

Combining metabolic and protein engineering of a terpenoid biosynthetic pathway for overproduction and selectivity control

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A common strategy of metabolic engineering is to increase the endogenous supply of precursor metabolites to improve pathway productivity. The ability to further enhance heterologous production of a desired compound may be limited by the inherent capacity of the imported pathway to accommodate high precursor supply. Here, we present engineered diterpenoid biosynthesis as a case where insufficient downstream pathway capacity limits high-level levopimaradiene production in *Escherichia coli*. To increase levopimaradiene synthesis, we amplified the flux toward isopentenyl diphosphate and dimethylallyl diphosphate precursors and reprogrammed the rate-limiting downstream pathway by generating combinatorial mutations in geranylgeranyl diphosphate synthase and levopimaradiene synthase. The mutant library contained pathway variants that not only increased diterpenoid production but also tuned the selectivity toward levopimaradiene. The most productive pathway, combining precursor flux amplification and mutant synthases, conferred approximately 2,600-fold increase in levopimaradiene levels. A maximum titer of approximately 700 mg/L was subsequently obtained by cultivation in a bench-scale bioreactor. The present study highlights the importance of engineering proteins along with pathways as a key strategy in achieving microbial biosynthesis and overproduction of pharmaceutical and chemical products.

GGPP synthase | levopimaradiene synthase | metabolic engineering | *Escherichia coli* | molecular reprogramming

Metabolic engineering is the enabling technology for the manipulation of organisms to synthesize high-value compounds of both natural and heterologous origin (1–4). In the case of heterologous production, well-characterized microorganisms are used as production hosts because targeted optimization can be performed using widely available genetic tools and synthetic biology frameworks (5, 6). One important application of engineered microbial systems is geared toward the synthesis of terpenoid natural products (7–9). Terpenoids represent one of the largest classes of secondary metabolites that includes pharmaceuticals, cosmetics, and potential biofuels candidates (8, 10–12). Metabolic engineering approaches to produce terpenoids in microbial systems such as *Escherichia coli* and yeast have commonly focused on increasing the precursor flux into the heterologous terpenoid pathway by rerouting endogenous isoprenoid metabolism (13–15). These engineering strategies have relied heavily on changing the enzyme concentrations in the product pathway.

Many properties of a metabolic pathway, however, are not limited solely by the enzyme concentration, as is particularly true for the terpenoid pathway. In nature, terpenoid biosynthesis is regulated at multiple metabolic branch points to create large structural and functional diversity (16–18). In the major metabolic branch point in terpenoid biosynthesis, the prenyl transferases and terpenoid synthases catalyze the formation of a wide range of structurally diverse acyclic and cyclic terpenoid molecules (17).

Sequence analysis of these enzymes showed that they are paralogous proteins evolved through gene duplications that subsequently diverged in functional roles to catalyze the formation of different terpenoid structures (16, 17, 19). Particularly, terpenoid synthases generate enzyme-bound carbocation intermediates that undergo a cascade of rearrangements and quenchings of carbocations to create structural diversity (20). These enzymes are highly promiscuous (21), and the functional promiscuity is often associated with unwanted product formation and poor catalytic properties (22). Thus in an engineered terpenoid pathway, these enzymes lead to low metabolic fluxes and large byproduct losses, limiting yield improvement of the desired product molecules. In some cases, the buildup of intermediate metabolites elicits stress responses detrimental to cell growth (23, 24). Thus, the ability to tune a heterologous terpenoid pathway at regulatory nodes would be a valuable approach both to confer an overproduction phenotype and to minimize toxicity in microorganisms.

In the present work, we engineered *Escherichia coli* to produce levopimaradiene, the diterpenoid gateway precursor of the pharmaceutically important plant-derived ginkgolides (25–28). The biosynthesis of levopimaradiene from simple carbon sources (glucose or glycerol) starts from the formation of the precursors isopentenyl diphosphate (IPP), and dimethylallyl diphosphate (DMAPP) derived from the 2-C-methyl-D-erythritol-4-phosphate (MEP) pathway in *E. coli*. Geranylgeranyl diphosphate synthase (GGPPS) then catalyzes the condensation of IPP and DMAPP to the linear diphosphate intermediate geranylgeranyl diphosphate (GGPP). In the final step, levopimaradiene synthase (LPS) catalyzes the conversion of GGPP to levopimaradiene via a complex reaction cascade of cyclization, rearrangement, and proton transfers (Fig. 1A). The promiscuous function of LPS also results in the formation of isomeric side products such as abietadiene, sandaracopimaradiene, and neoabietadiene (29, 30) (Fig. 1B). The functional expression of codon-optimized genes encoding for GGPPS and LPS in *E. coli* only generated minute quantities of levopimaradiene. Levopimaradiene synthesis was increased when GGPPS–LPS expression was coupled with the systematic amplification of genes in the upstream MEP pathway to elevate flux toward IPP and DMAPP; however, titers remained low. We postulated that the threshold of levopimaradiene

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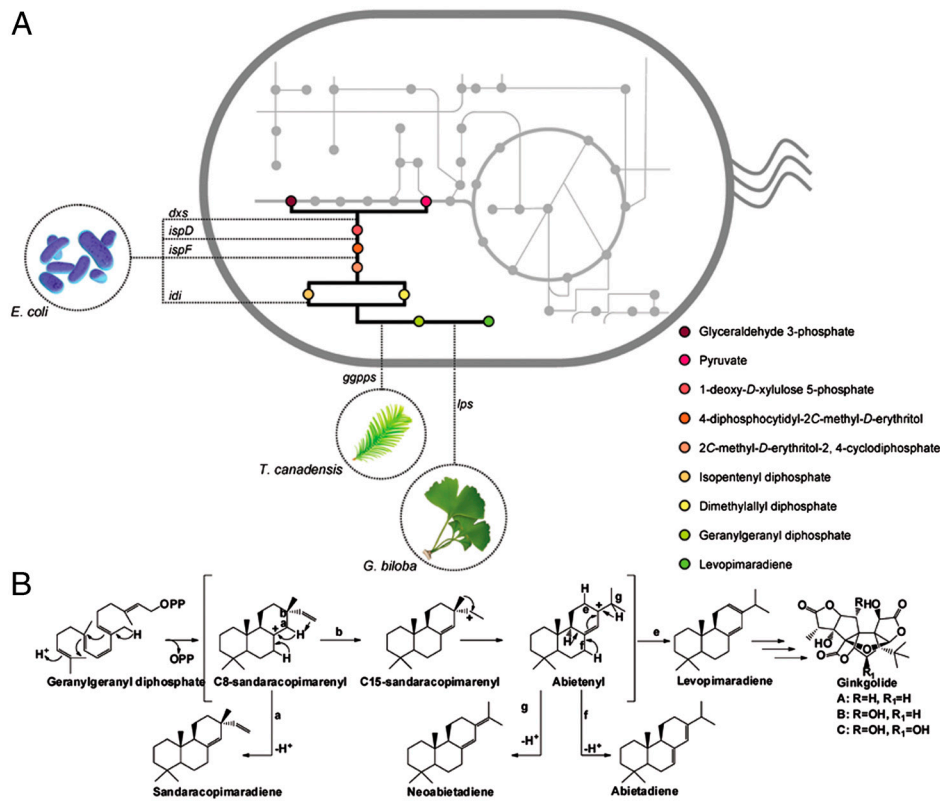


Fig. 1. (A) Engineering levopimaradiene synthesis in *E. coli*. A plant-derived pathway was constructed by introducing *T. canadensis* *gpps* and *G. biloba* *lps* codon-optimized genes. To amplify the endogenous precursor pools of GGPPS substrates (IPP and DMAPP), copy numbers of rate-limiting steps (*dxs*, *idi*, *ispD*, *ispF*) in the MEP pathway were amplified by additional episomal expression. (B) General reaction mechanism of “LPS-type” enzymes. Levopimaradiene, the major product of *G. biloba* LPS is the gateway precursor of ginkgolides. Coproducts of LPS include abietadiene, neoabietadiene, and sandaracopimaradiene that stem from the different deprotonation patterns throughout intermediates in the reaction cascade.

production was limited by inherent GGPPS–LPS capacity. To overcome this constraint, we adopted the principle of molecular reprogramming through engineering combinatorial mutations of the GGPPS–LPS pathway. This approach was inspired by natural systems, in which biosynthetic pathways undergo molecular reprogramming processes (e.g. via mutations of transcription regulators and enzymes) to accommodate important changes in metabolite concentrations (31–34). By combining protein and metabolic engineering, we achieved approximately 2,600-fold improvements in levopimaradiene productivity and demonstrated a strategy to harness the potential of engineered biosynthetic pathway for large scale microbial production of valuable molecules.

Results and Discussion

Levodipimaradiene Production Improvement via Precursor Pathway Amplification. The initial attempt to synthesize levopimaradiene from *E. coli* by coexpressing codon-optimized genes encoding for GGPPS and LPS resulted in only a small amount of levopimaradiene, 0.15 mg/L (Table S1), with no detectable amount of the related isomers produced by LPS. The first step taken to improve productivity was a metabolic engineering approach via incremental overexpression of the bottleneck enzymatic steps in the MEP pathway, namely *dxs*, *idi*, *ispD*, and *ispF* (Fig. 1A). Indeed, this approach improved levopimaradiene production (Table S1). The highest production of approximately 92 mg/L was achieved by inclusion of approximately 5 additional copies of the MEP pathway genes. At this level, the levopimaradiene isomers abietadiene, sandaracopimaradiene, and neoabietadiene (Fig. 1B) were also identified in the culture, at product fractions of 11%, 2%, and trace amounts, respectively (Fig. S1). However, further increasing the MEP pathway from approximately 5 to approximately 10 copies was not accompanied by additional increases in levopimaradiene production. In fact, the titer was lower (approximately 23 mg/L) than when MEP pathway was amplified by approximately 5-fold (Table S1). These results demonstrated that stepwise improvement of precursor flux, a strategy commonly employed in metabolic engineering, did not yield an incremental amplification of terpenoid molecules.

Hence, we postulated that the efficiency of the regulatory node in terpenoid biosynthesis, the GGPPS–LPS (prenyltransferase–terpenoid synthase) portion of the pathway, is rate-limiting under high IPP and DMAPP precursor flux (16–18, 20–22). Quantitative RT-PCR confirmed that higher MEP pathway transcript levels were achieved with 10-fold amplification of the MEP pathway, likely resulting in a buildup of toxic intermediates that negatively affected overall pathway flux (23). Thus, we set out to reprogram GGPPS and LPS to develop mutant pathways that confer high-level levopimaradiene production in the 10-copy MEP pathway background.

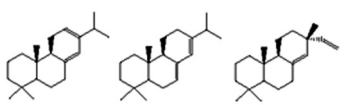
Probing the Putative Binding Pocket in LPS to Design Improved Variants. Fully combinatorial strategies to search for important mutations in LPS are impractical due to the lack of a suitable high-throughput screen. To circumvent this limitation, we first constructed a homology structure for the second active site of LPS that was used as a guide to probe residues important for catalytic function. In the second active site of an “LPS-type” enzyme, the bicyclic (+)-copalyl diphosphate (CPP) intermediate (derived from the deprotonation of GGPP in the first active site) undergoes a diphosphate-ionization cyclization. The resulting C8-sandaracopimaranyl cation intermediate is further deprotonated at two alternative sites to release isopimaradiene or sandaracopimaradiene end products. However, this intermediate can also undergo intramolecular proton transfer and 1,2-methyl migration to yield abietenyl cation. Subsequent deprotonation of abietenyl cation at four possible sites then produces abietadiene, levopimaradiene, neoabietadiene, and palustradiene (29, 30).

Following the construction of the LPS model, fifteen residues constituting the binding pocket were selected (Fig. S24). We perturbed these residues using phylogeny-based mutation (35, 36) to determine if they conferred a different production phenotype. Specifically, residue replacements were determined from paralogous LPS-type enzymes that are functionally different from LPS (Fig. S2B), namely *Abies grandis* abietadiene synthase (AS) (37), *Picea abies* AS, and *P. abies* isopimaradiene synthase (ISO) (38). Using this information, we created single mutations of M593I, C618N, L619F, A620T, L696Q, K723S, A729G, N838E, G854T,

and I855L based on residues in *A. grandis* and *P. abies* AS; whereas Y700H, A727S and V731L were created based on *P. abies* ISO. Alanine was used to replace Asn769 and Glu777 because these amino acids are conserved throughout LPS, AS, and ISO (Fig. 2).

The preengineered *E. coli* (with the addition of approximately 10 copies of the MEP pathway genes) expressing the wild-type GGPPS provided an in vivo screening system for titer and product distribution changes by the LPS mutations. We observed that the profiles of diterpenoid product distribution resulting from expressing LPS mutants M593I, C618N, L619F, A620T, L696Q, K723S, V731L, N838E, G854T, and I855L were similar to expression of wild-type LPS (Fig. 2). Hence, with respect to LPS product selectivity, these mutations were neutral or close to neutral. Diterpenoid productivities resulting from expressing LPS mutants L619F, A620T, and G854T were also not significantly changed compared to wild-type LPS (within 50%). However, diterpenoid production levels were notably altered by expressing mutants M593I, C618N, L696Q, K723S, V731L, N838E, and I855L (Fig. 2 and Table S2). The highest total diterpenoid production increase (approximately 3.7-fold) was mediated by expressing LPS M593I. In all cases, expression of these mutants did not significantly affect product distribution. Expression of LPS mutant Y700H, however, resulted in significant alteration of diterpenoid product distribution by abolishing abietadiene synthesis and increasing sandaracopimaradiene proportion (Fig. 2). Although a single mutation in *P. abies* AS, Y686H (corresponding to Tyr700 in LPS) did not result in product selectivity changes in vitro, it promoted isopimaradiene synthesis when combined with another mutation (Y686H/A713S) (38); hence Tyr700 may play an important role in mediating the evolvability of LPS-type enzymes. Additionally, the expression of the A729G mutant resulted in the exclusive production of sandaracopimaradiene; however, it was concomitant with a reduction in productivity of approximately 98% (Fig. 2). Finally, diterpenoid production was not observed in systems expressing LPS A727S, N769A, and E777A variants. These residues fell within approximately 4.7 Å from substrate in the homology model; therefore, it was not surprising that the mutations were deleterious to LPS activity given the close proximity to the substrate.

Mutational Enrichment of Tunable LPS Residues to Identify Variants Conferring Increased Productivity. The previous results pointed to mutations in LPS that significantly affected production phenotype, namely M593I and Y700H. Although the preliminary mutation of Ala729 imparted product selectivity changes, it was excluded from further analysis because even a conservative repla-



Mutation	1	2	3	Productivity (fold)
M593I	83	12	5	3.7
C618N	91	9	TA	0.2
L619F	94	6	TA	1.5
A620T	87	11	2	1.3
L696Q	86	7	7	1.6
Y700H	71	TA	29	0.4
K723S	90	7	3	1.8
A727S	ND	ND	ND	0.0
A729G	ND	ND	100	0.02
V731L	100	ND	ND	0.08
N769A	ND	ND	ND	0.0
E777A	ND	ND	ND	0.0
N838E	92	6	2	2.2
G854T	79	14	7	1.4
I855L	90	7	3	0.7

Fig. 2. Summary of LPS mutations and the impact with respect to product distribution and productivity of the engineered pathway. Trace amount (TA), not detected (ND). Numbers indicate percentage of each isomer (1-levipimaradiene; 2-abietadiene; 3-sandaracopimaradiene).

cement such as glycine was deleterious. From analyzing the structural model, we observed that Met593 is located at the posterior of the binding pocket, whereas Tyr700 is positioned at the entrance (in close vicinity of the DDXXD magnesium binding motif). To obtain the complete LPS evolvability profile by these residues, we sampled all amino acids through saturation mutagenesis. Additionally, we also explored the effects of expressing the saturation mutagenesis library of Ala620 because a mutation at this position in *A. grandis* AS changed its product selectivity in vitro (37).

From the saturation mutagenesis library of Met593, we found two substitutions that conferred significant productivity improvement (Fig. 3A and Table S3). In addition to isoleucine, which was discovered in the phylogenetic-based mutation, the replacement with leucine, another hydrophobic residue similar in size as methionine, increased diterpenoid productivity by approximately 2-fold without significantly changing product distribution (Fig. 3A). Based on the structural significance of this position, this productivity improvement appeared to be caused by the disruption of H-bonding at the end of the binding pocket, thus increasing the flexibility of the cavity to better fit the CPP substrate. Therefore, the M593I mutation likely resulted in the highest production increase (approximately 3.7-fold) because isoleucine is the most hydrophobic amino acid. Substitutions with smaller residues than methionine only yielded moderate production improvement (<2-fold in the case of cysteine, serine, and threonine), and were disruptive in the case of alanine, glycine, and valine. Furthermore, substitutions with amino acids longer than five heavy atoms and those with bulky rings such as phenylalanine, tyrosine, and tryptophan also consistently decreased or abolished activity. These trends are consistent with the requirement for the substrate to have an unobstructed cyclization pocket, as the center of the bend is proximal to this residue. Moreover, replacements with hydrophilic amino acids such as aspartic acid, glutamic acid, lysine, and arginine also generally reduced productivity possibly because their ability to form their own H-bonding may reduce the capacity of the binding pocket.

We also found that the replacement of Tyr700 with phenylalanine, methionine, and tryptophan improved productivity up to approximately 5-fold (Fig. 3B and Table S4). The reaction cascade toward the formation of abietenyl cation requires an energetically unfavorable transition from a tertiary to a secondary carbocation (30). Therefore it was postulated that the latter species is stabilized by the ionic interaction with the paired diphosphate anion that is chelated by the magnesium ion (37). Tyr700 is located within close proximity to the magnesium binding site, thus the absence of the hydroxyl group in amino acids that are similar to tyrosine may allow the repositioning of the magnesium closer to the aspartate-rich region, hence increasing reaction efficiency by improving the chelation of the diphosphate group. A few mutations, i.e. replacements with aspartic acid, histidine, proline, arginine, and lysine, abolished abietadiene synthesis in the product mixture, and conferred a decrease in productivity (Fig. 3B). The replacement with positively charged residues or a helix breaker (proline) might cause a misalignment of the diphosphate anion that impaired catalysis or prevented the deprotonation of abietenyl cation at carbon position f (Fig. 1B) to create abietadiene.

Finally, the sampling of all amino acid substitutions of Ala620 revealed that only replacement with residues similar to alanine (small or hydrophilic) (cysteine, glycine, serine, and threonine) as well as valine retained LPS activity; whereas other substitutions were destructive or deleterious (Fig. 3C and Table S5). A few destructive mutations (replacements with aspartic acid, leucine, asparagine) also destabilized abietenyl deprotonation to yield abietadiene. Therefore, Ala620 in LPS did not appear to control product selectivity and productivity in LPS, yet it was important for catalysis.

Combining Beneficial Mutations in LPS to Further Improve Productivity. In laboratory experiments, the beneficial effects of single

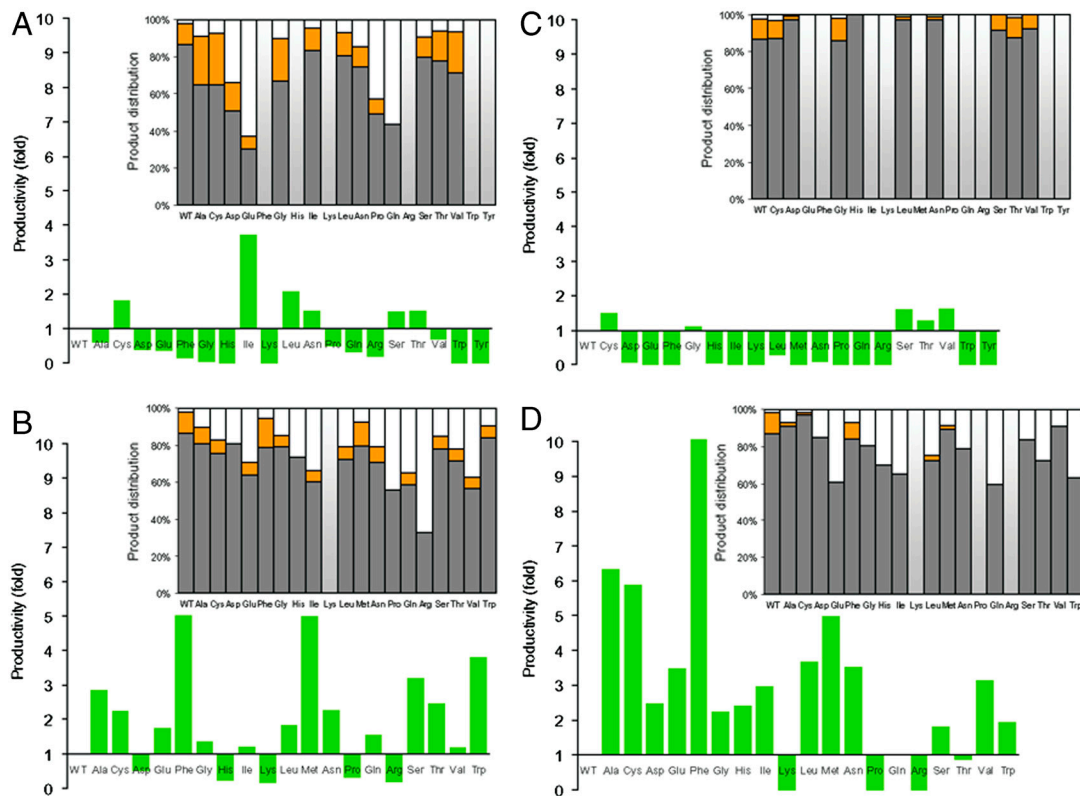


Fig. 3. Characteristics (productivity and product distribution) of the pre-engineered strains expressing wild-type *ggpps* and *lps* saturation mutagenesis library of: (A) Met593, (B) Tyr700, (C) Ala620, and (D) Tyr700 using *lps* M593I. In the product distribution charts, gray bars, orange bars, white bars represent proportion of levpimaradiene, abietadiene, and sandaracopimaradiene in the product mixture, respectively. Two-toned (white and light gray) bars represent nil production. WT represents the pre-engineered strain expressing wild-type *ggpps* and *lps*.

mutations are often additive (39, 40). Therefore, the production improvement resulting from expressing the LPS M593I variant encouraged us to explore the effect of this beneficial mutation in combination with saturation mutagenesis of Tyr700. As shown in Fig. 3D (Table S6), this combination successfully integrated the advantageous properties of the individual mutations, resulting in one variant (M593I/Y700F) that increased diterpenoid titer by approximately 10-fold over the expression of the wild-type enzyme without significant changes in product distribution. Interestingly, the expression of most LPS variants carrying the double mutations resulted in the reduction of abietadiene proportion (Fig. 3D). In two variants, M593I/Y700A and M593I/Y700C, the reduction of abietadiene was complemented by an increase in levpimaradiene, resulting in mixtures that contained up to 97% levpimaradiene. The combinations of M593I with Y700A and Y700C also conferred productivity improvements of approximately 6.3- and approximately 5.8-fold, respectively. Thus, it appeared that these mutations facilitated the stabilization of the intermediates that led to favoring abietenyl intermediate formation yet prevented proton extraction from route f (Fig. 1B). It is noteworthy that using the M593I mutant LPS as a parent for the subsequent saturation mutagenesis only produced three variants that decreased or abolished diterpenoid productivity (Fig. 3D). In contrast, previous saturation mutagenesis of Tyr700 resulted in five pathway variants that decreased/abolished diterpenoid production (Fig. 3B). Although a single M593I mutation was rendered neutral with respect to product selectivity, this mutation restored LPS activity upon subsequent defective mutations by aspartic acid and histidine replacement at residue 700. Thus M593I appeared to facilitate subsequent mutational robustness, a paradigm of neutral genetic drift (39).

Engineering Functional Mutations in GGPPS to Further Increase Diterpenoid Production. We next opted to mutate GGPPS, with the goal of further increasing pathway productivity. Although the structure of a plant GGPPS of angiosperm origin (from *Sinapis alba*) is available (41), the crystal structure for a gymnosperm GGPPS

has not been solved. Furthermore, the folding similarity of gymnosperm GGPPS enzymes and their angiosperm analogs is not known. Despite catalyzing essentially the same enzymatic reaction, GGPPS enzymes are known to exhibit wide structural diversity among organisms (41). Therefore, based on secondary structure analysis (42), the notable division of gymnosperm from angiosperm GGPPS enzymes may imply significant tertiary fold differences. In the case of *T. canadensis* GGPPS, its amino acid sequence only exhibited approximately 56% homology with that of *S. alba* GGPPS, with frequent gaps throughout the entire sequence (Fig. S3). As a result, the lack of a suitable structural guide prompted us to devise a random approach to mutate *T. canadensis* GGPPS. To enable a facile high-throughput screening method for isolating improved GGPPS variants, we utilized a lycopene biosynthetic pathway consisting of *crtB* and *crtI* as a colorimetric reporter (Fig. 4A). In this system, the expression of wild-type GGPPS resulted in colonies with light red coloration. Improved GGPPS variants from the mutagenesis were identified by the improvement of lycopene production in the cell, as determined by red coloration.

We isolated fifteen *ggpps* variants from colonies exhibiting red coloration. To assess the potential for improving levpimaradiene production in vivo, the fifteen mutant GGPPS isolates were coexpressed with the high-producing LPS M593I/Y700F mutant in the pre-engineered *E. coli* strain. Five GGPPS variants did not confer a levpimaradiene increase, indicating false positives obtained from the colorimetric screening. However, the coexpression of ten GGPPS mutants resulted in diterpenoid production improvement (Fig. 4B). The expression of mutant G10 resulted in the highest diterpenoid production increase of approximately 1.7-fold over the pathway harboring the wild-type GGPPS and the LPS M593I/Y700F, an equivalent of an approximately 17.7-fold increase over the pathway harboring wild-type GGPPS and LPS (Fig. 4B and Table S7). Sequence analysis of G10 revealed that two positions were mutated, namely S239C and G295D (Fig. S4). Amino acid alignment with GGPPS sequences from other plants (43) showed that most beneficial mutations are located in the region in between the two highly

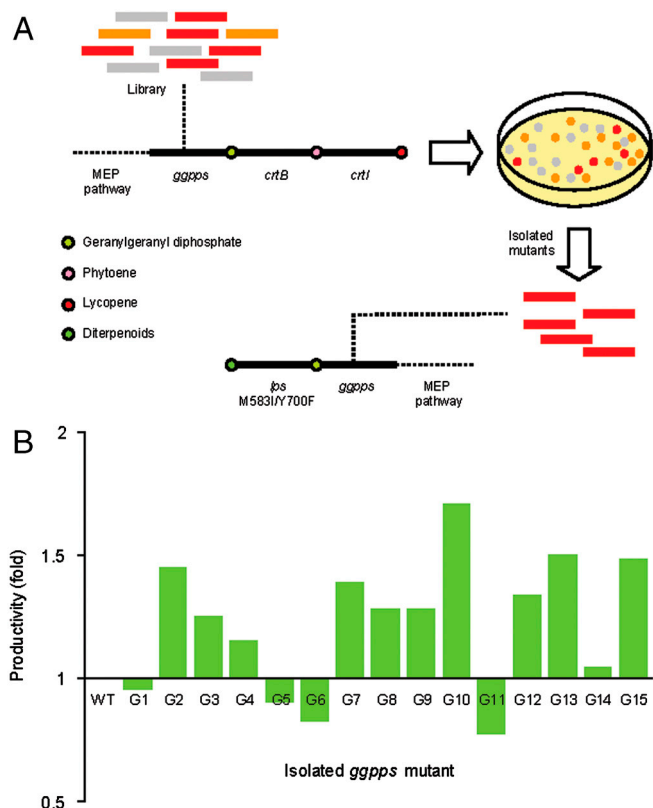


Fig. 4. Generation of GGPPS library based on stochastic mutation. (A) Creation of a facile high-throughput screening assay by fusing a lycopene pathway (*crtB* and *crtI*) with *ggpps* libraries. Mutant *ggpps* genes that conferred improved lycopene production (red colonies) were isolated. These variants were then coexpressed with *lps* carrying M5931/Y700F mutations for diterpenoid production assay. (B) Production phenotype of the preengineered *E. coli* strains coexpressing selected *ggpps* variants and *lps* M5931/Y700F. WT represents the strain expressing the wild-type *ggpps* and *lps* M5931/Y700F.

conserved aspartate-rich DDXXXXD and DDXXD domains (Fig. S4). A structural analysis of a prenyltransferase suggested that the two aspartate-rich regions bound three Mg^{2+} ions to facilitate the anchoring of the diphosphate groups of the IPP and DMAPP substrates (44). Therefore due to the close proximity to the aspartate motifs and Gly295 replacement with aspartate, the mutations in G10 may affect GGPPS catalysis by improving the binding efficiency of the magnesium ions needed for substrate anchoring. Overall, approximately 10-fold overexpression of the MEP genes and the use of mutant downstream enzymes consisting of GGPPS S239C/G295D and LPS M5931/Y700F increased levopimaradiene production approximately 2,600-fold over the expression of wild-type GGPPS and LPS alone (Table S7).

Levopimaradiene Overproduction in Controlled Culture Conditions.

The performance of the preengineered *E. coli* strain expressing the highest-producing levopimaradiene pathway consisting of GGPPS S239C/G295D and LPS M5931/Y700F was assessed in bioreactors under controlled conditions. The total diterpenoid titer reached a maximum of approximately 800 mg/L in 168 h, and levopimaradiene constituted approximately 700 mg/L (Fig. 5A). Using this engineered strain, 10 g/L glycerol was almost depleted after 56 h. Therefore 3 g/L glycerol was introduced into the culture every 8 h after this time point (Fig. 5B). Despite the relatively rapid consumption of glycerol, acetate only accumulated below 1 g/L throughout the cultivation. Overall, this experiment demonstrated that the production improvement obtained from the new pathway translated well toward larger cultivation.

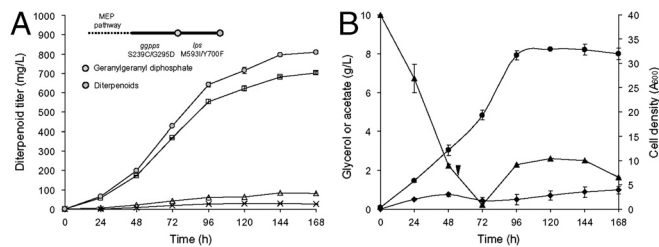


Fig. 5. Cultivation of the *E. coli* strain overexpressing the MEP pathway and the "reprogrammed" plant-derived pathway constituting GGPPS S239C/G295D and LPS M5931/Y700F mutants. (A) Diterpenoid production curves. Total diterpenoid, levopimaradiene, abietadiene, and sandaracopimaradiene are in circles, squares, triangles, and crosses, respectively. (B) Feed, fermentative by-product, and biomass curves. Glycerol, acetate, and cell density are in triangles, diamonds, and circles, respectively. Inverse triangle denotes the time point where 3 g of glycerol was added every 8 h.

Conclusions

Efforts to increase terpenoid production in *E. coli* previously focused on (i) overexpression of pathway enzymes, and (ii) optimizing the expression of enzymes by codon bias (7, 23, 45, 46). However, these approaches, which both aim to increase enzyme concentration to increase pathway flux, are still limited by the inherent low enzyme activity and specificity of the terpenoid pathways. Thus, in addition to metabolic engineering, the molecular reprogramming of key metabolic nodes such as prenyl transferase (GGPPS) and terpenoid synthase (LPS) though protein engineering is required to achieve substantial overproduction of a desired terpenoid product. Our approach has wide applicability not only in engineering of terpenoid pathways but also in many other secondary metabolic pathways, especially those with promiscuous enzymes that act as regulatory nodes. Our results also dispute the current notion that the MEP pathway is not effective for high-level production of terpenoid molecules (23, 47). In fact, the stoichiometry of the bacterial MEP pathway is 12–14% more efficient in consuming glucose or glycerol without redox imbalance compared to the eukaryotic mevalonate pathway for IPP/DMAPP synthesis. In a broader sense, because terpenoid pathways lead to compounds used in flavors, cosmetics, and potentially biofuels, our engineering approach is directly applicable for the high-level production of many commercially important compounds using microbial biotechnology.

Materials and Methods

Cloning and pathway construction. All cloning procedures were carried out in *E. coli* strain DH5alpha (Invitrogen), and pathway engineering was performed in *E. coli* MG1655 Δ (*endA*, *recA*) strains (SI Appendix). Genes were custom-synthesized (DNA 2.0) to incorporate *E. coli* codon bias, remove restriction sites for cloning purposes, and establish an approximately 50% GC-content. All strains carried the native chromosomal copy of the MEP pathway. Additional copies of pathway genes were inserted as operon *dxs-idi-ispD-ispF* under a Trc promoter. The single copy MEP strain was constructed by chromosomal localization of the MEP pathway and higher copy numbers were achieved through plasmid-based expression (SI Appendix and Table S8). Relative expression levels were verified through quantitative RT-PCR.

Culture Growth and Library Analysis. Single transformants of preengineered *E. coli* strains expressing pTrcGGPPS-LPS, or their mutant variants were cultivated for 18 h at 30 °C in LB. For library characterization, these preinocula were used to seed fresh 2 mL cultures at a starting A_{600} of 0.1 in rich medium (SI Appendix). Scale-up experiments (1-L cultures) were done in 3-L bioreactors (SI Appendix). To minimize the loss of diterpenoids due to air-stripping, 20% dodecane was added into the culture. The diterpenoid production was characterized by GC-MS analysis (SI Appendix).

Molecular Modeling. The homology model of LPS was built based on the structure of 5-epi-aristolochene synthase (48) [EAS (Protein Data Bank ID code 5EAT)]. Sequence alignment (Fig. S5) was performed with the ClustalW (49) method with standard gap penalties. Whereas LPS contains 323 residues in excess of EAS, they aligned almost exclusively at the proximity of the

second active side (toward the C-terminus), with a virtually gapless alignment. The CHARMM molecular modeling software (50, 51) with the CHARMM27 parameter set was used to mutate residues. Partial atomic charges needed for the substrate were obtained quantum mechanically with the Gaussian program using the 6-31G* basis set. Fifteen residues within a 10 Å distance from the substrate that contours the binding pocket were determined by using visual molecular dynamics (VMD) (52) (<http://www.ks.uiuc.edu/Research/vmd>).

Mutant Library Generation and Screening. The introduction of point mutations and saturation mutagenesis in *lps* were performed using QuikChange II XL (Stratagene). Nucleotide changes were set by custom designed oligonucleotides (Table S9). Subsequent to sequencing to verify nucleotide changes, the *lps* variants were used to replace the wild-type *lps* in pTrcGGPPS-LPS and subjected to expression in the preengineered *E. coli* for production analysis. The random mutagenesis library of *ggpps* was created by error-prone (EP) PCR at low mutation rate using GeneMorph II (Stratagene). A pool of plasmid pTrcGGPPS*-CRT was isolated from more than approximately 10⁶ transformants of *E. coli* DH10B. The plasmid library was then used to transform the *E. coli* strain overexpressing the MEP pathway for colorimetric screening.

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Colonies that displayed bright red coloration were isolated after incubation at 25°C for 3 d (as visualized on LB containing 75 µg/mL ampicillin and 25 µg/mL chloramphenicol). Following plasmid extraction and sequencing, the mutant *ggpps* genes were used as a pool in the next round of EP PCR. As a control, the integration of wild-type *ggpps* into the lycopene pathway gave rise to orange colored transformants. The iteration of mutation and screening was stopped after the second round of mutant collection, as no colony that displayed higher red coloration was identified in the third round of EP PCR.

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