

22PO-am060

ツルバギアの含硫二次代謝物生合成への関与が推測される *S*-酸化酵素遺伝子の同定

○王 吉晨¹, 鈴木 秀幸², 斉藤 和季¹, 吉本 尚子¹ (¹千葉大学医学薬学府, ²かずさDNA 研究所)

Tulbaghia violacea Harv. (Amaryllidaceae) is a small bulbous herb, which is commonly known as “wild garlic” because of the special garlic-like flavor. The different plant parts of *T. violacea* have traditionally been used in varieties of diseases conditions such as fever and colds, asthma, and tuberculosis for centuries. *S*-(Methylthiomethyl)cysteine sulfoxide (marasmin) is the major sulfur-containing secondary metabolites found in *T. violacea*. It will convert into a series of sulfur-containing compounds upon tissue damage, which possessing antimicrobial, antifungal, and antithrombotic activities.

This study aims to identify the genes that encode *S*-oxygenases involved in marasmin biosynthesis in *T. violacea*. Using a deep transcriptome-based approach, we have cloned two genes encoding clade III flavin-containing monooxygenase (FMO), *TvFMO1* and *TvFMO2*. The cDNA of *TvFMO1* and *TvFMO2* coded for polypeptides of 437 and 470 amino acids, respectively, that possess FAD-binding, NADP-binding, TGY, and FMO-identifying motifs characteristically found in plant FMOs. The deduced amino acid sequences of *TvFMO1* and *TvFMO2* showed approximately 50% similarity with that of *AsFMO1*, a garlic gene encoding a clade III FMO responsible for the stereoselective *S*-oxygenation in the biosynthesis of *S*-allylcysteine sulfoxide (alliin). These data suggested that *TvFMO1* and *TvFMO2* may encode *S*-oxygenases catalyzing stereoselective *S*-oxygenation reaction against a predicted biosynthetic intermediate *S*-(methylthiomethyl)cysteine to form marasmin in *T. violacea*. The plasmid of these two genes that for the protein expression system have been built and transformed into *yeast*. The functional analysis of these two genes is currently in progress, and the results will be discussed in the presentation.