Manipulation of the precursor supply for high-level production of longifolene by metabolically engineered *Escherichia coli*

Yujin Cao ^{1,*}, Rubing Zhang ^{1,*}, Wei Liu ¹, Guang Zhao ¹, Wei Niu ², Jiantao Guo ², Mo Xian ¹, Huizhou Liu ¹

¹ CAS Key Laboratory of Biobased Materials, Qingdao Institute of Bioenergy and Bioprocess Technology, Chinese Academy of Sciences, Qingdao, China

² Department of Chemistry, University of Nebraska-Lincoln, Lincoln, Nebraska, United States

Supplementary figure captions

Figure S1 Codon optimization of the longifolene synthase gene. wlgfs, wild-type longifolene synthase gene; olgfs, codon-optimized longifolene synthase gene. The identical codons are shown in dark blue and the optimized codons are shown in light blue. The amino acid encoded by each codon is shown as its abbreviation.

Figure S2 Time-course profiles for cell density (OD_{600}) and mevalonate production during shake-flasks culture of strain BL21/pA-mvaES. Cultures were performed in 500 ml shake flasks containing 50 ml liquid M9 mineral medium supplemented with 1 mM MgSO₄ and 20 g/L glucose. Error bars represent the range of three independent fermentations.

Figure S3 Schematic diagram of the expression constructs containing the genes encoding longifolene biosynthesis pathway. lgfS, longifolene synthase; ispA, *E. coli* FPP synthase; isoA, *B. trispora* FPP synthase; erg20, *S. cerevisiae* FPP synthase; mvaE, acetoacetyl-CoA synthase/HMG-CoA reductase; mvaS, HMG-CoA synthase gene; erg19, mevalonate kinase; erg8, phosphomevalonate kinase; erg12, mevalonate pyrophosphate decarboxylase; idi1, IPP isomerase.

Figure S1

wlgfS	ATGGCTCAGAT <mark>TTC</mark> TAAATG <mark>TTCGTCA</mark> CTGTC <mark>CGCGAGT</mark> TGAACGAATC <mark>C</mark> TCCATCATC M A Q I S K C S S L S A E L N E S S I I	60
olgfS	ATGGCTCAGAT <mark>CA</mark> GTAAATG <mark>CTCT</mark> TCTCTGTCTGCTGA <mark>AC</mark> TGAACGAATCTTCTATCATC	60
wlgfS	TCTCATCATCATGGAAATCTGTGGGGACGACGATTTCATACAATCTCTTAAGTCGTCCAAT SHHHGNLWDDDFIQSLKSSN NATACATGGAAAATCTGTGGGGGGGGGGGGGGGGGGGGGG	120
olgis		120
wigis	GGGGCACCTCAATATCATGAACGCGCTGCGAAACTTGTTGAAGAAATCAAGAATTTAGTT G A P Q Y H E R A A K L V E E I K N L V GGTGCTCCGCAGTACCACGAACGTGCTGCTAAACTGCTTGAAGAAATCAAAAACCTGGTT	180
wlafs		240
olgfS	V S E M K D C N D D L I R R L Q M V D I GTTTCTGAAATGAAAGACTGCAACGACGACCTGATCCGTCGTCTGCAGATGGTTGACATC	240
wlqfS	TTTGAATGTCT <mark>A</mark> GG <mark>A</mark> ATTGATCG <mark>G</mark> CACTTTCAGCATGAAAT <mark>A</mark> CA <mark>A</mark> GTTGCTCTTGATTAC	300
olgfS	F E C L G I D R H F Q H E I Q V A L D Y TTCGAATGCCTGGGTATCGACCGTCACTTCCAGCACGAAATCCAGGTTGCTCTCGACTAC	300
wlgfS	GT <mark>GTAC<mark>AG</mark>ATATTGGAACCAGCTGGAAGG<mark>C</mark>ATCGGTAT<mark>TGG</mark>ATC<mark>AAG</mark>AGATTC<mark>C</mark>CTTATC</mark>	360
olgfS	V Y R Y W N Q L E G I G I G S R D S L I GT <mark>CTAC</mark> CGCTA <mark>C</mark> TGGAACCAGCTGGAAGGTATCGGTATCGGTTCTCGTGACTCTCTGATC	360
wlgfS	AAAGATTTCAATGCTAC <mark>A</mark> GCTTTGGG <mark>A</mark> TTTCG <mark>G</mark> GCTCT <mark>C</mark> CGACTGCATCG <mark>A</mark> TATAACGTT	420
olgfS	K D F N A T A L G F R A L R L H R Y N V AAAGA <mark>CTTCAAC</mark> GCTACCGCTCTGGGTTTCCGTGCTCTGCGCGTCTGCACCGTTACAACGTT	420
wlgfS	TCCTCAGATGTCTTGGAGAATTTCAAGAACGAAAACGG <mark>G</mark> CAGTTCTTCTGCAGTTCCACG S S D V L E N E K N E N G O E E C S S T	480
olgfS	TCTTCTGACGTTCTGGAAAACTTCAAAAACGAAAACGGTCAGTTCTTCTGCTCTTCTACC	480
wlgfS	GTTGAAGAAAAAGAAGT <mark>GA</mark> GATGCATGTTGACGTTATTTC <mark>AGCTTCA</mark> GAAATTTCATTT V E E K E V R C M L T L F R A S E I S F	540
olgfS	GTTGAAGAAAAAGAAGTTCGTTGCATGCTGACCCTGTTCCGTGCTTCTGAAATCTCTTTC	540
wlgfS	CC <mark>CGG</mark> AGAAAAGT <mark>GATGGACGAG</mark> GCAAAAGGC <mark>GTTCACAAGAATATCTA</mark> ACCAAAGTT P G E K V M D E A K A F T T E Y L T K V	600
olgfS	CC <mark>GGGT</mark> GAAAAAGTTATGGACGA <mark>A</mark> GCTAA <mark>A</mark> GCTTTCAC <mark>CAC</mark> CGAATA <mark>C</mark> CTGACCAAAGTT	600
wlgfS	TTAACGGGAGTGGATGTAACGGACGTCAATCAAAGCCTTTTGAGAGAAGTGAAGTATGCC L T G V D V T D V N Q S L L R E V K Y A	660
olgfS	CTGACCGGTGTTGACGTTACCGACGTTAACCAGTCTCTGCGTGAAGTTAAATACGCT	660
wlgfS	CTGGAGTTTCCATGGCATTGCAGTTTGCCGAGATGGGAGGCAAGGAGCTTTATCGAAATA L E F P W H C S L P R W E A R S F I E I	720
olgfS	CTGGA <mark>ATTCCCGTGGCACTGCTCTCTGCCGCGTTGGGAAGC</mark> TCGTTCTTTCATCGAAATC	720
wlgfS	TGTGGACAAAACGATTCATGGCTCAAGTCGATTATGAACAAACGAGTTTTAGAGTTGGCG C G Q N D S W L K S I M N K R V L E L A	780
olgiS	TGCGGTCAGAACGACTCTTGGCTGAAATCTATCATGAACAAACGTGTTCTGGAACTGGCT	780
wlgfS	AAATTGGACTTCAATATTTTGCAATGGGCACATCATAGAGAACTACAGCTTCTGTCAAGT K L D F N I L Q W A H H R E L Q L L S S	840
olgis	AAACTGGACTTCAACATCCTGCAGTGGGCTCACCACCGTGAACTGCAGCTGCTGTCTCT	840
wlgfS	TGGTGGTCACAATCGGATATAGCGCAGCAGCAGAATTTCTATCGGAAGCGTCACGTGGAATTT WWSQSDIAQQNFYRKRHVEF TGGTGGTGACATCACATCACCACAACTTCTACCCTAAACCTCAACCTTCAATTC	900
olgis		000
olats	TACTTATGGGTGGTTATAGGCACGTTCGAGCCGGAGTTTTGAACATGCAGAATCACCTTT Y L W V V I G T F E P E F S T C R I T F TACCTGTGGGGTTGTTATCGGTACCTTCGAACCGGAATCACCTGCCGTATCACCTTC	960 960
wlafs	CCAAAAATCTCTACACTGATGACTATTCTAGATGACCTCTACGATACTCACGGAACGTTG	1020
olgfS	A K I S T L M T I L D D L Y D T H G T L GCTAAAATCTCTACCCTGATGACCATCCTGGACGACCTGTACGACACCCACGGTACCCTG	1020
wlqfS	GAACAACT <mark>C</mark> AAAATCTTCAC <mark>AGAGGGGGGGGGGGGAGTGGGATCTTTCGTTAGTA</mark> GACCG <mark>C</mark>	1080
olgfS	E Q L K I F T E G V K R W D L S L V D R GAACA <mark>gCTgAAAATCTTCAC</mark> CGA <mark>AGGTGTTAAACGTTGGGACCTGTCTGGTTGACCG</mark> T	1080
wlgfS	CTTCC <mark>A</mark> GACTACAT <mark>A</mark> AA <mark>GATTACA</mark> TTCGAATTCTTCCT <mark>C</mark> AACAC <mark>A</mark> TCTAATGAATTGATT	1140
olgfS	L P D Y I K I T F E F F L N T S N E L I CT <mark>GCC</mark> GGACTACATCAA <mark>AATC</mark> ACCTTCGAATTCTTCCTGAACACCTCTAACGAACTGATC	1140
wlgfS	GCTGAAGTTGC <mark>G</mark> AAAAC <mark>GCAA</mark> GA <mark>GCGGGAT</mark> ATGTC <mark>A</mark> GC <mark>C</mark> TACAT <mark>A</mark> CG <mark>A</mark> AAAAC <mark>A</mark> TGGGAA	1200
olgfS	A E V A K T Q E R D M S A Y I R K T W E GCTGAAGTTGCTAAAAC <mark>CCA</mark> GGA <mark>ACGTGACATGTC</mark> TGCTTACATCCGTAAAACCTGGGAA	1200
wlgfS	CG <mark>A</mark> TACCT <mark>T</mark> GAAGCTTA <mark>TTTGCAA</mark> GAAGC <mark>G</mark> GAATGGAT <mark>A</mark> GC <mark>A</mark> GCTCG <mark>A</mark> CACGT <mark>CCCT</mark> ACG	1260
olgfS	R Y L E A Y L Q E A E W I A A R H V P T CGTTACCT <mark>G</mark> GAAGCTTA <mark>CC</mark> TGCAGGAAGCTGAATGGATCGCTGCTCGTCACGTTCCGACC	1260
wlgfS	TTTGATGAGTACATGAAGAATGG <mark>C</mark> AT <mark>A</mark> TC <mark>CA</mark> GTTCTGG <mark>G</mark> ATGTGTAT <mark>ACTA</mark> AATTTGTAT	1320
olgfS	F D E Y M K N G I S S S G M C I L N L Y TT <mark>CGACGAATACATGAAAAACGGTATCTCTTCTTCTGGTATGTGCATCCTGAACC</mark> TGTAC	1320
wlgfS	TC <mark>GCTTCTGTTA</mark> ATGGG <mark>GCAA</mark> CTTCT <mark>A</mark> CCTGACGACGTTCTGGA <mark>GCAA</mark> ATACACTCTCCA	1380
olgfS	S L L L M G Q L L P D D V L E Q I H S P TCTCTGCTGCTGATGGGTCAGCTGCCGGACGACGTTCTGGA <mark>ACAGATCCACTCTCC</mark> G	1380
wlgfS	TC <mark>C</mark> AA <mark>GATCCACGAGCTTGTA</mark> GAATTGACGGC <mark>CAGACTGGTA</mark> GACGACTC <mark>A</mark> AAGGATTTT	1440
olgfS	SKIHELVELTARLVDDSKDF TCTAAAATCCACGAACTGGTTGAACGACTCTGAAAGACTTC	1440
wlgfS	GAGACGAAGAAGGTTGGTGG <mark>G</mark> GAGTT <mark>A</mark> GCTTC <mark>A</mark> GGTAT <mark>A</mark> GA <mark>GTG</mark> TTACGT <mark>G</mark> AAAGACAAC	1500
olgfS	E T K K V G G E L A S G I E C Y V K D N GA <mark>AACCAAAAAA</mark> GTTGGTGGTGG <mark>ACTGGCTTC</mark> TGGTATC <mark>GAATGCTACGTTAAAGACAAC</mark>	1500
wlgfS	CCTGAATGTAC <mark>A</mark> CTGGAAGATGCTTC <mark>A</mark> AATCATCT <mark>A</mark> AATGG <mark>CCTC</mark> CTTGATCTTACCGTT	1560
olgfS	P E C T L E D A S N H L N G L L D L T V CC <mark>GGAATGCAC</mark> CTGGAAGA <mark>CGCTTCTAACCACCTGAACGGTCTGCTGGACCTG</mark> ACCGTT	1560
wlgfS	AAGGAATTGAATTGGGAGTTTGT <mark>AA</mark> GGCATGAC <mark>AGCGTG</mark> GC <mark>C</mark> TTGTGTTTCAAGAAGTTC	1620
olgfS	K E L N W E F V R H D S V A L C F K K F AAAGAACTGAACTGGGAATTCGTCGTCGTCACGACTCTGTGCTCTGTGCTTCAAAAAATTC	1620
wlgfS	GC <mark>CTTCAACGTTGC<mark>ACG</mark>AGG<mark>CCTCCGACT</mark>TATCTACAAATAC<mark>AGAGACGG</mark>CTTTGACGTT</mark>	1680
olgfS	A F N V A R G L R L I Y K Y R D G F D V GCTTTCAACGTTGCTCGTGGTCTGCGTCTGATCTACAAATACCGTGACGGTTTCGACGTT	1680
wlafs	TCTAACCAGGAGATGAAAACCCACATATTCAAAATTCTCATCCATC	1737
olgfS	S N Q E M K T H I F K I L I D P L T * TCTAACCAGGA <mark>A</mark> ATGAAAACCCACATCTTCAAAATCCTGATCGA <mark>CCCGCTGACCTAA</mark>	1737

Figure S2



