
ABSTRACTS (MASTER THESIS)

Isolation of cDNAs encoding prenyltransferase for flavonoid from *Macaranga tanarius*

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Prenylation of an aromatic compound is a critical step to diversify the chemical structures and biological activities of secondary metabolites, and this reaction step is also involved in the biosynthesis of important endogenous quinone compounds like coenzyme Q and plastoquinone. The diversification of aromatic compounds by prenylation is via differences in prenylation position on the aromatic ring, various lengths of prenyl chain, and further modifications of the prenyl moiety, e.g. cyclization and hydroxylation, resulting in the occurrence of more than 1,000 prenylated compounds in plants.¹⁾ This biosynthetic reaction represents the crucial coupling process of the shikimate or polyketide pathway providing an aromatic moiety and the isoprenoid pathway derived from the mevalonate or MEP (methyl erythritol phosphate) pathways, which provides the prenyl (isoprenoid) chain.²⁾

In particular prenylated flavonoids have been actively studied as they show various biological activities beneficial for human health. These compounds frequently occur in some limited plant families like Moraceae and Leguminosae, while some other plant families are also known to contain prenylated flavonoids depending on the genus. *Macaranga tanarius* (Euphorbiaceae) is a tropical tree grown in Okinawa in Japan, which is a source of propolis in Okinawa area. Okinawan propolis contains characteristic prenylflavonoids, which are geranylated eryodictiol derivatives.

In this study we have found several candidate cDNAs coding for prenyltransferases from a cDNA library prepared from glandular trichomes of *M. tanarius* fruits. They contain three characteristic sequences, i. e., putative transit peptide at the N-terminus, D-rich motif conserved among Mg-dependent prenyltransferases, and membrane-spanning domain. We have tried to express them in yeast and detected the enzyme activity of prenyltransferase using eryodictiol as the flavonoid substrate.

1) Yazaki, et al., Phytochemistry, 70: 1739 – 1745, 2009

2) Akashi, et al., Plant Physiol. 149: 683 – 693, 2009