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To cite this version:

Benoit Boachon, Yannick Burdloff, Ju-Xin Ruan, Rakotoharisoa Rojo, Robert R. Junker, et al.. A Promiscuous CYP706A3 Reduces Terpene Volatile Emission from Arabidopsis Flowers, Affecting Florivores and the Floral Microbiome. The Plant cell, 2019, 31 (12), pp.2947-2972. 10.1105/tpc.19.00320 . hal-02335215

HAL Id: hal-02335215

https://hal.science/hal-02335215v1

Submitted on 15 Dec 2020

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RESEARCH ARTICLE

A Promiscuous CYP706A3 Reduces Terpene Volatile Emission from Arabidopsis Flowers, Affecting Florivores and the Floral Microbiome

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Short Title: Floral terpene metabolism in Arabidopsis

One sentence summary: A gene cluster encoding two promiscuous enzymes modulates volatile emissions from *Arabidopsis thaliana* flowers, formation of insect-deterring terpene oxides, and the composition of the floral microbiome.

The author responsible for distribution of materials integral to the findings presented in this article in accordance with the policy described in the Instructions for Authors (www.plantcell.org) is Nicolas Navrot (navrot@unistra.fr).

ABSTRACT

Flowers are essential but vulnerable plant organs, exposed to pollinators and florivores; however, flower chemical defenses are rarely investigated. We show here that two clustered terpene synthase and cytochrome P450 encoding genes (*TPS11* and *CYP706A3*) on chromosome 5 of *Arabidopsis thaliana* are tightly co-expressed in floral tissues, upon anthesis and during floral bud development. TPS11 was previously reported to generate a blend of sesquiterpenes. By heterologous co-expression of *TPS11* and *CYP706A3* in yeast and *Nicotiana benthamiana*, we demonstrate that CYP706A3 is active on TPS11 products and also further oxidizes its own primary oxidation products. Analysis of headspace and soluble metabolites in *cyp706a3* and *35S:CYP706A3* mutants indicate that CYP706A3-mediated metabolism largely suppresses sesquiterpene and most monoterpene emissions from opening flowers, and generates terpene oxides that are retained in floral tissues. In flower buds, the combined expression of *TPS11* and *CYP706A3* also suppresses volatile emissions and generates soluble sesquiterpene oxides. Florivory assays with the *Brassicaceae* specialist *Plutella xylostella* demonstrate that insect larvae avoid feeding on buds expressing *CYP706A3* and accumulating terpene oxides. Composition of the floral microbiome appears also to be modulated by *CYP706A3* expression. *TPS11* and *CYP706A3* simultaneously evolved within *Brassicaceae* and form the most versatile functional gene cluster described in higher plants so far.

Introduction

Flowers are essential reproductive organs of plants, but also comprise their most vulnerable tissues and thus require sophisticated defense strategies to preserve plant fertility. The “optimal defense theory” predicts that tissues within a plant are defended in proportion to their fitness value and risk of attack (McKey, 1979). Indeed, flowers are vehicles of Darwinian fitness due to their involvement in pollen and seed production, and at the same time are particularly exposed to attack by insects and pathogens (Li et al., 2017). In addition, pollinators are often florivores at another stage of their life cycle (Abdalsamee and Müller, 2015). Surprisingly, however, flower defense mechanisms have rarely been investigated, especially at the metabolic level (Junker, 2016). For example, it has been known since the Middle Ages that one of the most potent natural insect repellents (presently identified as pyrethrin) is generated mainly by the buds and flowers of some *Asteraceae*, in particular *Tanacetum cinerariifolium* (Katsuda, 2012). Although the metabolic pathway leading to pyrethrin has now been elucidated (Kikuta et al., 2012; Xu et al., 2018), its direct impact on plant defenses has not been reported. In *Nicotiana attenuata*, one of the best described models of flower chemical ecology, a complex interplay between several plant pathways, signaling, and insects or hummingbirds has been observed in field studies, revealing different plant strategies to attract pollinators, and to deter or attract florivores (Kessler et al., 2010, 2015; Euler and Baldwin, 1996; Li et al., 2017, 2018). In *Brassicaceae* and especially the *Arabidopsis thaliana* model, such a multipartite interplay largely remains to be investigated.

A. thaliana is a selfing species, with flowers emitting an essentially terpenoid volatile bouquet that is complex but weak in intensity (Chen et al., 2003; Tholl and Lee, 2011). It is produced by six terpene synthases (Chen et al., 2003; Tholl and Lee, 2011) (Figure 1) and is dominated by (*E*)-β-caryophyllene generated by TPS21 (Tholl et al., 2005). The next two most significant contributors to Arabidopsis floral emissions are TPS24, which generates monoterpenes such as α-pinene or β-myrcene, and TPS11, which produces a complex mixture of sesquiterpenes dominated by (+)-α-barbatene and (+)-thujopsene (Tholl et al., 2005). The only metabolic process so far reported to prevent excessive damage from pollinators and florivores in flowers from wild-type *A. thaliana* is the oxidative metabolism of linalool, which generates both volatile and soluble repellent compounds (Boachon et al., 2015). The production of volatile linalool by the flower-expressed terpene synthases TPS10 and TPS14, which attract insects, is significantly reduced by P450-mediated oxidative metabolism depending on CYP76C1, leading to the production of repellent lilac aldehydes, lilac alcohols and carboxylinalool. These oxygenated metabolites are largely converted to glucosides, which facilitates their storage in flower tissues. It thus seems reasonable to speculate that this oxidative metabolism constitutes an adaptation for fitness optimization and decreased risk of attack by consumers.

A second mechanism for Arabidopsis flower protection is associated with the production of the sesquiterpene (*E*)-β-caryophyllene (Huang et al., 2012). In this case, (*E*)-β-caryophyllene was demonstrated to protect flowers from bacterial pathogens, although its impact on insect herbivory was not tested. The antibacterial activity of (*E*)-β-caryophyllene against *Pseudomonas syringae pv. tomato* DC3000 (*Pto* DC300) was demonstrated *in vitro*, and *tps21* mutants lacking (*E*)-β-caryophyllene showed enhanced growth of (*Pto* DC300) on their stigmas, and production of lighter seeds upon infection with the pathogen.

To uncover further metabolic processes associated with floral defense in *A. thaliana*, in particular those relying on oxygenated non-volatile compounds, we investigate here the function of a small gene cluster of two genes encoding a sesquiterpene synthase (*TPS11,* At5g44630*)* and a cytochrome P450 (*CYP706A3,* At5g44620), which are tightly co-expressed in Arabidopsis flowers and flower buds. We demonstrate that CYP706A3 efficiently oxidizes TPS11 products and the products of other flower-expressed mono- and sesquiterpene synthases, thereby suppressing floral volatile emissions. We show that expression of *CYP706A3* impacts the composition of the floral microbiome, as well as the feeding behaviour of *Plutella xylostella* on flower buds. Flower protection provided by the *TPS11-CYP706A3* cluster starts well before anthesis and extends throughout floral bud development. This cluster of two physically and functionally linked genes is unusual and CYP706A3 represents the most promiscuous plant P450 oxygenase reported to date.

Results

CYP706A3 and *TPS11* are clustered on chromosome 5 and tightly co-expressed in flowers

Co-expression of *CYP706A3* and *TPS11* in Arabidopsis flowers was first evidenced by an *in silico* analysis aimed at identifying P450s involved in specific metabolic pathways. *CYP706A3* and *TPS11* emerged as among the most tightly co-expressed terpene synthase and cytochrome P450 genes (correlation coefficient $r = 0.94$) in the plant organ dataset (Ehlting et al., 2008) (http://www-ibmp.u-strasbg.fr/~CYPedia/CYP706A3/CoExpr_CYP706A3_Organs.html). This result was confirmed and refined using BAR Expression Angler (Toufighi et al., 2005) with *CYP706A3* as the bait, which indicated that *TPS11* was the gene most tightly co-regulated with *CYP706A3* when using the "Extended Tissue Compendium" data set (Figure 2A, Supplemental Dataset 1). Conversely, *CYP706A3* was the P450 gene the most tightly co-regulated with *TPS11*. Both genes were spatially and developmentally co-expressed, with the highest levels detected in carpels from flower stage 12 to 15, and in samples from the shoot apical meristem and inflorescence apex. Co-expression in flowers and especially carpels at anthesis was further validated by RT-qPCR (Figure 2B). While suggesting that both genes might contribute to reproductive fitness, their expression patterns also provided a first hint that CYP706A3 might be acting on TPS11 products.

Genomic organization further supported this hypothesis: *CYP706A3* and *TPS11* are two adjacent genes on chromosome 5 of *A. thaliana*, separated only by 5 kb of non-coding sequence and

transcribed in opposite directions (Figure 2C). As this hinted that these two genes might form the core of a larger metabolic cluster (Nützmann and Osbourn, 2014; Nützmann et al., 2016), neighboring genes were also inspected. Two genes coding for *S*-adenosyl methyltransferases, and both predicted to be located in plastids, showed expression profiles not matching those of *TPS11* and *CYP706A3*. Other genes were unlikely to contribute to a terpenoid-tailoring pathway (Figure 2C, Supplemental Figure 1). Moreover, no relevant metabolic gene(s) closely associated with the *TPS11/CYP706A3* locus was part of the list of most co-expressed genes in BAR Expression Angler. It thus seems likely that *TPS11* and *CYP706A3* form a minimal metabolic cluster of two co-transcribed genes. Both proteins are located in the cytoplasmic compartment, with CYP706A3 anchored to the endoplasmic reticulum (Supplemental Figure 2).

CYP706A3 oxidizes major TPS11 products in yeast

TPS11 was previously reported to generate a complex blend of more than sixteen sesquiterpenes, including (+)-α-barbatene and (+)-thujopsene as major components, when expressed in *E. coli* (Tholl et al., 2005). To test the hypothesis of a functional link between the two clustered genes, we tested the activity of CYP706A3 on TPS11 products in yeast, a more suitable host for expression of P450 enzymes (see Supplemental Figure 3). The full coding sequences of *TPS11* and *CYP706A3* were independently expressed in yeast. Headspace, collected from yeast cultures expressing *TPS11* alone and analyzed by gas chromatography coupled to mass spectrometry (GC-MS), featured the expected mixture of volatile compounds, with (+)-α-barbatene (**a**) and (+)-thujopsene (**b**) as major products (Figure 3A). Headspace collected from mixtures of co-cultivated yeasts expressing *TPS11* and *CYP706A3* revealed up to 22 additional products, likely resulting from CYP706-dependent oxidation of TPS11 products (Figure 3A; Supplemental Figure 3D). None of the major products **1**, **2**, **3** and **4** shown in Figure 3A could be identified by comparing their mass spectra (MS) (Supplemental Figure 4) with those of compounds present in the NIST library. Thus, headspace from scaled-up cultures of yeasts expressing *TPS11* and *CYP706A3* was collected for 8 days (Supplemental Figure 3B). Up to 0.7 mg/L of major TPS11 products (+)-α-barbatene (**a**) and (+)-thujopsene (**b**), and 0.3 mg/L of major CYP706A3 product **1** were collected at the peak of production. Pooled compounds were analyzed and separated on semi-preparative high-pressure liquid chromatography coupled to mass spectrometry (LC-MS). A total of 28 fractions were recovered (Supplemental Figure 5) and subsequently checked for purity by GC-MS. Only four fractions were further analyzed, two of them containing the major TPS11 products (+)-α-barbatene (**a** = fraction 28) and (+)-thujopsene (**b** = fraction 25), and two others containing the major CYP706A3 oxidized products (**1** and **3** in fraction 16, and **2** and **4** in fraction 11) (Figure 3B; Supplemental Figure 5).

To identify the compounds serving as substrates in formation of the major CYP706A3 products, fractions containing (+)-α-barbatene and (+)-thujopsene (fractions 28 and 25, respectively) were incubated with microsomal membranes prepared from yeast expressing *CYP706A3* (Figure 3C;

Supplemental Figure 6). (+)-α-barbatene was converted by CYP706A3 into products **1** and **3** of purified fraction 16, and into two other products (**7**) and (**8**) previously detected in headspace of mixed yeast cultures (numbering according to Supplemental Figure 3). (+)-thujopsene (Figure 3C), as well as pure (-)-thujopsene (as the only commercially available product) were both transformed into products **2** and **4** (Supplemental Figure 6B to D). Retention times (RT) and MS of these products were compared with those of corresponding compounds present in fractions 11 and 16 and in headspace from mixed yeast cultures (Supplemental Figure 4). Products **1** and **3**, derived from (+)-α-barbatene, yielded distinct fragmentation spectra, suggesting different structures. Products **2** and **4**, derived from (-/+)-thujopsene, had similar fragmentation spectra and were thus most likely stereoisomers.

NMR spectroscopy enabled identification of the major CYP706A3 products as 2 diastereoisomers of (+)-1-oxo-thujopsene (products **2** and **4** in fraction 11), and as a mix of 2 diastereoisomers of (+)-6-oxo-α-barbatene and (+)-6-OH-α-barbatene (products **3** and **1** in fraction 16, respectively) (Figure 3; Supplemental Figure 7).

Samples from yeast headspace, purified fractions and *in vitro* incubations were analyzed and compared by LC-MS and LC-MS/MS (Supplemental Figure 8). Mass spectra of compounds **1**, **2**, **3** and **4** in fractions 11 and 16 confirmed GC-MS and NMR structure assignments (Supplemental Figure 9). The purified fractions 11 and 16, respectively containing CYP706A3-generated thujopsene oxides and barbatene oxides, were then incubated with microsomal membranes isolated from yeast expressing *CYP706A3*. LC-MS/MS analysis of the resulting reaction medium extracts revealed activity of CYP706A3 on both thujopsene and barbatene oxides. The primary products of (+)-α-barbatene oxidation (fraction 16) were further converted by CYP706A3 into products **5**, **6**, **7** and **8**, while those of (+)-thujopsene (fraction 11) were converted into products **9**, **10** and **11** (Figure 3D and Supplemental Figure 8C). RT and MS of these secondary products indicated that most of them were further oxygenated compounds (Supplemental Figure 10).

Taken together, these data suggest a scenario involving a sequential activity of CYP706A3 on (+)-α-barbatene, (+)-thujopsene and on their respective oxides, as summarized in Figure 4.

***CYP706A3* expression in *Nicotiana benthamiana* reveals more extensive promiscuous activity on TPS11 products**

To confirm the activity of CYP706A3 on TPS11 products in a plant environment, the corresponding genes were transiently co-expressed in leaves of *Nicotiana benthamiana*. The same set of sesquiterpenes emitted by *TPS11*-transformed yeast, and in similar proportions, was detected in the headspace of *N. benthamiana* leaves expressing *TPS11* alone (Figure 5A). Co-expression of *CYP706A3* along with *TPS11* in *N. benthamiana* leaves resulted in the emission of the major CYP706A3 products **1**, **2**, **3** and **4** previously detected in yeast headspace, with concomitant decreased emission of all TPS11 products, although to different extents (Figure 5A-B). Terpene

structures had a major impact on emission decrease that was more pronounced for multi-cyclic compounds such as barbatene, thujopsene, chamigrene, cuprenene, isobazzanene and acoradiene (the emission of which decreased by more than 50%) than for monocyclic and acyclic compounds such as cuparene, sesquiphellandrene, zingiberene and farnesene (Figure 5B; Supplemental Table 1).

Decreased emission of TPS11 products was not due to the reduced production of TPS11 potentially resulting from its co-expression with another protein, since co-expression of *TPS11* and *CYP76C1* (the endogenous Arabidopsis linalool hydroxylase P450 inactive on TPS11 products), did not result in decreased emissions of TPS11 products (Supplemental Table 1).

To summarize, *TPS11* and *CYP706A3* co-expression in *N. benthamiana* confirmed CYP706A3-dependent formation of barbatene and thujopsene oxides *in planta,* and also revealed the promiscuity of CYP706A3 allowing oxidation of most TPS11 products, with a preference for more bulky multi-cyclic sesquiterpenoid structures.

CYP706A3 suppresses sesquiterpene and monoterpene emissions in Arabidopsis flowers

The functional relevance of the *TPS11* and *CYP706A3* cluster and role in Arabidopsis flowers was then investigated using *cyp706a3* and *35S:CYP706A3* mutants. Two independent T-DNA insertion lines in *CYP706A3*, one in the promoter (*cyp706a3-1*) and one in the coding sequence (*cyp706a3-2*), resulted in a total absence of *CYP706A3* transcripts in floral tissues. The ectopic over-expressor line was generated by transformation of Col-0 with a *cauliflower mosaic virus (CaMV) 35S:CYP706A3* construct. Null mutant validation and selection of the over-expressing line are documented in Supplemental Figure 11. Comparison of volatiles collected from mutant inflorescences with that of the wild-type Col-0 provided clear evidence that *CYP706A3* suppression leads to a dramatic increase in the emission of TPS11 products (Figure 6A). More surprisingly, this suppression also increased emission of other sesquiterpenes and monoterpenes generated by flower-expressed mono- and sesquiterpene synthases such as TPS21 or TPS24. Overall, the amounts of total flower-emitted volatile organic compounds (VOCs) more than doubled in the insertion mutants (Figure 6B). Conversely, in the *CYP706A3* over-expressing line, total emission of flower VOCs was strongly decreased. A more precise quantification of the different compounds identified in the mutant headspace confirmed the data obtained in *N. benthamiana* for *TPS11* and *CYP706A3* co-expression, indicating that all volatile terpenes were not oxidized by CYP706A3 with the same efficiency (Figure 6C-D). Furthermore, emission of the barbatene oxides **1** and **3** and of the thujopsene oxides **2** and **4** (primary products of CYP706A3-dependent barbatene and thujopsene oxidation) was drastically reduced from *cyp706a3* flowers relative to the wild-type (Figure 6E). These primary oxidized products were nevertheless not increased in the over-expressing line, in agreement with their further oxidation observed in the *in vitro* experiments.

Analyses of the headspace collected from the flowers of the *CYP706A3* mutants (Figure 6A) further suggested an unexpected promiscuous activity of CYP706A3 on TPS21 (sesquiterpene) and TPS24 (monoterpene) products. CYP706A3 activity was thus further investigated by co-expression with TPS21 or TPS24 in yeast cultures and *N. benthamiana* leaves. Mixing yeasts producing terpene synthases and CYP706A3 and co-expressing *TPS21* or *TPS24* with *CYP706A3* in *N. benthamiana* largely reduced terpene emissions compared to levels emitted by yeast or *N. benthamiana* leaves producing only terpene synthases (Supplemental Figures 12 and 13). CYP706A3 activity on TPS21 products resulted in the emission of oxidized derivatives in yeast and *N. benthamiana* (Supplemental Figures 12A-B). Some of these oxidized compounds were also generated by the incubation of (-)-*E*-β-caryophyllene (major TPS21 product) with the microsomal fraction of *CYP706A3*-transformed yeast. Among those, some were found at decreased levels in the headspace of *cyp706a3* flowers as compared to the wild type (Supplemental Figures 12C-E). By contrast, no volatile oxidation products were detected in yeast or *N. benthamiana* headspace when both *TPS24* and *CYP706A3* were expressed (Supplemental Figure 13A-B). CYP706A3 activity on TPS24 monoterpene products was nevertheless observed following incubation of four pure standards (α-pinene, (+)-sabinene, β-pinene, and α-phellandrene) with a microsomal fraction of *CYP706A3*-transformed yeast, revealing the formation of several unknown oxygenated products (Supplemental Figure 13C). Taken together, these results confirm the promiscuous activity of CYP706A3 on a large subset of sesquiterpenes and monoterpenes generated by Arabidopsis flowers, still with a preference for cyclic compounds as substrates.

CYP706A3-dependent VOC metabolism results in accumulation of oxygenated terpenoids in floral tissues

Only minor amounts of oxygenated terpenoid derivatives were detected in the headspace of wild-type and over-expressing *35S:CYP706A3* flowers, whereas CYP706-dependent conversion of primary oxygenated metabolites was observed *in vitro*. This raised the question of the fate of CYP706A3 products in flowers. We hypothesized that they might be retained in the floral tissues. Flowers were thus extracted with MeOH after headspace collection, and the extracts were analyzed by targeted LC-MS/MS (Figure 7, Supplemental Figure 14), focusing on potential oxygenated sesquiterpene products. Up to thirty-three potential hydroxy-, oxo-, dihydroxy- and carboxy-sesquiterpene derivatives were detected (**FS1** to **FS33**: for Flower Soluble compounds), most of them essentially reduced in the flowers of *cyp706a3* insertion mutants compared to the wild type. Conversely, sixteen of them were increased in the over-expressing line. None of the primary and secondary barbatene and thujopsene oxides (products **1** to **11**) were detected in the MeOH extracts of wild-type or mutant flowers, suggesting they were further metabolized. The same trend was observed for oxidation products accumulating in leaf tissues of *N. benthamiana* co-infiltrated with *TPS11* and *CYP706A3* (Supplemental Figure 15) (**NbS1** to **NbS21**: for *N. benthamiana* soluble

compounds). β–glycosidase treatment did not reveal new metabolites or increased amounts of detected oxidation products. This led us to conclude that most CYP706A3 products are sequentially oxidized, subjected to downstream modification, and become soluble enough to be stored in plant tissues.

CYP706A3 activity is high in developing floral buds

In silico transcriptome analysis shown in Figure 2 pointed to an intriguing expression pattern of *CYP706A3* and *TPS11* in the shoot apex, starting at the floral transition. In an attempt to determine the role of such gene expression during the early stages of inflorescence development, VOC emission and expression of terpene synthases and *CYP706A3* were further evaluated (Figure 8). Unlike other floral terpene synthases, *TPS11* was expressed upon floral transition and in the developing inflorescence, with concomitant, higher expression of *CYP706A3*. In agreement with these expression profiles, traces of (+)-α-barbatene and (+)-thujopsene were found in the headspace of bolting wild-type plants, and a dramatic increase was observed for *cyp706a3* insertion mutants (Figure 8B). Conversely, accumulation of sesquiterpene oxides was detected in Col-0 flower buds (**BS1** to **BS22**: for bud soluble compounds), and suppressed in *cyp706a3* mutants (Figure 8C, Supplemental Figure 16). The observed inversion of relative gene expression at anthesis is interesting, suggesting that CYP706A3 almost completely prevents TPS11 product emissions in developing inflorescences to generate oxidation products (Figure 8A-B). The *TPS11/CYP706A3* cluster and associated formation of sesquiterpene oxidation products are thus expected to play an important role during the early stages of flower development.

Structural basis of CYP706A3 activity

Compared to most other P450 enzymes, CYP706A3 shows an unusual promiscuity. It acts upon both sesqui- and monoterpenes and, in addition, catalyzes successive oxidation reactions on the same substrates. In an effort to understand the structural basis of this promiscuity, a 3D homology model of the enzyme was generated using a multiple template approach, with an iterative search of templates based on sequence identity and on the search of distant homologs by HMM profiles (see Methods). CYP706A3 models rebuilt from various combinations of the detected templates (listed in Supplemental Table 2) were assessed and compared. The best homology model, yielding the highest QMEAN4 score (Benkert et al., 2008), was obtained from a three-template construction (PDB codes 3czh, 5irq and 2hi4, alignment displayed in Supplemental Figure 17). This structure exhibited two main access channels as computed by Mole 2.5 (Pravda et al., 2018) (Figure 9A, Supplemental Figure 18), one markedly hydrophobic channel connected to the membrane, the other less hydrophobic pointing towards the membrane–water interface, corresponding respectively to channels 2f and 2c of Cojocaru et al., 2007. The CYP706A3 heme pocket revealed a rather small, constrained and essentially hydrophobic cavity (Figure 9B) composed of mainly apolar residues

(Ile130, Ala383, Val382, Val387, Gly318, Leu386), with the exception of the only polar residue Thr322 in the first crown above the heme plane (Figure 9B and C). The upper part of the cavity was also predominantly hydrophobic (Val497, Ile496, Trp131, Leu317 and Leu229), with a single charged residue (Asp321). Together, these properties make the active site well-adapted to terpenoids such as sesquiterpenes, as exemplified by the good modelled fit of (+)-thujposene and (+)-α-barbatene in the heme vicinity (Figure 9C-9D).

Docking of different sesquiterpenes in this structural model yielded strikingly homogeneous distributions (Supplemental Figure 19), with a major or unique best-ranked cluster of poses corresponding in most cases to the observed metabolism. (+)-thujopsene was found stacked to the heme porphyrin ring by its double bond, with the shortest iron–carbon distances observed for allylic (C11, Figure 9E) and vinyl positions (C1), in agreement with the primary oxidation product 1-oxo-thujopsene. Similarly, the best affinity histogram cluster for docked (+)-α-barbatene contained poses fully consistent with observed primary products (+)-6-OH- and (+)-6-oxo-α-barbatene, with the shortest iron–carbon distances observed for allylic (C5) and vinyl (C6) carbons (Figure 9F). The model is also consistent with re-uptake and further conversion of primary oxidation product 1-oxo-thujopsene (Figure 9G), with the best docking pose displaying a favorable heme–ligand distance (shortest distances observed for positions C11 and C15), with a slightly better binding score for (+)-thujopsene. This conformation is likely favored by the stabilizing presence of the polar Thr322 in the heme pocket. The low binding energies for docking of (*E*)-β caryophyllene, (*E*)-β-farnesene, α-pinene, and (+)-sabinene all indicate overall good affinities for the active site (Supplemental Table 3), with a preference for cyclic sesquiterpenes, fully supporting the CYP706A3-dependent oxidative conversions observed *in vitro* and *in vivo*, and the experimentally uncovered promiscuity of CYP706A3.

CYP706A3 activity on TPS11 products results in flower protection against insects

Oxidation of volatile floral terpenes can affect the behavior of flower visiting insects, as previously reported for the attractant linalool metabolized by CYP76C1 into repellent lilac compounds (Boachon et al., 2015). Thus, a potential role of *TPS11/CYP706A3* in flower defence was investigated on the pollinator hoverflies that naturally visit Arabidopsis flowers (Jones, 1971; Snape and Lawrence, 1971; Hoffmann et al., 2003). Their preference for the blends of VOCs generated by yeast expressing *TPS11* alone, or by mixed yeasts expressing *TPS11* and *CYP706A3* was tested in an olfactometer. Purified fractions of CYP706A3 products were also investigated (Supplemental Figure 20). Tests comparing TPS11 and CYP706A3 products as a blend or isolated fractions over the neutral field (control without scents) did not yield significant differences, but results all converged to suggest that non-oxidized sesquiterpenes tend to attract hoverflies, while oxidized sesquiterpenes repel them. In line with this trend, hoverflies significantly preferred TPS11 products over the mix of TPS11 and CYP706A3 products, thus confirming the repellent activity of the oxidized products.

TPS11 and *CYP706A3* were shown to be co-expressed during floral transition, suggesting a defensive role of the accumulated sesquiterpene oxides in developing buds (Figure 8). Thus, we tested the feeding behavior of the *Brassicaceae* specialist herbivore *Plutella xylostella* with dual-choice tests on T4 stage flower buds (as defined in Figure 8) of *cyp706a3* and *35S:CYP706A3* compared to wild-type plants (Figure 10A). *P. xylostella* was previously shown to feed on Arabidopsis flowers (Boachon et al., 2015) and is a natural florivore on wild *Brassicaceae* (Knauer et al., 2018). Caterpillars clearly avoided wild-type buds, and favored foraging on buds of the *cyp706a3-2* mutant lacking sesquiterpene oxides. Conversely, caterpillars preferred feeding on wild-type rather than *35S:CYP706A3* buds with increased sesquiterpene oxide content. Together, our data thus suggest that the CYP706A3 products can alter the preference of *P. xylostella* for developing buds and modify the behavior of insects visiting open flowers.

CYP706A3 expression affects flower-associated bacterial communities

There is growing evidence for a close interplay between flower metabolites and the associated microbiome (Junker and Tholl, 2013; Boachon et al, 2019). Thus, we analyzed the effect of *CYP706A3* expression on the floral microbiome by a non-targeted approach employing commonly accepted methods (Bringel and Couée, 2015; Junker and Keller, 2015). DNA from bacterial communities colonizing wild-type, *cyp706a3-2* and *35S:CYP706A3* flowers was extracted, and the 16S rRNA gene was used as a marker and sequenced to identify bacterial operational taxonomic units (OTU) based on DNA sequence similarities. OTU identities and counts were used to compare richness, diversity and composition of the microbiomes present on the three flower types (Figure 10B-D). The average number of the different OTUs detected did not significantly differ between flower types (Col-0 = 337 ± 28 OTUs (mean ± SD), *cyp706a3-2* =342 ± 41 and *35S:CYP706A3* = 360 ± 20 OTUs ; Kruskal-Wallis rank sum test: Chi^2_2= 1.00, p= 0.61). Still, a Chao rarefaction analysis, which estimates the maximum number of OTUs to be expected after additional sampling, suggested a lower expected number of OTUs on wild-type flowers compared to *cyp706a3-2* and *35S:CYP706A3* (Figure 10B). The lower rarefaction curve of OTU richness from wild-type flowers did not overlap with those of the *cyp706a3-2* and *35S:CYP706A3*. The abundance of the OTUs detected on each flower line was then further investigated with a multivariate analysis using the Partial Least Square Discriminant test (PLS-DA) (Hervé et al., 2018). Clearly, the five biological replicates of each of the wild-type, *cyp706a3-2* and *35S:CYP706A3* flowers were significantly separated in three different clusters, each corresponding to a respective genotype (Figure 10C). The two first discriminant axes of the PLS-DA explained 99% of the variance between the flower lines and the permutation test indicated a significant difference between the composition of the microbial communities among the three flower lines (P = 0.001).

To identify the OTUs specifically colonizing each of the flower lines, a univariate analysis was then performed (Figure 10D and Supplemental Table 4). It revealed that 47 OTUs had significantly

different colonization patterns on the flowers of the three lines. Specifically, 20 and 25 OTUs were significantly enriched in the microbiome colonizing *cyp706a3-2* and *35S:CYP706A3* flowers relative to wild-type flowers, out of which 20 were barely detectable or absent on wild-type. By contrast, 19 and 19 OTUs found in wild-type flowers were significantly depleted from *cyp706a3-2* and *35S:CYP706A3* flowers, respectively, out of which 14 and 6 were barely detectable or absent.
Such data suggest that the CYP706A3-generated metabolites play a role in the assembly of specific bacterial taxa colonizing Arabidopsis flowers.

The*TPS11/CYP706A3* cluster is specific to *Brassicaceae*

To evaluate the significance and conservation of the *TPS11/CYP706A3* cluster, the emergence, phylogeny and association of its constituents were examined, with a primary focus on *Brassicales* and related plants. *TPS11* homologs were detected in all *Brassicaceae* from both lineages I and II (with one to four duplications in *Arabidopsis lyrata*, *Eutrema salsugineum, Brassica rapa* and *Capsella rubella*), but not in earlier diverging *Brassicales* (Figure 11A). The *TPS11* clade thus appears specific to *Brassicaceae*. Phylogenetic analysis also revealed that the *CYP706A* subfamily is specific to *Brassicales*, but that the *CYP706A3* clade is represented only in *Brassicaceae* where it seems to be fixed, since *CYP706A3* homologs (with a single duplication in *A. lyrata* and *B. rapa*) are present in all species of sequenced genomes (Figure 11B).
TPS11/CYP706A3 clustering is observed in all *Brassicaceae* belonging to lineage I and in *Eutrema salgineum* belonging to lineage II (Figure 11C). *TPS11* and *CYP706A3* clustering thus occurred early in the evolution of *Brassicaceae*, before the split between sister lineages around 45 million years ago. The cluster is duplicated in *C. rubella,* while tandem duplications of *TPS11* are observed in several wild species. In domesticated members of the lineage II *Brassica* genus (thus submitted to a less stringent environment), *TPS11* and *CYP706A3* are still present, but no longer clustered (Figure 11C).

Discussion

A minimal and versatile functional cluster evolving within *Brassicaceae*

Functional gene clusters have been defined as groups of at least three non-homologous biosynthetic genes for a distinct biosynthetic pathway adjacent to one another in the genome (Nützmann and Osbourn, 2014; Nützmann et al., 2016). We show here that a combination of just two physically clustered and co-regulated genes can form an efficient functional unit, generating a whole range of terpenoid oxides that protect the plants against florivorous insects and selectively alter the flower microbiome. This gene combination still matches the criteria defined for metabolic gene clusters, since it contains the first committed step of the pathway generating initial chemical scaffolds (a terpene synthase) and a subsequent P450 tailoring. The originality of this uncommon cluster associated with a sesquiterpenoid-derived pathway is that both the terpene synthase and

cytochrome P450 enzymes yield several products and/or transform a large set of substrates. CYP706A3, alone, catalyzes not only the oxidation of a broad range of sesqui- and monoterpenes, but also a cascade of reactions on the same original substrate. Our data suggest that both *TPS11* and *CYP706A3* evolved early within *Brassicaceae*, and became clustered before the split of *Brassicaceae* lineages I and II. This minimal functional cluster is possibly representative of an early stage of the formation of more complex metabolic gene clusters, such as those reported in angiosperms. It may also be representative of a more flexible and transient organization suited to the inherent promiscuity of enzymes involved in small isoprenoid (mono- and sesquiterpenes) metabolism for swift plant adaptation.

CYP706A3 generates a versatile defense arsenal exapted from flower scent

Both *TPS11* and *CYP706A3* seem to be fixed in *Brassicaceae*, and their clustering is maintained in wild species. This might result from a dual selective advantage for such a structural arrangement. One is reduced emission and enhanced detoxification of membrane-damaging terpenes abundantly formed in flower tissues essential for reproduction. Another is the formation of defense molecules that protect flower organs from pathogens and herbivores. Our data demonstrate that CYP706A3 not only acts upon products of TPS11, but also on mono- and sesquiterpenes generated by other flower-expressed TPS enzymes, such as (*E*)-β-caryophyllene or α-pinene. Remarkably, primary oxidation products are further transformed by CYP706A3. The reason for this unusual activity of CYP706A3 with a broad range of olefins and oxygenated compounds is found in its predicted active site properties (Figure 9; Supplemental Table 3), and in the orientations of the enzyme on the membrane and of the two main access channels. Orientations of the two access channels, together with their physicochemical properties (Figure 9; Supplemental Figure 18), suggest that CYP706A3 has been evolutionarily adapted to facilitate uptake of small and hydrophobic/non-polar substrates from the membrane, and release of polar products into the membrane–water interface. This configuration would also be compatible with the reported activities of three previously functionally characterized CYP706 enzymes, catalyzing oxidation of (+)-valencene in Alaska cedar (*Callitropsis nootkatensis*; Cankar et al., 2014), (+)-δ-cadinene in cotton (Luo et al., 2001), and phenylacetaldoxime in eucalyptus (*Eucalyptus cladocalyx*; Hansen et al., 2018), respectively. In addition, the CYP706A3 structural characteristics enable re-uptake of moderately polar metabolites from the membrane–water interface for further oxidation. As a result, CYP706A3-dependent metabolism of flower-emitted terpenes leads to a large variety of oxygenated products.

The production of such a large diversity of oxygenated terpenoids may provide the plant with a selective advantage and also bears potential for development of synergistic effects in support of flower defense. *A. thaliana* is a selfing species and thus not dependent on pollinators. Our results support the hypothesis that the flowers of this species benefit from reducing the number and frequency of flower visitors, including taxa otherwise known to be pollinators and florivores.

Interestingly, duplications of *TPS11* or of the whole cluster are observed in several *Brassicaceae* species. Such duplications are expected to generate even broader chemical diversity of VOCs, possibly for adaptation to specific ecological niches, or to face increased ecological challenges. In favor of the latter hypothesis, *C. rubella* and *A. lyrata* show whole cluster and/or *TPS11* duplications (Figure 11C). The *C. rubella* ancestor, *C. grandiflora* and *A. lyrata* are both outcrossing and emit strong scents dominated by benzenoid compounds (Abel et al., 2009; Raguso, 2016). The selfing *C. rubella* only recently evolved from outcrossing *C. grandiflora* with concomitant loss in benzaldehyde emission, but keeps emitting significant amounts of benzoic acid (Sas et al., 2016). *TPS11* and *CYP706A3* duplications may thus have been required to reinforce the defense arsenal of floral tissues against visiting insects in outcrossing species. Terpene oxides have been shown earlier to serve as protections against florivores (Boachon et al., 2015). This is supported in the current study. Although we could not measure the development of *P. xylostella* larvae by feeding them with flower buds, nor test pure CYP706A3 products, our choice-test experiments show that flower buds containing lower amounts of oxidized sesquiterpenes were clearly preferred by insect larvae over buds with higher concentrations of these compounds. Scent, like outbreeding, is considered as an ancestral trait in angiosperms. A shift from outbreeding to selfing is one of the most common evolutionary transitions in flowering plants (Thien et al., 2009; Doubleday et al., 2013; Sicard et al., 2011) and is well documented for *Brassicaceae* (Sicard and Lenhard, 2018; Vekemans et al., 2014). Following emergence of *TPS11* and *CYP706A3*, their clustering and duplication might thus represent ancestral events in *Brassicaceae*. The multiple instances of gene or cluster duplications and loss observed in different taxa were potentially favored by the presence of transposable elements on both sides of the cluster (Boutanaev and Osbourn, 2018), as reported in Arabidopsis (http://signal.salk.edu/cgi-bin/tdnaexpress?GENE=At5g44620&FUNCTION=&TDNA=).

So far, flower defense and interactions have essentially been discussed with respect to volatile compounds emitted at anthesis, and their impact on insects or microbial pathogens. Our results support the notion that soluble oxygenated metabolites, diverted from flower-emitted volatiles and retained in flower tissues, also contribute to a versatile and complex defense line against insects (Figure 10A; Supplemental Figure 20). Together with our previous demonstration of the conversion of linalool generated by Arabidopsis flowers into soluble defensive compounds (Boachon et al., 2015), our results contribute to solving the long-standing puzzle of the modest residual amount of scent emitted by selfing plants (Raguso, 2016), by revealing the exaptation of floral volatile mono- and sesquiterpenes to raise antifeedant flower defense.

Flower defense starts with the onset of floral bud development

Previous investigations on floral defense focused on anthesis without considering the earlier stages of flower development. Worthy of note, *TPS11* and *CYP706A3* expression starts with floral transition, resulting in an accumulation of oxygenated sesquiterpenes already in young flower buds.

Our data thus associate initiation of the defense of reproductive organs to early stages of flower development. In young buds, moreover, the ratio of *TPS11* to *CYP706A3* expression is inverted compared to open flowers, preventing emission of insect-attracting volatile terpenes and ensuring their complete conversion into soluble defense compounds. The observed ratio inversion also indicates that whilst both genes are essentially co-regulated, independent developmental modulation of their respective expression is also possible.

***CYP706A3* most likely shapes flower-associated bacterial communities**

Our data indicate a selective impact of CYP706A3-dependent terpenoid oxidative metabolism on the flower microbiome. Analyses of bacterial abundance, diversity and composition suggest distinct microbial community characteristics for each flower genotype (Figure 10C). Flowers of both the *cyp706a3* and *35S:CYP706A3* lines host OTU-enriched bacterial communities compared to the wild type (Figure 10B), which would be in agreement with a contribution of terpenoid oxidative metabolism to reduce bacterial colonization and thus diversity in wild-type flowers. Visual inspection of the ordination plot (PLS-DA) enables a clear separation of the communities associated with the flower genotypes. Such differences in community composition of the genotypes raise the possibility that all OTUs are equally not affected. Accordingly, we found plant line-specific effects on individual OTUs. For example, among OTUs found in higher abundance on the *35S:CYP706A3* plant, OTU_532 affiliated with *Pseudomonas* was detected (Figure 10D). In line with this observation, an OTU affiliated with *Pseudomonas* was found to be enriched in *Petunia* stigmas impaired in the accumulation of sesquiterpenes (Boachon et al., 2019). Strains from this genus were also recently described to stimulate conversion of terpenoid hydrocarbons to oxygenated sesquiterpenoids in the plant *Atractylodes lancea* (Zhou et al., 2018). Conversely, we found that specific OTUs colonizing wild-type flowers were depleted on *cyp706a3* and the *35S:CYP706A3* flowers.

Only 47 out of 1485 OTUs detected significantly differed between the flower lines. This potentially reflects the selective effects of CYP706A3-dependent metabolic alterations in the different genotypes. Analysis from single mutant lines might cast doubt on the reliability of our data. The latter are nevertheless supported by the good reproducibility among replicates. Our sampling procedure might, in addition, conceal larger differences. *CYP706A3* expression is mainly detected in the flower stigma, but due to the small size of Arabidopsis flowers, we analyzed the microbiome from whole inflorescences. Bacterial communities were previously shown to differ between flower organs (Junker and Keller; 2015). Pooling floral organs is thus expected to reduce visibility of microbiota modifications specifically associated with stigma biochemistry.

Altogether our results suggest that the *TPS11* and *CYP706A3* cluster may contribute to modulate bacterial communities on Arabidopsis flowers. This would be in concordance with earlier findings that volatile organic compounds shape bacterial community diversity and composition (Junker an Tholl, 2013; Burdon et al., 2018; Boachon et al., 2019). Recent studies demonstrated that removal

of the floral microbiome resulted in a decrease of floral terpene emission (Peñuelas et al. 2014) and modified the floral metabolome (Gargallo-Garriga et al. 2016). In addition, epiphytic bacteria altered floral scent emissions (Helletsgruber et al. 2017). Conversely, floral volatiles can also affect microbes colonizing flowers, such as (*E*)-β-caryophyllene generated by TPS21 in Arabidopsis flowers that was shown to confer protection against the bacterial pathogen *Pseudomonas syringae* (Huang et al., 2012). The organ-specific ecological role of bacterial sub-populations and their advantage for flower fitness thus remain to be determined. Furthermore, the selective effects of CYP706A3 substrates and products on relevant microbial species merit further investigations. More complex levels of multi-organism interactions may also be considered to link the flower-associated microbiome and flower visitors (Farré-Armengol and Junker, 2019).

Methods

Plant growth

A. thaliana Col-0 and *N. benthamiana* plants were cultivated in growth chambers under standard conditions as described previously (Boachon et al., 2015). Seeds were sown on a standard soil compost mixture in 7 cm diameter pots and cultivated in growth chambers under white fluorescent lamps with a light intensity of 100-150 $\mu mol.m^{-2}.s^{-1}$ at 22°C during the 12 h day period and 19°C during the 12 h night period for Arabidopsis, and at 24°C during the 16 h day period and at 20°C during the 8 h night period for *N. benthamiana*.

Gene co-expression analysis and quantification of gene expression

CYP706A3 and *TPS11* co-expression patterns were investigated using the 'Expression Angler' tool (Toufighi et al., 2005). Quantification of expression of *CYP706A3*, *TPS03*, *TPS10*, *TPS11*, *TPS14*, *TPS21* and *TPS24* genes was performed by RT-qPCR as previously described (Boachon et al., 2015). Primers used for each gene are listed in Supplemental Table 5. Relative transcript levels were calculated using the $E^{\Delta Ct}$ method (Pfaffl, 2001), taking the specific amplification efficiency of each primer pair into account, and were normalized with four reference genes whose stable expression is validated (Czechowski et al., 2005). Four biological replicates (pooled organs collected from individual plants) were used for plant organ tissues and flower organs, and three for floral transition analysis.

Generation of vector constructs

To express *CYP706A3* and terpene synthase genes in plant and yeast, plasmids were constructed as previously described (Höfer et al., 2014; Boachon et al., 2015) using the USER™ cloning system (New England Biolabs) according to Nour-Eldin et al. (Nour-Eldin et al., 2006). Coding sequences

(CDS) were inserted into the yeast expression plasmid pYeDP60u2 and into the plant expression vector pCAMBIA3300u. To study subcellular localization, *CYP706A3* and *TPS11* CDSs with modified 3' ends were inserted in Gateway binary vectors 5' to the sequence of G3GFP in pGWB451 and of RFP in pGWB461, respectively (Nakagawa et al., 2007). Plants and yeasts were transformed as previously described (Ginglinger et al., 2013; Höfer et al., 2014; Boachon et al., 2015). Primers used for cloning are listed in Supplemental Table 5.

Confocal microscopy of CYP706A3 and TPS11 in *N. benthamiana*

Fluorescent protein fusion constructs were transformed into the hypervirulent *A. tumefaciens* strain LBA4404. The leaves of three-week-old *N. benthamiana* plants were co-transformed by agro-infiltration with cultures of equal density of agrobacteria harboring the genes of interest or the p19 gene (silencing suppressor) (Voinnet et al., 2003) in a ratio of 1/1 (v/v) for transient expression as described in Bassard et al. (Bassard et al., 2012). Four days post-infiltration, leaf discs were excised for observation by laser scanning confocal microscopy. Cell imaging was performed using the A1R confocal system microscope (Nikon, Japan). Images were recorded with a 40x water immersion Apochromat Long Working Distance (LWD) objective lens and a 1.15 numerical Aperture objective (Nikon, Japan). Excitation/emission wavelengths were 488/500-550 nm for G3GFP and CYP706A3:G3GFP constructs, and 561/570-620 nm for the TPS11:mRFP construct, respectively. Z-stack image series were sequentially acquired using the A1R confocal system with NIS-Element software (Nikon, Japan). Images were processed via contrasts and brightness corrections with ImageJ software version 1.51n (NIH, USA; http://rsb.info.nih.gov/ij).

Heterologous expression in yeast, VOCs collection and purification

To test the activity of CYP706A3 on products formed by terpene synthases, yeast expression plasmids carrying *CYP706A3*, *TPS11* and *TPS21* CDSs were each transformed into the WAT11 yeast strain (Höfer et al., 2014; Boachon et al., 2015), while expression plasmid carrying *TPS24* CDS was transformed into the K197G yeast strain as previously described (Fischer et al., 2011; Ginglinger et al., 2013). Individual colonies were verified by PCR and cultivation was carried out in the appropriate media as previously described for WAT11 (Höfer et al., 2014; Boachon et al., 2015) and K197G yeast strains (Fischer et al., 2011; Ginglinger et al., 2013). Individual transformed colonies were grown in minimum selection medium for at least 24 hours, and then 10 times diluted in complete medium and grown for 30 hours. 250 mL of yeast culture of each transformant in co-culture with 250 mL of yeast culture of the corresponding strain transformed with the empty vector, or co-cultures of 250 mL of yeast transformed with *CYP706A3* CDS mixed with 250 mL of yeast culture transformed with plasmids carrying either *TPS11*, *TPS21* or *TPS24* CDSs were then induced overnight with galactose (20 g/L). Cultures were poured in 1L glass bottles equipped with a lid with 2 entries (in and out) on which was inserted a TEFLON tube inserted in the culture at the inlet and

a glass cartridge containing 500 mg of Poropak Q (80-100 mesh) (Sigma-Aldrich, St Louis, MO, USA) at the outlet. Cultures were stirred with a magnetic bar, and a vacuum pump was used to pump out VOCs through the Poropak Q cartridges, enabling oxygenation of the cultures by bubbling the air flux through the inlet tube as shown on the scheme in Supplemental Figure 3. VOCs were collected from the yeast cultures for 2 days, and cartridges were eluted every 24 hours with 1 mL dichloromethane spiked with nonyl acetate as internal standard before analysis by GC-MS. To produce and purify TPS11 products further converted by CYP706A3, yeast cultures were grown under similar conditions, but with optimization and upscaling. Briefly, 100 mL of a culture of yeast co-transformed with both *TPS11* and *CYP706A3* expression plasmids was mixed, at the start of galactose induction, with 900 mL of a culture of yeast transformed with only *CYP706A3* expression plasmid. Up to six 1 L cultures were grown at the same time in 2 L glass bottles for 8 days, and VOCs were collected as described above. Cartridges were eluted every day with 1 mL dichloromethane; eluates were then pooled and concentrated under a gentle stream of argon. After analysis of diluted samples by GC-MS to check for products, concentrated samples were diluted in MeOH and run on a semi-preparative High Performance Liquid Chromatography system (e2695 separation module Waters) coupled to an ACQUITY QDa Mass Spectrometer system (Waters). The semi-preparative system was equipped with a Kinetex® 5 µm C18 100 Å Column 250 x 10.0 mm, Ea (Phenomenex), a diode array detector (DAD) and a fraction collector. Chromatography was run with (A) water and (B) methanol as mobile phase, both containing 0.1% formic acid and starting for 1 min at 85% B. A linear gradient was applied to reach 100% B in 12 min, followed by 100% B for 10 min. Return to initial conditions was achieved in 1 min followed by 22 min of column conditioning with 85% B for a total run time of 45 min. The column was operated at 35°C with a flow rate of 3 mL/min, injecting 200 µL sample per run. Following separation on the column, 10% of the products were directed to the Q-da mass spectrometer while the remaining 90% was directed to the DAD and fraction collector through a split line. The Q-da mass spectrometer was set to ionize in positive mode and the cone voltage was set at 10 V. Products were identified based on their putative oxygenated mass, and fractions collected accordingly. Each collected fraction was enriched through several runs, and then diluted with pure water so as to reduce the concentration of eluting solvent MeOH to less than 5%. Sesquiterpene products in each fraction were subsequently concentrated by solid phase extraction (SPE) on Oasis HLB extraction cartridges (Waters) as previously described (Höfer et al., 2014). Products were eluted with $CDCl_3$ prior to GC-MS analysis to verify the purity of each fraction. Selected fractions were submitted to NMR analysis for product identification.

NMR characterization of products

Selected fractions containing substrates or products of CYP706A3 were analyzed on a 500 MHz Bruker Avance spectrometer equipped with a 5-mm DCH dual cryoprobe with z-gradient operating

at 500.13 MHz for ^{1}H and 125.758 MHz for ^{13}C. 1D ^{1}H, ^{1}H -^{1}H COSY, edited ^{1}H -^{13}C HSQC and ^{1}H -^{13}C HMBC were recorded for each sample, adding ^{1}H -^{1}H NOESY and 1D ^{13}C as required.

In vitro activity of CYP706A3 on purified sesquiterpenes

Yeast transformed with CYP706A3 expression plasmid was grown, expression induced, microsomal fraction extracted and P450 expression quantified as previously described (Höfer et al., 2014). To analyze CYP706A3 activity on different substrates, assays were carried out in 300 µL of 20 mM sodium phosphate buffer (pH 7.4) containing 100 µM substrates, 1 mM NADPH, and an adjusted amount of CYP706A3, as yeast microsomal fraction. To improve dissolution of sesqui- and monoterpenes, the latter were added directly to microsomal fractions before dilution with buffer containing up to 5% DMSO. Samples were incubated at 28°C for 1 hour and subsequently extracted with 600 µL ethyl acetate spiked with 10 µM nonyl acetate. After vortexing and short centrifugation at 4,000 g for 2 min at room temperature, the ethyl acetate phase was recovered, dried on anhydrous Na_2SO_4 (Sigma-Aldrich), and analyzed by GC-MS.

For Liquid Chromatography coupled to tandem Mass Spectrometry (LC-MS/MS) analysis of products, similar reactions were stopped by addition of 250 µL of MeOH, vortexed for 10 s, and centrifuged at 5,500 g for 5 min at room temperature. A volume of 400 µL of the supernatant was transferred into LC vials for analysis.

Isolation of insertion mutant and overexpression lines

Arabidopsis insertion lines *cyp706a3-1* (SALK_057031*)* and *cyp706a3-2* (SALKseq_052540) were identified using the T-DNA Express tool from SALK (Alonso et al., 2003), and requested from the Nottingham Arabidopsis Stock Center. Homozygous mutant lines were selected for absence of transcripts in insertion lines by RT-PCR amplifying the full CDS, and RT-qPCR in flower tissues as described above. Over-expressed lines (*35S:CYP706A3*) were generated by transforming the plant expression plasmid pCAMBIA3300 carrying the *CYP706A3* CDS into the *Agrobacterium* GV3101 strain, before transformation of Col-0 plants by floral dip. Transformants in the T1 progeny were selected by germination on phosphinothricin (BASTA) at 10 ug/mL, and resistant lines were screened by RT-qPCR for *CYP706A3* expression in flower tissues. Selected T1 lines showing highest expression were brought to T3 stable progeny by germination on BASTA. *CYP706A3* over-expression was analyzed on T3 lines by RT-qPCR in flower tissues as described above.

VOC collection from the headspace of Arabidopsis flowers and transformed *N. benthamiana* leaves

VOCs emitted from Arabidopsis flowers were collected as previously described, with minor changes (Boachon et al., 2015). About 50 to 60 inflorescences from each line were used for each sample collection, with at least three biological replicates. Detached inflorescences were placed in 12 mL

glass tubes filled with water and placed in 1 L glass jars equipped with an inlet and an outlet. Volatiles were pumped out from the jar with a vacuum pump at ~100 mL min^{-1} and trapped on a cartridge filled with 30 mg Porapak Q (80-100 mesh, Grace scientific) at the outlet. A similar cartridge was placed at the inlet to ensure purification of the incoming air. VOCs were sampled for 24 h. After volatile collection, flowers were cut from inflorescences and weighed before further analysis of soluble compounds. Porapak Q cartridges were eluted with 200 µL dichloromethane spiked with 10 µM nonyl acetate, and VOC analysis and quantification were performed by GC-MS.

To measure VOCs emitted from Arabidopsis plants during floral transition, plants were grown individually on Jiffy-7 peat pellets (Jiffy) under standard conditions, until the appearance of the first inflorescence. Four plants were used per sample, placed in 1 L glass jars, and VOCs were collected as described above. Porapak Q cartridges were eluted every day until the first inflorescence opened, and samples were analyzed by GC-MS.

For headspace analysis of VOCs emitted from transformed *N. benthamiana* leaves, plant expression constructs carrying the CDS of *CYP706A3*, *CYP76C1*, *TPS11, TPS21* or *TPS24* were transformed into hypervirulent *A. tumefaciens* LBA4404, which was used to infiltrate the *N. benthamiana* leaves as described previously (Ginglinger et al., 2013). After two days, infiltrated leaves were detached, and their petioles dipped into a 12 mL glass vial filled with water that was placed in a 1 L glass jar. VOCs emitted from the headspace were collected from 3 to 4 infiltrated leaves per sample for 24 hours following the same procedure as described above for Arabidopsis flower VOCs and subsequently analyzed by GC-MS.

GC-MS analysis

Capillary GC was performed as described previously (Boachon et al., 2015), on a PerkinElmer Clarus 680 gas chromatograph coupled to a PerkinElmer Clarus 600T mass spectrometer (PerkinElmer), using a HP-5ms column (30 m, 0.25 mm, 0.25 µm; Agilent technologies). Samples were injected by splitless injection, at 250°C injector temperature, using a program consisting of 0.5 min at 50°C, followed by 20°C min^{-1} to 320°C, then 5 min at 320°C, with a flow of 1.2 ml min^{-1} of He as carrier gas. Products were identified based on their retention times and electron ionization mass spectra (70 eV, *m/z* 50-300), and compared to those present in the NIST and WILEY libraries and to previously published Arabidopsis flower VOCs (Tholl et al., 2005).

Extraction of soluble compounds

Following collection of VOCs from Arabidopsis flowers and *N. benthamiana* transformed leaves, plant material was extracted with MeOH for analysis of the soluble compounds. The extraction procedure was as previously described (Boachon et al., 2015), and samples were analyzed by LC-MS/MS.

LC-MS/MS analysis of soluble compounds

LC-MS/MS analyses were essentially performed as described previously (Boachon et al., 2015). Quantitative analyses were carried out using several multiple reaction monitoring channels, each specific for a potential oxidized sesquiterpene mass (based on soluble products from yeast-expressed cultures), with specific MS/MS transition and tunes as listed in Supplemental Table 6.

Insect behavior

We tested florivory with the herbivore *Plutella xylostella,* since it is a Brassicaceae specialist that had been shown to feed on floral tissues of Arabidopsis in previous experiments (Boachon et al., 2015) and on Brassicaceae flowers in nature (Knauer et al., 2018). Preference of the *P. xylostella* L3 larvae for flowers from wild-type, *cyp706a3* or *35S:CYP706A3* mutants was tested using a dual-choice feeding test, essentially as described previously (Boachon et al., 2015), except that closed flowers at stage T3 (see Figure 8) were used. Briefly, five Col-0 and five *cyp706A3-2* or *35S:CYP706A3* closed buds were set in 1% agarose on opposite sides of a Petri dish. One insect was placed in the center of the Petri dish. The number of flowers (or flower parts) consumed by the insect was recorded after three hours.

The behavior of adult hoverflies (*Episyrphus balteus*) was tested with headspace collected from yeast cultures expressing *CYP706A3* alone, together with *TPS11*, or with purified fractions, in a star-shaped olfactometer described previously (Junker et al., 2010). Experiments were carried out as described previously (Boachon et al., 2015). The field of the olfactometer defined as substance field was supplied with an air stream from a desiccator in which 100 µg of compounds dissolved in MeOH was placed on a filter. The field of the olfactometer defined as neutral was supplied with an air stream from a control desiccator in which the same amount of MeOH was placed on a filter. Hoverflies were placed one by one for 4 min in the olfactometer and time spent in the neutral or substance fields was measured. Substances in the desiccator were replaced every 20 min.

Phylogenetic analysis

Sequences of CYP706 and TPS11 from different available *Brassicales* genomes were retrieved using a Blast homology search with AtTPS11 and AtCYP706A3 as bait on the Phytozome website (http://phytozome.jgi.doe.gov/), the BrassicaDB page (http://brassicadb.org), or Dr. David Nelson's website (http://drnelson.uthsc.edu/CytochromeP450.html). Homologous sequences were then aligned with other representative TPS (AtTPS12, 13, 23) and CYP76 family members, and more distantly related sequences as outgroup (CYP76C1, CYP76G1, CYP71A12). Sequences were discarded if not grouping with TPS11 or CYP706 in alignments including these outgroup sequences. Short incomplete sequences were manually curated and removed, and remaining sequences were then aligned using MUSCLE and default settings with Seaview (Gouy et al., 2010; Edgar, 2004),

and Gblocks sets defined on protein sequence alignments. Phylogenetic trees were then built using PhyML (Guindon et al., 2010), using the LG model for TPS, and JTT model for CYP706, and consistency was tested by performing 100 bootstrap iterations. If not specifically named to date, sequences were referred to according to their position in the different branches of the tree.

Microbiome analysis

For microbial DNA extraction, micro-organisms were collected from inflorescences of 5- to 6-week-old Arabidopsis plants. For each sample, 5 fully opened inflorescences were harvested from one plant using sterile forceps. Each biological replicate was collected from a different plant. Inflorescences were placed in BashingBeads Lysis tubes from the Xpedition™ Fungal/Bacterial DNA Miniprep kit (Zymo Research) containing lysis solution. Lysis tubes were shaken for 5 min at 20 Hz using TissueLyser II (Qiagen, Hilden, Germany) to extract DNA following the manufacturer's guidelines (Zymo Research). After DNA extraction, the 16S rRNA gene V5-V7 hypervariable region was PCR amplified using primers 799F/1193r as previously described (Supplemental Table 5; Bodenhausen et al., 2013). Amplicon DNA libraries were constructed by the Illumina TruSeq DNA library preparation protocol. Sequencing was performed at MR DNA (www.mrdnalab.com, Shallowater, TX, USA) by MiSeq (2x300bp) following the manufacturer's guidelines. Sequence data were processed using the MR DNA analysis pipeline (MR DNA, Shallowater, TX, USA). In summary, sequences were joined, barcodes removed, and sequences <150 bp or with ambiguous base calls were discarded. Sequences were denoised, OTUs generated and chimeras removed. Operational taxonomic units (OTUs) were defined by clustering at 3% divergence (97% similarity). Final OTUs were taxonomically classified using BLASTn against a curated database derived from GreenGenes, RDPII and NCBI (www.ncbi.nlm.nih.gov, DeSantis et al. 2006, http://rdp.cme.msu.edu). The resulting OTU table was used to determine taxonomic relative abundances and subsequent statistical analyses of alpha- and beta-diversity using the R package vegan (Dixon, 2003) (Supplemental Table 4). The Kruskal-Wallis rank sum test was performed to probe differences in the OTU richness in wild-type, *cyp706a3* mutant and complemented flowers. Chao rarefaction analysis was used to estimate the maximal number of OTUs associated with the flowers of specific lines given a complete sampling. Partial Least Square Discriminant Analysis (PLS-DA) was performed to discriminate the entire bacterial community composition between the flowers of the three Arabidopsis lines. The PLS framework is suited to analyzed data when the number of variables is equal to or greater than samples, which was the case in our data with 15 samples and 1485 variables (number of OTUs) (Hervé et al, 2018). Furthermore, this framework can be applied to quantitative data without any assumption on their distribution. PLS-DA tests whether lines have different bacterial communities. To validate the PLS-DA model, we used a permutation test to evaluate significant differences between groups (Hervé et al, 2018). Finally, a Kruskal-Wallis rank

sum test was performed to identify OTUs that significantly differed between all lines and a Wilcoxon rank sum test was performed to identify OTUs being significantly different between a pair of lines.

Construction of 3D models of CYP706A3

Modeller9v14 and Autodock4 calculations were performed using the computing facilities of the CEA-DRF-Joliot (cluster Gabriel) at Saclay. GROMACS (2016.1) calculations were performed on the I2BC (CNRS/CEA-Gif) cluster.

3D models of *A. thaliana* CYP706A3 (519 amino acids) were rebuilt without the N-terminal membrane segment (catalytic domain 38-519) using Modeller9v14 (Webb and Sali, 2014) and the crystal structures of Protein Data Bank (PDB) selected as templates. Choice of templates was guided by an iterative process that optimized both the multiple sequence alignment (MSA) between the CYP706A3 sequence and templates, and the quality score of models implied by each alignment. The protocol started with 6 templates selected on the basis of the best similarity according to Blast-PDB, HMMER (https://www.ebi.ac.uk/Tools/hmmer/search/hmmscan) and HHPRED (https://toolkit.tuebingen.mpg.de/#/tools/hhblits), summarized in Supplemental Table 2, and on the basis of other criteria such as highest alignment length, best atomic resolution, and highest quantitative model energy analysis (QMEAN) scores. All suitable templates proved to be human isoforms, and exhibited rather low sequence identities with AtCYP706A3 (24-25%). However, corresponding 3D structures were well-aligned by structure alignment algorithms MUSTANG (Konagurthu et al., 2006) and PROMALS3D (Konagurthu et al., 2006; Pei et al., 2008). Resulting MSA were consistent with those obtained with the MAFFT-L-INS-I algorithm (Pei et al., 2008; Katoh and Standley, 2013). As a result of the iterative process, final construction giving rise to the best model involved the three templates CYP2R1 (pdb 3czh), CYP17A1 (pdb 5irq), and CYP1A2 (pdb 2hi4) (see features in Supplemental Table 2). The validated MSA used as input for MODELLER is shown in Supplemental Figure 17.

Several runs of 100 models each were performed, and generated models sorted by the MODELLER objective function were also evaluated by their DOPE (Discrete Optimized Protein Energy) and GA341 scores calculated by MODELLER. The best models having the lowest DOPE score or best objective function issued from each run were pooled and submitted to the online metaserver SAVES (Structural Analysis and Verification Server (http://services.mbi.ucla.edu/SAVES), and finally to the QMEAN scoring function (Benkert et al., 2008) server (Benkert et al., 2009) for model quality assessment. The final model selected for docking studies was the best one according to a good compromise between the scores calculated by the SAVES server scoring programs and the QMEAN4 value and Z-score. As a result, the selected AtCYP706A3 model had a QMEAN4 value and Z-score equal to 0.71 and -2.2 respectively, which are reasonably good scores when compared to the QMEAN scores of individual PDB templates (Supplemental Table 2). The Ramachandran plot exhibited only one residue in disallowed regions (Ile55), located in the disordered N-terminal

segment, upstream of A helix. RMSDs calculated between a-carbons of each template and of the model ranged between 0.61 and 0.88 Å.

Preparation of AtCYP706A3 structures for docking studies

Protein structures generated by Modeller were first stripped of all hydrogen atoms, and then atom charges and hydrogen atoms were added to the protein with the UCSF Chimera package (www.cgl.ucsf.edu/chimera) UCSF chimera 2004 (Pettersen et al., 2004) using AMBER ff14SB parameters. Parameters (geometry and atom charges) applied for the heme in the initial step of the catalytic cycle (defined as Fe^{III} protoporphyrin IX) were taken from an AMBER-compatible heme model developed by Shahrokh *et al*. (Shahrokh et al., 2012), and in some docking experiments with (+)-thujopsene the heme cofactor was also defined as the highly reactive intermediate *compound I* $(Fe^{IV}=O)^{+\cdot}$. The atom charges of the proximal cysteine thiolate were taken from the same work.

Docking procedure of sesquiterpenes

Molecular docking experiments with sesquiterpene molecules into the CYP706A3 active site were performed using AutoDock 4 (release 4.2.6) in the semi-flexible mode, and prepared with AutoDock Tools (Morris et al., 2009). Ligand molecules were parameterized under the UCSF Chimera molecular modeling suite using AM1-BCC charges model, and the structure files saved under MOL2 format as input files for AutoDock. Usually, the semi-flexible mode in Autodock means that the ligand is fully flexible and the receptor kept rigid. In multi-cyclic sesquiterpenoid structures, however, there is no rotatable bond detected by Autodock in the torsion tree. For handling unsaturated ring flexibility, several conformations of the non-aromatic rings were generated by short molecular dynamics (MD) simulations and minimization steps performed under Chimera, and used as a starting point for docking to allow better conformational sampling of the ligands under Autodock 4. The MOL2 format files created in Chimera for the receptor and ligands was converted into PDBQT format with merging all nonpolar hydrogen atoms, and with original charges (AMBER 14ff and AM1-BCC) maintained. The receptor was kept either rigid or flexible. The modeled structure of AtCYP706A3 was also optimized by short 30 ns MD runs (GROMACS 2016) to generate various relaxed conformations of the protein, in addition to the initial MODELLER structure. As a whole, in most cases, the best docking results were obtained using different conformations of multi-cyclic compounds docked in the rigid receptor mode, onto the initial MODELLER structure, with the heme in the Fe^{III} state.

The docking box, in which grid maps were computed using the program AutoGrid (Morris et al., 2009), included the active site with the iron-protoporphyrin group on one edge, and the whole distal moiety of the enzyme to allow a large sampling of potential poses. A “blind” docking test was first done with a grid built by AutoGrid with 64, 88, and 80 points in the x, y, and z directions and a grid spacing of 0.37Å to allow for a good compromise between the resolution of the explored volume and the size of the binding area. In most cases and remarkably, the docking experiments revealed

a unique pose in the active site, close to the heme iron (Supplemental Figure 19A and B). The docking box size was then decreased to 52x54x54 points (x,y,z) with a grid spacing of 0.27Å to allow for a more detailed view of conformations docked in the active site (Supplemental Figure 19C as example). For each sesquiterpene conformer, 100 independent runs were performed using the Lamarckian genetic algorithm (Fuhrmann et al., 2010). The default settings were applied for all other parameters.

The resulting poses were assigned a score calculated by Autodock that can be considered as an estimated free energy of ligand binding (indicative of binding affinity), then clustered as a function of the closeness of their positions and conformations with Root Mean Square Deviation (RMSD) set at 2.0 Å or 1.0 Å, and finally ranked by their binding score (for the best pose in the cluster). The resulting histograms of 100 poses of (+)-thujopsene docked into AtCYP706A3 shown in Supplemental Figure 19 revealed solutions markedly focused in the first cluster, sometimes gathered in a unique cluster within 2Å of RMSD as for conformer 2 of (+)-thujopsene (Supplemental Figure 19A). To resolve slightly different positions of the ligand in the vicinity of the heme, it proved to be more informative to cluster at 1Å of RMSD (Supplemental Figure 19B and C).

Accession Numbers

Sequence data from this article can be found in the Arabidopsis Genome Initiative or GenBank/EMBL databases under the following accession numbers: CYP706A3 (AT5G44620), TPS11 (AT5G44630), TPS21 (AT5G23960), TPS24 (AT3G25810), CYP76C1 (At2g45560), TPS03 (AT4G16740), TPS10 (At2g24210), TPS14 (AT1G61680). Microbiome SRA accession: PRJNA562511.

Supplemental Data

Supplemental Figure 1. *CYP706A3-TPS11* cluster on chromosome 5 of *A. thaliana*.

Supplemental Figure 2. CYP706A3 and TPS11 subcellular localizations.

Supplemental Figure 3. Activity of yeast-expressed CYP706A3 on TPS11 products detected by GC-MS.

Supplemental Figure 4. Mass spectra confirm the identity of compounds detected and further used in our experiments.

Supplemental Figure 5. Identification, separation and enrichment of TPS11 and CYP706A3 products from yeast headspace by semi-preparative LC-Qda.

Supplemental Figure 6. Activity of yeast-expressed CYP706A3 on (-)-thujopsene.

Supplemental Figure 7. Structure of sesquiterpene oxide products formed by CYP706A3 according to NMR spectra.

Supplemental Figure 8. Sequential activity of yeast-expressed CYP706A3 on TPS11 products analyzed by LC-MS/MS.

Supplemental Figure 9. LC-MS of CYP706A3 primary products.

Supplemental Figure 10. LC-MS of CYP706A3 secondary products

Supplemental Figure 11. Genotyping of *CYP706A3* mutants.

Supplemental Figure 12. Activity of CYP706A3 on TPS21 products.

Supplemental Figure 13. Activity of CYP706A3 on TPS24 products.

Supplemental Figure 14. Targeted LC-MS/MS profiling of the sesquiterpene oxide metabolites present in the flowers of wild-type Arabidopsis and *CYP706A3* mutants.

Supplemental Figure 15. Targeted LC-MS/MS profiling of the sesquiterpene oxide metabolites in *N. benthamiana* leaves transiently co-expressing *TPS11* and *CYP706A3*.

Supplemental Figure 16. Targeted LC-MS/MS profiling of sesquiterpene oxide metabolites in buds of wild-type Arabidopsis and *cyp706a3-2* insertion mutant.

Supplemental Figure 17. Multiple sequence alignment of templates used for homology modelling.

Supplemental Figure 18. Channel profiles of physico-chemical properties calculated by Mole2.5.

Supplemental Figure 19: Examples of clustering of 100 docking runs of two different initial conformations of (+)-thujopsene performed by Autodock 4.2.6 on the rebuilt 3D model of AtCYP706A3.

Supplemental Figure 20: Ecological impact of CYP706A3 products on hoverflies.

Supplemental Table 1. Quantification of sesquiterpene emissions upon heterologous expression in *Nicotiana benthamiana.*

Supplemental Table 2. List of potential templates for AtCYP706A3 modelling detected by remote homology methods (based on HMM profiles, or structure prediction by HMM-HMM comparison).

Supplemental Table 3. Binding energy scores obtained by docking the mentioned sesqui- and monoterpene substrates with the AtCYP706A3 model.

Supplemental Table 4. Detailed taxonomic designation for bacterial OTUs that are significantly different between a pair of Arabidopsis lines (Col-0, *cyp706a3-2*, and *35S:CYP706A3*).

Supplemental Table 5: PCR primer list.

Supplemental Table 6: MS/MS conditions and set-up for the LC analysis in multiple reaction monitoring (MRM) of putative sesquiterpene oxides.

Supplemental Dataset 1. Raw and complete data for the fifty most co-expressed genes identified using BAR expression Angler (Toufighi et al., 2011) and *CYP706A3* as bait.

Supplemental Dataset 2: Flower microbiome raw data.

Supplemental Dataset 3: Statistical analysis.

Supplemental Dataset 4: Protein sequence alignment used to generate TPS11 phylogeny.

Supplemental Dataset 5: Tree resulting from alignment in Dataset 4.

Supplemental Dataset 6: Protein sequence alignment used to generate CYP706A3 phylogeny.

Supplemental Dataset 7: Tree resulting from Dataset 6.

Author contributions

BB: designed experiments, performed experiments and interpreted results; YB performed experiments and analyzed data; RJ, X-YC: generated and provided mutants; BV, LA and LM: RMN analysis and interpretation; SM: constructed vectors and mutants; FB, SV, RRJ, FN, FB and SV: microbiome analysis; LH, JEB: confocal microscopy; RR, FA: modeling and docking studies; AL: yeast expression; NN: phylogenomic analysis; BB, YB, RRJ, ND, and IK: designed insect behaviour experiment and analyzed data; DW-R funding and work design; BB and DW-R wrote the manuscript. All authors read and edited the manuscript.

Acknowledgments

BB, YB and DW acknowledge the support of the European Fund for Regional Development in the program INTERREG IVA Broad Region EU invests in your future to the SaarLorBiotech project. The authors acknowledge the use of the facilities of the Bindley Bioscience Center, a core facility of the NIH-funded Indiana Clinical and Translational Sciences Institute. We thank Todd Blevins for contributing to the editing of the manuscript.

References

Abdalsamee, M.K. and Müller, C. (2015) Uncovering different parameters influencing florivory in a specialist herbivore. Ecol. Entomol. **40**: 258-268.

Abel, C., Clauss, M., Schaub, A., Gershenzon, J., and Tholl, D. (2009). Floral and insect-induced volatile formation in *Arabidopsis lyrata* ssp. *petraea*, a perennial, outcrossing relative of *A. thaliana*. Planta **230**: 1–11.

Alonso, J.M. et al. (2003). Genome-wide insertional mutagenesis of *Arabidopsis thaliana*. Science **301**: 653–657.

Bassard, J.-E. et al. (2012). Protein-protein and protein-membrane associations in the lignin pathway. Plant Cell **24**: 4465–4482.

Benkert, P., Künzli, M., and Schwede, T. (2009). QMEAN server for protein model quality estimation. Nucleic Acids Res. **37**: W510–4.

Benkert, P., Tosatto, S.C.E., and Schomburg, D. (2008). QMEAN: A comprehensive scoring function for model quality assessment. Proteins **71**: 261–277.

Boachon, B. et al. (2015). CYP76C1 (cytochrome P450)-mediated linalool metabolism and the formation of volatile and soluble linalool oxides in Arabidopsis flowers: a strategy for defense against floral antagonists. Plant Cell **27**: 2972–2990.

Boachon, B., Lynch, J.H., Ray, S., Yuan, J., Clado, K.M.P., Junker, R.R., Kessler, S.A., Morgan, J.A and, Dudareva, N. (2019) Natural fumigation as a mechanism for volatile transport between flower organs. Nature Chemical Biology 15 583-588.

Boutanaev, A.M. and Osbourn, A.E. (2018) Multigenome analysis 2018implicates miniature inverted-repeat transposable elements (MITEs) in metabolic diversification in eudicots.Proc Natl Acad Sci U S A. 115:E6650-E6658.

Bringel, F. and Couée, I. (2015) Pivotal roles of phyllosphere microorganisms at the interface between plant

functioning and atmospheric trace gas dynamics. Front. Microbiol., 6:486.

Burdon, R.C.F., Junker R.R., Scofield, D.G., and Parachnowitsch, A.L. (2018) Bacteria colonising *Penstemon digitalis* show volatile and tissue-specific responses to a natural concentration range of the floral volatile linalool. Chemoecology 28 :11-19.

Bodenhausen, N., Horton, M.W., and Bergelson, J. (2013). Bacterial communities associated with the leaves and the roots of *Arabidopsis thaliana*. PLoS One **8**: e56329.

Cankar, K., van Houwelingen, A., Goedbloed, M., Renirie, R., de Jong, R.M., Bouwmeester, H., Bosch, D., Sonke, T., and Beekwilder, J. (2014). Valencene oxidase CYP706M1 from Alaska cedar (*Callitropsis nootkatensis*). FEBS Lett. **588**: 1001–1007.

Chen, F., Tholl, D., D'Auria, J.C., Farooq, A., Pichersky, E., and Gershenzon, J. (2003). Biosynthesis and emission of terpenoid volatiles from Arabidopsis flowers. Plant Cell **15**: 481–494.

Cojocaru, V., Winn, P.J., and Wade, R.C. (2007). The ins and outs of cytochrome P450s. Biochim. Biophys. Acta **1770**: 390–401.

Czechowski, T., Stitt, M., Altmann, T., Udvardi, M.K., and Scheible, W.-R. (2005). Genome-wide identification and testing of superior reference genes for transcript normalization in Arabidopsis. Plant Physiol. **139**: 5–17.

Dixon, P. (2003). VEGAN, a package of R functions for community ecology. J. Veg. Sci. **14**: 927-930.

Doubleday, L.A.D., Raguso, R.A., and Eckert, C.G. (2013). Dramatic vestigialization of floral fragrance across a transition from outcrossing to selfing in *Abronia umbellata* (*Nyctaginaceae*). Am. J. Bot. **100**: 2280–2292.

Edgar, R.C. MUSCLE: multiple sequence alignment with improved accuracy and speed. In Proceedings. 2004 IEEE Computational Systems Bioinformatics Conference, 2004. CSB 2004.

Ehlting, J., Sauveplane, V., Olry, A., Ginglinger, J.-F., Provart, N.J., and Werck-Reichhart, D. (2008). An extensive (co-)expression analysis tool for the cytochrome P450 superfamily in *Arabidopsis thaliana*. BMC Plant Biol. **8**: 47.

Euler, M. and Baldwin, I.T. (1996). The chemistry of defense and apparency in the corollas of *Nicotiana attenuata*. Oecologia **107**: 102–112.

Farré-Armengo, G. and Junker, J.J. (2019) Bacteria associated with flowers affect the reproductive success of *Brassica napus*L. *via* scent-mediated interactions with pollinators. https://www.biorxiv.org/content/10.1101/685453v1.

Fischer, M.J.C., Meyer, S., Claudel, P., Bergdoll, M., and Karst, F. (2011). Metabolic engineering of monoterpene synthesis in yeast. Biotechnol. Bioeng. **108**: 1883–1892.

Fuhrmann, J., Rurainski, A., Lenhof, H.-P., and Neumann, D. (2010). A new Lamarckian genetic algorithm for flexible ligand-receptor docking. J. Comput. Chem. **31**: 1911–1918.

Gargallo-Garriga, A., Sardans, J., Pérez-Trujillo, M., Guenther, A., Llusià, J., Rico, L., Terradas, J., Farré-Armengol, G., Filella, I., Parella T. and Peñuelas J. (2016) Shifts in plant foliar and floral metabolomes in response to the suppression of the associated microbiota. BMC Plant Biol. **16**:78.

Ginglinger, J.-F. et al. (2013). Gene coexpression analysis reveals complex metabolism of the monoterpene alcohol linalool in Arabidopsis flowers. Plant Cell **25**: 4640–4657.

Gouy, M., Guindon, S., and Gascuel, O. (2010). SeaView version 4: A multiplatform graphical user interface for sequence alignment and phylogenetic tree building. Mol. Biol. Evol. **27**: 221–224.

Guindon, S., Dufayard, J.F., Lefort, V., Anisimova, M., Hordijk, W. and Gascuel, O. (2010). New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. Syst. Biol. **59**:307-321.

Hansen, C.C., Sørensen, M., Veiga, T.A.M., Zibrandtsen, J.F.S., Heskes, A.M., Olsen, C.E., Boughton, B.A., Møller, B.L., and Neilson, E.H.J. (2018). Reconfigured cyanogenic glucoside biosynthesis in involves a cytochrome P450 CYP706C55. Plant Physiol. **178**: 1081–1095.

Helletsgruber, C., Dötterl, S., Ruprecht, U. and Junker, R.R. (2017) Epiphytic Bacteria Alter Floral Scent Emissions. J. Chem. Ecol. **43**:1073-1077**.**

Hervé, M.R., Nicolè, F. and Lê Cao, K.A. (2018) Multivariate Analysis of Multiple Datasets: a Practical Guide for Chemical Ecology. J. Chem. Ecol. **44**: 215-234.

Höfer, R., Boachon, B., Renault, H., Gavira, C., Miesch, L., Iglesias, J., Ginglinger, J.-F., Allouche, L., Miesch, M., Grec, S., Larbat, R., and Werck-Reichhart, D. (2014). Dual function of the cytochrome P450 CYP76 family from *Arabidopsis thaliana* in the metabolism of monoterpenols and phenylurea herbicides. Plant Physiol. **166**: 1149–1161.

Hoffmann, M.H., Bremer, M., Schneider, K., Burger, F., Stolle, E., and Moritz, G. (2003). Flower visitors in a natural population of *Arabidopsis thaliana*. Plant Biol. **5**: 491-494.

Huang, M., Sanchez-Moreiras, A.M., Abel, C., Sohrabi, R., Lee, S., Gershenzon, J., and Tholl, D. (2012). The major volatile organic compound emitted from *Arabidopsis thaliana* flowers, the sesquiterpene (E)-β-caryophyllene, is a defense against a bacterial pathogen. New Phytol. **193**: 997–1008.

Jones, M.E. (1971). The population genetics of *Arabidopsis thaliana* I. The breeding system. Heredity **27**: 39-50.

Junker, R.R. (2016). Multifunctional and diverse floral scents mediate biotic interactions embedded in communities. *Deciphering Chemical Language of Plant Communication*, eds Blande J, Glinwood R (Springer, Cham), pp 257–282.

Junker, R.R., Heidinger, I.M.M., and Blüthgen, N. (2010). Floral scent terpenoids deter the facultative florivore *Metrioptera bicolor* (Ensifera, Tettigoniidae, Decticinae). J. Orthoptera Res. **19**: 69–74.

Junker, R.R. and Keller, A. (2015). Microhabitat heterogeneity across leaves and flower organs promotes bacterial diversity. FEMS Microbiol. Ecol. **91**: fiv097.

Junker, R.R. and Tholl, D. (2013). Volatile organic compound mediated interactions at the plant-microbe interface. J. Chem. Ecol. **39**: 810–825.

Katoh, K. and Standley, D.M. (2013). MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol. Biol. Evol. **30**: 772–780.

Katsuda, Y. (2012). Progress and future of pyrethroids. Top. Curr. Chem. **314**: 1–30.

Kessler, D., Diezel, C., and Baldwin, I.T. (2010). Changing pollinators as a means of escaping herbivores. Curr. Biol. **20**: 237–242.

Kessler, D., Kallenbach, M., Diezel, C., Rothe, E., Murdock, M., and Baldwin, I.T. (2015). How scent and nectar influence floral antagonists and mutualists. Elife **4**.

Kikuta, Y., Ueda, H., Takahashi, M., Mitsumori, T., Yamada, G., Sakamori, K., Takeda, K., Furutani, S., Nakayama, K., Katsuda, Y., Hatanaka, A., and Matsuda, K. (2012). Identification and characterization of a GDSL lipase-like protein that catalyzes the ester-forming reaction for pyrethrin biosynthesis in *Tanacetum cinerariifolium*- a new target for plant protection. Plant J. **71**: 183–193.

Knauer, A.C., Bakhtiari, M. and Schiestl, F.P. (2018) Crab spiders impact floral-signal evolution indirectly through removal of florivores. Nat Commun. **9**: 1367.

Konagurthu, A.S., Whisstock, J.C., Stuckey, P.J., and Lesk, A.M. (2006). MUSTANG: a multiple structural alignment algorithm. Proteins **64**: 559–574.

Li, R., Schuman, M.C., Wang, Y., Llorca, L.C., Bing, J., Bennion, A., Halitschke, R., and Baldwin, I.T. (2018). Jasmonate signalling makes flowers attractive to pollinators and repellant to florivores in nature.

J. Integr. Plant Biol. **60**: 190–194.

Li, R., Wang, M., Wang, Y., Schuman, M.C., Weinhold, A., Schäfer, M., Jiménez-Alemán, G.H., Barthel, A., and Baldwin, I.T. (2017). Flower-specific jasmonate signalling regulates constitutive floral defenses in wild tobacco. Proc. Natl. Acad. Sci. U. S. A. **114**: E7205–E7214.

Luo, P., Wang, Y.H., Wang, G.D., Essenberg, M., and Chen, X.Y. (2001). Molecular cloning and functional identification of (+)-delta-cadinene-8-hydroxylase, a cytochrome P450 mono-oxygenase (CYP706B1) of cotton sesquiterpene biosynthesis. Plant J. **28**: 95–104.

McKey D. (1979) The distribution of secondary compounds within plants. *Herbivores: Their Interaction with Secondary Plant Metabolites* (Academic, New York), pp 55–133.

Morris, G.M., Huey, R., Lindstrom, W., Sanner, M.F., Belew, R.K., Goodsell, D.S., and Olson, A.J. (2009). AutoDock4 and AutoDockTools4: Automated docking with selective receptor flexibility. J. Comput. Chem. **30**: 2785–2791.

Nakagawa, T. et al. (2007). Improved Gateway binary vectors: high-performance vectors for creation of fusion constructs in transgenic analysis of plants. Biosci. Biotechnol. Biochem. **71**: 2095–2100.

Nour-Eldin, H.H., Nørholm, M.H.H., and Halkier, B.A. (2006). Screening for plant transporter function by expressing a normalized Arabidopsis full-length cDNA library in Xenopus oocytes. Plant Methods **2**: 1-17.

Nützmann, H.-W., Huang, A., and Osbourn, A. (2016). Plant metabolic clusters - from genetics to genomics. New Phytol. **211**: 771–789.

Nützmann, H.-W. and Osbourn, A. (2014). Gene clustering in plant specialized metabolism. Curr. Opin. Biotechnol. **26**: 91–99.

Pei, J., Tang, M., and Grishin, N.V. (2008). PROMALS3D web server for accurate multiple protein sequence and structure alignments. Nucleic Acids Res. **36**: 2295–2300.

Peñuelas, J., Farré-Armengol, G., Llusia, J., Gargallo-Garriga, A., Rico L., Sardans, J., Terradas, J. and Filella I. (2014) Removal of floral microbiota reduces floral terpene emissions.Sci. Rep. **4**:6727.

Pettersen, E.F., Goddard, T.D., Huang, C.C., Couch, G.S., Greenblatt, D.M., Meng, E.C., and Ferrin, T.E. (2004). UCSF Chimera--a visualization system for exploratory research and analysis. J. Comput. Chem. **25**: 1605–1612.

Pfaffl, M.W. (2001). A new mathematical model for relative quantification in real-time RT-PCR. Nucleic Acids Res. **29**: e45.

Pravda, L., Sehnal, D., Toušek, D., Navrátilová, V., Bazgier, V., Berka, K., Svobodová Vareková, R., Koca, J., and Otyepka, M. (2018). MOLEonline: a web-based tool for analyzing channels, tunnels and pores (2018 update). Nucleic Acids Res. **46**: W368–W373.

Raguso, R.A. (2016). Plant evolution: Repeated loss of floral scent - A path of least resistance? Curr. Biol. **26**: R1282–R1285.

Sas, C., Müller, F., Kappel, C., Kent, T.V., Wright, S.I., Hilker, M. and Lenhard, M. (2016) Repeated Inactivation of the First Committed Enzyme Underlies the Loss of Benzaldehyde Emission after the Selfing Transition in Capsella. Curr Biol. **26**:3313-3319.

Shahrokh, K., Orendt, A., Yost, G.S., and Cheatham, T.E., 3rd (2012). Quantum mechanically derived AMBER-compatible heme parameters for various states of the cytochrome P450 catalytic cycle. J. Comput. Chem. **33**: 119-133.

Sicard, A. and Lenhard, M. (2018). Capsella. Curr. Biol. **28**: R920–R921.

Sicard, A., Stacey, N., Hermann, K., Dessoly, J., Neuffer, B., Bäurle, I., and Lenhard, M. (2011). Genetics, evolution, and adaptive significance of the selfing syndrome in the genus *Capsella*. Plant Cell **23**: 3156–3171.

Slotte, T. et al. (2013). The *Capsella rubella* genome and the genomic consequences of rapid mating system evolution. Nat. Genet. **45**: 831-835.

Snape, J.W., and Lawrence, M.J. (1971). The breeding system of *Arabidopsis thaliana*. Heredity **27**: 299-302.

Thien, L.B., Bernhardt, P., Devall, M.S., Chen, Z.-D., Luo, Y.-B., Fan, J.-H., Yuan, L.-C., and Williams, J.H. (2009). Pollination biology of basal angiosperms (ANITA grade). Am. J. Bot. **96**: 166–182.

Tholl, D., Chen, F., Petri, J., Gershenzon, J., and Pichersky, E. (2005). Two sesquiterpene synthases are responsible for the complex mixture of sesquiterpenes emitted from Arabidopsis flowers. Plant J. **42**: 757–771.

Tholl, D. and Lee, S. (2011). Terpene specialized metabolism in *Arabidopsis thaliana*. Arabidopsis Book **9**: e0143.

Toufighi, K., Brady, S.M., Austin, R., Ly, E., and Provart, N.J. (2005). The botany array resource: e-Northerns, expression angling, and promoter analyses. Plant J. **43**: 153–163.

Vekemans, X., Poux, C., Goubet, P.M., and Castric, V. (2014). The evolution of selfing from outcrossing ancestors in *Brassicaceae*: what have we learned from variation at the S-locus? J. Evol. Biol. **27**: 1372–1385.

Voinnet, O., Rivas, S., Mestre, P., and Baulcombe, D. (2003). An enhanced transient expression system in plants based on suppression of gene silencing by the p19 protein of tomato bushy stunt virus. Plant J. **33**: 949–956.

Webb, B. and Sali, A. (2014). Comparative protein ptructure modeling using MODELLER. Curr. Protoc. Bioinformatics **47**: 5.6.1–32.

Xu, H., Moghe, G.D., Wiegert-Rininger, K., Schilmiller, A.L., Barry, C.S., Last, R.L., and Pichersky, E. (2018). Coexpression analysis identifies two oxidoreductases involved in the biosynthesis of the monoterpene acid moiety of natural pyrethrin insecticides in *Tanacetum cinerariifolium*. Plant Physiol. **176**: 524–537.

Zhou, J.-Y., Sun, K., Chen, F., Yuan, J., Li, X., and Dai, C.-C. (2018). Endophytic Pseudomonas induces metabolic flux changes that enhance medicinal sesquiterpenoid accumulation in *Atractylodes lancea*. Plant Physiol. Biochem. **130**: 473–481.

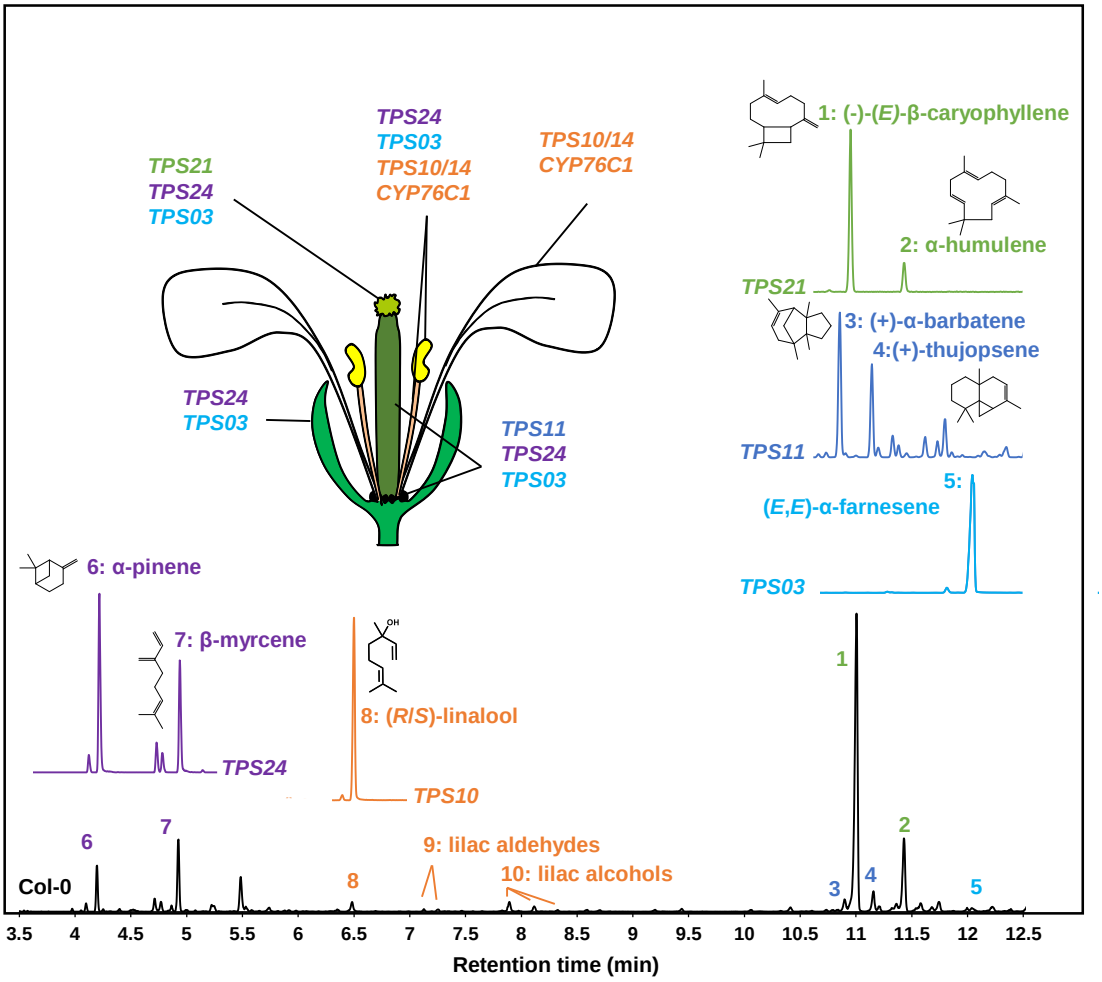

Figure 1. Flower-expressed terpene synthases in Col-0 *Arabidopsis* and resulting flower-emitted terpenoids.

Top: GC-MS chromatograms of products generated by different TPS expressed in *N. benthamiana*. Expression in specific flower organs is indicated. Bottom: Representative GC-MS chromatogram of headspace collected from Col-0 flowers focusing on major mono- and sesquiterpenes (m/*z*: 93) produced by flower-expressed TPSs.

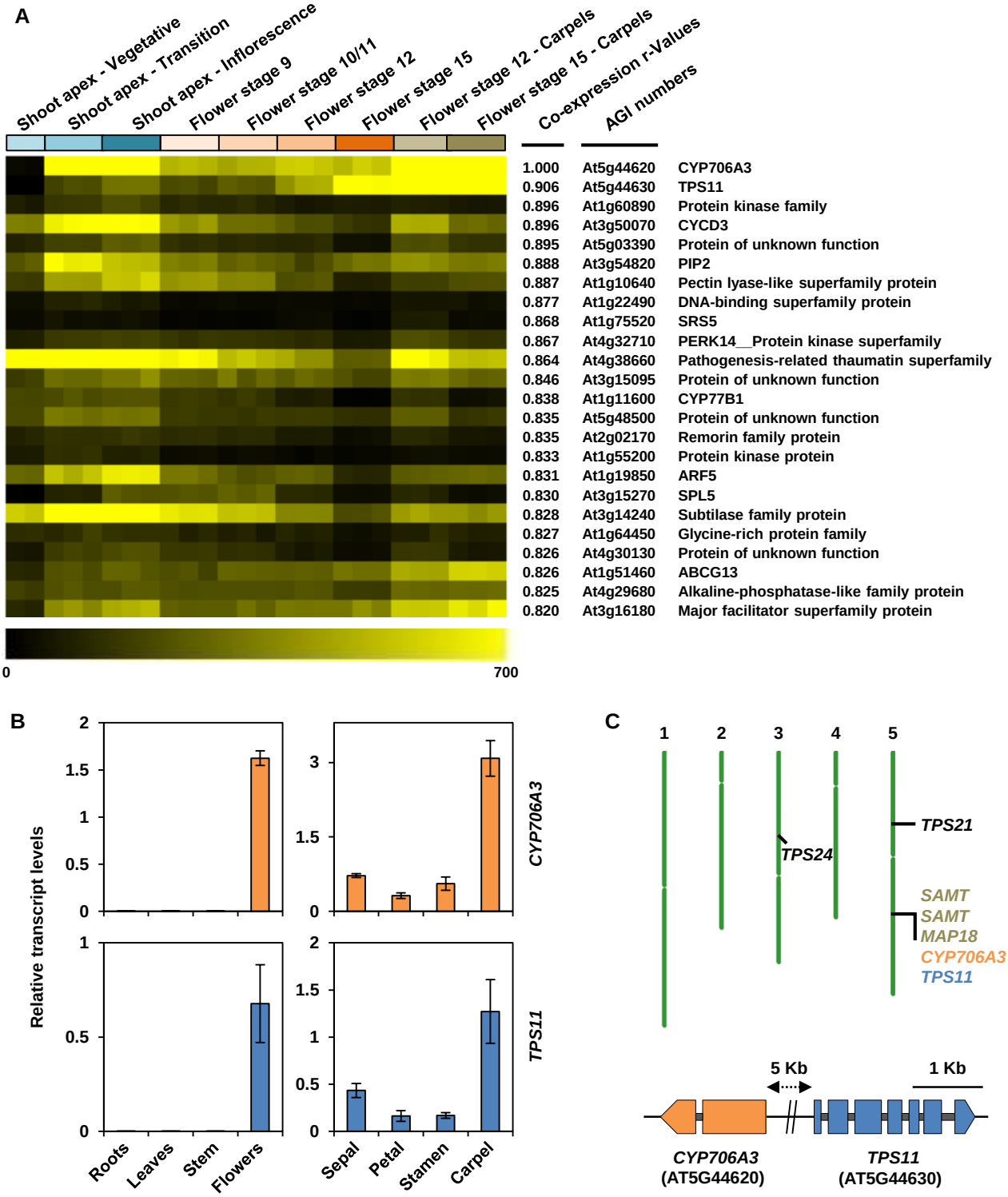

Figure 2. *CYP706A3* and *TPS11* are co-expressed and physically clustered on chromosome 5 in *A. thaliana*. (A) Expression heatmap of the 25 genes most coregulated with *CYP706A3*. Analysis was performed using the Expression Angler tool and the AtGenExpress extended Tissue Compendium data set (Toufighi et al., 2005). The heatmap shows expression levels in selected flowers' tissues: vegetative shoot apex, transition and inflorescence tissues, flower stages 9, 10/11, 12, 15, and carpels of flower stages 12 and 15. Pearson correlation coefficients (r values) of each gene co-expressed with *CYP706A3,* AGI numbers of the genes, and gene annotations from TAIR are shown. (B) Relative transcript levels of *CYP706A3* and *TPS11* in plant (left panel) and flower (right panel) organs. Relative transcript levels were determined by RT-qPCR (details in Methods section). Results represent mean ± SE of four biological replicates (pooled tissues from individual plants). (C) Map of the *CYP706A3* and *TPS11* gene cluster on chromosome 5 (top) and representation of introns/exons and genomic distances between both genes (bottom). The genomic localizations of *TPS24*, *TPS21* and cluster-neighboring genes are also indicated. Numbers 1–5 indicate chromosomes 1–5 . Line represents chromosome 5 on which are located the exons (*CYP706A3*: orange-filed, TPS11: blue-filled boxes) and introns (gray-filled boxes).

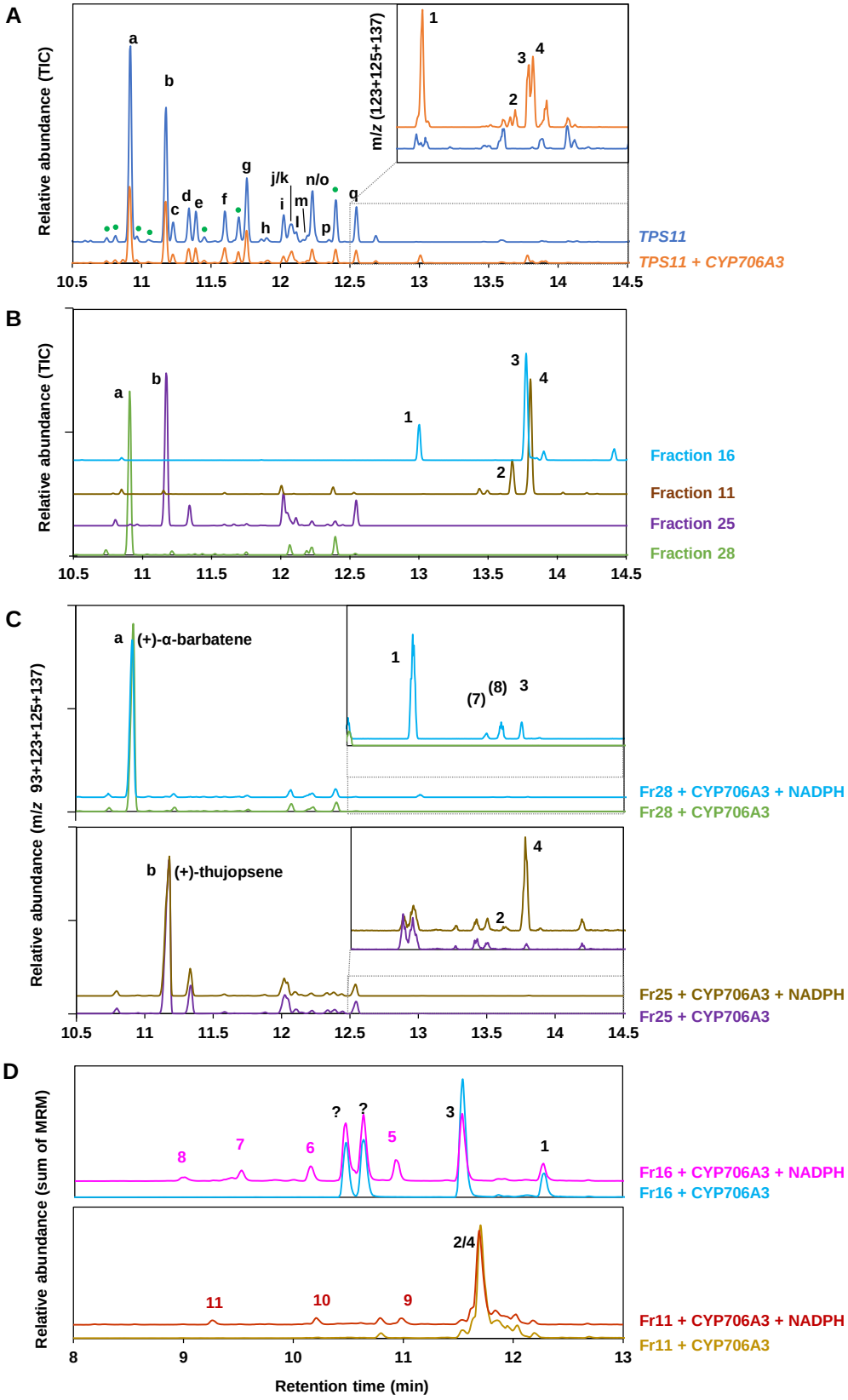
A
Relative abundance (TIC)
m/z (123+125+137)
TPS11
TPS11 + CYP706A3
B
Relative abundance (TIC)
Fraction 16
Fraction 11
Fraction 25
Fraction 28
C
Relative abundance (m/z 93+123+125+137)
(+)-α-barbatene
(+)-thujopsene
Fr28 + CYP706A3 + NADPH
Fr28 + CYP706A3
Fr25 + CYP706A3 + NADPH
Fr25 + CYP706A3
D
Relative abundance (sum of MRM)
Fr16 + CYP706A3 + NADPH
Fr16 + CYP706A3
Fr11 + CYP706A3 + NADPH
Fr11 + CYP706A3
Retention time (min)

Figure 3. Yeast-expressed CYP706A3 oxidizes TPS11 products.

(A) GC-MS chromatograms of headspace collected from cultures of yeast expressing *TPS11* or from mixtures of yeast expressing *TPS11* or *CYP706A3*. Chromatograms show the relative abundance of total ion current (TIC) and the sum of extracted ion current as insets (*m/z* 123 + 125 + 137). See Methods section for detailed protocol.

(B) GC-MS chromatograms of fractions purified from (A) and containing TPS11 and CYP706A3 products.

(C) GC-MS chromatograms of ethyl acetate extracts from incubations of purified TPS11 products (fraction 28 containing (+)-α-barbatene (upper panel) or fraction 25 containing (+)-thujopsene (lower panel)) with microsomal membranes prepared from yeast expressing CYP706A3 in the presence or absence (negative control) of NADPH. Chromatograms show the sum of extracted ion current (*m/z* 93 + 123 + 125 + 137). Insets show expanded chromatogram scale. CYP706A3-dependent metabolism of TPS11 products is probably underestimated due to low solubility of substrates in the incubation buffer.

(D) LC-MS/MS chromatograms of MeOH extracts from incubations of purified CYP706A3 primary products (fraction 16 containing barbatene oxides (**1**) and (**3**) (upper panel) or fraction 11 containing thujopsene oxides (**2**) and (**4**) (lower panel)) with microsomal membranes prepared from yeast expressing *CYP706A3* in the presence or absence (negative control) of NADPH. Chromatograms show the sum of different multiple reaction monitoring (MRM) listed in Supplemental Table 6.

TPS11 products are indicated with letters: (**a**) (+)-α-barbatene, (**b**) (+)-thujopsene, (**c**) isobazzanene, (**d**) (+)-β-barbatene, (**e**) (*E*)-β-farnesene, (**f**) β-acoradiene, (**g**) (+)-β-chamigrene, (**h**) α-zingiberene, (**i**) α-cuprenene, (**j**) α-chamigrene, (**k**) (-)-cuparene, (**l**) 1,2-dihydrocuparene, (**m**) (-)-zingiberene, (**n**) 1,2-dihydrocuparene, (**o**) β-sesquiphellandrene, (**p**) (*E*)-γ-bisabolene, and (**q**) δ-cuprenene. The products were identified based on a comparison of their MS and RT with libraries and published work (Tholl et al., 2005). CYP706A3 products are indicated by numbers and defined in Figure 4. Peaks labelled with question marks could not be identified, but their mass suggests that they are oxygenated sesquiterpenoids. These peaks appeared only after storage. See Supplemental Figure 3 and 4 for more extensive data.

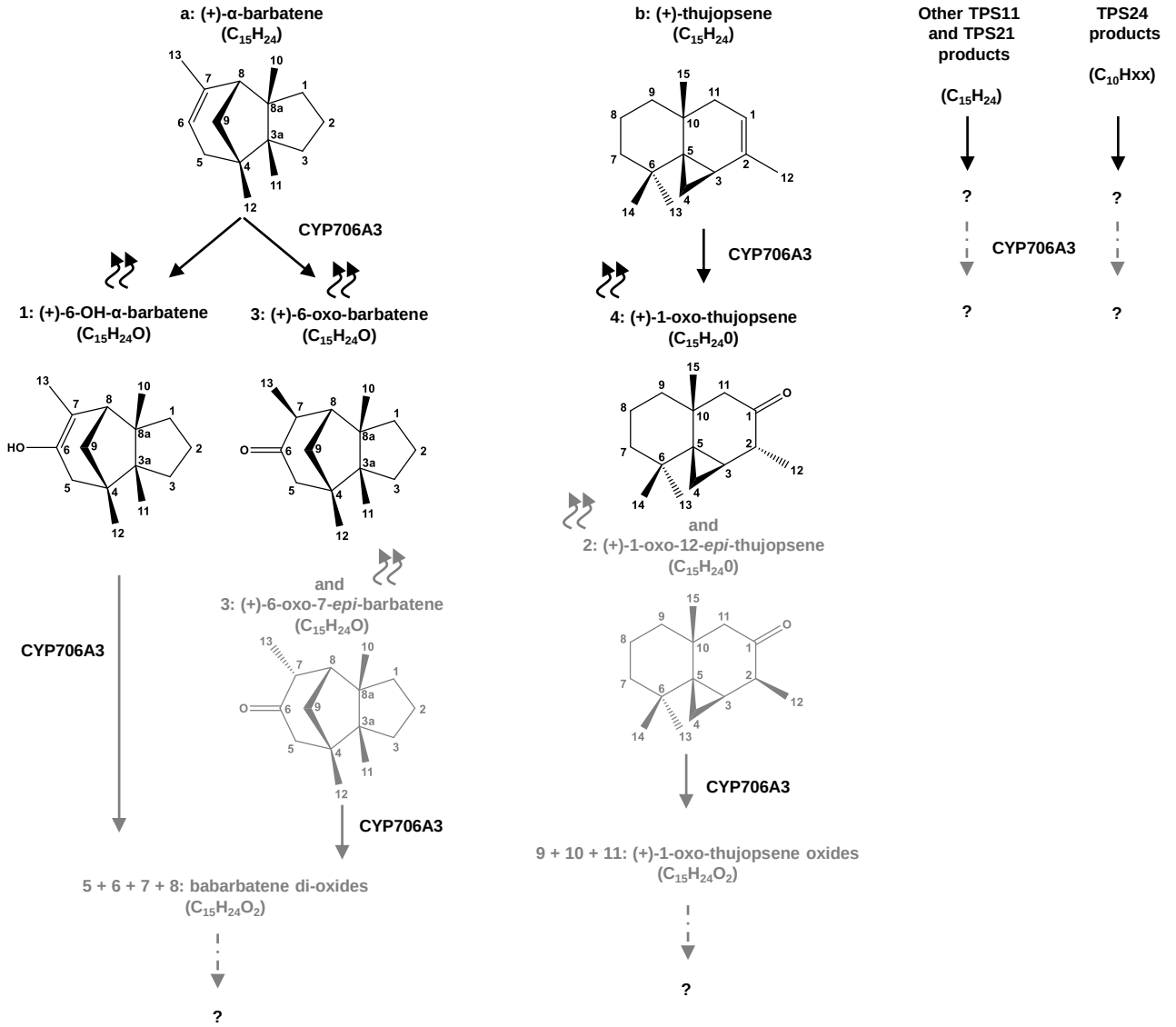

Figure 4. Reactions catalyzed by CYP706A3 on floral TPS products.
Wavy arrows indicate volatile compounds. Black arrows indicate primary and NADPH-dependent activities of CYP706A3 on TPS11 ((+)-α-barbatene and (+)-thujopsene), TPS21 and TPS24 products confirmed *in vitro*. Primary products **1**, **2**, **3** and **4** (in black and grey) were validated by NMR spectroscopy and represent the major CYP706A3 products emitted from Arabidopsis flowers. Grey arrows indicate secondary NADPH-dependent activities of CYP706A3 on primary products derived from (+)-α-barbatene and (+)-thujopsene obtained *in vitro*. Raw formulae of secondary products in grey were deduced from LC-MS spectra. Dashed -dotted grey arrows indicate CYP706A3 putative activities deduced from flower metabolic profiling. Unidentified compounds are indicated by question marks.

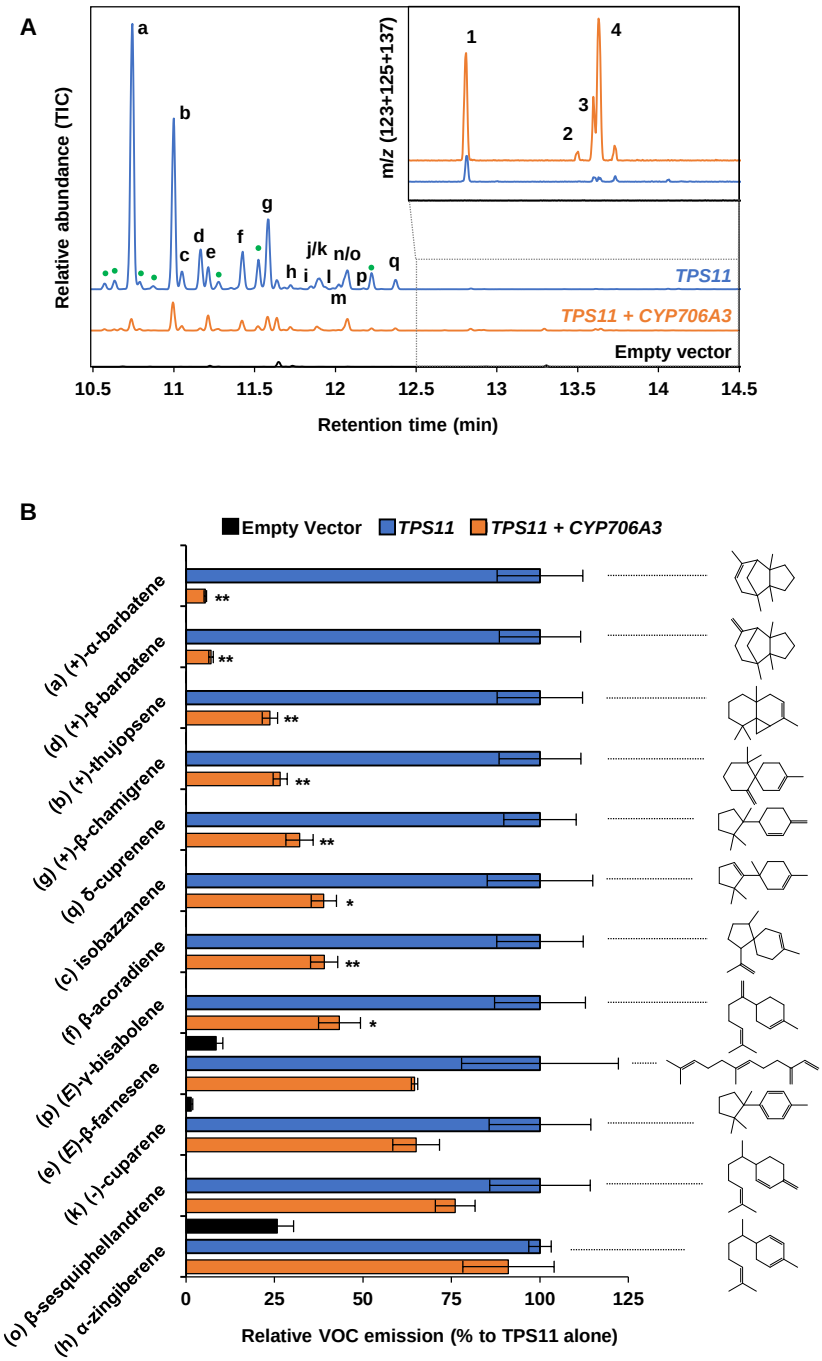

Figure 5. Transient co-expression in *N. benthamiana* reveals CYP706A3 activity on multiple TPS11 products.

Headspace was collected on four leaves for 24 hours, three days after agroinfiltration (see detailed protocol in Methods section).

(A) Representative GC-MS chromatograms of headspace from *N. benthamiana* transiently expressing the empty vector, *TPS11* alone or co-expressing *TPS11* and *CYP706A3*. Chromatograms show the relative abundance of total ion current (TIC) and the sum of extracted ion current in the inset (*m/z* 123 + 125 + 137).

(B) Relative quantification of emitted TPS11 products in the headspace of *N. benthamiana* expressing *TPS11* alone and co-expressing *TPS11* and *CYP706A3* (only compounds for which quantification was not biased by low emission or co-elution with compounds having similar MS are shown). Histograms represent relative emission levels from 3 biological replicates (pooled leaves from individual transformed plants) ± SE compared to levels of the same sesquiterpene emitted by *N. benthamiana* leaves expressing *TPS11* alone (set at 100%). Statistically significant differences between leaves expressing *TPS11* alone and leaves co-expressing *TPS11 and CYP706A3* are indicated (two-tailed Student's *t* test : $*p < 0.05$; $**p < 0.01$). Compounds are sorted from the most to the least transformed by CYP706A3. Chemical structure of each compound is shown on the right. Absolute quantifications and additional data are provided in Supplemental Table 1.

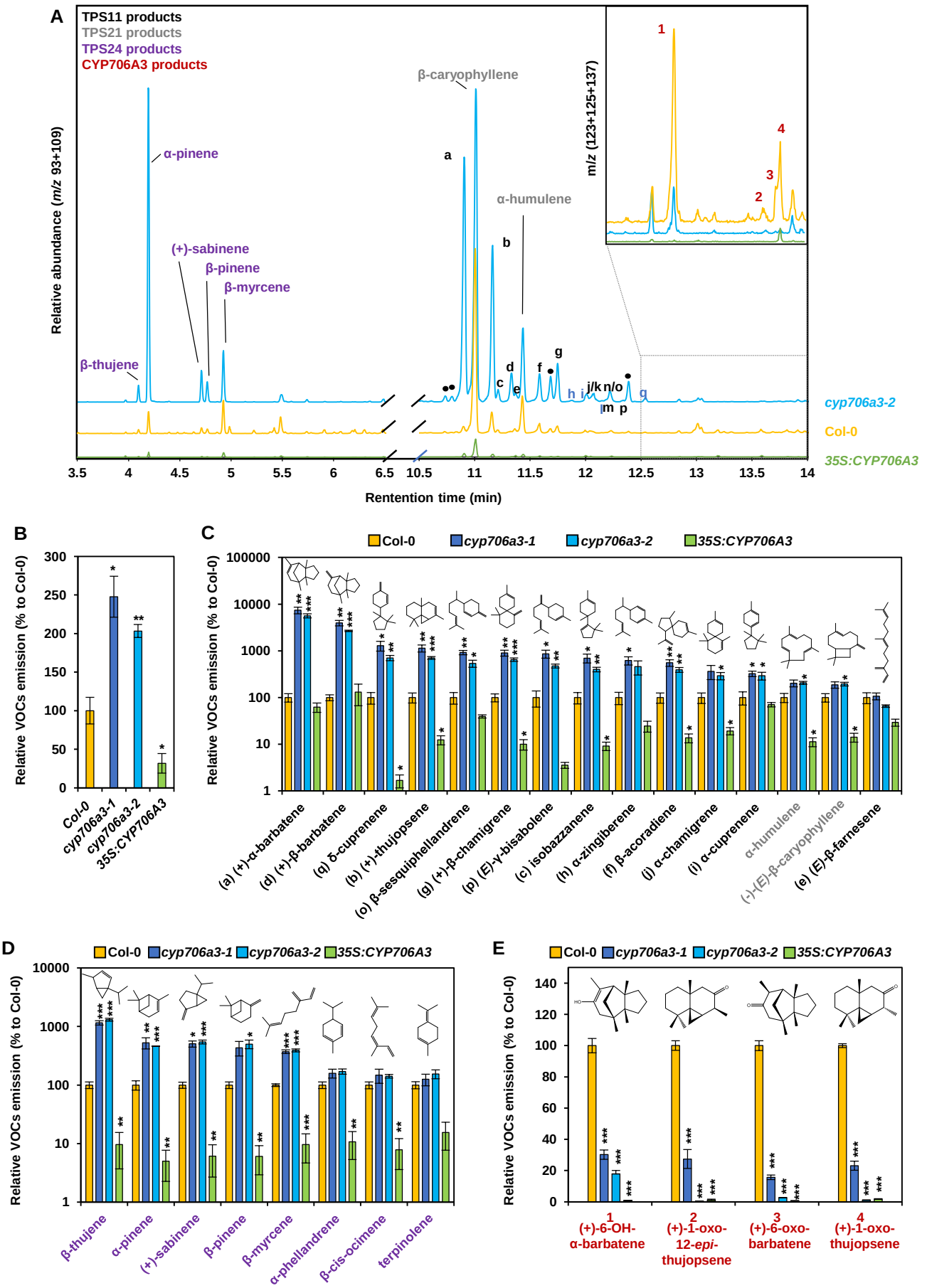
A
TPS11 products
TPS21 products
TPS24 products
CYP706A3 products
Relative abundance (m/z 93+109)
β-caryophyllene
α-pinene
α-humulene
(+)-sabinene
β-pinene
β-myrcene
β-thujene
m/z (123+125+137)
cyp706a3-2
Col-0
35S:CYP706A3
Rentention time (min)
B
Relative VOCs emission (% to Col-0)
Col-0
cyp706a3-1
cyp706a3-2
35S:CYP706A3
C
(a) (+)-α-barbatene
(d) (+)-β-barbatene
(q) δ-cuprenene
(b) (+)-thujopsene
(o) β-sesquiphellandrene
(g) (+)-β-chamigrene
(p) (E)-γ-bisabolene
(c) isobazzanene
(h) α-zingiberene
(f) β-acoradiene
(j) α-chamigrene
(i) α-cuprenene
α-humulene
(-)-(E)-β-caryophyllene
(e) (E)-β-farnesene
D
β-thujene
α-pinene
(+)-sabinene
β-pinene
β-myrcene
α-phellandrene
β-cis-ocimene
terpinolene
E
1 (+)-6-OH-α-barbatene
2 (+)-1-oxo-12-epi-thujopsene
3 (+)-6-oxo-barbatene
4 (+)-1-oxo-thujopsene

Figure 6 . Flower-emitted VOCs in *CYP706A3* mutants.

(A) GC-MS chromatograms of headspace collected from flowers of Col-0, *cyp706a3* and *CYP706A3* over-expressing lines. Chromatograms show the relative abundance of the sum of extracted ion current (*m/z* 93 + 109) to display the major mono- and sesquiterpenes. Chromatograms in the inset show the relative abundance of the sum of extracted ion current (*m/z* 123 + 125 + 137) to highlight the major CYP706A3 primary and volatiles products.

(B–E) GC-MS relative quantification of (B) total VOCs emissions, (C) TPS11 and TPS21 products, (D) TPS24 products, (E) and CYP706A3 oxygenated products **1**, **2**, **3**, and **4**. VOCs emitted by flowers of different lines were compared to those emitted by Col-0 (100%). Note that the y-axis in (C) and (E) are in logarithmic scale. Compounds in (C) and (D) are sorted from the most to least increased in insertion mutants. Data are the mean ± SE of three biological replicates (pooled inflorescences from individual plants). Statistically significant differences relative to Col-0 are indicated (two-tailed Student's *t* test: $*p < 0.05$; $**p < 0.01$, $***p < 0.001$).

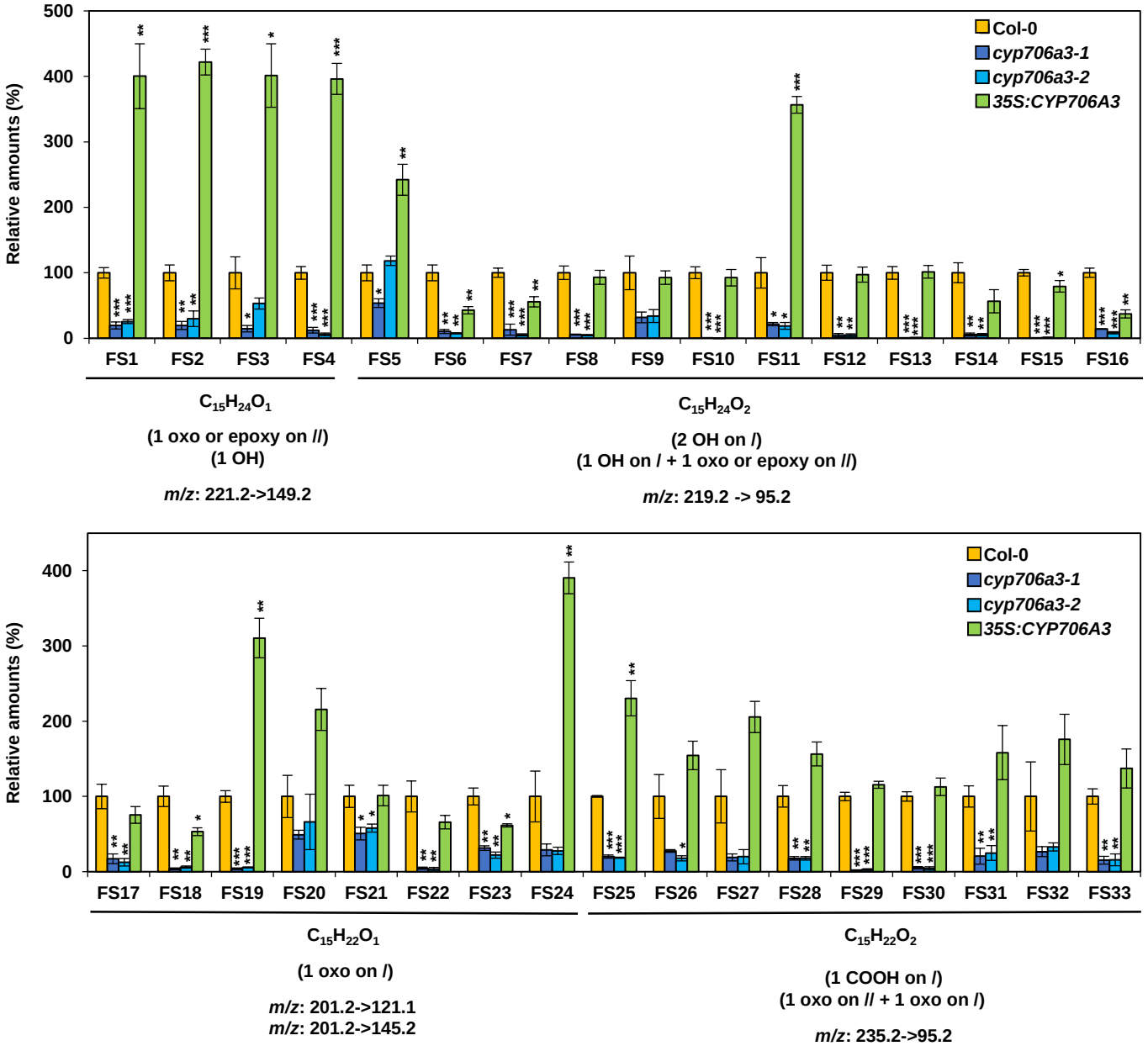

Figure 7. Soluble products of CYP706A3-dependent sesquiterpene oxygenation detected in flower tissues.

Sesquiterpene oxides from wild-type and *CYP706A3* mutant plants were quantified in flower methanol extracts. LC-MS/MS using multiple reaction monitoring of specific MS/MS transitions was targeted to identify sesquiterpene oxides resulting from single or multiple oxidations. For each compound differentially detected in mutant lines, the specific MS/MS transitions used are shown, as well as the expected raw formula. Data are given as the mean ± SE of three biological replicates (pooled inflorescences from individual plants), and expressed relative to Col-0 set at 100%. Statistically significant differences relative to Col-0 are indicated (two-tailed Student's *t* test: **p* < 0.05; ***p*< 0.01, ****p* < 0.001). Representative chromatograms and identification of numbered sesquiterpene oxides are shown in Supplemental Figure 14. FS stands for flower soluble compounds.

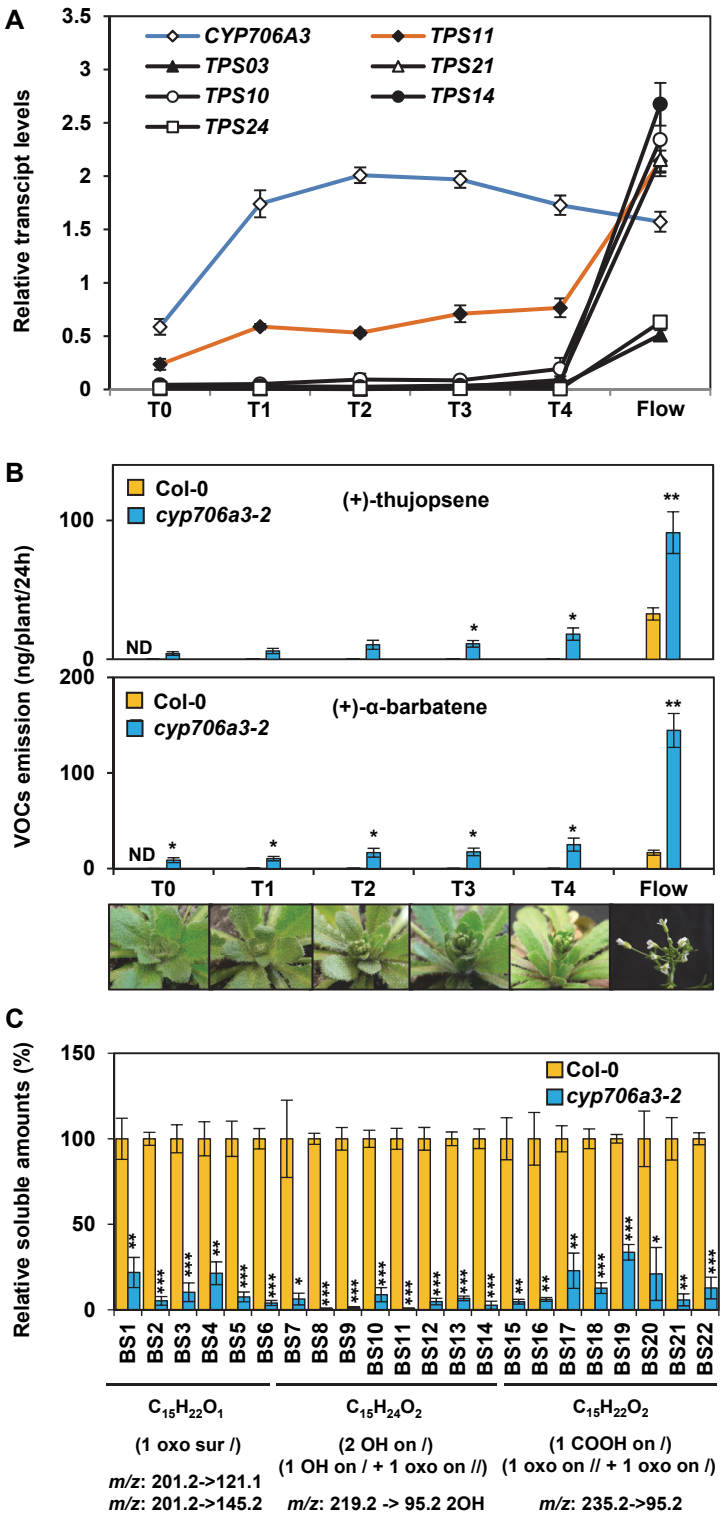

Figure 8. The *TPS11/CYP706A3* cluster is active in developing floral buds.
(A) Relative expression of *CYP706A3* and of major flower-expressed terpene synthase genes (Figure 1) during floral transition and inflorescence development evaluated by RT-qPCR. (B) Quantification of (+)-thujopsene (upper panel) and (+)-α-barbatene (lower panel) emission from wild-type and *cyp706a3-2* mutant plants at the same development stages as in (A). VOCs were collected for 24 hours from four plants per sample at the six stages of flower development shown in the photographs below from floral transition (T0) to opened inflorescence (Flow). T indicates the different transition phases. (C) LC-MS/MS quantification of soluble sesquiterpene oxides identified in MeOH extracts of stage T4 buds from wild-type and *cyp706a3-2* mutant plants (as described in Figure 7). For each compound, specific MS/MS transitions used are indicated, as well as expected raw formulae. Representative chromatograms and identification of the numbered sesquiterpene oxides are shown in Supplemental Figure 16. BS stands for bud soluble compounds. Data in (B) are given as the mean ± SE (n = 4 individual plants). Data in (A) and (C) are given as the mean ± SE of three biological replicates (pooled inflorescences from individual plants). Statistically significant differences relative to Col-0 are indicated (two-tailed Student's *t* test: **p* < 0.05; ***p* < 0.01, ****p* < 0.001).

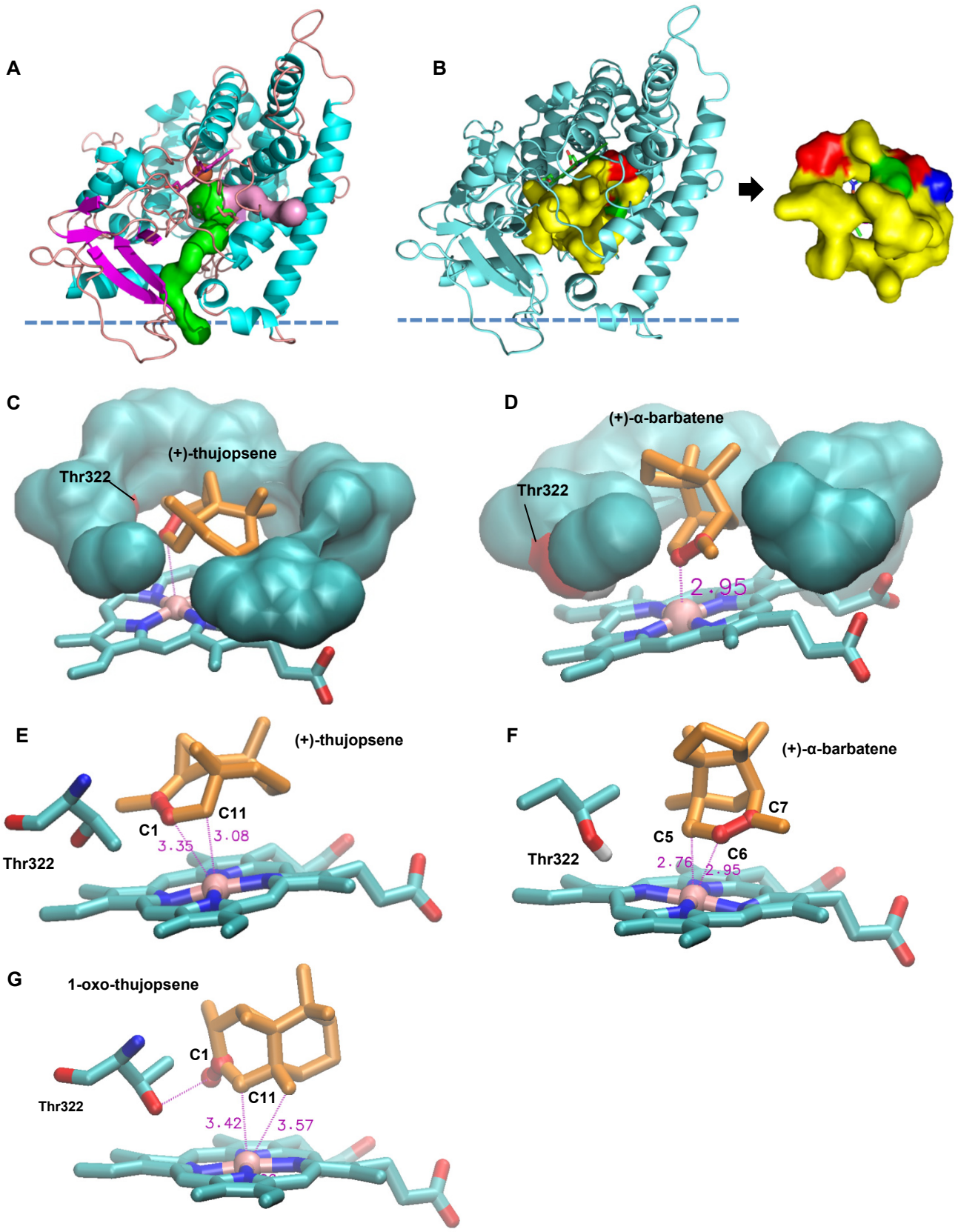
A
B
C
(+)-thujopsene
Thr322
D
(+)-α-barbatene
Thr322
2.95
E
(+)-thujopsene
C11
C1
3.35
3.08
Thr322
F
(+)-α-barbatene
C7
C5
C6
Thr322
2.76
2.95
G
1-oxo-thujopsene
C1
C11
Thr322
3.42
3.57

Figure 9. 3D structural model of the CYP706A3 active site and comparative docking of relevant substrates.

Structural model of AtCYP706A3 (segment 38-519) showing potential channels for substrate access, active site topology/characteristics, and docking positions for (+)-α-barbatene, (+)-thujopsene, and (+)-1-oxo-thujopsene determined by Autodock4.

(A) Overall structure displaying the two main channels (represented in surface mode in pink and green) with bottleneck values of 1.4 Å, positive hydropathy indexes, and logP values higher than 1. The predicted position of the membrane surface calculated by the PPM server of the OPM database (https://opm.phar.umich.edu/ppm_server) is schematized by the horizontal dashed line. The most hydrophobic channel (green) connects directly to the membrane bilayer while the other channel (pink) connects the active site to the interfacial medium.

(B) Display of the small internal cavity mostly delineated by hydrophobic residues (in yellow, surface mode). Two apertures are visible, corresponding to egress channels. Polar (green) and charged (red) residues correspond to Thr322 and Asp314, respectively. Thr322 is the only non-hydrophobic residue in contact with the active site cavity.

(C) View of (+)-thujopsene buried in the small hydrophobic pocket. Only the first crown of interacting residues is displayed. The only polar residue Thr322 of the cavity is shown on the left (red surface). The thujopsene double bond is indicated in red.

(D) View of (+)-α-barbatene in the small hydrophobic pocket. Only the first crown of residues is displayed. The only polar residue Thr322 of the cavity is shown on the left (red surface). The barbatene double bond is indicated in red. Distance (≈3Å) between the oxidation site and heme iron is indicated.

(E) Predominant docking pose of (+)-thujopsene, with high affinity energy binding of –9.2 $kcal.mol^{-1}$. The two atoms closest to the heme iron are C1 and C11, in full agreement with oxidation site. Distances to heme iron are indicated in red with dotted lines, and double bond C1-C2 is shown in red.

(F) Predominant docking pose of (+)-α-barbatene, with high affinity energy binding of –9.39 $kcal.mol^{-1}$. Two atoms (red ball-and-stick) closest to heme iron (pink) C5 and C6 are at equivalent distances. The polar side chain of Thr322 is displayed.

(G) Predominant docking pose of (+)-1-oxo-thujopsene, with high affinity energy binding of –9.8 $kcal.mol^{-1}$. The keto group (C1=O), shown in red, is oriented on the same side as the polar side chain of Thr322.

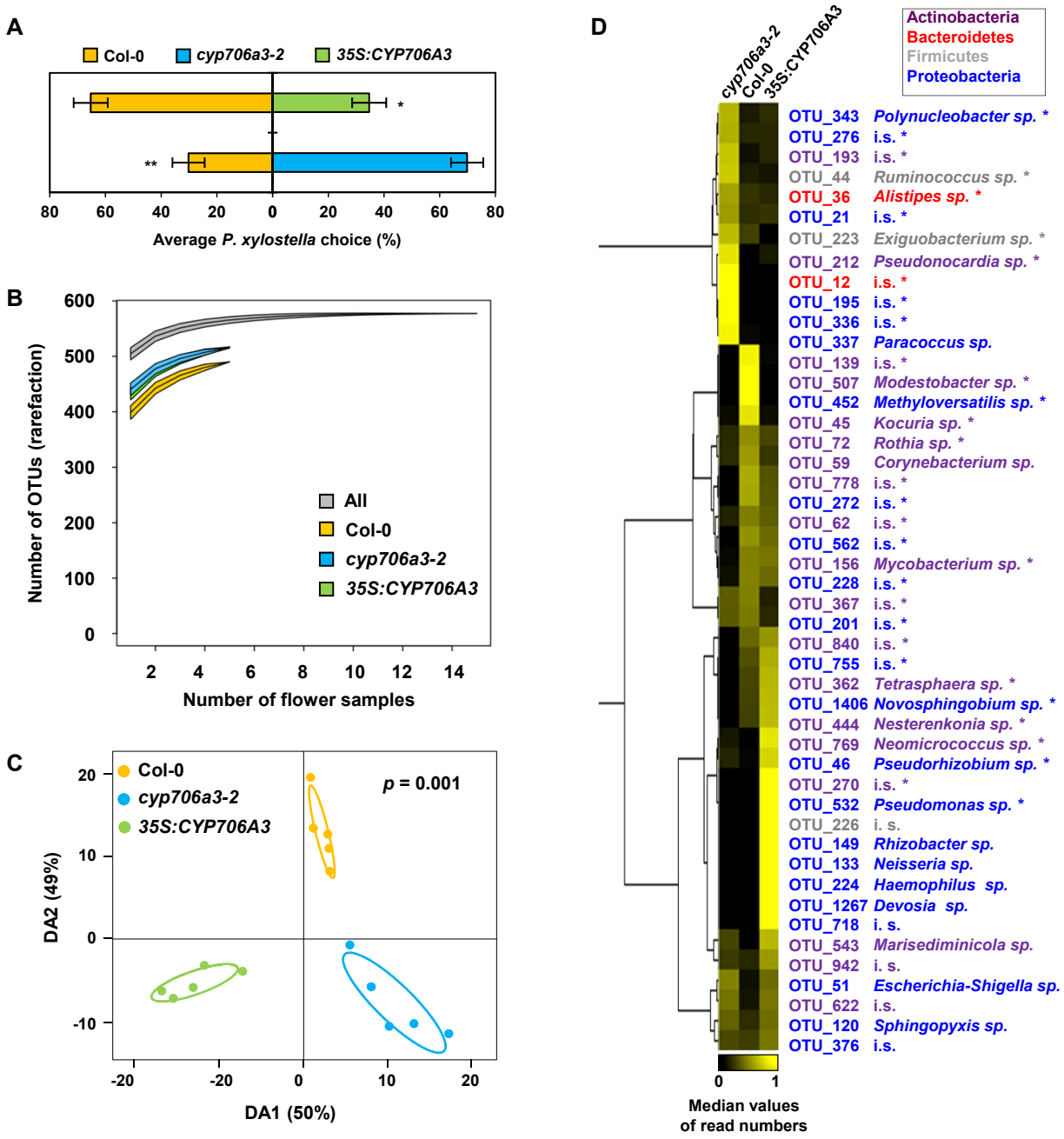

Figure 10. The cluster oxidation products influence florivore behaviour and floral microbial populations. (A) Feeding preference of larvae of *Plutella xylostella* for buds from Col-0, *cyp706a3-2* and *35S:CYP706A3* in dual-choice test. Data represent the average proportion of consumed buds for 30 individual insects (± SE). Statistically significant differences are indicated (Wilcoxon: *p = 0.0265, **p = 0.0019). (B) Diversity of OTUs present on Col-0 flowers was lower than those of *cyp706a3-2* and *35S:CYP706A3* when analyzed using a Chao rarefaction test. Graph shows OTUs accumulation curves for each flower line when increasing the number of flower samples analyzed (rarefaction). Data are mean ± SE from 5 biological replicates (pooled inflorescences from 5 individual plants): Col-0 = 538 ± 13, *cyp706a3-2* = 565 ± 13 and *35S:CYP706A3* = 571 ± 15. Curve thickness represents ± SE. (C) Abundance of OTUs (counts) detected on the flowers of Col-0, *cyp706a3-2* and *35S:CYP706A3* was analyzed by a Partial Least Square Discriminant Analysis (PLS DA) using the three lines as discriminant factor. Graph shows the difference in overall bacterial communities for each of five replicates from the three different lines . A cross-validation test with 999 permutations confirms the significant difference between bacterial communities among lines (p = 0.001). (D) Differential flower-associated bacterial populations between Col-0, *cyp706a3-2* and *35S:CYP706A3* flowers. Heatmap represents the relative abundance of specific OTUs being significantly different between a pair of lines based on a Wilcoxon rank sum test (n = 5, $p < 0.05$). OTUs that significantly differed between all lines are marked with an asterisk (Kruskal-Wallis rank sum test, n = 5, $p < 0.05$). OTUs are hierarchically clustered based on the averaged number of reads per flower line with uncentered correlation. Each row gives the median proportional number of reads in each of the flower lines, i.e., each row sums up to 1 to facilitate comparison between lines and OTUs despite differences in total read counts. Each color represents a phylum (Actinobacteria, Bacteroidetes, Firmicutes or Proteobacteria) as indicated in the box. Taxonomic designation was based on the percentage of identity to reference sequences in the SILVA database and indicated at the genus level unless unknown (i.s. *incertae sedis*). Detailed taxonomic identification is presented in Supplemental Table 4.

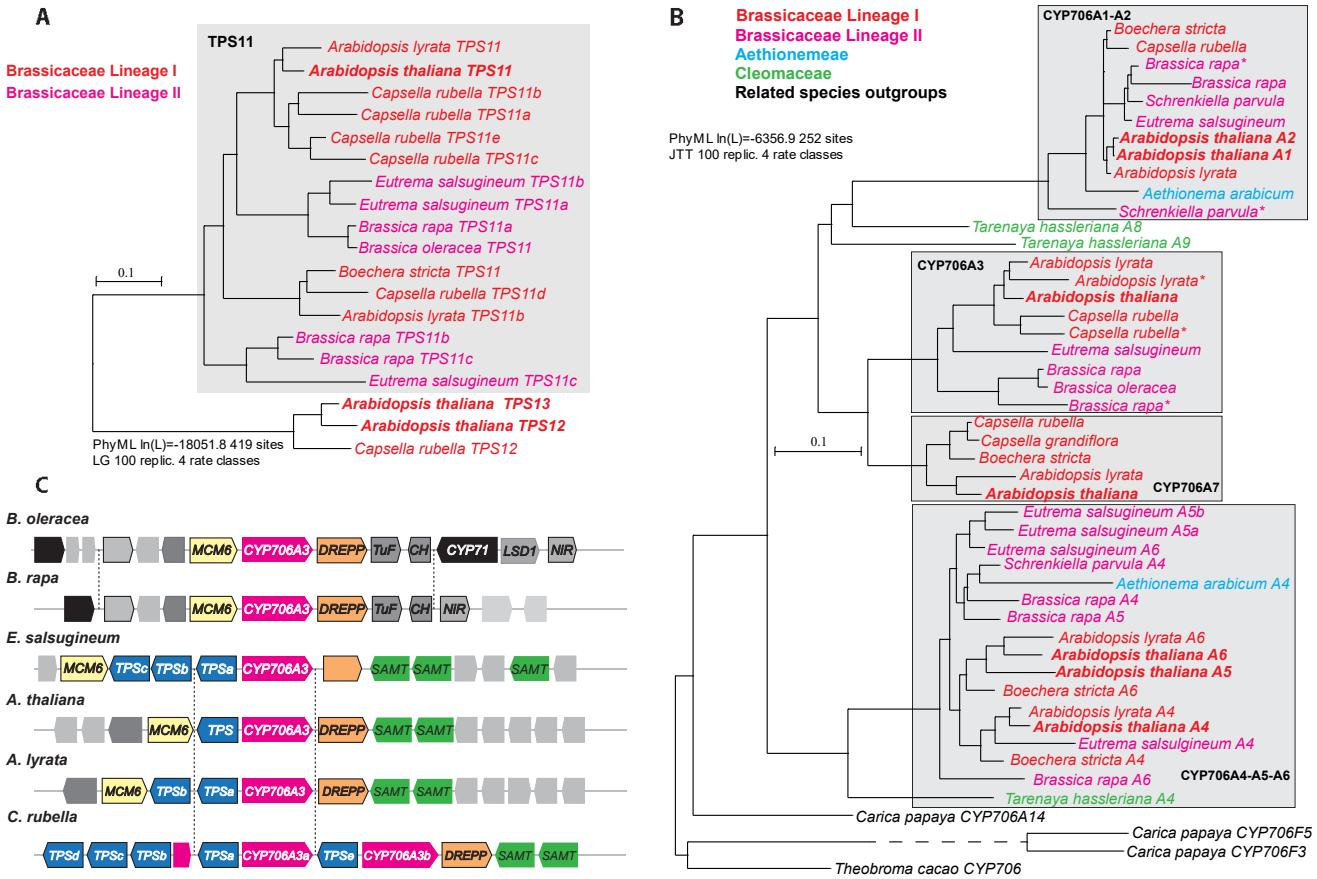

Figure 11. Evolution of the *TPS11/CYP706A3* gene cluster in *Brassicaceae*.
TPS11 (A) and CYP706A (B) phylogeny in *Brassicales*. Protein sequences were retrieved using a homology search with *A. thaliana* TPS11 or CYP706A3 sequences as a template, from the Phytozome website (http://phytozome.jgi.doe.gov/), the BrassicaDB page (http://brassicadb.org), or Dr D. Nelson's website (http://drnelson.uthsc.edu/CytochromeP450.html), and used to build the tree using PhyML on Gblocks sets defined on the multiple alignment of protein sequences using Seaview. (A) Phylogeny of TPS11. TPS sequences closest to TPS11 in Capsella and Arabidopsis are used as an outgroup. (B) Phylogeny of the available sequences assigned to the CYP706A subfamily of *Brassicales* and some closest homologs use as an outgroup. If not specifically named yet, sequences were referred to according to their position in the different branches of the tree. Bootstrap values for the different branches are available in Supplemental Data 5 and 7. (C) Structure of the *TPS11/CYP706A3* locus. Species possessing a *CYP706A3* homolog were aligned at the genome level to show potential gene clusters. *TPS11* and homologs were given different names corresponding to their position in the phylogenetic tree below. Conserved features and neighboring genes were highlighted by similar box shape, color or putative annotation. *CYP706A3* and duplicates (magenta); *TPS11* and duplicates (blue); *SAMT* (green): *S*-adenosyl methyltransferase domain; *MCM6* (yellow): DNA replication licensing factor; *DREPP* (orange): PF05558 DREPP plasma membrane polypeptide; *TuF* (grey): elongation factor Tu; *CH* (grey): charged multivesicular body protein 2A; *LSD1* (grey); *NiR*: unnamed nitrate dehydrogenase. Light gray boxes: no annotation available. Scale bar: substitutions per site.