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Cloning and characterization of a farnesyl pyrophosphate synthase from *Matricaria recutita* L. and its upregulation by methyl jasmonate

S.S. Su, H.M. Zhang, X.Y. Liu, G.F. Pan, S.P. Ling, X.S. Zhang, X.M. Yang, Y.L. Tai and Y. Yuan

College of Life Sciences, Anhui Agricultural University, Hefei, China

Correspondence author: Y. Yuan
E-mail: zhiwuxue239@163.com

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ABSTRACT. *Matricaria recutita* (L.), commonly known as chamomile, is one of the most valuable medicinal plants because it synthesizes a large number of pharmacologically active secondary metabolites known as α-bisabolol and chamazulene. Although the plant has been well characterized in terms of chemical constituents of essential oil as well as pharmacological properties, little is known about the genes responsible for biosynthesis of these compounds. In this study, we report a new full-length cDNA encoding farnesyl diphosphate synthase (FPS), a key enzyme in the pathway of biosynthesis of isoprenoids, from *M. recutita*. The cDNA of MrFPS comprises 1032 bp and encodes 343 amino acid residues with a calculated molecular mass of 39.4 kDa. The amino acid sequence homology and phylogenetic analysis indicated that MrFPS belongs to the plant FPS super-family and is closely related to FPS from the Asteraceae family. Expression of the MrFPS gene in *Escherichia coli* yielded FPS activity. Using real-time quantitative PCR, the expression pattern of the MrFPS gene was analyzed in different

tissues of *M. recutita* as well as in response to methyl jasmonate. The expression analysis demonstrated that MrFPS expression varies in different tissues (with maximal expression in flowers and stems) and was significantly elevated in response to methyl jasmonate. This study will certainly enhance our understanding of the role of MrFPS in the biosynthesis and regulation of valuable secondary metabolites in *M. recutita* at a molecular level.

Key words: Farnesyl pyrophosphate synthase; Secondary metabolite; Methyl jasmonate; *Matricaria recutita* L.

