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Monoterpene Synthase from *Lavandula angustifolia* and Solid-Phase Microextraction- Gas Chromatography-Mass Spectroscopy Analysis of its Aroma Profile

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ABSTRACT

Lavandula angustifolia Mill. (Labiatae) is commercially used as a fragrance and flavor in cosmetics, food and pharmaceutical industries. This aromatic species is widely grown and cultivated in various temperate regions of Persia. There are diverse reports around composition of the oil of this plant in Iran representing linalool derivatives or 1,8-cineol and camphor as the major compounds. In addition, some mono- and sesquiterpene synthases have been cloned and identified from *L. angustifolia*. In the present study, the aroma profile of one cultivated plant in Tehran has been extracted and analyzed via Headspace Solid-Phase Microextraction technique coupled with gas chromatography- mass spectroscopy. In order to determine the sequence of the active terpene synthase in this plant, mRNA was prepared, 3' and 5'-RACEs-PCR Method employed, cDNA sequenced and finally aligned with other recognized terpene synthases. The results showed that the cultivated plant leaves mainly comprised linalool (31.0%), linalyl acetate (18.2%) and lavandulyl acetate (10.7%) apposite of the essential oil of plant reported from dry and temperate areas. Sequencing the cDNA cloned from this plant revealed the presence of a monoterpene synthase absolutely similar to limonene synthase, responsible in formation of limonene, terpinolene, camphene and some other cyclic monoterpenes in *L. angustifolia* young leaves.

Keywords: Monoterpene synthase, *Lavandula angustifolia*, Labiatae, Headspace Solid phase Microextraction, Essential oil.

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INTRODUCTION

Terpenes and terpenoids are classified among the important bioactive natural compounds. Most of them exhibited biological activity such as sterols, saponins and volatile oils. Recent genetic approaches are capable of isolation and characterization of the biosynthetic enzymes especially by development of molecular biological techniques. For example, sequence comparison of mono-, sesqui- and diterpene synthases revealed that they have a similar structure [1, 2]. Purification and identification of a number of monoterpene synthases indicated that they all have similar properties (like molecular mass, a divalent metal ion and neutral pH optimum requirements). The interesting point is that a terpene synthase is able to form multiple products [1, 3]. For example the pinene synthases (from sage and grand fir) can catalyze the production of both α - and β -pinenes [4].

Geranyl diphosphate (GDP) is well known as a natural substrate for monoterpene synthases. It is found that all terpene synthases employ GDP without the formation of free intermediates [5]. Since GDP could not be directly cyclized, because of the C₂-C₃ (*trans*) double bond, both isomerization and cyclization have to be created in biosynthesis [1, 4]. For this reason, monoterpene cyclases are able to catalyze both the isomerization and cyclization reactions. There have been a few monoterpene synthases involving in production of acyclic products such as myrcene and linalool [4, 6].

Most of the Lamiaceae (Labiatae) plant species produce considerable amounts of essential oils. Essential oils contain a complex mixture of aromatic and volatile compounds and are widely used in cosmetics as fragrance, in the food industry as flavoring and in the household products as scenting agents [7]. The genus *Lavandula* comprises 30 known species, three of them are economically important including *Lavandula angustifolia*, *Lavandula latifolia* and the hybrid *L. angustifolia* × *L. latifolia* [8]. The constituents of the essential oil of lavender have been frequently reported and linalool and linalyl acetate are mainly described as the most abundant compounds. Other characteristic components that have been identified are limonene, 1, 8-cineol, camphor, lavandulol, lavandulyl acetate and α -terpineol [9].

Literature review show that two monoterpene synthases (LaLIMS and LaLINS) and one sesquiterpene synthase (LaBERS) were cloned from lavender. LaLIMS catalyze the formation of (R)-(+)-limonene, terpinolene, (1R, 5S)-(+)-camphene, (1R, 5R)-(+)- α -pinene, β -myrcene and traces of α -phellandrene. The second enzyme LaLINS produce exclusively (R)-(-)-linalool, the main component of lavender essential oil [8]. In the present study, we aimed to analyze the aroma profile of a cultivated *L. angustifolia* in Tehran, *via* Headspace Solid-Phase Microextraction technique coupled with gas chromatography- mass spectroscopy (SPME-GC-MS), in order to determine the main components compared to other reports from diverse arid and temperate areas. Furthermore, the cloning of a monoterpene synthase related to the flavor of *L. angustifolia* essential oil has been described for the first time from Iranian cultivated plant leaves.

MATERIALS AND METHODS

General Procedure

Chemical reagents and solvents were purchased from Merck Co. (Germany). Gel and plasmid extraction kits were from Invitrogen Co. (UK). RNeasy Plant Mini Kit was prepared from Qiagen (USA), and vectors and E. coli competent cells were from Invitrogen. Polymerase chain reactions were performed on a Primus 25 (Peqlab, Germany) thermal cycler.

Plant Materials

The plant used in this study was grown in the Herboratum of Faculty of Pharmacy, Tehran University of Medical Sciences. The plant identified by Dr. Gholamreza Amin, Department of Pharmacognosy (the same institution) as *Lavandula angustifolia*. Lavender young leaves were harvested from one *L. angustifolia* plant grown outside in a mini-garden under natural conditions.

cDNA Preparation

Total RNA was extracted from the early growing stage of the *L. angustifolia* leaves using RNeasy Plant Mini Kit and reverse transcribed with oligo (dT) primer [ad: 5'-GCT GTC AAC GAT ACG CTA CGT AAC GGC ATG ACA GTG TTT TTT TTT TTT TTT TTT-3'] designed to have an adaptor sequence at the 5'-end to obtain the cDNA for the 3'-RACE method. The resulting cDNA of the leaves was used as a template in subsequent PCR with Taq or KOD Dash DNA polymerases with various combinations of sense and antisense degenerate primers. The temperature program was designed on thermal cycler and started at 94°C (3 min), followed by 33 cycles (94°C for 30 s, 46°C for 30 s and 72°C for 1min), then 72 °C for 2 min. Elongating times were different (30-60 s) based on the expected length of the amplified fragment. The size of monoterpene synthase sequences (partial not complete) was estimated by gel electrophoresis. PCRs were repeated using the same primers to obtain more amounts of DNA, for cloning into the vector. The similarity of cloned sequences to known sequences was checked with NCBI pBLAST.

3'and 5'-RACEs-PCR Method

The 3'-RACE method was used to amplify the 3'-end of the monoterpene synthase. First, the polymerase chain reaction for 3'-RACE was carried out with degenerate primer [5'- TAG ATG ATG TTT ACG AT-3'] and an adaptor primer [amm: 5'- GGC CAC GCG TCG ACT AC-3']. The PCR was performed by KOD Dash DNA polymerase (0.2 µL), amm primer (0.3 µL), degenerate primer (0.6 µL), dNTP (0.1mM, 2 µL), DNA template (1 µL) and appropriate amounts of recommended buffer, DMSO and water by the temperature program (94°C for 20 s, 40°C for 15 s and 72°C 30 s, 33 cycles). The subsequent PCR gave a 900 bp product, which was electrophoresed on 0.8% agarose gel and purified using the Gel-M™ Gel Extraction System (Viogene). The resulting DNA fragment was cloned into the plasmid vector pCR 2.1 using the

TOPO TA cloning kit (Invitrogen). Specific antisense primer [LAV-I: 5'-ACC CCA TTC GTA GTT GTC GCA GAA CG-3'] designed on the basis of the sequence obtained from 3'-RACE.

A poly C tail was appended to the cDNA for 5'-RACE by terminal dideoxynucleotidyl transferase, and the cDNA was purified on a PCR-M column (Viogene). To clone the 5'-end of the transcript (5'-RACE), cDNA was synthesized from mRNA with Reverse Transcriptase and gene specific reverse primers based on the known sequence parts (LAV-I). The purified product (64 μ L) was amplified with terminal deoxynucleotidyl transferase (1 μ L), dCTP (10 mM, 5 μ L) and 16 μ L of TdT buffer in PCR at 37°C for 90 min, 70°C for 10 min and 4°C for 10 min to synthesize an oligo (dC) -tail. The cDNA (1 μ L) was used as a template in PCR (temperature program: 94°C for 30 s, 52°C for 20 s, 74°C 50 s, 35 cycles) with dNTPs (10 mM, 2 μ L), oligo (dT) anchor primer as for 3'-RACE (0.3 μ L), gene specific primer (10 μ M, 0.3 μ L), KOD Dash DNA polymerase (0.8 μ L) and appropriate amounts of buffer and water. Furthermore, a touchdown protocol similar to that of used for 3'-RACE was applied.

SPME- GC-MS Analysis

Head space Solid-phase microextraction (SPME) coupled to gas chromatography and mass spectrometry has been applied for analyzing the essential oil directly evaporated from *L. angustifolia* young leaves. GC-MS was performed on a cross-linked 5% methyl phenyl siloxane (HP-5, 30 m \times 0.25 mm i.d., 0.25 μ m film thickness), carrier gas, He; split ratio, 1:15; quadruple mass spectrometer Hewlett-Packard 6890) operating at 70 eV ionization energy. In order to obtain the retention index for each compound, normal alkanes (C8-C25) were injected at the same temperature and condition. The components were identified by comparison of their retention indices (RI, DB-5) and mass fragmentation with those reported in the literature [10]. Percentage of each component was calculated on the basis of the peak area.

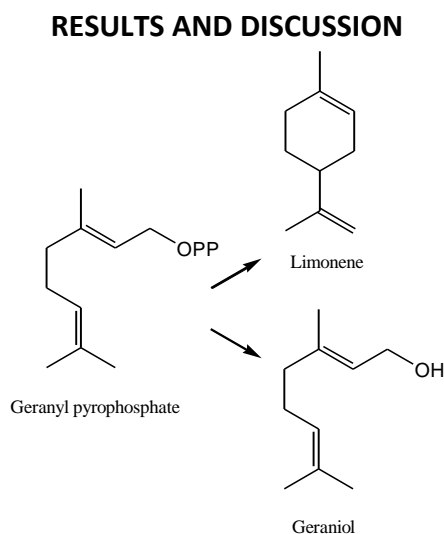


Fig 1: Cyclic and linear monoterpenes biosynthetic pathway.

In the present study, PCR process were performed with degenerate primers designed regarding to the conserved amino acid sequence in various plant terpene synthases. Sequence analysis was carried out using the cDNA prepared from the young leaves of *L. angustifolia* as a template. The results of partial cloning revealed the core sequence containing the 3'-flanking region of limonene synthase, on the other hand the partial sequence was similar to monoterpene synthase genes reported in GenBank in advance, so that the 5'- and 3'-ends were cloned by RACE-PCR to get the full-length sequences. In order to clone the full length of limonene synthase cDNA, the 5'-RACE technique was utilize to complete the remained 5'-region (Figs 1, 2). The transcript from leaves' mRNA was identical and previously designed as LaLIMS [8].

The open reading frame of the above mentioned limonene synthase consists of 1809 bp, coding for protein with 602 amino acids and the predicted molecular mass of 70.3 kDa. Literature review shows two characteristic motives for monoterpene synthases as DDxxD and (N,D)D(L,I,V)x(S,T)xxxE, which are reported to completely conserved in limonene synthase sequences [8]. These motives are essential for substrate (*e.g.* Mn²⁺, Mg²⁺) binding and ionization [11]. A distinguished part of the active site of such enzymes, which are frequently found in monoterpene synthases, is LQLYEASFL and well conserved in LaLIMS [12].

M. longifolia	-----GAAAAACA-TAGAAAGAGAGCGGAAGG---AAAGATTAATCATGGCTCTCAA	48
P. citriodora	AATCCAAGAAAAATAACAGATAAAAAAGGGAAATCTAAAGATTAATC---GATCTCAA	57
L. angustifolia_lin	-----ATGTCGATCA-----ATA-	13
L. angustifolia_lim	-----ATGTCTATCA-----TTAG	14
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M. longifolia	AGTGTTTAGTGTGCAACTCAAATGGCGATTCTAGCAAGCTAACGAGATGTCTTC--AA	106
P. citriodora	AAATGTATACCGGTGTGATGAATATGGCGTTTCTATGAAGCCAGCTAATATCTTCATAA	117
L. angustifolia_lin	-----TCAACATG-----CCTGC--AGCC-----GCCGCTC	39
L. angustifolia_lim	CATGCATGTGGGAATCCTTAATAG-----CCTGC--AGCTTA-TAACCATCTTCGCAA	65
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M. longifolia	CCCTCACACTTGAAATCCTCTCCAAAATTGT---TAT-----CTAGCACTA--ACA	152
P. citriodora	CTCCGGCAGTAGCAA--CTCTCAAATTTGTGCGGTGTCTCTCTACTAGTACTAGAGCA	175
L. angustifolia_lin	-----CGCC-----TTT---C-	49
L. angustifolia_lim	CTTGACAGGAGAG-----CTTCAAAGCCGCGCCATGT-----CT---CTT---CT	105
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M. longifolia	GTAGTAG-TCGGTCTCGCCTCCGTGTGTATTGCTCCTCCTCGCAACT-----C	199
P. citriodora	GCTACAGCTCGCCTCCGCTCCGGTGCCTGCTCGTT--GCAACT-----C	220
L. angustifolia_lin	GCTGCT-----C---ACAACACTACA-----T	66
L. angustifolia_lim	ACTGCCGCCCACTCGCCTCCGGTTTCTTGCGCCAC---ACAACACTAGAATTAAGTCC	162
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M. longifolia	ACTACTGAG---AGACGATCCGGAACACTACAACCCTTCTCGTTGGGATGTGCAATTCATC	256
P. citriodora	AGTGATCAA---CGACGATCTGGAACTACAGTCTCCTTTTGGAAATACCGATTATAT	277
L. angustifolia_lin	GTGATGAAACCCGACGCTCCGGAACACTACCGCCCTCGGCTTGGGATFCCAACACTACATC	126
L. angustifolia_lim	GTCGATGAAACCCGACGCTCCGGAACACTACAACCCTACCGCTTGGGATFCCAACACTACATC	222
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M. longifolia	CAATCCCTCCACAGTGATTATGAGGAGGACAAACACGCGATTAGGGCTTCT--GAGCTG	313
P. citriodora	CTATCTCTCAACTGTGACTATGAGGACGAGAGACGCATGAGAGGGGCTGCTGGTGAGCTG	337
L. angustifolia_lin	CAATCTCTCAATTTCTAGTATAAGGAAAAGAAGTGCTTGACAAGGCTAGAA---GGGCTG	183
L. angustifolia_lim	CAATCCCTCGACAATCAGTATAAGAAAGAGAGGTACTCGACAAGACACGCT---GAGCTG	279
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M. longifolia	GTCACCTTGGTGAAGATGGAATTGGAGAAAAGAAACGATCATATTCGACAACCTTGAGTTG	373
P. citriodora	GTTGAGCAAGTGAAGATGCTGATGGAGAAAAGAAACAGATCCTATTGTACAGCTTGAGTTG	397
L. angustifolia_lin	ATTGAGCAAGTGAAGAACTGAAGGGGACAAAAATGGAGGCTGTTCAACAATTGGAGTTG	243
L. angustifolia_lim	ACTGTGCAAGTGAAGAAGCTGCTGGAGGAAGAAATGGAAGCGGTTCAAAAAGTTGGAATTG	339
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M. longifolia	ATCGATGACTTGACAGAGSATGGGCTGTCCGATCATTTCCAGAAATGAGTTCAAAGAATC	433
P. citriodora	ATTGATGACCTTCAAAGCTGGCTCTCTCTCACTATTTTCGAGAAAAGAAATCAAGGAAATA	457
L. angustifolia_lin	ATTGATGACTCGCAGAATCTGGGATATCATATATTTTCAAGATAAAAATTAACATATC	303
L. angustifolia_lim	ATTGAGGATTTGAAGAACCTGGGAATATCTTACCATTAAAGGACAATATCCAACAGATT	399
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M. longifolia	TTGCTCTATATATCTCGACCAT---CACTATTACAAGAACCCTTTTCCAAAAGAAGAA	490
P. citriodora	TTATTCA---ACATCAGTACTATA--TATGATGACAAGAAC-----AGGGAG	499
L. angustifolia_lin	TTGAATTTGATATATAATGATCACAATATTTTACGATAGTGA-----AGCTGAAGGA	357
L. angustifolia_lim	TTAAATCAAATATATAATGACCAAAATGTTGCCACAACAGTGA-----AGTGAAGAA	453
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M.longifolia	TGGGATCATCGAGCCACGTCAGCATGCAAGTGAAGGATAATGATGGGCAAAGTCAACGC	1073
P.citriodora	TGGGATCATTGAGCCCTCGTCAACATGAAAATGAAGGATAATGATGGCAAAGCTCTTGC	1091
L.angustifolia_lin	TCCACTCTTTGAGCCCTCATCAATATGGATATCAAAGAAAAGTGGCCACCAAGATCATAAC	941
L.angustifolia_lim	GGGAACCTTTGAGCCCTCATCAATATGGTTATCAGAGAGAACTTGTCGCCAAGATTATTGC	1049
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M.longifolia	TCTGATTACGGTGATCGATGATATTTATGATGTCTATGGCACCTTAGAAGAACTCGAACA	1133
P.citriodora	TCTAATAACCACGTTAGATGATGTTTACGATGTCTACGGTACCTTAGAAGAACTCGAGCT	1151
L.angustifolia_lin	CCTAATCACATCTTTAGACGATGTTTACGATATCTATGGCACGTTAGATGAATTGCAACT	1001
L.angustifolia_lim	TCTAGCAACAGTTGTAGATGATGTTTACGATGTATATGGTACGTTAGAGGAACTGGAAC	1109
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M.longifolia	ATTCACGTACCTCATTTCGAA-GATGGGATATAAACTCAATCGACCAACTTCCCATTACA	1192
P.citriodora	GTTCCACCGAGGCGATTAGAA-GATGGGAAATCAGTTCAATTGACCAACTTCCTAACTACA	1210
L.angustifolia_lin	ATTTACGAAC-TTATTTGAAAGATGGGATAATGCATCAATCGGCCGACTTCCTGAATACT	1060
L.angustifolia_lim	ATTTACAGATGCCATTTCGGA-GATGGGATCGTGAATCAATCGACCAACTTCCTTACTACA	1168
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M.longifolia	TGCAACTGTGCTTTCTTGCACTCAACAACCTCGTCGATGATACATCGTACGATGTTATGA	1252
P.citriodora	TGCAACTCTGTTTTCTTACAATCAACAACCTTTGTCGACGATACTGCCTACGATGTCATGA	1270
L.angustifolia_lin	TGCAATTGTTCTATTTTCGCAATCCACAACCTTTGTTTTCCGAGGTGGCTTACGACATTCTCA	1120
L.angustifolia_lim	TGCAGCTATGCTTTTTGACTGTCAACAACCTTTGTTTTTCGAGCTTGCTCATGATGTTCTTA	1228
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M.longifolia	AGGAGAAAGGCGTCAACGTTATACCCTACCTGCGGCAATCGTGGGTGGATTGGCGGATA	1312
P.citriodora	AAGAGAAAGATATCAACATCATCCCCTATCTACGAAAATCGTGGGTGGATTGGCTGAGG	1330
L.angustifolia_lin	AAGAAAAGGTTTTCACTAGTATTGTATATTTACAGAGATC-TGGGTGGATTGCTAAAAG	1179
L.angustifolia_lim	AGGATAAGAGTTTCAACTGCTTACCACATTTACAGAGATCGTGGCTAGACTTGGCTGAAG	1288
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M.longifolia	AGTATATGGTAGAGGCACGGTGGTTCTACGCGGACACAAACCAAGTTTGAAGAGTATT	1372
P.citriodora	CATATCTGGTAGAGGCGAAATGGTTCTATGGCGGATATAAACCAAAATTTG-----	1380
L.angustifolia_lin	GATACCTAAAAGAGGCAAAG-GGTACAATAGTGGATACACGCCAACCTCGAGGAATATT	1238
L.angustifolia_lim	CATATCTGTGCGAGGCTAAGTGGTACCACAGTAGATATACACCGAGCTCGAGGAATATC	1348
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M.longifolia	TGGAGAACTCATGGCAGTCGATAAGTGGGCCCTGTA-TGTTAACGCACATATCTTCCGA	1431
P.citriodora	-----	
L.angustifolia_lin	TCGACAACGCATTCATGACAAT-AGGGGCCCTCCGGTACTATCGCAAGCTTATTTTACA	1297
L.angustifolia_lim	TCAATATTGCAAGAGTTTCAGTTACGTGTCCCACTA-TAGTTTCACAAATGTACTTTGCA	1407
M.longifolia	GTAACAGATTCGTTTACAAAGGAGACCGTCGACAGTTTGTACAAATACCACGATTTAGTT	1491
P.citriodora	-----	
L.angustifolia_lin	TTA-----GGAAGCTCATCATCGAGAGCATGTACGAATATGACAACATACTT	1344
L.angustifolia_lim	TTACCAATTCGATAGAGAAACCGGTCATCGAGATCATGTACAAATACCACGACATACTT	1467
M.longifolia	CGTTGGTCATCCTTCGTTCTGCGGCTTGCTGATGATCTGGGAACCTCGGTGGAAGAGGTG	1551
P.citriodora	-----	
L.angustifolia_lin	CGCGTTTCGGGAATGCTCGTGAGGCTTCCCGATGACCTAGGAACATCATCGTTTCGAGATG	1404
L.angustifolia_lim	TACCTCTCAGGAATGCTTCTAAGGCTTCCCTGATGATCTAGGAACAGCATCGTTTGAGTTG	1527

M.longifolia	AGCAGAGGCGATGTGCCGAAATCACTTCAGTGTACATGAGTACTACAATGCATCGGAG	1611
P.citriodora	-----	
L.angustifolia_lin	GAGAGAGGCGACGTGCCGAAATCGGTCCAGCTATACATGAAGGAAACAAATGCTACGGAG	1464
L.angustifolia_lim	AAGAGAGGTGATGTGCAAAAAGCAGTCCAGTGTATATGAAGGAAAGAAATGTTCTTGAA	1587
M.longifolia	GCGGAGGCGCGGAAGCACGTGAAATGGCTGATAGCGGAGGTGTGGAAGAAGATGAATGCG	1671
P.citriodora	-----	
L.angustifolia_lin	GAGGAGGCGGTGGAGCACGTGAGGTTTTTGAATCGGGAGGCGTGAAGAAGATGAACACG	1524
L.angustifolia_lim	AATGAGGCACGAGAACATGTGAAGTTTCTGATTCGGGAGGCGTGAAGCAGATAAACACC	1647
M.longifolia	GAGAGGGTGTGCAAGGATTCTCCATTCGGCAAA-GATTTTATAGGATGTGCAGCTGATTT	1730
P.citriodora	-----	
L.angustifolia_lin	GCGGAGGCGGCGGTGATTCTCCGTT-AGTGAGTGACGTGGTGGCGGTGGCGGCAATCT	1583
L.angustifolia_lim	GCGATGGCGACCG---ATTGTCCATTTACTGAA-GATTTTGCTGTGGCTGCAGCGAATCT	1703
M.longifolia	AGGAAGGA-GGCGCAGTTGATGTACCATAATGGAGATGGGCACGGCACACAACATCCTAT	1789
P.citriodora	-----	
L.angustifolia_lin	TGGAAGGGCGGCGCAGTTTATGTATTTTCGACGGAGATGGTA-----ACCAGTCTAG	1634
L.angustifolia_lim	TGGAAGAGTGGCGAATTTGTGTACGTGACGGAGATGGTTTTGGCGTGAACACTCAA	1763
M.longifolia	AATACATCAACAAATGACCAGAACCTTATTCGAGCCCTTTGCATGAGAGGTGATGATGAT	1849
P.citriodora	-----	
L.angustifolia_lin	TTTGCAGCAGTGGATTGTGAGCATGCTGTTCGAGCCGTACGCATGA-----	1680
L.angustifolia_lim	AATATATGAACAGATTGGAACCCCTGATGTTCGAGCCATATCCCTAA-----	1809
M.longifolia	GAGCCATCGTTTACTTACTTAAATTTACCAAAGTTTTTCGAAGGCATAGTTTGAATTC	1909
P.citriodora	-----	
L.angustifolia_lin	-----	
L.angustifolia_lim	-----	
M.longifolia	TTCAAGCACCAAAATGGAATAAGGAGAATCGGCTCAAACAACGTGGCATTGCCACCACGT	1969
P.citriodora	-----	
L.angustifolia_lin	-----	
L.angustifolia_lim	-----	
M.longifolia	GAGCACAAGGAGAGTCTGTGTCGTTTATGGATGAACTATTCATTTTATGCATGTAATA	2029
P.citriodora	-----	
L.angustifolia_lin	-----	
L.angustifolia_lim	-----	
M.longifolia	ATTAAGTTCAAGTTCAAGAGCCTTCTGCATATTTAACTATGTACTTG	2076
P.citriodora	-----	
L.angustifolia_lin	-----	
L.angustifolia_lim	-----	

Fig 2: Alignment of nucleotide sequences (cDNA) of the isolated monoterpene synthase (*L. angustifolia_lim*) with other limonene synthases (*M. longifolia* and *P. citriodora*) and linalool synthase of lavender (*L. angustifolia_lin*). Alignment was carried out using free ClustalW software (<http://www.ch.embnet.org/index.html>).



Fig 3: Tree view for cloned cDNA from *Lavandula angustifolia* in comparison to other similar monoterpene synthase mRNA (using free software of BLAST, NCBI).

Limonene is one of the cyclic monoterpenes, found in plant kingdom, as the simple example for cyclization of terpenoids. Its biosynthesis is started from geranyl pyrophosphate (GPP), which is a common precursor for all monoterpenes. Limonene synthases promote the cyclization of GPP into limonene and have been identified and reported from *Perilla*, *Mentha* and *Abies* [4, 13, 14]. Terpene synthases (TPS) have been cloned from several plant species and their phylogenetic relationships well found. These enzymes have been classified into six sections TPSa-f. Although there have been some differences among the various groups, there are several conserved motifs in all TPSs such as mTPSs signature arginine-rich N-terminal RR(x8)W motif [15, 16].

Table 1: Chemical composition of the essential oil of *Lavandula angustifolia* young leaves obtained by SPME

Compound Names	Retention Indices DB-5	Percentage (%)
myrcene	987	3.0
limonene	1030	1.3
1,8-cineole	1034	0.9
<i>trans</i> -ocimene	1057	2.2
linalool	1099	31.0
camphor	1140	0.9
borneol	1165	1.2
terpinen-4-ol	1180	2.9
α -terpineol	1190	6.3

linalyl acetate	1260	18.2
lavandulyl acetate	1289	10.7
Caryophyllen+	1404	5.2
cyclic monoterpenes	-	13.5
linear monoterpenes	-	65.1
sesquiterpenes	-	5.2
total	-	83.8

The results of head space SPME-GC-MS analysis of the aroma profile of *L. angustifolia* showed that linalool (31.0%), linalyl acetate (18.2%), lavandulyl acetate (10.7%) and alpha-terpineol (6.3%) were found as the major compounds (Table 1). Although the profile of the main components is in agreement with those reported in the literature [7, 17, 18], there is a wide variation in the quantitative composition of lavender oil. Genotype, altitude, microclimate and cultivation condition can affect the composition of the oil [19, 20]. For instance, 1, 8-cineole, camphor and borneol were found as the major compounds from *L. angustifolia* which had been collected from Yazd, an arid and temperate area located at the central part of Iran [21].

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