Supplementary Table S1. Further bibliographic reference data on biochemistry, molecular biology and functional role of plant volatiles. Reviewing the literature between 1989 and February 2011.

VOC class	Sub-class	Topic	Key words	Key topics	Ref.
Terpenoids					
	General concepts				
		Acquired immunity to herbivory caused plant volatiles	Allelopathy, defense, plant communication, priming, volatiles	Discusses whether more plants eavesdrop on infochemical cues, and if these cues that allow them to adjust their defenses to suit their risk also increase their fitness as a result.	[1]
		Attraction of parasitoids	Parasitoids, diamondback moth, *Brassica*, signals, plant-insect interactions.	The flight response of female parasitoids to volatiles released from plants that are attacked by their host herbivores are tested under laboratory conditions. Parasitoids significantly preferred plants that had been under attack by herbivores (currently attacked plants) over intact plants. After removal of the larvae, the plants (formerly attacked plants) were still significantly preferred by parasitoids over intact plants.	[2]
		Biogenic volatile organic compound (BVOC) emissions from arctic ecosystems	Climate warming, heath, litter, monoterpene, sesquiterpene, subarctic, tundra	The relatively low emissions of monoterpenes and sesquiterpenes were doubled in response to an air temperature increment. BVOC emissions were seasonal, and warming combined with litter addition triggered emissions of specific compounds. The observed changes have implications for ecological interactions and feedback effects on climate change via impacts on aerosol formation and indirect greenhouse effects.	[3]
		Elevated terpene production in plants	terpene production, tobacco, cytosolic and plastidic isopentenyl diphosphate, increased sesquiterpene synthesis.	Natural-product biosynthetic platforms yielding thousands of times more of a novel chemical target than observed heretofore can be engineered into plants by diverting key metabolic intermediates in different intracellular compartments.	[4]
		Evolution of plant communication by VOCs	Chemical information-transfer, systemic acquired-resistance, herbivore-induced volatiles, extrafloral nectar, indirect defense, interplant communication, attract parasitoids.	Discusses four possible non-exclusive explanations involving the role of volatiles: in direct defense, as within-plant signals, as traits that synergistically interact with other defenses, and as cues among kin.	[5]
		Evolutionary context for herbivore-induced plant VOCs	Indirect defenses, adaptive value, HIPV-'mute' and HIPV-'deaf' plants, fitness value of HIPV emissions under natural conditions.	Considers the different community members that react to HIPVs and how their responses could alter selective regimes for emissions. Evaluates the mechanisms responsible for the activation of HIPVs and considers the fitness consequences of HIPV emissions in the rich community context that occurs in the real world.	[6]
		Genetic aspects of floral fragrance	biosynthesis, floral scent compound, gene cloning, evolution, genetic manipulation, metabolic engineering.	Summarizes the reported floral fragrance-related genes and the biosynthesis of floral scent compounds, introduces the origin of new modification enzymes for flower scent, compares different methods for	[7]

VOC class	Sub-class	Topic	Key words	Key topics	Ref.
				floral fragrance-related gene cloning, and discusses the metabolic engineering of floral scent. The perspectives and prospects of research on floral fragrance are presented.	
		Genomic organization of terpene synthases	Functional expression, cdna cloning, isoprenoid biosynthesis, sesquiterpene cyclase.	A model presented for the evolutionary history of plant terpene synthases suggests that this superfamily of genes responsible for natural products biosynthesis derived from terpene synthase genes involved in primary metabolism by duplication and divergence in structural and functional specialization. This novel molecular evolutionary approach focused on genes of secondary metabolism may have broad implications for the origins of natural products and for plant phylogenetics in general.	8
		Homoterpene volatiles biosynthesis and P450 (CYP82G1)	Arabidopsis, floral scent, herbivory, terpene biosynthesis	CYP82G1 (At3g25180), encoding a P450 enzyme of the Arabidopsis thalianaCYP82 family, is responsible for the conversion of (*E*,*E*)-geranyllinalool to TMTT. The recombinant CYP82G1 enzyme is able to convert (*E*)-nerolidol, the C_{15}-analog of geranyllinalool, to the respective C11-terpene DMNT.	9
		Induced VOCs	Climate–herbivory interactions, VOCs-emitting plants, atmospheric feedback.	proposed strategy for inclusion of invertebrate–VOCs relationships in terrestrial ecosystem models	10
		Instrumentation applied in plant metabolomic analyses	gas chromatography mass spectrometry (GC-MS), proton nuclear magnetic resonance ((1)H-NMR) spectroscopy, liquid chromatography (LC)-MS, ultra high performance liquid chromatography (UHPLC).	As well as covering the theory behind modern day LC-MS, the review also discusses the most relevant metabolomics applications for the wide range of MS instruments that are currently being applied to LC	11
		Intra- and intercellular translocation	monoterpene biosynthesis, glandular trichomes, secretory-cells, pathway.	Highly ordered, protein-mediated processes that involve intra- and intercellular translocation need be considered when attempting to understand how a plant can regulate the formation and accumulation of complex but well-defined natural product profiles.	12
		MYB transcription factors in conifer trees contribution to the isoprenoid- and flavonoid-oriented responses.	Gene family expansion, gymnosperms, isoprenoid metabolism, MYB transcription factors, microarray RNA profiling, *Picea glauca*, plant evolution, stress response, terpenes, tissue-specific expression.	Histological, metabolite, and transcript (microarray and targeted quantitiative real-time PCR) analyses of PtMYB14 transgenics, coupled with mechanical wounding and JA application experiments on wild-type plantlets, allowed identification of PtMYB14 as a putative regulator of an isoprenoid-oriented response that leads to the accumulation of sesquiterpene in conifers.	13
		Plant communication	Plant fitness, signaling, resistance, herbivory, cost/benefit analysis, eavesdropping.	Hypothetical benefits ofemitting cues include: repelling herbivores; attracting predators ofherbivores; suppressing germination ofcompetitors; communicating with other branches of the same plant; and communicating with genetic relatives.	14
		Plant volatile terpenoid	Volatile terpenoids, terpene synthase, subcellular localization, spatio-	Summarizes recent progress in the characterization of volatile terpenoid biosynthetic genes, their spatio-temporal expression patterns and	15

VOC class	Sub-class	Topic	Key words	Key topics	Ref.
		metabolism	temporal expression, metabolic engineering.	subcellular localization of corresponding proteins. In addition, recent information obtained from metabolic engineering is discussed.	
		Subcellular compartmentation of isoprenoids	biosynthesis of terpenoids in plants, single and multiple enzymatic steps, metabolic engineering, monoterpene and sesquiterpene synthases.	Evaluates the exploiting of the subcellular compartmentation of plant isoprenoid metabolism as a mean to boost terpenoid production.	16
		Terpenoid synthase (AtTPS) gene family of Arabidopsis	gene evolution, secondary metabolism, isoprenoid, terpene cyclase, prenyl transferase.	Arabidopsis has the largest and most diverse group of TPS genes currently known for any species. Phylogenetic analyses highlight events in the divergence of the TPS paralogs and suggest orthologous genes and a model for the evolution of the TPS gene family.	17
		VOCs and global change	Atmospheric chemistry and physics, climate and global changes, high atmospheric CO_2 concentrations, ozone and enhanced UV radiation.	Direct and indirect effects of environmental factors associated with global and climate change on VOC Emissions. Analysis of alterations in the physiology of organisms, ecological interactions between organisms, and atmospheric chemistry and climate arising from global change-altered VOC emissions.	18
		VOCs and pollution	Extrafloral nectar, herbivore, multitrophic interactions, Phaseolus lunatus, pollutant, terpene, Tetranychus urticae, troposphere, two-spotted spider mites, volatile	Ozone degrades several herbivore-induced VOCs, a likely mechanism reducing communication distances. High ozone concentrations induced extrafloral nectar secretion in exposed plants, this suggests that ozone can play a complex role in the indirect defence of plants..	19
		VOCs and UV-B irradiation	*Mentha piperita*, UV-B irradiation, terpenoid gene expression, quantitative real-time PCR, essential oil composition, flavonoids	UV-B irradiation differentially modulates the expression of genes involved in peppermint essential oil biogenesis and the content of UV-B absorbing flavonoids. Plants grown in field were better adapted to increasing UV-B irradiation than plants cultivated in growth chambers. The interplay between terpenoid and phenylpropanoid metabolism is also discussed.	20
		Volatile emissions and ozone	*Populus nigra*, ozone uptake, VOC, surface compounds, phenolic compounds	The emission of isoprene and oxygenated six-carbon (C6) volatiles were inhibited by ozone, whereas methanol emission was increased, especially in developing leaves.	21
	Hemiterpenes				
		Isoprene emissions and herbivory	avoidance, dose response, herbivory, threshold, tobacco hornworm, transgenic tobacco.	Both in vivo and in vitro experiments showed that isoprene can activate feeding avoidance behaviors.	22
		Isoprene emission and atmospheric CO_2 concentration	atmospheric chemistry, CH_4, climate change, forests, global change, O_3.	A new model of isoprene emission describes its response to changes in atmospheric CO_2 concentration.	23
		Isoprene biosynthesis and ozone tolerance	antioxidants, biogenic volatile organic compounds, green leaf volatiles, photosynthesis, alpha-tocopherol.	non-isoprene emitting poplars might benefit from changes within the antioxidative system by providing them with enhanced ozone tolerance.	24
		Isoprene synthase	Isoprene synthase promoter, Light	ISPS promoter activity, which correlates with basal isoprene emission	25

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		(ISPS)	regulation, Temperature regulation, Developmental regulation.	capacity, is not uniformly distributed within leaf tissue and that it can adapt rapidly towards internal as well as external environmental stimuli.	
		Isoprene diurnal variation in the basal emission rate	Ambient light and temperature, atmospheric chemistry, modeling, basal emission rate, diurnal patterns, Eucalyptus, hydrocarbon emission, biogenic, isoprene, Populus, Quercus.	Diurnal fluctuations in emission are large and species specific, and must be considered when estimating emission rates for use in short-term regional atmospheric-chemistry models.	26
		Structure of isoprene synthase	Protein crystallography, terpenoid biosynthesis, hemiterpene synthase, enzyme mechanism.	The crystal structure of native PcISPS [isoprene synthase from gray poplar hybrid *Populus×canescens*] has been determined at 2.7 Å resolution, and the structure of its complex with the unreactive substrate analogue dimethylallyl-S-thiolodiphosphate and three Mg^{2+} has been determined at 2.8 Å resolution.	27
	Monoterpenes				
		(-)-limonene-7-hydroxylase	*Perilla frutescens*, Lamiaceae, (-)-Perillyl alcohol, Perillaldehyde, Cytochrome P450.	Reports on a homology-based approach to acquiring the cDNA encoding a (-)-limonene-7-hydroxylase, and describes the basic properties of this cytochrome P450 monoterpene oxygenase from the glandular trichomes of *Perilla frutescens*.	28
		(-)-Pinene synthase	*Abies grandis*, monoterpene cyclases, terpene cyclase structure-function, geranyl diphosphate cyclization, turpentine biosynthesis, directed mutagenesis.	Directed mutagenesis was used to replace amino acid residues in (-)-pinene synthase with the corresponding (-)-camphene synthase residues to define those responsible for mechanistic differences, and to better understand their role in catalysis. Several mutants with variously altered activities, most notably mutated pinene synthases in which the majority of product passes through the alternative bornyl cation intermediate are reported.	29
		(-)-α-terpineol synthase	*Vitis vinifera*, wine flavour and aroma, terpene cyclase.	Describes the identification and functional characterization of two *V. vinifera* cv. Gewürztraminer cDNAs that encode multi-product (-)-α-terpineol synthases.	30
		(+)-α-pinene synthase and (-)-α-pinene synthase	*Pinus taeda*, monoterpene synthase, turpentine biosynthesis, loblolly pine.	Reports the isolation of cDNAs encoding (+)-α-pinene synthase, (-)-α-pinene synthase, and three other related synthases of turpentine formation in loblolly pine, describing their functional expression in *Escherichia coli* and properties of the recombinant enzymes, and providing a comparative structural evaluation based on computer modeling with implications for the origin and control of stereochemistry in monoterpene biosynthesis.	31
		1,8-cineole synthase	*Arabidopsis thaliana*, functional expression, antifungal activity, cDNA isolation.	Report the characterization of a monoterpene synthase encoded by two identical, closely linked Arabidopsis genes, At3g25820 and At3g25830, whose transcripts are detected almost exclusively in roots.	32
		3-Carene synthase	*Salvia stenophylla*, glandular trichome isolation, homology-based cDNA cloning, recombinant protein	A homology-based cloning strategy yielded the target cDNA for 3-carene synthase which was characterized and functionally expressed in *Escherichia coli*. The recombinant synthase was shown to catalyze the	33

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			expression, geranyl diphosphate cyclization.	divalent metal ion-dependent conversion of geranyl diphosphate to (+)-3-carene (73% of the product mix), and to lesser amounts of limonene, myrcene, 4-carene and β-phellandrene, thereby suggesting that this single enzyme is responsible for the production of all of the monoterpenes of *S. stenophylla* essential oil.	
		Bornyl diphosphate synthase	*Salvia officinalis*, enzymatic cyclization, geranyl pyrophosphate, monoterpene cyclases,.	Reports an x-ray crystal structure of a monoterpene cyclase, recombinant (+)-bornyl diphosphate synthase (BPPS) from *Salvia officinalis* and the structures of several BPPS–ligand complexes that, taken together, map out the reaction coordinate of isoprenoid diphosphate cyclization.	[34]
		Characterization of (*E*)-β-ocimene and 1,8 cineole synthases	*Citrus*, gene expression.	Contains information of the cloning and functional analysis of 1.8 cineole and (*E*)- β-ocimene synthase genes, isolated in *Citrus* species. The expression profile and molecular evolution of monoterpene synthases in *Citrus* is also discussed.	[35]
		Chrysanthemyl diphosphate synthase	Presqualene pyrophosphate, squalene biosynthesis, crystal-structure, farnesylpyrophosphate synthetase, irregular monoterpenes.	Reports the isolation and characterization of the gene for chrysanthemyl diphosphate (CPP) synthase from *Chrysanthemum cinerariaefolium*, that produces CPP as an intermediate in the biosynthesis of the naturally occurring pyrethrin insecticides, construction of an Escherichia coli strain for production of recombinant enzyme, purification and characterization of the enzyme, and product studies that conclusively establish the function of the enzyme.	[36]
		Functional expression and characterization of (-)-limonene synthase and (+)-alpha-pinene synthase	*Cannabis sativa*, monoterpene synthase, geranyl pyrophosphate.	Two recombinant, stereospecific monoterpene synthases, a (+limonene synthase (CsTPS1) and a (+)-alpha-pinene synthase (CsTPS2), encoded by *Cannabis sativa* L. cv. 'Skunk' trichome mRNA, are isolated and characterized.	[37]
		Functional expression of a myrcene/(*E*)- β-ocimene synthase	*Arabidopsis thaliana*, monoterpene synthase, terpene cyclase.	Reports on the expression of two TPS genes in Arabidopsis, the cloning and expression in *Escherichia coli* of the AtTPS10 cDNA, and functional characterization of active AtTPS10 monoterpene synthase as myrcene/(*E*)- β-ocimene synthase.	[38]
		Geraniol synthase	*Cinnamomum tenuipilum*, Lauraceae, camphor tree, functional expression, monoterpene synthases.	Reports the isolation of a cDNA clone from *Cinnamomum tenuipilum*, which was functionally expressed in *Escherichia coli* and identified as a geraniol synthase.	[39]
		Heterodimeric geranyl(geranyl)diphosphate synthase	*Humulus lupulus*, trichome, enzyme evolution, subunit interactions.	Report the functional expression of heterodimeric GPPS large and small subunits from Hop. Biochemical and phylogenetic analyses reveal the existence of a previously undescribed class of heterodimeric G(G)PPS.SSUs with broad distribution in both angiosperms and gymnosperms.	[40]

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		Molecular cloning of geranyl diphosphate synthase	Monoterpene compartmentation, plastid, cytosol, secretory tissue.	Describes the cloning and functional characterization of a cDNA of a homodimeric GPPS and its *in situ* localization using GPPS- specific antibodies.	41
		Monoterpene synthases	*Lavandula*, glandular trichomes, floral scent, functional-characterization, linalool synthase.	Molecular and chemical analyses suggest that changes in TPS expression occur during lavender inflorescence development and lead to changes in VOC composition. Both molecular data and terpene analysis support the findings that changes in biosynthesis of terpene occurred during inflorescence development.	42
		Myrcene synthase	*Perilla frutescens*, homology-based cDNA cloning, Labiatae.	Functional expression of a clone of a monoterpene synthase from *Perilla frutescens* in *Escherichia coli* yielded an active monoterpene synthase enzyme, which converted geranyl diphosphate into 53.8% myrcene, 20.9% sabinene, 19.8% linalool and 5.5% limonene.	43
		Spearmint (-)-limonene hydroxylase	*Mentha*, cytochrome P450, trans-carveol, trans-isopiperitenol.	Describe the application of a systematic molecular strategy for the identification of a single amino acid residue responsible for the difference in the regiospecificity of (2)-limonene C3- and C6-hydroxylases.	44
		Structure of 1,8-cineole synthase	*Arabidopsis thaliana*, diphosphate synthase, bornyl diphosphate, crystal-structure, cyclases.	Provides the structural evidence for a mechanism where plants, instead of using a different dedicated gene for the production of each different terpene, may employ a highly flexible simple scaffold that can, with only very few substitutions, provide the complete spectrum of activities required.	45
		Up-regulation of 1-deoxy-D-xylulose-5-phosphate synthase in transgenic lavender	*Lavandula latifolia*, MEP-pathway, isoprenoid biosynthesis, 4-phosphate pathway, plant volatiles, reductoisomerase.	The DXS enzyme plays a crucial role in monoterpene precursor biosynthesis and, thus, in VOC production in spike lavender. Provides a strategy to increase the essential oil production in spike lavender by metabolic engineering of the MEP pathway without apparent detrimental effects on plant development and fitness.	46
		Biosynthesis of linalyl acetate	*Mentha aquatica* var. *citrata* AATs, lemon mint, linalool.	Cell-free extracts of lemon mint (*Mentha aquatica* var. *citrata*) efficiently catalyzed the formation of linalyl acetate from linalool and acetyl-coenzyme A.	47
		Constitutive and induced monoterpene biosynthesis in grand fir.	*Abies grandis*, cortical oleoresin, turpentine, monoterpene synthases, wound-induction, conifer defense.	Describes the distribution of monoterpene synthase activities in non wounded (control), wounded, and Ethrel-treated stems. Quantitative differences were observed 'chemotypes' were defined based on in vitro assessment of monoterpene biosynthetic capability.	48
		Cyclization of geranyl pyrophosphate to (+)-cis- and (+)-trans-sabinene	Sweet marjoram, ionization of substrate analogs, inhibition of sabinene hydrate cyclase, l,2-hydride shift, stereochemistry.	Addresses several specific features of the cyclization mechanism, and provides evidence for the cationic nature of the reaction and for the hydride shift step.	49

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		hydrate			
		Cyclization of geranyl pyrophosphate to (+)-Sabinene	*Mentha* x *piperita*, soluble enzyme preparations, neryl pyrophosphate, substrate-analog, cyclases, stereochemistry, isomerization.	The results obtained define the overall stereochemistry of the coupled isomerization-cyclization of geranyl pyrophosphate (via 3R-linalyl pyrophosphate) to (+)-sabinene, demonstrate a 1,2-hydride shift in the construction of the thujane skeleton, and confirm the electrophilic nature of this enzymatic reaction type.	50
		Cytochrome-P-450 catalyzed monoterpene hydroxylation	Microsomes, geraniol, nepetalactone, iridoid monoterpenes.	A microsomal preparation isolated from leaves of *Nepeta mussinii* catalysed the hydroxylation of the monoterpene alcohol, geraniol, to 10-hydroxygeraniol. This reaction is a key step in the biosynthesis of iridoid monoterpenes, such as nepetalactone.	51
		Dynamics of monoterpene emissions	VOC emissions, quercus-ilex leaves, isoprene emission, scots pine, populus-deltoides, rate variability.	Dynamic models describing temporal fluctuations in Scots pine monoterpene emissions. The models accurately predicted the measured monoterpene flux. A good agreement was found with measured emissions and the model involving photorespiration.	52
		Fructose and (-)-carvone biosynthesis	Essential oil, radiolabelled sugars, sugar uptake, non-mevalonate pathway.	Feeding of *Mentha spicata* cuttings with ^{14}C-sucrose, ^{14}C-glucose, and ^{14}C-fructose resulted in labelled (-)-carvone biosynthesis. Among sugars, fructose feeding caused the highest (-)-carvone biosynthesis.	53
		Impact of ozone on monoterpene emissions	Chlorophyll fluorescence, fosmidomycin, isoprenoids, photosynthesis, reactive oxygen species	Monoterpenes produced by *Quercus ilex* leaves share the same biosynthetic pathway and function as isoprene. Furthermore, all volatile isoprenoids may have similar antioxidant properties and may be stimulated by the same stress-inducing conditions.	54
		Induction of monoterpene biosynthesis by soil bacteria.	*Origanum* x *majoricum*, plant growth promoting rhizobacteria.	Plant inoculation with three species of plant growth-promoting rhizobacteria (PGPRs) (*Pseudomonas fluorescens*, *Bacillus subtilis*, *Azospirillum brasilense*), causes systemic induction of monoterpene pathways in *Origanum*, suggesting a possible significantly increase productivity and reduction of fertilizer required for economically crop production.	55
		Limonene synthase localization in leucoplasts of oil gland secretory cells	*Mentha* x *piperita*, 4s-limonene synthase, isolated chromoplasts, precursor proteins.	The leucoplastidome of the oil gland secretory cells is the exclusive location of limonene synthase, and almost certainly the preceding steps of monoterpene biosynthesis, in peppermint leaves. However, succeeding steps of monoterpene metabolism in mint appear to occur outside the leucoplasts of oil gland cells.	56
		Linalool synthase induction by jasmonic acid	*Lycopersicon esculentum*, jasmonic acid, trichomes, linalool, terpenes, defence.	Describes the identification and characterization of the first two monoterpene synthases from a solanaceous species (tomato), LeMTS1 and LeMTS2. Provides evidence that these genes are differentially regulated and more importantly, that expression of linalool synthase LeMTS1 is restricted to trichomes and induced by JA.	57
		Molecular characterization of	Orchid, MEP pathway, fragrance.	This is the first report on the full-length gene isolation and the expression profile of DXR in a vandaceous orchid.	58

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		a new 1-deoxy-D-xylulose 5-phosphate reductoisomerase			
		Monoterpene accumulation in leaves of peppermint	glandular trichomes, essential oil, developmental-changes, enzyme preparations, emission rates.	Shows the accumulation of monoterpenes in peppermint leaves and investigates several physiological processes that could regulate their accumulation: the rate of biosynthesis, the rate of metabolic loss, and the rate of volatilization.	59
		Monoterpene alcohol acetylation	*Origanum dayi*, Lamiaceae, enantioselective acetyl transferase, (S)-linalyl acetate, (R)-linalyl acetate.	Reports on the enzymatic and stereoselective formation of linalyl acetate in eight selected species of the Lamiaceae family, evaluates the formation of additional tertiary acetates and investigates the possibility of stereoselective acetate formation.	60
		Monoterpene emission from coniferous trees and climate warming	Pinus ponderosa, *Pseudotsuga menziesii*, atmospheric chemistry, carbon dioxide, climate change, nitrogen.	Demonstrates that although growth at elevated CO_2 may not affect the rate of monoterpene emission per unit biomass, the effect of elevated CO_2 on leaf area index, and the effect of climate warming on monoterpene biosynthesis and volatilization, could increase canopy monoterpene emission rate.	61
		Monoterpene glycoside biosynthesis	*Vitis vinifera*, berries, N^6-benzyladenine, grape, indoleacetic acid, in vitro culture.	Demonstrates their ability of isolated grape berries to biosynthesize monoterpene glycosides.	62
		Monoterpene regulation of Ras and Ras-related protein expression	Rap1a, RhoA, RhoB, perillyl alcohol, down-regulation.	The ability of monoterpenes to regulate the expression of the Ras-related proteins suggests a role for these plant-derived compounds in altering signal transduction elements.	63
		Monoterpene synthase transformation in tobacco	lemon monoterpene synthases, transgenic tobacco, fragrance.	Tobacco can easily and efficiently be transformed and is a suitable model to study the release of plant volatiles. Isolated monoterpene synthases from lemon were used to transform tobacco to study the change in fragrance of the transgenic in comparison to the wild type plants.	64
		Monoterpene-induced molecular responses in Arabidopsis	jasmonate/JAZ signaling, transcriptome, plant-insect interaction, plant-plant interaction.	Assesses the extent to which exposure to monoterpene volatiles affects the transcriptome of *A. thaliana* using a genome-wide transcriptome analysis.	65
		Neryl diphosphate precursor rather than geranyl diphosphate	Terpene synthases, cis-prenyltransferases, biochemical diversity, specialized metabolism.	Contrary to the textbook view of geranyl diphosphate as the "universal" substrate of monoterpene synthases, in tomato glands neryl diphosphate serves as a precursor for the synthesis of monoterpenes.	66
		Transgenic manipulation of monoterpene	mevalonate-independent pathway, glandular trichomes, functional expression, transcription factors.	Discusses strategies for engineering monoterpene metabolism and summarizes recent developments in this field.	67

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		biosynthesis			
	Sesquiterpenes				
		(3S)-(*E*)-nerolidol synthase	*Cucumis sativus*, enzyme isolation and product identification, headspace analysis.	Investigates a nerolidol synthase that catalyzes the first dedicated step in the biosynthesis of 4,8-dimethyl-1,3(E),7-nonatriene in response to herbivory.	68
		5-Epi-aristolochene synthase	*Capsicum annuum*, sesquiterpene cyclase gene, cell-suspension cultures, Dna-binding proteins, *Nicotiana tabacum*.	Reports on a partial *Capsicum annuum* var. *annuum* Epi-aristolochene synthase (PEAS) cDNAs from total RNA isolated from pepper fruits elicited with cellulase. Differences and similarities of this gene in comparison with those from tobacco, H. muticus, and the UV-inducible PEAScDNA are carried out. Southern blot analysis demonstrates a chili pepper 5-epi-aristolochene synthase gene family.	69
		Amorpha-4,11-diene synthase	*Arabidopsis thaliana*, amorpha-4,11-diene synthase promoter (ADSpro).	To determine the subcellular localization of Amorpha-4,11-diene synthase (ADS), an open reading frame (ORF) of ADS was fused to the green fluorescent protein (smGFP) gene and introduced into the *A. thaliana* protoplasts. GFP fluorescence was located exclusively in the cytosol, an indication that ADS is a cytosol-localized protein.	70
		Epicubenol synthase	Sesquiterpene synthases, labeled precursosrs.	Describes experiments with (+)-epicubenol synthase which confirm the proposed intermediacy of (3R)-nerolidyl diphosphate in the cyclization reaction and which establish the stereochemical course of the conversion of famesyl diphosphate to (+)-epicubenol. Confirms the intermediacy of NPP in the formation of related cadinane, picrotoxane and sativane sesquiterpenes and fully support previously developed stereochemical models of sesquiterpene biosynthesis.	71
		(-)-α-gurjunene synthase	*Solidago canadensis*, cyclization mechanism, labeled substrates, multiproduct sesquiterpene synthase.	Describes the enzymatic activity which catalyzes the formation of (-)-α-gurjunene as major product from the common isoprenoid intermediate FDP. In addition, incubations of a partially purified enzyme preparation with deuterated substrate analogues are used to propose a cyclization mechanism for the formation of α-gurjunene from FDP.	72
		α-zingiberene synthase	*Lycopersicon esculentum*, volatiles, metabolic engineering.	Shows that the synthesis of sesquiterpenes can be enhanced by the ectopic expression of a single transgene in tomato fruit, and it further demonstrates the interconnection between the pools of terpenoid precursors in the plastids and the cytosol.	73
		β-bisabolene synthase cloning	*Zingiber officinale*, rhizomes, (S)-β-bisabolene,	ZoTps1, the (S)-β-bisabolene synthase gene in ginger, was suggested to catalyze (S)-β-bisabolene formation with the conversion of farnesyl diphosphate to nerolidyl diphosphate followed by the cyclization between position 1 and 6 carbons. The ZoTps1 transcript was detected in young rhizomes, but not in leaves, roots and mature rhizomes of ginger.	74
		β-caryophyllene synthase of *Mikania*	Allelopathy, *Brassica campestris*, *Raphanus sativus*, wounding.	A partial cDNA for β-caryophyllene synthase gene is isolated from the expressed sequence tag (EST) library of *Mikania micrantha* leaves. The	75

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		micrantha		full length cDNA is 1898 bp in full length and it encodes a putative protein of 547 amino acids. Its expression was significantly increased in *M. micrantha* leaves after wounding.	
		(+)-δ-Cadinene synthase	*Gossypium arboretum*, site-directed mutagenesis, farnesyl-diphosphate synthase, aristolochene synthase, terpenoid cyclase, isoprenoid biosynthesis, sesquiterpene cyclase, pentalenene synthase.	Reports the X-ray crystal structure of (+)-δ-cadinene synthase (DCS) from *G. arboreum* and the structure of its complex with 2-fluorofarnesyl diphosphate (2F-FPP). Presents product distribution and kinetic data for DCS mutants with aspartate → alanine and glutamate → alanine substitutions in the $D^{307}DTYD^{311}$ and $D^{451}DVAE^{455}$ segments. These results taken together illuminate aspects of metal binding in an unusual terpenoid cyclase active site and provide inferences regarding conformational changes that may occur upon substrate binding and catalysis.	76
		δ-cadinene synthase cloning	Phytoalexins, fungal elicitation, cadinene, cyclase, cotton	Reports on the isolation and characterization of a cDNA clone which encodes a protein with a high degree of amino acid sequence identity to three related terpene cyclases. The translated of this cDNA is shown to be an active FPP cyclase that produces the bicyclic compound (+)-δ-cadinene. In cotton cells the levels of enzyme and the corresponding mRNA are found to be inducible upon treatment with fungal elicitors, consistent with their role in the production of phytoalexins.	77
		δ-cadinene synthase induction	*Gossypium hirsutum*, *Gossypium barbadense*, phytoalexins, desoxyhemigossypol, delta-cadinene synthase, plant-pathogen interaction.	Plants are inoculated with defoliating strain V-76 of *Verticillium dahliae*. The concentrations of phytoalexins in inoculated plants is compared to those in a control group that had been inoculated with sterile water. Tissues from these plants are divided into two groups. One group is analyzed for phytoalexin concentrations, and the second is used to assay the level of δ-cadinene synthase.	78
		Maize sesquiterpene synthase	Parasitoid attraction, plant defense signal, terpene biosynthesis, volatile terpenes.	A terpene synthase, TPS10, that forms the herbivore-induced sesquiterpene volatiles of maize is isolated and overexpressed in *Arabidopsis thaliana*, generating plants that emit high levels of sesquiterpenes. Use of these transgenic plants in bioassays with parasitic wasps demonstrated that the sesquiterpenes produced by TPS10 can provide a volatile signal for the indirect defense of the plant against herbivore attack.	79
		Sesquiterpene synthases catalytic landscape	Evolution, protein, enzyme, cyclase, phytoalexins, promiscuity, expression.	Systematic quantitative characterization of the catalytic landscape underlying the evolution of sesquiterpene chemical diversity.	80
		Sesquiterpene synthases from sunflower	*Helianthus annuus*, antimalarial-drug precursor, germacrene-a synthase, western corn-rootworm, (+)-delta-cadinene synthase, cDNA isolation,	This study functionally identifies sesquiterpene synthase genes predominantly expressed in sunflower trichomes.	81

VOC class	Sub-class	Topic	Key words	Key topics	Ref.
			amorpha-4,11-diene synthase.		
		Sesquiterpene synthases of kiwifruit	*Actinidia*, α-farnesene, floral volatiles, germacrene D.	Describes the comparative analysis of the terpene volatiles produced in male and female kiwifruit flowers (*Actinidia deliciosa* 'Hayward') and the isolation and functional characterization of two terpene synthases responsible for the formation of major terpenoid compounds produced in these flowers is reported.	82
		Sesquiterpene synthases of lettuce	*Lactuca sativa*, Compositae, phytoalexin, germacrene A synthase, gene expression.	Reports the cloning of sesquiterpene synthase genes from lettuce. Two induced sesquiterpene synthases were cloned, expressed in *Escherichia coli* and found to produce germacrene A from FPP.	83
		(+)-δ-cadinene-8-hydroxylase inhibition	*Gossypium arboreum*, enzyme inhibition, substrate specificity, cytochrome P450 monooxygenase, clotrimazole, miconazole, α-muurolene, α-cubebene, α-copaene, α-humulene.	Sesquiterpene olefins δ-cadinene, α-cubebene, α-muurolene, α-humulene, and a mixture of (-)- and (+)-α-copaene were inhibitory to hydroxylation of (+)-δ-cadinene. In addition, α-cubebene, α-muurolene, α-humulene, and, to a smaller extent, δ-cadinene served as alternative substrates for (+)-δ-cadinene-8-hydroxylase and were converted to mono-hydroxylated products.	84
		5-Epi-aristolochene 1,3-dihydroxylase	*Arabidopsis thaliana*, substrate recognition sites, P450-dependent monooxygenase, functional expression, directed mutagenesis, heterologous expression.	Describes the successive region and stereospecific hydroxylation of epiaristolochene (EA) by its dihydoxylase (EAH). The results demonstrate a preferred reaction order and provide evidence that Ser368 and Ile486 play a significant role in orchestrating the successive hydroxylation of EA to capsidiol.	69
		Germacrene A oxidase	capitate glandular trichomes, antimalarial-drug precursor, functional-characterization, heterologous expression, eudesmane derivatives.	Germacrene A oxidase (GAO), evolutionarily conserved in all major subfamilies of Asteraceae, catalyzes three consecutive oxidations of germacrene A to yield germacrene A acid. Furthermore, it is also capable of oxidizing non-natural substrate amorphadiene. GAO activity is widely conserved in Asteraceae including the basal lineage.	85
		Hydroxylation of sesquiterpenes	*Cichorium intybus*, bioconversion, nootkatone, cytochrome P450, dehydrogenase.	A microsomal enzyme preparation of chicory roots catalyses the hydroxylation of various sesquiterpene olefins in the presence of NADPH. Discusses the involvement of (+)-germacrene A hydroxylase (a cytochrome P450 enzyme) and other enzymes.	86
		Inhibition of sesquiterpene cyclase by mevinolin	Inhibitor of sterol and sesquiterpene metabolism, [^{3}H]mevalonate incorporation, kinetic analysis.	Demonstrates that mevinolin inhibits radioactive acetate, but not mevalonate, incorporation into sterols, but inhibits both acetate and mevalonate incorporation into sesquiterpenoids. By directly assaying selected enzymes, mevinolin inhibited HMGR and sesquiterpene cyclase activities, but not squalene synthetase. Mevinolin may inhibit branch pathways of isoprenoid metabolism by selectively inhibiting branch point enzymes in addition to HMGR.	87
		Recombinant sesquiterpene cyclases	Trichodiene synthase, *Escherichia coli*, kinetic-analysis, rapid quench, biosynthesis, stereochemistry.	A mechanism that involves an initial, rapid equilibration of enzyme with substrate to form an enzyme-substrate complex, followed by a slower conversion of FPP to an enzyme-bound hydrocarbon and a subsequent	88

VOC class	Sub-class	Topic	Key words	Key topics	Ref.
				rate-limiting step, is proposed.	
		Regulation of sesquiterpene cyclase gene expression	*Medicago sativa*, systemic acquired-resistance, cell-suspension cultures, hypersensitive disease resistance, dna-binding proteins, plant defense genes.	Demonstrates that the EAS4 promoter (EAS is a sesquiterpene cyclase located at a putative branch point in the isoprenoid biosynthetic pathway) contains cis-acting elements capable of conferring qualitative and quantitative expression patterns that are exclusively associated with pathogen-, elicitor-, or wound induction patterns. A possible role of SA, MJ, and H,O, as regulators of EAS4-specific expression or expression of other endogenous sesquiterpene cyclase genes is examined.	89
		Biosynthesis of sesquiterpenes in carrot	*Daucus carota* L., 1-deoxy-D-xylulose, mevalonic acid, stir bar sorptive extraction, thermal desorption-multidmensional gas chromatography-mass spectrometry (TD-enantio-MDGC-MS).	In vivo feeding experiments were used to study the intra-plant variation of cytosolic mevalonate and plastidial methylerythritol phosphate pathways. A separate investigation of phloem and xylem was carried out to localize the site of terpene biosynthesis and to clarify the question whether the presence of oil ducts is mandatory for terpene biosynthesis.	90
		Chamomile sesquiterpenes	*Matricaria recutita*, mevalonic acid pathway, methylerythritol phosphate pathway, isopentenyl diphosphate,, C-13-labeling.	Describes the specific incorporation of 1-[1-^{13}C]deoxy-D-xylulose into the sesquiterpenes of chamomile, their isolation, and quantitative ^{13}C NMR spectroscopic analysis.	91
		Induction of sesquiterpenes in tobacco	Methyl jasmonate-defense response, phytoalexins	Provides evidence that MeJA induces a subset of genes coding for the biosynthesis of sesquiterpene phytoalexins.	92
		Induction of sesquiterpenes in Zea mays	bioassay (excised vs. intact tissues), Jasmonic acid, Spodoptera, plant volatiles, volicitin, Zea (herbivory).	Examines the mechanical damage, JA and volicitin treatment effects on sesquiterpene release in corn seedlings and the differences between intact-plant and excised-leaf bioassays.	93
		Sesquiterpene phytoalexin biosynthetic enzymes	Beta-glucuronidase reporter gene, pathogen-associated molecular patterns, pepper 5-epi-aristolochene synthase gene, reactive oxygen species.	Reports on a highly localized systemic gene expression of enzymes directly involved in sesquiterpene phytoalexin biosynthesis in leaves of tobacco (*Nicotiana tabacum*) and chili pepper (*Capsicum annuum*) elicited by pathogen-associated molecular patterns.	94
Oxylipins					
	GLVs				
		9/13-Hhydroperoxide lyase	*Medicago truncatula*, subcellular localisation of 9/13-hydroperoxide lyase, CYP74C enzymes.	Investigates the endocellular localisation of *M. truncatula* 9/13-HPL (HPLF), a member of the CYP74C subfamily and its localisation pattern. Proposes a link between the unexpected localisation of a member of the CYP74C subfamily and the possible activation of the enzyme in vivo.	95
		Allene oxide cyclase	*Arabidopsis thaliana*, jasmonate, 12-oxo-phytodienoic acid, oxylipins, X-ray structure.	Focuses on the structural and molecular mechanisms underlying the AO cyclization reaction. Discusses the crystal structure of AOC2 of *A. thaliana* with respect to putative binding sites of the instable substrate, 12,13-epoxy-9(Z),11,15(Z)-octadecatrienoic acid (12,13-EOT), as well as possible intermolecular rearrangements during the cyclization reaction.	96

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		Allene oxide synthase	*Parthenium argentatum* , crystal-structure, prostacyclin synthase, guayule, conformation, oxylipins, protein, cloning.	Eeport the crystallization of guayule AOS purified from overexpressing E. coli, and the preliminary X-ray diffraction analysis.	97
		Antisense lipoxygenase	*Nicotiana attenuata*, jasmonates, herbivore resistance, lipoxygenase, nicotine, trypsin protease inhibitors, quantitative PCR.	Isolation and characterization of three classes of the lipoxygenase gene family. Demonstrated the reduced expression of genes involved in defense activation and altered expression of growth-related genes.	98
		Biosynthesis of trans-2-hexenal	*Fragaria x ananassa fruit*, wounding, total fatty acids, free fatty acids, linolenic acid, lipoxygenase, hydroperoxide lyase, C-6 aldehydes, cis-3-hexenal, trans-2-hexenal.	Analyzes the composition and quantity of total and free fatty acids of control and wounded strawberry fruit. Determines activities of the key enzymes of the LOX pathway, LOX and HPL, and production of C6 aldehydes.	99
		Defense gene induction	*Zea mays*, C-6-volatiles, (Z)-3-Hexenol, methyl jasmonate, terpenes.	Compares differences in phytochemical release and mRNA levels for several previously characterized enzymatic steps in defense pathways for insect damage, MeJA or C6-alcohol treatment. Postulates that applied (*Z*)-3-hexenol can be taken up by maize plants and metabolized into a less active acetylated form. Synthetic (*Z*)-3-hexenyl acetate is applied to maize and its efficacy as a signaling molecule is compared to that of other synthetic C6-volatiles.	100
		Dynamics of GLV precursors	*Brassica oleracea* var. *gemmifera*, hexenyl acetate, dimethyldisulphide, lipoxygenase, stable isotope analysis, compartmentation.	Investigates the dynamics of precursor compounds of GLVs and other biogenic compounds released by mechanically damaged *Brassica oleracea* leaves. The labelling pattern found in most GLVs indicates a low turnover of the precursor α-linolenic acid.	101
		Fatty acid hydroperoxide lyase silencing	*Nicotiana attenuata*, CYP74, oxylipin signaling, jasmonates, feeding stimulant, *Manduca sexta*, *Manduca quinquemaculata*, *Spodoptera exigua*, Lepidoptera.	Analyzes the wound- and herbivore-induced release of GLVs and characterize the expression of an HPL gene from *N. attenuata* (NaHPL). Extensive overlap of GLV- and JA-regulated transcript accumulation suggests crosstalk between signals derived from two oxylipin pathways.	102
		Lipoxygenase 2 supplies substrates for green leaf volatile production.	Nicotiana, green leaf volatiles, jasmonic acid, lipoxygenase, oxylipins	Demonstrates that *Nicotiana attenuata* channels the flux of fatty acid hydroperoxides through the activities of different lipoxygenases, leading to different direct and indirect defence responses mediating the plant's herbivore resistance.	103
		Lipoxygenase gene family of Arabidopsis	Fatty acid, fatty acid hydroperoxide, lipoxygenase, oxylipins.	Comprises the systematic characterization of the regio- and stereo-specificity of the fatty acid oxygenations catalyzed by the complete family of lipoxygenases of *A. thaliana*.	104
		Lipoxygenase metabolic pathway in plants	Lipoxygenase, hydroperoxide lyase, green leaf volatiles, enzymes engineering, natural flavor production,	Describes the different enzymes involved in the bioconversion of lipids to natural GLVs with regards to their chemical and enzymatic properties. Biotechnological techniques to enhance their production potentialities are	105

VOC class	Sub-class	Topic	Key words	Key topics	Ref.
			bioconversion.	discussed along with their implication in a complete bioprocess, from the lipid substrate to the corresponding aldehydic or alcoholic flavors.	
		Oxylipin pathway in rice and Arabidopsis	Aldehydes, allene oxide synthase, hydroperoxide lyase, jasmonates, oxylipin pathway.	Provides new insights into the evolution of JAs and aldehydes signaling pathways, and the complex network of processes responsible for stress adaptations in monocots and dicots	[106]
		Oxylipin structural diversity	Cyp74, fatty acid peroxides, lipid metabolism, lipid peroxidation, lipid signaling, lipoxygenase pathway.	Aims at giving an overview of plant oxylipins and the multitude of enzymes responsible for their biosynthesis.	[107]
		Pentacyclic oxylipins	12-oxo-phytodienoic acid (12-oxo-PDA), 15,16-dihydro-12-oxo-PDA, jasmonic acid, 9,10-dihydrojasmonic acid, 12-oxo-PDA reductase, biological activity, secondary metabolite induction, plant defense, plant cell cultures.	Analyses the significance of the postulated dihydro-pathway. Evaluates the secondary metabolite inducing activity of the oxylipins and their dihydro-compounds in seven plant cell culture species and examines the in vivo formation and metabolism of the dihydro-oxylipins.	[108]
		Peroxygenase pathway	acid epoxide hydrolase, unsaturated fatty-acids, rice blast disease, hydroperoxide-dependent oxygenase, self defensive substances, substrate hydroxylation, xenobiotic metabolism, soybean peroxygenase, cytochrome P-450.	The peroxygenase pathway involves two enzymes i) a peroxygenase, which catalyzes an intramolecular transfer of oxygen from hydroperoxides yielding epoxyalcohols, and (or) intermolecular oxygen transfer (cooxidation reactions) resulting for example in the epoxidation of double bonds of unsaturated fatty acids, ii) an epoxide hydrolase, which hydrates preferentially the epoxides formed by the peroxygenase.	[109]
		Use of 'mute' plants	*Nicotiana attenuata*, genetic silencing, eavesdropping,	GLV-dependent genes have been identified by complementing a GLV-deficient volatile blend with a mixture of synthetic GLVs. Blends deficient in GLVs regulated numerous genes in receiver plants that did not respond to the complete VOC blends of WT emitters, indicating a suppressive effect of GLVs.	[110]
		Role of ethylene	*Zea mays*, plant-plant signaling, ethylene, (Z)-3-hexen-1-ol, herbivore-induced volatile organic compounds, sesquiterpenes.	Demonstrates that ethylene synergizes HI-VOC emission in maize plants exposed to (Z)-3-Hexen-1-ol but has no volatile inducing effect on its own.	[111]
		Triggering of local and systemic VOC emissions	*Lycopersicon esculentum*, Solanaceae, herbivores, monoterpenes, sesquiterpenes, C-6-volatiles.	Examines the role of C6-aldehydes/alcohols in the emission of plant volatiles and compares this response with activated VOC emissions triggered by insect damage. Report on the activation of volatile emissions from the monoterpene and sesquiterpene pathways by a series of C6-volatiles. Supports the theory that green leaf volatiles activate a systemic signaling cascade triggering volatile emissions in untreated leaves.	[112]
	Jasmonates				
		Enzymes in	Allene oxide cyclase, allene oxide	Until recently, jasmonic acid has been viewed as the end product of the	[113]

VOC class	Sub-class	Topic	Key words	Key topics	Ref.
		jasmonate biosynthesis	synthase, crystal structure, CYP74, oxylipins, oxophytodienoate reductase, substrate specificity.	pathway and as the bioactive hormone. It becomes increasingly clear, however, that biological activity extends to and may even differ between the various jasmonic acid metabolites and conjugates as well as its biosynthetic precursors. Oxygenated fatty acids give rise to a vast variety of bioactive compounds including but not limited to jasmonates. Shows insights into the structure, function, and regulation of the enzymes involved in jasmonate biosynthesis.	
		12-Oxophytodienoate reductase	flavoprotein, jasmonic acid biosynthesis, plant defense, oxylipin signature, 12-oxophytodienoic acid.	Presents the high-resolution crystal structures of LeOPR3 and of two mutant proteins. The active-site architecture of LeOPR3 provides insight into the remarkable stereoselectivity of the different OPR isoforms and the substrate specificity of the OYE family in general. The structural data suggest that dimerization, which also occurs in solution, may be regulated by reversible phosphorylation.	114
		Hydroxyjasmonate sulfotransferase	*Arabidopsis thaliana*, allene oxide cyclase, jasmonic acid, gene-expression, flavonol 3-sulfotransferase, oxylipin signature, plant defense, cis-jasmone.	Reports the characterization of a ST (AtST2a) from *A. thaliana* exhibiting strict specificity for hydroxyjasmonates. This is the first report of a ST involved in jasmonate metabolism. Demonstrates that 12-OHJA and its sulfate derivative are natural constituents in *A. thaliana*. Proposes a role for the hydroxyjasmonate ST in the regulation of the levels of JA and/or 12-OHJA in plants.	115
		Silencing the jasmonate cascade	*Nicotiana attenuata*, Arabidopsis, gene expression, resistance, evolution.	Shows that lipoxygenase-dependent signaling determines host selection for opportunistic herbivores and that induced defenses influence herbivore community composition.	116
		Indirect defense of *Arabidopsis thaliana*	Herbivory, oxylipin, herbivore-induced volatile, metabolite analysis, behavioral analysis, *Pieris rapae.*	The involvement of several intermediates from the jasmonate pathway in the induction of plant volatiles by leaf-feeding herbivores is studied. The contribution of the two sub-pathways that originate from galactolipids (16:0) or phospholipids (18:0), with special interest in dnOPDA, OPDA, and JA is studied. Mutants with altered production levels of dnOPDA, OPDA, and JA were selected. For caterpillar-infested mutants and their corresponding wild-type plants, the levels of dnOPDA, OPDA, and JA were quantified. The effects of the observed differences in oxylipin profiles and HIPV blend composition after caterpillar feeding on species interactions are described.	117
		Arabidopsis Jasmonate Signaling Pathway	Receptor, defense, repression, coronatine, proteins, mediator, targets, complex, growth.	The degradation of JAZ proteins liberates transcription factors that function in the presence of the RNA polymerase II coregulatory complex Mediator to permit the expression of a number of jasmonate-regulated genes. Recent developments include the identification of COI1 as a receptor for jasmonates. Upstream of the signaling events, microRNA319 (miR319) negatively regulates the production of JA and JA-derived signals	118
		Jasmonate	*Arabidopsis thaliana*, Metabolomics,	Wounded specimens of Arabidopsis are analysed by mass spectrometry	119

VOC class	Sub-class	Topic	Key words	Key topics	Ref.
		glucoside	mass spectrometry, UHPLC/TOFMS, wounding, jasmonates, OPC-4.	(MS)-based metabolomics to screen for wound-induced metabolites belonging to the jasmonate family. Reveales the presence of a novel jasmonate metabolite. Its accumulation over time following wounding is monitored and compared with that of known jasmonates.	
		Response to wounding	*Arabidopsis thaliana*, methyl jasmonate, oxylipin signal, male-sterile, resistance, transport.	Accumulation in the midveins of several polar derivatives of JA and JA-Ile correlated with the polarity of the molecules. Apparent differences in the level of JA in resting leaves are found.	120
		Jasmonate amino acid conjugates	Plant defense, secondary metabolism, jasmonic acid, jasmonoyl-isoleucine, coronalon	Offers a survey of both natural and synthetic mimetics of the natural hormone which can be used for a selective manipulation and the study of the plant's secondary metabolism.	121
Volatile phenolics					
		Phenylpropanoid biosynthetic pathway.	Flavonoid, anthocyanin, tannin, coumarin, volatiles, lignin.	Gives an update on the various facets of the general phenylpropanoid pathway, which is not only restricted to common lignin or flavonoid biosynthesis, but feeds into a variety of other aromatic metabolites like coumarins, phenolic volatiles, or hydrolyzable tannins.	122
		New insights into the shikimate and aromatic amino acids biosynthesis	Carbon metabolism, metabolomics, metabolic regulation, primary metabolism, secondary metabolism-phenylpropanoids and phenolics, volatiles	Plants can also synthesize phenylalanine via the intermediate metabolite phenylpyruvate (PPY), similarly to many microorganisms. Recent studies also identified a number of transcription factors regulating the expression of genes encoding enzymes of the shikimate and aromatic amino acids pathways as well as of multiple secondary metabolites derived from them in Arabidopsis and in other plant species	123
		Biosynthesis of Phenolic Glycosides	*Populus nigra*, Isotope labeling, Phenolic glycosides, Herbivore defense, Carbon-13, LC-MS.	A revised metabolic grid model of phenolic glycosides biosynthesis in *Populus* is proposed, providing a guide for functional genomic analysis of the phenolic glycosides biosynthetic pathway.	124
		Chorismate mutase and VOCs	Chorismate mutase, petunia, benzenoid/phenylpropanoid, volatiles, flower, chloroplast	To understand the regulation of ‘upstream’ components in the floral volatile benzenoid/phenylpropanoid (FVBP) system, two chorismate mutase (PhCM1 and PhCM2) cDNAs from petunia have been cloned and characterized. The results show that PhCM1 is the principal chorismate mutase responsible for the coupling of metabolites from the shikimate pathway to the synthesis of FVBPs in the corolla of Petunia.	125
		3-Ketoacyl-CoA thiolase	*Petunia hybrida* cv. Mitchell, Benzoic acid, 3-ketoacyl-CoA thiolase, beta-oxidation, benzenoids, floral volatiles.	Describes the identification and characterization of a petunia 3-ketoacyl-CoA thiolase (PhKAT1), which plays an important role in the β-oxidative pathway leading to the production of benzoyl-CoA from 3-oxo-3-phenylpropionyl-CoA (benzoylacetyl-CoA). Transgenic plants were generated suppressing PhKAT1 expression (ir-PhKAT1). Analysis indicates that the β-oxidative pathway plays a major role in the production of benzoic acid and thus of precursors for C6–C1 volatiles. This 3-ketoacyl-CoA thiolase is present in the peroxisomes of petunia petals,	126

VOC class	Sub-class	Topic	Key words	Key topics	Ref.
				adding the involvement of this organelle in volatile benzenoid biosynthesis.	
		Allylphenol O-methyltransferase	Ocinum basilicum L., Lamiaceae, sweet basil, essential oils, estragole, methyl eugenol, O-methyltransferase.	Provides evidence that in sweet basil leaves, chavicol and eugenol can be enzymatically O-methylated, to generate methyl chavicol and methyl eugenol, respectively, by SAM dependent O-methyltransferase activities.	127
		Biosynthesis and metabolism of salicylic acid	systemic acquired resistance, salicylic acid glucoside, benzoic acid 2-hydroxylase, udp-glucose-salicylic acid glucosyltransferase	Enzymology and molecular biology of SA biosynthesis and metabolism provide a better understanding of signal transduction pathway involved in plant disease resistance.	128
		Chemically synthesized salicylate derivative	*Taxus chinensis*, cell-suspension cultures, methyl jasmonate,, tropane alkaloids, root cultures, acid, enhancement, expression, induction.	A novel fluoro-containing salicylate, trifluoroethyl salicylate (TFESA), is chemically synthesized and evaluated by bioassay as a potential elicitor for inducing the biosynthesis of plant secondary metabolites. A high taxuyunnanine C (Tc)-producing cell line of T. chinensis is used as a model plant cell system, where Tc is a physiologically active substance with a neuron growth factor-like activity.	129
		Foliar emission of methyl salicylate	*Agelastica alni*, *Euceraphis betulae*, monoterpenes, sesquiterpenes, volatile.	MeSA has been shown to have aphidrepellent qualities and has been shown recently to have impact on formation of secondary organic aerosols in the atmosphere. The paper discusses results in relation to these two phenomena.	130
		Methyl salicylate esterase	salicylic acid, salicylic-acid-binding protein, systemic acquired resistance, alpha/beta hydrolase.	The 3D structure of a salicylate-binding protein (SABP2) in the absence and presence of SA at up to 2.1-Å resolution is determined. Demonstrates that SABP2 has esterase activity with a physiologically relevant Km value for MeSA, and that SA is a potent product inhibitor of this activity. Suggest that MeSA may have an important role in SAR that is distinct from the role of SA.	131
		O-methyltransferases	*Rosa hybrida* cv Fragrant Cloud and cv Golden Gate, floral scent, evolution, emission, aroma, specificity.	Describes the biochemical characterization of the enzymes encoded by two cDNAs of rose cv Golden Gate and cv Fragrant Cloud petals that are very similar to each other and also exhibit homology to known O-methyltransferases (OMTs). Shows that they catalyze the last two steps of the formation of orcinol dimethyl ether.	132

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