phenolics and alkaloid as substrates and share the common domains for S-adenosyl-L-methionine (AdoMet) and substrate binding. We searched the *Arabidopsis* genome and found 17 OMTs genes (AtOMTs). Some of AtOMTs showed as high as 96 % sequence similarity. AdoMet binding domain of AtOMTs is highly conserved while the substrate binding domain is diverse, indicating that they use different substrates. Expression of seven AtOMT genes (*AtOMT1*, *AtOMT7*, *AtOMT8*, *AtOMT8*, *AtOMT10*, *AtOMT11*, *AtOMT12*, and *AtOMT16*) in response to UV and in different tissues was investigated using the real-time quantitative reverse transcriptase-polymerase chain reaction. All the AtOMTs except AtOMT 7 were expressed but expression of AtOMT7 was only detected after UV illumination. On the other hand, only AtOMT1 and AtOMT8 were expressed in all the tissues whereas AtOMT10 showed flower specific expression. These results add new insights on the expression and the distinct function of AtOMTs.

### References

1. *Arabidopsis* Genome Initiative (2000) Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. *Nature* **408**, 796-815.

2. Cacace, S., Schröder, G., Wehinger, E., Strack, D., Schmidt, J., and Schröder, J. (2003) A flavonol *O*-methyltransferase from *Catharanthus roseus* performing two sequential methylations. *Phytochem.* **62**, 127-137.