International Journal of Current Research in
Biosciences and Plant Biology
Volume 5 • Number 2 (February-2018) • ISSN: 2349-8080 (Online)
Journal homepage: www.ijcrbp.com

Original Research Article **doi:** https://doi.org/10.20546/ijcrbp.2018.502.002

Cloning and Sequence Analysis of Phosphomevalonate Kinase Gene (*McPMK*) from *Matricaria chamomilla*

Yishan Xu[1], Xiaomeng Liu[1], Jie Chang[2,3] and Feng Xu[1]*

[1]College of Horticulture and Gardening, Yangtze University, Jingzhou 434025, China
[2]Hubei Collaborative Innovation Center of Targeted Antitumor Drug, Jingmen, Hubei 448000, China
[3]College of Chemical Engineering and Pharmacy, Jingchu University of Technology, Jingmen, Hubei 448000, China

***Corresponding author.**

Article Info

Date of Acceptance:
14 January 2018

Date of Publication:
06 February 2018

Keywords

Matricaria chamomilla
Molecular cloning
Phosphomevalonate kinase
Sequence analysis

ABSTRACT

The phosphomevalonate kinase gene (*PMK*) is one of the core enzymes in the biosynthetic pathway of sesquiterpenoids and catalyzes the formation of mevalonate-5-diphosphate (MVAPP). In order to isolate and identify the *PMK* gene, a specific primer was designed based on the *McPMK* gene sequence in the transcriptome of *Matricaria chamomilla*. The full-length cDNA was 1782 bp of *PMK* gene and named *McPMK* (GenBank Accession No.MG778909). *McPMK* contains a 1479 bp open reading frame (ORF) encoding a total of 493 amino acids. McPMK proteins were analyzed online with molecular weights and isoelectric points of 53.58 KDa and 5.55, respectively. Amino acid multiple alignment showed that the *McPMK* encoded amino acid sequence is highly similar to other plant PMK proteins and has a GHMP kinase superfamily-specific ATP binding site. Phylogenetic tree analysis showed that *McPMK* clustered with Asteraceae *PMKs* in dicotyledonous species, and had the closest genetic relationship with *Chamemelum nobile*. The gene fragment of PMK amplified from *M. chamomilla* laid the foundation for the analysis of its function in the biosynthesis of terpenoids.

Introduction

Matricaria chamomilla L., a year-old herb of Asteraceae, is one of the most commonly used medicinal plants in Europe (Raal et al., 2012; Sayadi et al., 2014). *M. chamomilla* is rich in essential oils, pharmacological evidence shows that its essential oil has a significant anti-inflammatory, inhibit fungi, antispasmodic and analgesic, improving lung cancer and other effects. Thus is widely used in medicine, cosmetics, medicine and other fields (Pirzad et al., 2006). *M. chamomilla* flowers contain 0.24-2.0 percent volatile oil that is blue in color. a-Bisabolol and chamazulene are their main active pharmaceutical ingredients. a-Bisabolol, a sesquiterpenoid compound, has the pharmacological effects of sedation, anti-

inflammatory, anti-oxidation and is an important component of topical health products and skin care products (Murti et al., 2012; Son et al., 2014). Medically, it is often used to treat conditions such as vomiting, headache, and indigestion (Chadwick et al., 2013; Bonifacio et al., 2012). In general, *M. chamomilla* is a kind of medicinal plant with great development and utilization value.

Terpenoids are one of the most abundant type secondary metabolites (Yonekura-Sakakibara and Saito, 2009). Over 60,000 terpenes and derivatives are found in nature (Cheng et al., 2007; Bohlmann and Keeling, 2008). Terpenoids are synthesized in plants through two independent pathways: the mevalonate (MVA) pathway in the cytoplasm and the 2Cmethyl-D-erythritol 4-phosphate (MEP) pathway in the plastids (Vranová et al., 2013). MVA pathway is the main source for the synthesis of terpenoids. Acetyl-CoA is formed by two molecules of acetyl-CoA under the action of acetoacetyl-CoA transporter (AACT), 3-hydroxy-3-methylglutaryl-CoA synthase (HMGS) catalyzes the formation of 3-hydroxy-3-methylglutaryl CoA (HMG-CoA) and then forms mevalonate (MVA) catalyzed by the 3-hydroxy-3-methylglutarylCoA reductase (HMGR), followed by mevalonate kinase (MVK), phosphomevalonate kinase (PMK) and diphosphomevalonate decarboxylase (MVD) to form isopentenyl-diphosphate (IPP) or dimethylpropenyl pyrophosphate (DMAPP) (Zhang et al., 2007). IPP and DMAPP condense to form geranyl pyrophosphate (GPP). The combination of GPP and one IPP unit generates farnesyl pyrophosphate (FPP) as a precursor to sesquiterpene, eventually forming a sesquiterpenoid by means of isomerization, cyclization, complexation and so on (Yun-Fei et al., 2011).

PMK, a member of the GHMP kinase superfamily, is an important site of regulation of terpenoid metabolism in organisms that synthesize terpenoid skeletons by the traditional MVA pathway, is an essential enzyme in the synthesis pathway and the catalytic reaction step is the rate-limiting step in the MVA to IPP pathway(Chang et al., 2008). There are three rate-limiting reactions that are continually dependent on ATP in this pathway, where PMK catalyzes the second rate-limiting reaction, which acts to transfer the gamma phosphate group on ATP to mevalonate-5-phosphate (MVAP) generation of mevalonate-5-diphosphate (MVAPP). PMK is one of the key enzymes that control the entire metabolic pathway (Garcia and Keasling, 2014).

We analyzed the data of the *M. chamomilla* transcriptome data obtained by our group in the early stage and found a large number of genes involved in the MVA pathway. In this study, we first cloned the cDNA sequence of *PMK* gene (*McPMK*) from *M. chamomilla* and analyzed the bioinformatics, which laid the foundation for the further study on the role of *PMK* gene in terpenoids synthesis pathway in *M. chamomilla*.

Materials and methods

Plant material and reagents

In this study, we used the *M. chamomilla* cultivated in glass greenhouse of college of horticulture and gardening of Yangtze University as material to collect the leaves. After frozen in liquid nitrogen, and stored in -80 ℃ refrigerator for the cloning of *McPMK*. MiniBEST Plant RNA Extraction kit, PrimeScript ™ 1st Strand cDNA Synthesis Kit, one-step RTPCR kit, Agarose Gel DNA Purification Kit Ver. 4.0, pMD19-T vector, dNTP, RNase and DNA polymerase were purchased from Dalian Bao Bio Co. (TaKaRa). Primer synthesis and DNA sequencing were entrusted to Shanghai Sangon Biotechnology Company, China.

Cloning of *McPMK*

Total RNA was isolated from frozen plant tissues using the TaKaRaMiniBEST Plant RNA Extraction kit. Based on the *PMK*unigene sequence of *M. chamomilla* transcriptome data (GenBank accession No. MG778909), a pair of specific primers, McPMK-u: 5'GTGAAAAAAGATGGCTGTGGTTGC-3' and McPMK-d: 5'-CTTCTGGGAGTGGAAGTGCAAATG-3' were designed and synthesized. The first-strand cDNA was synthesized using PrimeScript cDNA Synthesis Kit.

McPMK cDNA was amplified with the one-step RTPCR kit under the following conditions: 94°C for 4 min; 30 cycles of amplification at 94°C for 30 s, 62°C for 30 s, and 72°C for 90 s; and a final extension at 72°C for 10 min. The amplified products purified using agarose gel DNA purification Kit Ver. 4.0. The purified PCR product was cloned into the pMD19-T vector, and then transformed into Escherichia coli DH5α. Positive clones were selected and sent to Shanghai Sangon Biotechnology Company for sequencing.

Bioinformatic analysis of McPMK

The obtained nucleotide sequence and deduced amino acid sequence were compared by a BLAST tool on the http://www.ncbi.com (NCBI) website. The isoelectric point (pI) and molecular weight of the deduced McPMK protein were computed using the software of Compute pI/Mw Tool at http://web.expasy.org/compute_pi/. Multiple sequence alignment was performed using the Vector NTI 10.0 program. A phylogenetic tree was constructed through the neighbor-joining (NJ) method with CLUSTALX 2.0 and MEGA 6.0 software.

Results

Cloning and characterization of *McPMK*

According to the sequence of the transcriptome of *M. chamomilla*, a pair of specific primers was designed and the *McPMK* gene was cloned using thetemplate of reverse transcribed cDNA. The sequencing results showed that the full-length cDNA was 1782 bp and contained a 1479 bp ORF, which encodes a total of 493 amino acids (Fig. 1). The results of BLASTN analysis at NCBI site showed that the nucleotide sequence of *McPMK* had a high similarity to those of other *PMK* genes. The nucleotide sequence of *McPMK* was 93%, 85%, 84%, 76%, 75%, 74%, 74% and 72% identical to those of the PMK genes from *Chamaemelum nobile*, *Helianthus annuus*, *Taraxacum kok-saghyz*, *Citrus sinensis*, *Ziziphus jujuba*, *Hevea brasiliensis*, *Prunus avium* and *Spinacia oleracea*, respectively (Table 1). Collectively, these results indicated that the gene we cloned is the cDNA sequence of *McPMK*.

Characterization of the deduced McPMK protein

ExPASy-ProtParam online analysis of *McPMK* gene encoded protein, the results showed that the protein molecular weight and PI were 53.58KDa and 5.77. Multiple alignment results showed that the protein sequence of *McPMK* gene shared high homology with PMK protein sequences of other plants, all of which were more than 70%. The McPMK protein showed 93%, 83%, 76%, 73%, 73%, 75% and 74% identical to the counterparts of *C.nobile* (ASJ80966.1), *H.annuus* (XP_021970137.1), *Panaxnoto ginseng* (AIK21784.1), *Populus euphratica* (XP_011028097.1), *Vitis vinifera* (XP_002275808.1),*Daucus carota* (XP_017223228.1) and *Ziziphus jujube* (XP_015868326.1), respectively. Meanwhile, McPMK protein was found to have a GHMP kinase superfamily-specific ATP binding site (Fig. 2). The above analysis further shows that the *McPMK* gene is a member of the PMK gene family.

Molecular evolution analysis

Based on the deduced amino acid sequence of *McPMK* and the amino acid sequence of other plant *PMK* genes, phylogenetic tree was constructed to study the evolutionary relationships among different plant *PMK* genes. As shown in Fig. 3, the evolutionary tree is divided into two major categories, one is monocotyledonous, *Zea mays* of Poaceae; one is dicotyledonous plants, including Asteraceae, Araliaceae, Cucurbitaceae and Malvales. Phylogenetic analysis of PMK protein showed that McPMK was clustered in Asteraceae, and the closest relationship with the *C. nobile*, the most distant genetic relationship with *Z. mays*. Probably because both *M. chamomilla* and *C. nobile* belong to Asteraceae dicotyledonous plants, while *Z. mays* belongs to Poaceae monocotyledonous plants. Explaining the PMK genes of Asteraceae plant have a common evolutionary ancestor.

```
1       GTAAACGGTTACTGTTTCATTCTCAGTCCCATTTGCTTGTTCTAAGGTATCTCCGTCAACAATCCATAACTT
73      GTTCTAGGTTGTTCGAGGTTAATCTTTCAAACACAGACTGTAAACTTGTGAAAAAAGATGGCTGTGGTTGCT
25                                                              M  A  V  V  A
145     TCGGCTCCGGGGAAGGTTTTAATGGCTGGTGGTTATTTGGTATTGGAGAGGCCTAATGCAGGAATCGTGCTT
49       S  A  P  G  K  V  L  M  A  G  G  Y  L  V  L  E  R  P  N  A  G  I  V  L
217     AGTACTAATGCCCGGTTTTATGCGATTCTTAAGCCTCTTTATGATGCACTTGAATCTGACATTTTGGCAGCG
73       S  T  N  A  R  F  Y  A  I  L  K  P  L  Y  D  A  L  E  S  D  I  L  A  A
289     GAGTGGATGGATCTTAAAGTCAACTCTCCTCAAATGTCAAGAGAAACTACATACAAATTGTCATTAAAAGAT
97       E  W  M  D  L  K  V  N  S  P  Q  M  S  R  E  T  T  Y  K  L  S  L  K  D
361     TTTACACTACAGTGTTTGAGTGAATCAAGGAACCCCTTTGTCGAGTATGCAGTCCAATATTCCATAGCAGCA
121      F  T  L  Q  C  L  S  E  S  R  N  P  F  V  E  Y  A  V  Q  Y  S  I  A  A
433     GCATATGCCACACTCGACAAGAATGAAAGGAATAGATTGCTTAAATTACTGTCACAAGGTATGGATATTACA
145      A  Y  A  T  L  D  K  N  E  R  N  R  L  L  K  L  L  S  Q  G  M  D  I  T
505     ATCCTAGGTTGCAATGACTTCTATTCATATCGGAATCAGATTGAAGCACGTGGCCTCCCTTTAGTCCCAGAC
169      I  L  G  C  N  D  F  Y  S  Y  R  N  Q  I  E  A  R  G  L  P  L  V  P  D
577     TCATTAGCGACTCTTCAGCCATTCACATCAATTACTTTCAATGCCGAAGAATCAAATGTAGAAAACTCCAAA
193      S  L  A  T  L  Q  P  F  T  S  I  T  F  N  A  E  E  S  N  V  E  N  S  K
649     CCAGAAGTTGCAAAAACTGGATTAGGGTCGTCTGCGGCTATGACAACTGCTGTAGTAGCTGCTTTGCTAAAT
217      P  E  V  A  K  T  G  L  G  S  S  A  A  M  T  T  A  V  V  A  A  L  L  N
721     TATCTAGGAGTTGTTGATCTTCCGCTTTATAGTACAAATCAAAAGAATGATAAAATTTTGGATCTTGATTTA
241      Y  L  G  V  V  D  L  P  L  Y  S  T  N  Q  K  N  D  K  I  L  D  L  D  L
793     GTACATATGATCGCTCAAACAGCGCATTGTATCGCTCAAGGGAAAGTTGGCAGTGGATTTGATGTTAGCTCT
265      V  H  M  I  A  Q  T  A  H  C  I  A  Q  G  K  V  G  S  G  F  D  V  S  S
865     GCTGTTTATGGCAGTCATCGTTATGTTCGTTTTTCGCCGAATATCATTTCTTCAGCTCAGGAAACTGTCGGT
289      A  V  Y  G  S  H  R  Y  V  R  F  S  P  N  I  I  S  S  A  Q  E  T  V  G
937     AACACACCCTTAGAAGAAGTCATTGGCGATGTCTTGAAGGGAAAGTGGGATCATGAAAGGACTAAATTCTCG
313      N  T  P  L  E  E  V  I  G  D  V  L  K  G  K  W  D  H  E  R  T  K  F  S
1009    TTGCCACCATTAATGAATCTGATTTTGGGAGAACCAGGAAGTGGAGGATCGTCTACACCGTCAATGGTTGGC
337      L  P  P  L  M  N  L  I  L  G  E  P  G  S  G  G  S  S  T  P  S  M  V  G
1081    GCTGTCAAGAAATGGCAAAAGTCTGACCCACAAAAGTCAAAGGATACGTGGAACAAGTTGTCAGAGGCAAAT
361      A  V  K  K  W  Q  K  S  D  P  Q  K  S  K  D  T  W  N  K  L  S  E  A  N
1153    TCAGCACTTGTAGCACAGTTTAACTTGTTAAGTAAATCAGCTGCAGATAGCTGGGACTCGTACAAAGCTGTC
385      S  A  L  V  A  Q  F  N  L  L  S  K  S  A  A  D  S  W  D  S  Y  K  A  V
1225    ATCACCGGCTGCAGCATGTTAAAATCAGAAAAGTGGATGGAGCAATTCAGTGAAGCAACTCATGTAGAAATC
409      I  T  G  C  S  M  L  K  S  E  K  W  M  E  Q  F  S  E  A  T  H  V  E  I
1297    GTTAAAGCATTATTGGGAGCTAGAGATGCAATGCTTAAGATTCGGTTCCATATGAGGCAGATGGGCGACGCT
433      V  K  A  L  L  G  A  R  D  A  M  L  K  I  R  F  H  M  R  Q  M  G  D  A
1369    GCAGGCATTCCGATCGAACCTGAATCACAAACTCGACTCCTGGACGTGACCATGAACACAGAAGGTGTCTTG
457      A  G  I  P  I  E  P  E  S  Q  T  R  L  L  D  V  T  M  N  T  E  G  V  L
1441    TTAGGTGGAGTTCCTGGTGCAGGTGGATTTGATGCCGTTTTTGCTATTACTTTAAGTGACTCAAGTACAAAT
481      L  G  G  V  P  G  A  G  G  F  D  A  V  F  A  I  T  L  S  D  S  S  T  N
1513    TTGACCAAAATATGGAGTTTCCATAATGTTTTGGCCATGCTAGTGCGGGAAGATCCGCGCGGTGTTTCTATA
505      L  T  K  I  W  S  F  H  N  V  L  A  M  L  V  R  E  D  P  R  G  V  S  I
1585    GAAAGTGGTGATCCTCGGGCCAAGTAATATATCTCAAGTAACGCATTCTTGTTCATTGTATTGTCATATCAA
529      E  S  G  D  P  R  A  K  *
1657    TGGCACATTTGCACTTCCACTCCCAGAAGTATGGTGTTTATTCATTGACGGTTTCTCATTTCTTATACGTGA
```

Fig. 1: Nucleotide sequence and deduced amino acid sequence of *McPMK*. The initial codon and the stop codon are highlighted in red square box.

Table 1. Nucleotide sequence of *McPMK* similarity to the *PMK* genes from other plant species.

Species	Accession No.	E-value	Identity/%
Chamaemelum nobile	KX894316.1	0.0	93
Helianthus annuus	XM_022114445.1	0.0	85
Taraxacum kok-saghyz	KT899411.1	0.0	84
Citrus sinensis	XM_006471412.2	0.0	76
Ziziphusjujuba	XM_016041830.1	0.0	75
Hevea brasiliensis	AF429385.1	5e-155	74
Prunus avium	XM_021952904.1	4e-151	74
Spinacia oleracea	XM_021996129.1	9e-98	72

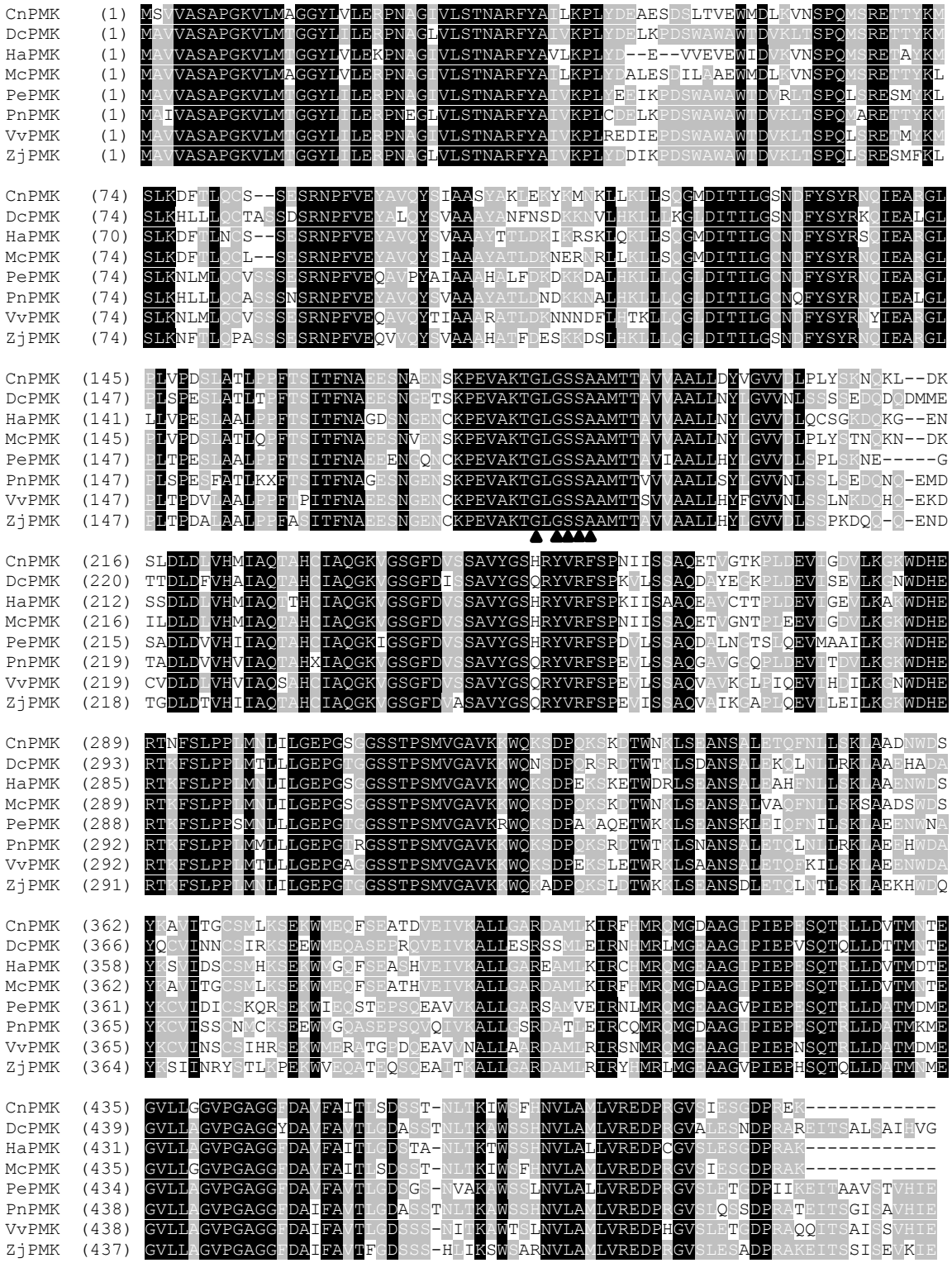

Fig. 2: Sequence multi-alignment of the deduced McPMK protein with other PMK proteins. The species name and GenBank accession number are shown as following: CnPMK, *C. nobile* (ASJ80966.1); DcPMK,D. carota (XP_017223228.1); HaPMK, *H. annuus* (XP_021970137.1); McPMK, *M. chamomilla*; *P. euphratica* (XP_011028097.1); PnPMK, *P. notoginseng* (AIK21784.1); VvPMK, *Vitis vinifera* (XP_002275808.1); ZjPMK, *Z. jujube* (XP_015868326.1). The black triangle indicates the ATP binding site.

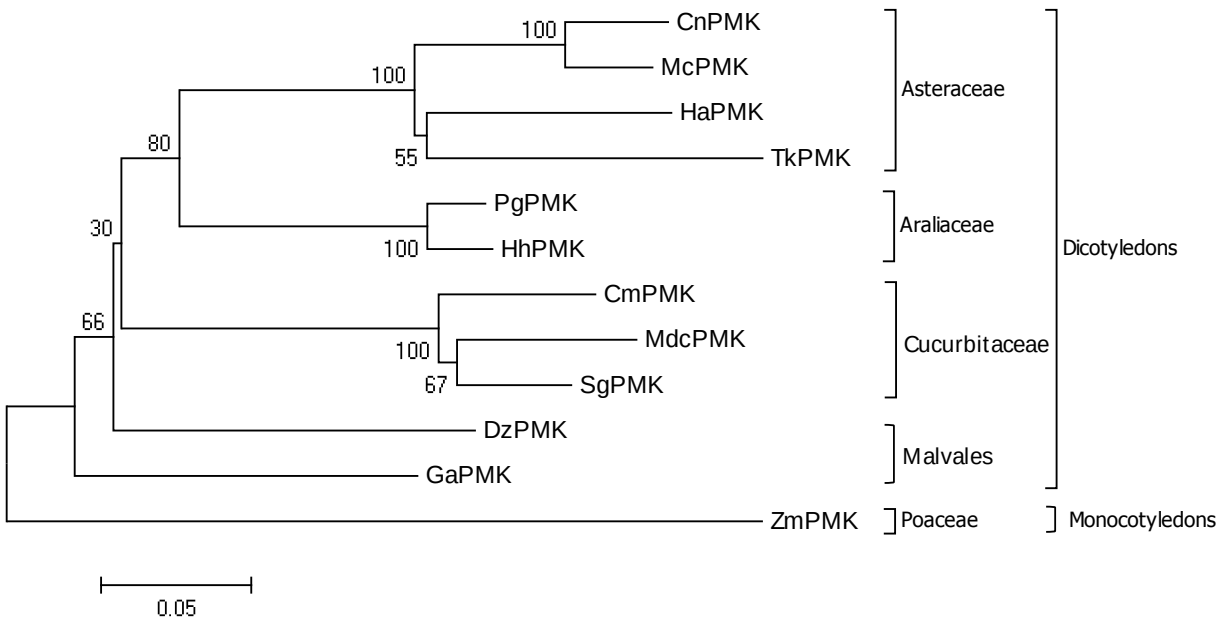

Fig. 3: Phylogenetic tree of PMKs from different species using the neighbor-joining method.The species, protein names and GenBank accession number are as following: *M. chamomilia*: McPMK; *C. nobile:* CnPMK (ASJ80966.1); *H. annuus*: HaPMK (XP_021970137.1);*T. kok-saghyz*: Tkpmk (AMB19700.1); *Panax ginseng*: PgPMK (AGZ15314.1); *Hedera helix*: HhPMK (APY22352.1); *Cucurbita moschata*: CmPMK (XP_022951530.1); *Momordica charantia*: MdcPMK (XP_022145447.1); *Siraitia grosvenorii*: SgPMK (AEM42973.1); *Durio zibethinus*: DzPMK (ALD84323.1); *Gossypium arboretum*: GaPMK (XP_019080389.1); *Z. mays*: ZmPMK (NP_001149345.1).

Discussion

Terpenoids are the most abundant natural products and 60% of known natural products can be attributed to these substances (Buntrock, 2012). Terpenoids are one of the largest families of plant secondary metabolites that have important physiological roles in living organisms and are widely used in industrial and agricultural production and in medical and health care (Henry et al., 2015). However, the amount of terpenoids in organisms is very low, often reaching only one part per million in the plant, and it is extremely difficult to chemically synthesize most of the natural products with important biological activity. The extraction of these active ingredients from raw materials such as plants can no longer satisfy people's needs. In recent years, along with the research on terpenoid biosynthesis pathway and its key enzyme, synthetic biology and metabolic engineering based on molecular biology technology have become one of the most potential ways to improve the production of terpenoid in plants.

Tanshinones, paclitaxel, a-Bisabolol, chamazulene and other terpenoids have important medicinal and economic value, while there are few reports on the terpenoid biosynthesis pathway in *M. chamomilla*. The whole plant of *M. chamomilla* can be used as medicine. In this study, *McPMK* gene with 1782 bp in length was cloned from leaves of *M. chamomilla*. The amino acid sequence of *McPMK* gene is highly homologous to the PMK protein of MVA pathway in other plants. And it also contains a GHMP kinase superfamily-specific ATP binding site, suggesting that the *McPMK* gene is the second rate-limiting enzyme in the MVA pathway and is also one of the key enzymes that control the entire MVA metabolic pathway (Zhang et al., 2007). The McPMK protein as terpenoid biosynthetic pathway key enzyme, has important research value. Studies have shown that the *MK* and *PMK* gene expression is low in plants

MVA pathway, increased their expression can increase the production of terpenoids in plants, while if PMK overexpression in plants can increase the content of isoprenoid derivatives (Redding-Johanson et al., 2011; Ajikumar et al., 2008; Singh et al., 2012).

Therefore, in the follow-up experiment, the eukaryotic expression vector of *McPMK* gene will be constructed by means of genetic engineering and transformedto *M. chamomilla* by *Agrobacterium tumefaciens*-mediated genetic transformation system, and genetically modifying it. We hope to obtain transgenic plant with high content of terpenoid, ultimately improve the medicinal and economic value of *M. chamomilla*. This research will help to understand the pathway and regulation mechanism of terpene biosynthesis and provide candidate gene for further study.

Conflict of interest statement

Authors declare that they have no conflict of interest.

Acknowledgement

This work was supported by the National Natural Science Foundation of China (31400603).

References

Akbar Ajikumar, P. K., Tyo, K., Carlsen, S., Mucha, O., Phon, T. H., Stephanopoulos, G., 2008. Terpenoids: opportunities for biosynthesis of natural product drugs using engineered microorganisms. Mol. Pharm. 5(2), 167-190.

Bohlmann, J., Keeling, C. I., 2008. Terpenoid biomaterials. Plant J. Cell Mol. Biol. 54(4), 656-669.

Bonifacio, M., Rigo, A., Guardalben, E., Bergamini, C., Cavalieri, E., Fato, R., 2012. α-Bisabolol is an effective proapoptotic agent against bcr-abl+ cells in synergism with imatinib and nilotinib. Plos One. 7(10), 1172-1178.

Buntrock, R. E., 2012. Review of nature's chemicals: the natural products that shaped our world. J. Chem. Educ. 89(5), 580-581.

Chadwick, M., Trewin, H., Gawthrop, F., Wagstaff, C., 2013. Sesquiterpenoids lactones: Benefits to plants and people. Int. J. Mol. Sci. 14(14), 12780-12805.

Chang, Q., Yan, X. X., Gu, S. Y., Liu, J. F., Liang, D. C., 2008. Crystal structure of human phosphomevalonate kinase at 1.8 a resolution. Proteins Struct. Funct.Bioinform. 73(1), 254-258.

Cheng, A. X., Lou, Y. G., Mao, Y. B., Lu, S., Wang, L. J., Chen, X. Y., 2007. Plant terpenoids: biosynthesis and ecological functions. J. Integr. Plant Biol. 49(2), 179-186.

Garcia, D. E., Keasling, J. D., 2014. Kinetics of phosphomevalonate kinase from, saccharomyces cerevisiae. Plos One. 9(1), e87112.

Henry, L. K., Gutensohn, M., Thomas, S. T., Noel, J. P., Dudareva, N., 2015. Orthologs of the archaeal isopentenyl phosphate kinase regulate terpenoid production in plants. P. Natl. Acad. 112(32): 10050-10055.

Murti, K., Panchal, M. A., Gajera, V., Solanki, J., 2012. Pharmacological properties of Matricariarecutita: A review. Pharmacologia. 3(8), 348-351. Pirzad, A., Alyari, H., Shakiba, M. R., Zehtabsalmasi, S., 2006. Essential oil content and composition of german chamomile (*Matricaria chamomilla* L.) at different irrigation regimes. J. Agron. 5(3), 451-455.

Pirzad, A., Alyari, H., Shakiba, M. R., Zehtabsalmasi, S., 2006. Essential oil content and composition of german chamomile (*Matricaria chamomilla* L.) at different irrigation regimes. J. Agron. 5(3), 451-455.

Raal, A., Orav, A., Püssa, T., Valner, C., Malmiste, B., Arak, E., 2012. Content of essential oil, terpenoids and polyphenols in commercial chamomile (*Chamomilla recutita, L.*Rauschert) teas from different countries. Food Chem. 131(2), 632-638.

Redding-Johanson, A. M., Batth, T. S., Chan, R., Krupa, R., Szmidt, H. L., 2010. Targeted proteomics for metabolic pathway optimization:

Application to terpene production. Metab. Eng. 13(2), 194-203.

Sayadi, V., Mehrabi, A. A., Saidi, M., Nourollahi, K., 2014. In vitro culture and callus induction of chamomile (*Matricaria chamomilla* L.) explants under different concentrations of plant growth regulators. Int. J. Biosci. 4(10), 206-211.

Singh, P., Batth, T. S., Juminaga, D., Dahl, R. H., Keasling, J. D., Adams, P. D., Petzold, C. J., 2012. Application of targeted proteomics to metabolically engineered escherichia coli. Proteomics. 12(8), 1289-1299.

Son, Y. J., Kwon, M., Ro, D. K., Kim, S. U., 2014. Enantioselective microbial synthesis of the indigenous natural product (−)-α-bisabolol by a sesquiterpene synthase from chamomile (*Matricaria recutita*). Biochem. J. 463(2), 239-248.

Vranová, E., Coman, D., Gruissem, W., 2013. Network analysis of the mva and mep pathways for isoprenoid synthesis. Annu. Rev. Plant Biol. 64(1), 463-476.

Yonekura-Sakakibara, K., Saito, K., 2009. Functional genomics for natural product biosynthesis. Nat. Prod. Rep. 26(11), 1466-1487.

Yun-Fei, H. E., Gao, W., Liu, T. S., Wen-Yuan, L. I., Huang, L. Q., 2011. Research advances of diterpene synthase. Acta Pharmaceut. Sin. 46(9), 1019-1025.

Zhang, C. B., Sun, H. X., Gong, Z. J., 2007. Plant terpenoid natural metabolism pathways and their synthases. Plant Physiol. Commun. 43(4), 779-786.

How to cite this article:
Xu, Y., Liu, X., Chang, X., Xu, F., 2018. Cloning and sequence analysis of phosphomevalonate kinase gene (McPMK) from *Matricaria chamomilla*. Int. J. Curr. Res. Biosci. Plant Biol. 5(2), 10-17. **doi:** https://doi.org/10.20546/ijcrbp.2018.502.002