

Diversity, regulation, and genetic manipulation of plant mono- and sesquiterpenoid biosynthesis

Fengnian Yu · Ryutaro Utsumi

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Abstract Among plant secondary metabolites, terpenoids are the most abundant and structurally diverse group. In addition to their important roles in pollinator attraction and direct and indirect plant defense, terpenoids are also commercially valuable due to their broad applications in the cosmetic, food, and pharmaceutical industries. Because of their functional versatility and wide distribution, great efforts have been made to decipher terpenoid biosynthetic pathways, to investigate the molecular mechanism determining their structural diversity, and to understand their biosynthetic regulation. Recent progress on the manipulation of terpenoid production in transgenic plants not only holds considerable promise for improving various plant traits and crop protection but also increases our understanding of the significance of terpenoid metabolites in mediating plant-environment interactions.

Keywords Plant terpenoid biosynthesis · Structural diversity · Regulation · Genetic manipulation · Transgenic plants

Introduction

Terpenoids are the most abundant and structurally diverse group, comprising over 40,000 individual compounds [1]. A large number of these compounds are of plant origin and play numerous biological roles in higher plants. Some terpenoids are present in most of the plant species, and they

are essential for plant growth and development [2]. For example, sterols (C_{30}) are essential components of membranes, carotenoids (C_{40}) function as photosynthetic pigments, gibberellins (C_{20}) and abscisic acid (C_{15}) are phytohormones, and ubiquinones are involved in mitochondrial electron transport. On the other hand, many terpenoids including monoterpenoids (C_{10}), sesquiterpenoids (C_{15}) and diterpenoids (C_{20}) are only found in certain species or taxonomically related groups. They are considered secondary metabolites and play important roles in plant-plant and plant-environment interactions [3, 4].

Terpenoids are extremely variable in chemical structure, exhibiting hundreds of different carbon skeletons. However, they share a common feature of biosynthesis, and the classification of terpenoids is based on the number of common five-carbon isoprene units in the skeletal structure. The specific focus of this review is on the origins of the mono- and sesquiterpenoids, the C_{10} and C_{15} members of the terpenoid family. Mono- and sesquiterpenoids are two of the most heavily studied classes, largely due to their wide distribution throughout the plant kingdom and their essential roles in both plants and human society. They are the common components of floral scents and essential oils that can function as pollinator attractants [5–7] or as repellents or phytoalexins against herbivores or pathogens [8, 9]. Importantly, some volatile mono- and sesquiterpenoids can be emitted from leaves or flowers in response to herbivore attack to attract natural enemies of herbivores, either predators or parasitoids [10–12]. In addition, herbivore-induced volatile monoterpenoids can also act as airborne signals to prime neighboring plants against future insect attack. For example, three terpenoids including the monoterpene (E)- β -ocimene were emitted from lima bean leaves in response to damage by spider mites (*Tetranychus urticae*). These volatile terpenoids elicited defense-related

F. Yu · R. Utsumi (✉)
Department of Bioscience, Graduate School of Agriculture,
Kinki University, Nakamachi, Nara 631-8505, Japan
e-mail: utsumi@nara.kindai.ac.jp

gene expression in neighboring uninfested lima bean leaves [13]. While terpenoids are usually studied in above-ground tissues, the novel functions of sesquiterpenoids as signal molecules in the below-ground environment have also been identified recently. For example, the sesquiterpene β -caryophyllene was found to be released from maize roots in response to attack by the beetle *Diabrotica virgifera virgifera* as a volatile signal to attract predatory nematodes, which indirectly protect the plant from further damage [14].

The functional versatility of mono- and sesquiterpenoids is reflected in their great structural diversity. For example, maize contains as many as 100 different terpenoids, most of which are sesquiterpene hydrocarbons. Interestingly, terpenoid composition can not only be markedly different from one species to another, but within a single species it often exhibits pronounced qualitative or quantitative variations among different varieties or ecotypes [15, 16]. Although recent progress in terpenoid biosynthesis has provided new insights into the mechanisms determining terpenoid diversity and distribution, we do not yet have a comprehensive understanding of this immense diversity.

Humans have also benefited from many terpenoids. For example, the monoterpene limonene is widely used as a fragrance in cosmetics products. Nootkatone, an important flavor constituent of grapefruit, is commonly used in the beverage industry as a flavor additive [17]. Artemisinin, a sesquiterpenoid in wormwood, has proved to be an effective antimalarial compound [18]. The anti-inflammatory and potential anticancer compound zerumbone from shampoo ginger has recently become the attractive subject of pharmacological investigations [19–22].

The ecological and commercial importance of terpenoids has prompted the rapid development of engineering terpenoid production in transgenic plants. Recent progress in deciphering terpenoid biosynthetic pathways and the identification of genes and enzymes involved in these pathways has made genetic manipulation in plants highly feasible. This manipulation can improve a large number of traits in crops, including pest resistance, weed control, increased aroma of fruits and vegetables, and the production of medicinal compounds. In addition, transgenic plants with modified terpenoid profile can provide a valuable tool for studying the biosynthesis and regulation of these compounds and their ecological functions in plant-environment interactions.

In this article, we describe the recent advances in understanding the molecular mechanisms of plant terpenoid biosynthesis and regulation and the genetic manipulation of terpenoid production in transgenic plants. Here, we limit our review to the mono- and sesquiterpenoids as defined above.

Terpenoid biosynthesis and its subcellular compartmentation in plants

All terpenoids are derived from the five-carbon building blocks isopentenyl diphosphate (IPP) and its isomer dimethylallyl diphosphate (DMAPP). The sequential head-to-tail condensation of IPP and DMAPP generates *trans*- (or *E*-) isoprenyl diphosphates, 2*E*-geranyl diphosphate (GPP, C₁₀), 2*E*, 6*E*-farnesyl diphosphate (*E*, *E*-FPP, C₁₅), and 2*E*, 6*E*, 10*E*-geranylgeranyl diphosphate (*E*, *E*, *E*-GGPP, C₂₀). These reactions are catalyzed by short-chain *trans*- (or *E*-) prenyltransferases, GPP synthases (GPS), FPP synthases (FPS), and GGPP synthases (GGPS), respectively (Fig. 1). Subsequent cyclizations of prenyl phosphates by the action of terpene synthases (TPSs) generate the olefinic parent skeletons, monoterpenes (C₁₀), sesquiterpenes (C₁₅), and diterpenes (C₂₀), respectively. Pairwise condensation of FPP and GGPP generates the classes of triterpenes (C₃₀) and tetraterpenes (C₄₀), respectively. Further modifications of the parent skeleton types by a series of different enzymes (P450 hydroxylases, dehydrogenases, reductases, and methyl transferases) give rise to the large variety of different terpenoid metabolites [23]. Recently, a new pathway for mono- and sesquiterpene biosynthesis from *cis*- (or *Z*-) isoprenyl diphosphates has been reported. In wild tomato trichomes, a *cis*- (or *Z*-) FPP synthase (α FPS) catalyzes the formation of *Z*, *Z*-FPP from IPP and DMAPP, and a sesquiterpene synthase (Santalene and Bergamotene Synthase [SBS]) uses *Z*, *Z*-FPP as a substrate to produce the tomato class II sesquiterpenes. More surprisingly, SBS can also use neryl diphosphate (NPP), the *cis*-isomer of GPP, and convert it into a monoterpene. These novel findings provide new insights into terpene biosynthesis in higher plants [24].

It is well known that in higher plants two independent pathways, localized in different intracellular compartments, are involved in the biosynthesis of IPP and DMAPP. In the cytosol, IPP is derived from the classic mevalonic acid (MVA) pathway that begins with the condensation of acetyl-CoA [25], whereas in plastids, IPP is generated from pyruvate and glyceraldehyde 3-phosphate (GA-3P) through the methylerythritol phosphate (MEP) pathway [26, 27]. It was previously assumed that the cytosolic pool of IPP provides the precursor for the production of sesquiterpenes and triterpenes, while the plastidial pool of IPP serves as the precursor for the production of monoterpenes, diterpenes, and tetraterpenes. However, there is increasing evidence suggesting that cross-talk occurs between the two different biosynthetic pathways [28–34]. In glandular trichomes of peppermint, the cytoplasmic MVA pathway is blocked at 3-hydroxy-3-methylglutaryl-CoA reductase, a rate-controlling enzyme of the MVA pathway, and both plastidial

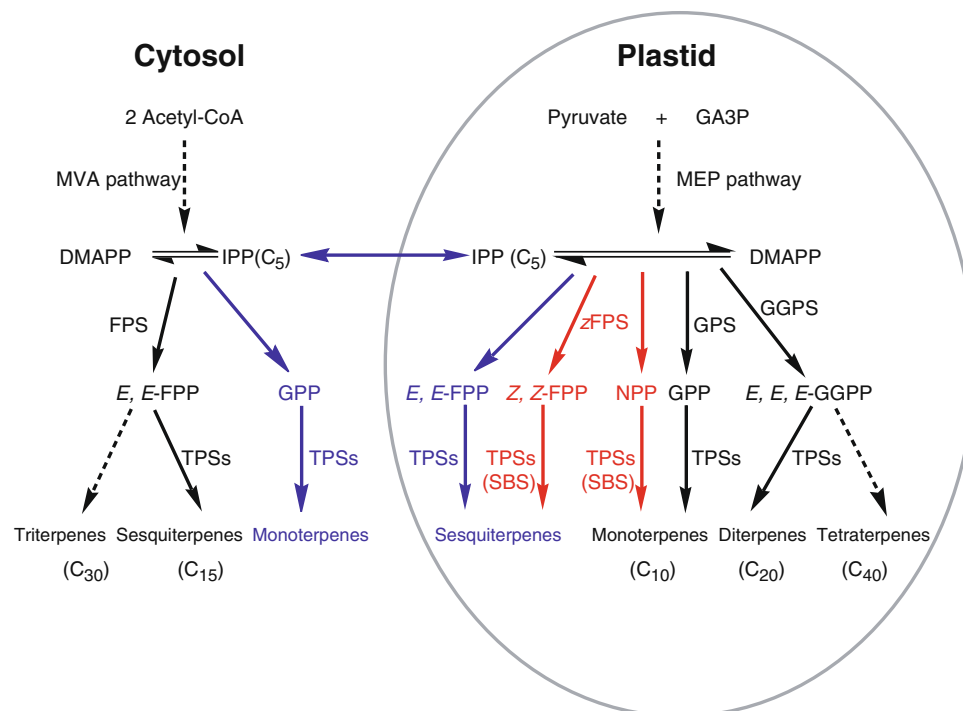


Fig. 1 The two terpenoid biosynthetic pathways producing different terpene classes in plants and their intracellular compartmentation. Both the cytosolic mevalonate (MVA) pathway and the plastidial methylerythritol phosphate (MEP) pathway lead to the formation of the C₅ units IPP and DMAPP. Generally, the MVA pathway is responsible for the production of sesquiterpenes (C₁₅) and triterpenes (C₃₀), whereas the MEP pathway is responsible for monoterpenes (C₁₀), diterpenes (C₂₀), and tetraterpenes (C₄₀). However, cross-talk

between the two pathways, including the exchange of IPP between two compartments, the cytosolic monoterpenoid biosynthesis and plastidial sesquiterpene biosynthesis, has been demonstrated (indicated in *blue*). In addition, the biosynthesis of terpenes from *cis*-isoprenyl diphosphates in chloroplasts of tomato trichomes has been recently discovered (indicated in *red*). Solid and dashed arrows represent single and multiple enzymatic steps, respectively

monoterpene and cytosolic sesquiterpene biosynthesis rely exclusively on plastidic-derived IPP [28]. Recent studies with snapdragon flowers have also indicated that the MEP pathway provides IPP precursors for both monoterpene and sesquiterpene biosynthesis, and the trafficking of IPP occurs unidirectionally from the plastids to cytosol [31]. In addition, in some cases, both pathways can even cooperate to supply IPP precursors for biosynthesis of certain terpenoids. For example, the chamomile sesquiterpenes consist of two C₅ isoprene units derived from the MEP pathway, with a third unit being formed via both pathways [32, 33]. Towler and Weathers [34] also provided the indirect evidence that artemisinin is probably biosynthesized from IPP pools derived from both the plastid and the cytosol. Despite these observations, the relative contribution of each pathway to the biosynthesis of the various classes of terpenoids remains largely unknown.

Besides the transport of the IPP precursors between different compartments, the intracellular localization of the different terpenoid biosynthesis is also not as strictly defined as previously believed. It has been well established

that monoterpene biosynthesis localizes in plastids, the formation site of the precursor GPP, whereas sesquiterpenes are synthesized in the cytosol/endoplasmic reticulum compartment, the site of FPP formation. However, two different strawberry monoterpene synthase proteins, which respectively generate linalool and several olefinic monoterpenes, lack the plastid-targeting signals and have been shown to be targeted to the cytosolic compartment [35]. Similarly, transgenic tomato plants carrying a lemon basil α -zingiberene synthase can also produce monoterpenes in the cytosol [36]. In contrast, two sesquiterpene synthases, STC1 and SBS from maize and tomato, respectively, contain putative N-terminal plastid-targeting peptides [24, 37]. Green fluorescent protein (GFP) experiments with SBS demonstrated that SBS is localized in the chloroplast, thus providing the evidence that sesquiterpene biosynthesis can take place in the plastids [24]. These findings raise new questions about the fundamental processes in plants that regulate how and where terpenoids are produced, transported and accumulated in the plant cell. An outline of the two terpenoid biosynthetic pathways in plants and their intracellular compartmentation is shown in Fig. 1.

Diversity and plasticity of terpenoid formation

Terpenoids exhibit a tremendous range of diversity in carbon skeletons and functional groups. Recent progress in terpenoid biosynthesis has provided valuable insights into the mechanisms determining terpenoid diversity. The most significant in this regard are studies of terpene synthases (TPSs), a large group of enzymes that are responsible for most of the structural varieties of terpenoids. As described above, TPSs are the branch point enzymes that convert diphosphates to the parent carbon skeletons of terpenoids. A striking feature of TPSs is their astonishing capability to produce multiple products from a single substrate with high regio- and stereospecificity. This ability results from their unique catalytic mechanism that involves manipulation of carbocations, intramolecular additions and rearrangements [38]. Generally, individual intermediates have a variety of metabolic fates in the reaction, resulting in the formation of multiple products. For example, in grand fir, δ -selinene synthase and γ -humulene synthase generate 34 and 52 different sesquiterpenes, respectively [39].

Despite the relatively high degree of structural relatedness among TPSs, comparative sequence analyses have indicated that there is no clear relationship between phylogenetic organization and catalytic specificities [40]. Therefore, it is extremely difficult to predict the product profiles of TPSs based solely on their primary sequence. Thanks to the availability of the three-dimensional structures of three plant TPSs [41–43], it has become possible to identify the active sites and to determine the regions or amino acid residues that control the product specificity and selectivity of TPSs. Domain-swapping experiments based on amino acid comparisons of two phylogenetically related sesquiterpene synthases, 5-epi-aristolochene (TEAS) and vetispiradiene synthases (HVS), demonstrated that the first 261 amino acids and the last 106 residues could be interchanged between the two proteins without affecting the product profile, and the middle regions between amino acids 261 and 342 of TEAS and amino acids 386 and 449 of HVS are responsible for the product specificity. Chimeric enzymes containing both of these functional domains unexpectedly generated products of both parent enzymes at various ratios [44]. Because TEAS and HVS share the first two catalytic reaction steps and differ in the terminal step, Greenhagen et al. [45] developed a contact mapping strategy to identify amino acids that contribute to discrete reaction steps. By employing this strategy as well as mutational replacement of variable residues within and surrounding the active sites of the two enzymes, the activities of TEAS and HVS could be interconverted. These results facilitated the use of homology modeling and site-directed mutagenesis to pinpoint which amino acid residues determine the product outcome.

TPS4 and TPS5 are two closely related maize sesquiterpene synthases that produce the same complex sesquiterpene mixture in different proportions. Comparative mutational analyses have indicated that the product selectivity of the two enzymes is controlled by only four amino acids at the catalytic site [16]. Additional studies of TPS4 by modeling and mutagenesis showed that two different functional pockets in the active site contribute to the formation of multiple products by TPS4. One pocket appears to be the site of the initial steps of the reaction including substrate binding, isomerization, and the first cyclization. A conformational change of the bisabolyl cation intermediate results in a shift from one pocket to the other, where it is then converted to a different group of products by further cyclization [46].

Studies of the maize TPS4 and TPS5 enzymes also found that, although both B73 and Delprim varieties contain TPS4 and TPS5 genes, each variety has only one functional allele, suggesting the contributions of gene duplication and allelic variation of TPSs to the terpenoid diversity and distribution [16]. Differences in the terpenoid profile between different varieties or cultivars have also been detected in other plant species. For example, in the headspace of cultivated strawberry, only the monoterpene linalool and the sesquiterpene nerolidol were observed. However, wild strawberry emitted several monoterpenes that are not detected in the cultivated varieties. This marked difference is due to two different TPSs, FaNES1 and FvPINS, that are expressed in the cultivated and wild varieties, respectively [35]. In another example, the glandular trichomes of two tomato species, *Solanum lycopersicum* and its wild relative *Solanum habrochaites* LA1777, also have different terpenoid profiles. *S. lycopersicum* mainly produces monoterpenes and traces of class I sesquiterpenes, whereas LA1777 produces mainly class II sesquiterpene carboxylic acids (SCAs), small amounts of class I sesquiterpenes, and traces of monoterpenes [47]. Class I sesquiterpenes comprise germacrene as well as α -humulene and β -caryophyllene, whereas class II sesquiterpenes consist of α -santalene, α -bergamotene, and β -bergamotene, which are the likely precursors of SCAs. The biosynthesis of the two distinct classes of sesquiterpenes is controlled by two independent loci. A locus on chromosome 6 consists of two gene clusters of sesquiterpene synthases, of which only one is genetically associated with the biosynthesis of class I sesquiterpenes. At a second locus of LA1777 on chromosome 8, SBS gene is responsible for the biosynthesis of class II sesquiterpenes [24, 48]. These studies shed light on the molecular mechanism resulting in terpenoid diversity under selective pressure during evolution and domestication.

TPSs not only can produce multiple products from a single substrate but also exhibit tremendously functional flexibility. For example, Yoshikuni et al. [49] identified the candidate ‘plasticity’ residues that are not essential for catalytic functionality but may determine product selectivity in grand fir γ -humulene synthase, and then they developed an approach for systematic recombination of these residues and successfully constructed seven novel sesquiterpene synthases with improved specificities by screening fewer than 2,500 mutants. This functional plasticity of TPSs would seem to be very important in natural evolution, allowing plants to adapt to various environmental changes.

Another intriguing feature of TPSs is that some of them, such as FaNES1 and SBS, can accept both GPP and FPP as their substrates to produce a mixture of mono- and sesquiterpenes [24, 35]. GFP localization experiment showed that FaNES1 localizes to the cytosol and a change in subcellular localization may lead to the enzyme encountering both GPP and FPP substrates. In another example, overexpression of the lemon basil α -zingiberene synthase (ZIS) gene in tomato fruits led to the unexpected enhanced accumulation of both mono- and sesquiterpenes. In vitro experiment also showed that the recombinant ZIS can accept GPP as a substrate to produce monoterpenes, suggesting that when sufficient GPP is available, ZIS could have monoterpene synthase activity in addition to sesquiterpene synthase activity [36]. These observations indicate that the subcellular sites of TPS activities and substrate availability also regulate the terpenoid diversity.

In addition to the contribution of TPSs, the diversity of terpenoids can be further amplified by the modification of the parent hydrocarbon skeletons, such as the addition of hydroxyl groups, further oxidation to ketones, demethylation, and methyl transference, which affect various chemical properties of the molecules that influence their biological activities. A good example of the action of terpene-modifying enzymes is the biosynthesis of a monoterpene (–)-menthol in peppermint. Briefly, menthol biosynthesis begins with the formation of (–)-limonene, a reaction catalyzed by a limonene synthase. Subsequent modifications include hydroxylation of (–)-limonene to (–)-*trans*-isopiperitenol by P450 limonene-3-hydroxylase, dehydrogenation of (–)-*trans*-isopiperitenol to (–)-isopiperitenone by isopiperitenol dehydrogenase, generation of (+)-*cis*-isopulegone by (–)-isopiperitenone reductase, isomerization of (+)-*cis*-isopulegone to (+)-pulegone by isopulegone isomerase, reduction of (+)-pulegone to (–)-menthone by (+)-pulegone reductase, and finally formation of (–)-menthol by (–)-menthone reductase [50].

Spatial and temporal regulation of plant terpenoid biosynthesis

Terpenoid biosynthesis in plants can be spatially and temporally regulated during development and in response to biotic and abiotic factors, such as insect or pathogen damage, light intensity, temperature, humidity and nutrient availability [51–57].

Mono- and sesquiterpenoids are often emitted from specific floral tissues at particular times or developmental stages to attract pollinators. In snapdragon, the emission of two main floral scent compounds, the monoterpene myrcene and (E)- β -ocimene, occurs in the upper and lower petal lobes and is regulated developmentally, following diurnal rhythms controlled by a circadian clock. The developmental and rhythmic emission of the two monoterpenes correlates with the weak diurnal oscillation of the corresponding monoterpene synthase genes [58]. In *Nicotiana suaveolens*, the nocturnal emission of several monoterpenes from petals and stigmas is a consequence of the transcriptional regulation of the 1,8-cineole synthase by the circadian clock [59]. These specific changes in terpenoid emission that follow diurnal, nocturnal, or circadian rhythms over the flower lifespan may be associated with the appearance of insects that pollinate the flowers. For example, flowers that are pollinated by night-active insects such as moths may have their scent output at maximum levels in the early evening, coincident with the period of maximum feeding activity of the nocturnal insects [60, 61].

Besides serving as attractants for species-specific pollinators, terpenoid volatiles are also known to play a significant role in plant defense. Tholl et al. [15] revealed that in *Arabidopsis* flowers, terpene volatiles consisting predominantly of sesquiterpenes are not synthesized in petals but in stigma, nectaries, sepals, and anthers. Given the fact that *Arabidopsis* is largely self-pollinating, these terpenoid volatiles may serve to inhibit microbial infection or herbivorous damage at the vulnerable sites. In addition, some terpenoids are also frequent constituents of essential oils and resins and are constitutively accumulated in highly specialized secretory structures, such as the glandular trichomes of mints [62, 63] and resin ducts of conifers [64–66]. Some of these constitutive terpenoids can be released from storage structures against herbivory [67, 68]. Furthermore, their biosynthesis can be restricted to a brief period during leaf development or fruit ripening [69, 70]. More commonly, de novo terpenoid biosynthesis, including the formation of new storage structures such as resin ducts or oil glands, can be induced locally and systematically in response to fungal elicitation or herbivore attack [14, 71–75]. For instance, in conifers, herbivore attack and jasmonate treatment triggered the production of oleoresin

containing mono-, sesqui-, and diterpenoid components, which is often accompanied by extensive cellular differentiation, leading to the de novo formation of traumatic resin ducts [71, 73]. More recently, Opitz et al. [76] also demonstrated that elevated levels of terpenoids in cotton leaves after real and simulated herbivory are due to the increased filling of existing glands as well as the production of additional storage glands.

Research over the past few decades has begun to unveil some of the regulatory mechanisms by which terpenoid biosynthesis is induced following damage. It has been discovered that induced terpenoid biosynthesis appears to be regulated by the activities of relevant biosynthetic enzymes. One of the best-studied examples is the induction of sesquiterpenoid accumulation in elicitor- or pathogen-challenged tobacco cell suspension cultures. The rapid increase of antibiotic sesquiterpenoids in challenged cells results from the coordinated induction of sesquiterpene synthase activities and suppression of squalene synthase, the first committed enzyme in sterol biosynthesis [77, 78]. These observations are consistent with a number of similar studies with other plant species [79, 80], suggesting that the induction of terpenoid biosynthesis may be associated with other branch pathways sharing the same precursor pools. Despite these findings, the signal transduction cascades resulting in the activation of the terpenoid biosynthetic pathways and the regulation elements that control the induced cellular differentiation leading to the new formation of secretory structures are far from being understood.

Manipulation of terpenoid production in transgenic plants

Genetic manipulation of terpenoid biosynthesis in plants is currently a very active research area. Over the past few years, many attempts have been made to manipulate terpenoid production in transgenic plants by genetic engineering to alter fragrance and flavor profiles of flowers and fruits and to improve direct and indirect defenses (reviewed in [81–85]). Although the feasibility of enhancing terpenoid yield by overexpressing the enzymes that produce terpene precursors or modify parent terpene structures has been demonstrated [86–89], most of the studies on manipulation of terpenoid production focused on the overexpression of TPSs in transgenic plants under constitutive promoters.

The introduction of three lemon monoterpene synthases into tobacco is one of the successful examples of altering scent profiles by genetic engineering. Transgenic tobacco plants emitted olfactorily detectable amounts of monoterpene volatiles from flowers and leaves [90]. Importantly, the relatively high levels of the introduced monoterpenoids

in flowers did not affect the endogenous linalool biosynthesis, suggesting that a precursor pool is available to introduced monoterpene synthases. The first attempt to improve the flavor of the fruits was performed by overexpression of a *Clarkia breweri* S-linalool synthase (LIS) gene in tomato under the control of the fruit-specific E8 promoter. This resulted in the accumulation of low levels of linalool and 8-hydroxylinalool in ripening fruits [91]. In a more successful experiment, the ectopic expression of the lemon basil geraniol synthase (GES) gene under the control of the fruit ripening-specific polygalacturonase (PG) promoter led to the accumulation of high levels of geraniol and its derivatives in tomato fruit, which profoundly affected tomato flavor [92].

In addition to the impact on the quality of flavor and scent, manipulation of terpenoid production in plants has also been proven to be an effective strategy for improving direct and indirect defenses. Overexpression of FaNES1, a strawberry linalool/nerolidol synthase gene in *Arabidopsis* produced high levels of linalool that significantly repelled aphids [93]. Moreover, transgenic potato plants that express the same gene were more attractive to beneficial predatory mites than the wild-type plants [83], thus indirectly protecting plants from insect damage. In another study, the introduction of a maize sesquiterpene synthase (TPS10) to *Arabidopsis* led to the strong emission of several herbivore-induced sesquiterpenoids, which are exploited by the females of the parasitoid *Cotesia marginiventris* to locate their lepidopteran hosts [94]. These studies indicated that metabolic engineering of terpenoids in plants also provides a valuable tool to evaluate the role of some volatile terpenoids in mediating tritrophic interactions.

Engineering of sesquiterpenoid production in plants seems more difficult and less successful than the generation of monoterpenoids due to the lack of sufficient precursor for the introduced sesquiterpene synthases. In a recent study, transgenic tomato fruits overexpressing ZIS gene under the control of the tomato PG promoter produced high levels of α -zingiberene and various quantities of 14 other sesquiterpenes without affecting plant phenotype except for a slight decrease in carotenoid content, implying that there was sufficient cytosolic supply of FPP in ripening tomato fruits [36]. In another study, enhancement of sesquiterpenoid production was achieved by switching the subcellular localization of FENS1 to the mitochondria. This manipulation resulted in substantial emission of (3S)-(E)-nerolidol and a degradation product of nerolidol, C11 homoterpene 4,8-dimethyl-1,3(E),7-nonatriene [(E)-DMNT] from *Arabidopsis*, and both of these terpenoids could attract carnivorous predatory mites, the natural enemies of spider mites [95]. More significantly, Wu et al. [96] developed a new engineering strategy for high-level sesquiterpenoid

biosynthesis in plants by coexpression of a FPP synthase and a sesquiterpene synthase, while diverting the subcellular compartment of the two enzymes from cytosol to plastids. This strategy boosted the production of two sesquiterpenes, patchoulol and amorpho-4,11-diene more than 1,000-fold, highlighting the importance of compartmentalization of both precursor pools and introduced enzymes in the regulation of terpenoid biosynthesis. This success also indicated the potential of using metabolic engineering to explore plant-based production platforms for commercially interesting terpenoids.

Although significant progress has been made in manipulation of terpenoid production in plants in the past few years, many studies have also revealed the limitations and problems that have to be surmounted. It has been shown that the introduction of a single gene has only limited value for substantial production of the desired compound [91, 97, 98]. In addition, in many cases, the intended terpenoids produced by transgenic plants were further modified by the endogenous enzymes, resulting in different terpenoid derivatives based on the entire biochemical repertoire of the plant used. For example, while engineering petunia and carnation plants with LIS gene, the synthesized linalool was partially converted into linalyl β -D-glucoside and linalyl oxides, respectively [97, 98]. Therefore, it is difficult to predict the metabolic fate of the introduced terpenoids. More importantly, high-level expression of an introduced gene in plants can lead to deleterious effects on plant growth and development [92, 93, 96]. In fact, transgenic tobacco plants producing exceptionally high levels of patchoulol exhibited leaf chlorosis, vein clearing, and a reduction in stature [96]. In another experiment, high geraniol accumulation in transgenic tomato fruits was at the expense of a 50% decrease in lycopene content [92]. These phenotypic changes result either from the toxicity of the newly synthesized terpenoids or from diversion of the carbon flux of the primary metabolism pathway, which causes a deficiency of some essential metabolites such as sterols and carotenoids.

Conclusions and prospects

Recent progress in the biochemical and molecular genetic analysis of terpenoid biosynthesis has provided new insight into the mechanism directing terpenoid diversity, distribution, and regulation. The two elaborate biosynthetic pathways localized in separate subcellular compartments and the cross-talk between the two pathways reflect the complexity of terpenoid biosynthesis in plants. The subcellular compartmentation of precursors and enzymes, the multifunctional feature of TPSs, and the evolutionary process of TPS genes, including gene duplication,

subsequent neo-functionalization, and the allelic variations all contribute to the remarkable diversity and plasticity of terpenoids, which might allow plants to adapt easily to continuous environmental changes.

The spatial and temporal regulation of terpenoid biosynthesis during development and in response to environmental stresses is closely related to their ecological or physiological functions, such as attracting pollinators, repelling pathogens and herbivores, and attracting the natural enemies of herbivores. The combination of genomic, proteomic and metabolomic tools, as well as the establishment of in vitro cell culture systems should help elucidate the regulatory mechanism of terpenoid biosynthesis.

Recent efforts to manipulate terpenoid production in plants have demonstrated the feasibility of enhancing plant defenses and improving the scent and aroma quality of flowers and fruits by metabolic engineering. However, many attempts have resulted in disappointing enhancement of terpenoids or in unpredicted metabolic consequences due to our insufficient understanding of plant metabolic networks and their regulation. To explore plant systems as an efficient terpenoid production platform, more sophisticated strategies for engineering multistep pathways should be developed either by simultaneously overexpressing multiple genes in a pathway and/or blocking those in another competing pathway, or through the use of transcriptional regulators to control several endogenous genes.

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