

Identification of methylation mechanisms of SaOMT5 from *Streptomyces avermitilis* based on molecular modeling and its deletion mutants

Youngdae Yoon, Yong-sub Yi¹, Youngshim Lee, Joong-hoon Ahn, and Yoongho Lim

Bio/Molecular Informatics Center, Konkuk University, Seoul 143-701, Korea

¹Seoul University of Venture and Information, Seoul 135-090, Korea

TEL: +82-2-450-3764, FAX: +82-2-446-9001

S-adenosyl-L-methionine (AdoMet) dependent O-methyltransferases are involving many biological functions in organisms. Most of all, plant OMTs are related in not only the biosynthesis of lignin monomer, but also participated in flavonoids biosynthesis. This is not a plant OMT and it is not able to classify by plant OMT classification, because it has characteristics of both class I and class II OMTs¹). This OMT methylated flavonoids which involve *ortho*-dihydroxy groups on one hydroxy group randomly. It is quite different characteristics from plant OMT. To verify the mechanism of SaOMT5, 3-D structure was designated by Modeller program using the structure of rat catechol OMT (COMT, 1vid) as a template, because it has 34% of amino acid sequence homology. And this enzyme is consisted in 6 alpha-helix and 7 beta-sheet, and it was known that C-terminal is more important than N-terminal to maintain its activities²). We make the deletion mutants which were deleted 15, 22, 30, 45, and 53 amino acids from N-terminal and 6, and 10 amino acids from C-terminal. Although the methylation activities are decreased, N53 mutant still maintained its activity. In case of C-terminal mutants, however, just 10 amino acids deletion is knocked out its activity. It is evidence that C-terminal is important to maintain its activity and to study the 3-D structures of each mutant will be helped to understand the mechanism of SaOMT5.

References

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