

Microbial Influence on Plant Volatile Organic Compound Emission and Its Ecological Impact

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Abstract

Plant volatile organic compounds (VOCs) are low-molecular-weight, high-vapour-pressure metabolites that mediate a large fraction of the chemical communication occurring above and below ground. plant growth-promoting rhizobacteria (PGPR), arbuscular mycorrhizal fungi (AMF), endophytes and the wider soil microbiome—reshape the composition, quantity and ecological function of plant volatiles. Across the collated evidence, microbial colonisation rarely leaves the volatilome unchanged. Bacterial inoculants such as *Bacillus* and *Pseudomonas* spp. prime the emission of green-leaf volatiles, terpenoids and methyl salicylate through induced systemic resistance (ISR) linked to jasmonic-acid, salicylic-acid and ethylene signalling. AMF symbioses (e.g. *Funneliformis mosseae*) elevated leaf VOC pools by as much as 85% and increased terpenoid content by roughly half in quantitative meta-analyses, while reductions in soil microbial diversity paradoxically raised total VOC flux but narrowed its chemical richness. The ecological consequences are multi-trophic: microbially reprogrammed blends alter herbivore performance, recruit parasitoids and predators, suppress phytopathogens, structure neighbouring microbial communities and feed back onto atmospheric chemistry through biogenic emissions. Five secondary-data tables summarise emission shifts, functional mechanisms and trophic outcomes. The synthesis argues that the plant volatilome is best understood as a holobiont trait, jointly encoded by host and microbiome, with direct relevance for sustainable pest management, biocontrol and climate-linked emission modelling.

Keywords: *microbial volatile organic compounds; induced systemic resistance; PGPR; arbuscular mycorrhizal fungi; plant–insect interactions; chemical ecology; holobiont*

1. Introduction

Volatile organic compounds are among the most versatile currencies of plant biology. A single plant may release hundreds of distinct volatiles spanning terpenoids, green-leaf volatiles (GLVs), aromatic compounds, fatty-acid derivatives and nitrogen- or sulphur-containing molecules, and these blends are continuously retuned in response to development, abiotic conditions and biotic interactions. For most of the twentieth century, the plant was treated as the sole author of its own volatilome. That view has been steadily overturned: plants are now understood as holobionts whose emitted chemistry emerges from a negotiated interaction between host genotype and an intimate community of bacteria, fungi and other microorganisms colonising roots, leaves and internal tissues.

This synthesis focuses specifically on how microorganisms influence plant VOC emission and what that influence means ecologically. The topic sits at the intersection of chemical ecology, microbiology and atmospheric science, and it has acquired practical urgency as agriculture searches for microbial alternatives to synthetic pesticides. The following three subsections frame the conceptual background, the significance of microbial modulation, and the objectives and scope of the review.

1.1 Plant Volatiles as a Chemical Communication Network

Plant VOCs function as an airborne signalling network linking plants to insects, microbes, neighbouring plants and the atmosphere. They are characterised by low molecular weight and high vapour pressure, which allows them to diffuse rapidly through air and soil pore space and to act as infochemicals between organisms. Constitutive emissions advertise resources to pollinators and seed dispersers, while inducible emissions—especially herbivore-induced plant volatiles (HIPVs)—signal damage. HIPV blends can repel ovipositing herbivores, prime defences in undamaged tissues and neighbouring plants, and recruit the natural enemies of herbivores in a form of indirect defence. Because the same molecular classes recur across these functions, small quantitative shifts in a blend can carry substantial ecological meaning.

The biosynthetic origins of these compounds explain much of their ecological flexibility. Terpenoids arise from the plastidial methylerythritol-phosphate and cytosolic mevalonate pathways; green-leaf volatiles are cleaved from membrane fatty acids by the lipoxygenase pathway within seconds of tissue damage; and aromatic volatiles such as methyl salicylate derive from the shikimate pathway. Each of these routes is a potential point of regulatory intervention, and it is precisely at these nodes—hormone signalling, enzyme activity and gene transcription—that microbial partners exert their influence. A blend is therefore not a fixed species trait but a dynamic readout of the plant's physiological state, integrating internal

signalling with the demands of the surrounding biotic environment. This plasticity is the substrate on which microbial modulation operates.

1.2 The Microbial Dimension of the Volatilome

Superimposed on host-controlled emission is a microbial layer of regulation. Root-associated PGPR and mycorrhizal fungi remodel host primary and secondary metabolism, thereby changing which volatiles are produced and in what quantity. Microorganisms also emit their own microbial VOCs (mVOCs)—more than 200 have been catalogued—that act as signals to plants and to other microbes, modulating growth, motility, biofilm formation and antibiotic tolerance. Microbial influence therefore operates through two coupled routes: indirectly, by reprogramming the plant's biosynthetic pathways, and directly, by contributing volatiles that mix into the emitted blend. Distinguishing these routes is analytically difficult and remains a central methodological challenge in the field.

The significance of this microbial layer has grown as agriculture confronts the limitations of synthetic chemical inputs. Broad-spectrum pesticides impose well-documented costs on human health, non-target organisms and environmental quality, and their efficacy is eroded by resistance. Microbial modulation of plant volatiles offers a fundamentally different strategy: rather than applying an external toxin, it recruits the plant's own defensive and communicative chemistry, often at low ecological cost and without leaving persistent residues. mVOCs and microbe-primed plant volatiles can suppress pathogens, deter or intoxicate herbivores, and recruit beneficial insects, positioning the plant–microbiome interface as a promising target for sustainable crop protection. Understanding how microorganisms reshape emission is thus not only a question of basic chemical ecology but also a prerequisite for designing the next generation of biological inputs.

2. Literature Review

The literature on microbial influence over plant volatiles has expanded rapidly since 2018, driven by advances in headspace sampling, gas chromatography–mass spectrometry (GC–MS) and community sequencing. Four themes organise this body of work: bacterial modulation via induced systemic resistance; mycorrhizal and endophytic reprogramming of secondary metabolism; whole-community and soil-diversity effects; and the multi-trophic ecological consequences of altered blends.

2.1 Rhizobacteria and Induced Systemic Resistance

Plant growth-promoting rhizobacteria are the most intensively studied microbial modulators of plant volatiles. Root colonisation by strains of *Bacillus*, *Pseudomonas*, *Paenibacillus* and related genera triggers induced systemic resistance, a primed defensive state that resembles the response to herbivory in its signalling architecture. ISR is classically dependent on jasmonic-acid and ethylene signalling, although salicylic-acid-dependent induction is also frequently observed, and the pathway engaged is strain- and host-specific. A recurrent outcome is that PGPR treatment elevates the emission of defence-associated volatiles—indole, β -caryophyllene, methyl salicylate and GLVs—thereby strengthening both direct and indirect defence.

Bacterial volatiles themselves act as ISR elicitors. Short-chain compounds such as 2,3-butanediol and acetoin, and longer-chain molecules such as the C13 volatile tridecane produced by *Paenibacillus polymyxa*, prime transcription of defence marker genes and confer protection against pathogens. Importantly, the magnitude and even the direction of these effects depend on plant genotype: studies in maize show that herbivory protection via VOCs is governed more strongly by cultivar than by the composition of an introduced bacterial community, underscoring that microbial modulation is contingent on host genetic background.

A useful distinction within this literature separates priming from direct induction. Priming does not necessarily elevate defence-volatile emission in the unchallenged plant; instead it conditions the plant to respond faster and more strongly when a herbivore or pathogen subsequently attacks. This explains why some PGPR studies report little constitutive change in the volatilome yet document markedly enhanced defensive output under challenge—a pattern observed, for example, in broad bean where *Bacillus amyloliquefaciens* FZB42 primed defence without conspicuous growth promotion. From an applied standpoint, priming is attractive because it minimises the metabolic cost of standing defence while preserving rapid inducibility, but it also complicates screening, since the benefit of an inoculant may be invisible until the plant is stressed. The strain-specificity of elicitation, combined with host-genotype dependence, means that effective microbial products will likely require matching of inoculant, cultivar and target pest rather than the deployment of a universal biocontrol strain.

2.2 Mycorrhizal and Endophytic Reprogramming of Secondary Metabolism

Arbuscular mycorrhizal fungi form symbioses with the roots of most terrestrial plants and exert some of the largest documented effects on plant volatile chemistry. In grapevine, colonisation by *Funneliformis mosseae* enhanced leaf-tissue VOC pools by around 85% and

specifically raised defence- and stress-associated volatiles including (E)-2-hexenal, geraniol, benzaldehyde and methyl salicylate. Quantitative meta-analysis across 233 paired observations found AMF inoculation increased medicinal active-ingredient content by 27% overall, with terpenoids rising by roughly 53% and flavonoids by 68%, and with belowground organs responding more strongly than aboveground tissues.

AMF effects are, however, species- and context-specific. Root VOC profiling in sorghum showed that different *Glomus* species altered both the quantity and identity of root volatiles in a fungus-specific manner, and colonisation of black pepper shifted the balance between sesquiterpene hydrocarbons and oxygenated sesquiterpenes over the course of the symbiosis. Endophytic fungi and bacteria add a further layer, colonising internal tissues and contributing secondary metabolites that participate in multidimensional interactions with the host and the wider microbiome. Across these systems the consistent message is directional plasticity rather than a fixed response: symbiosis reliably changes the volatilome, but the sign and size of change vary with partner identity, host organ and developmental stage.

2.3 Soil Microbial Diversity and Community-Level Effects

Beyond single inoculants, the structure of the whole soil community shapes both soil-derived and plant-derived volatiles. A counter-intuitive but well-replicated finding is that reduced microbial diversity increases total VOC flux from soils while decreasing the number of distinct compounds emitted, consistent with a shift from a balanced producer–consumer network toward net production. Taxa such as Proteobacteria, Bacteroidetes and fungi correlate positively with emission and appear to act mainly as producers, whereas several prokaryotic phyla behave as consumers that scrub volatiles from the pore space.

For plants, the identity of the soil inoculum can reshape foliar emission. In invasive lupin, soil-inoculum treatment significantly altered VOC composition—chiefly by raising green-leaf-volatile emission—in both native and invasive populations, and these shifts corresponded to differences in herbivore resistance. Such community-level effects position mVOCs both as drivers of soil ecological regulation and as potential non-destructive indicators of subsurface microbial activity, an emerging application termed volatilomics.

These findings caution against extrapolating directly from single-strain inoculation experiments to field conditions, where introduced organisms enter a resident community that may buffer, amplify or redirect their effects. The producer–consumer framing is particularly instructive: because a fraction of the soil community actively consumes volatiles, net emission reflects a balance rather than gross production, and any manipulation that removes consumers can raise apparent flux even without increasing synthesis. For applied microbiome

management this implies that outcomes depend not only on which beneficial strain is added but on the metabolic structure of the community it joins. The diagnostic promise of volatilomics—reading community activity from its volatile signature without destructive sampling—rests on the same principle and offers a route to monitoring soil health that complements genomic and biochemical profiling.

2.4 Multi-Trophic Ecological Consequences of Altered Blends

The ecological payoff of microbial modulation is realised across trophic levels. At the second trophic level, PGPR-primed plants can suppress herbivore performance: inoculation of broad bean with *Bacillus amyloliquefaciens* FZB42 reduced reproduction of one pea-aphid clone through defence priming, and PGPR-inoculated sweet basil showed enhanced biochemical and structural defence under aphid attack. At the third trophic level, microbially altered HIPV blends influence the recruitment of parasitoids and predators, linking belowground symbiosis to aboveground biological control.

Microbial volatiles also mediate plant–pathogen and microbe–microbe antagonism. Volatiles such as dimethyl disulfide exert bacteriostatic effects on plant pathogens, and bacterial and fungal mVOCs can inhibit fungal phytopathogens directly, offering a volatile-mediated route to biocontrol. Finally, biogenic VOC emission connects these micro-scale interactions to ecosystem and atmospheric processes, since terpenoids and isoprene influence aerosol formation and atmospheric oxidative capacity. The literature thus converges on a view of the plant volatilome as a holobiont-level trait with consequences that scale from the rhizosphere to the atmosphere.

It is worth stressing that these outcomes are not uniformly beneficial from every organism's perspective, and this is where the ecological framing becomes important. A blend that recruits parasitoids benefits the plant and the third trophic level but harms the herbivore; a volatile that suppresses one pathogen may simultaneously signal an opportunistic competitor. In invasion biology, microbially mediated shifts in emission can favour exotic plants by enhancing their defence in a novel range, as documented when invasive lupin populations associated with soil microbiota from the invaded range and displayed elevated green-leaf-volatile emission alongside greater herbivore resistance. The same mechanistic machinery, in other words, can serve conservation-relevant or agriculturally undesirable ends depending on context. Recognising this contingency guards against an over-optimistic reading of microbial modulation as inherently "good" for the plant or the ecosystem, and reframes it instead as a lever whose consequences depend on the community and the management goal.

3. Research Methodology

This study employs a secondary-data synthesis design. Rather than generating new empirical measurements, it collates, standardises and interprets quantitative and qualitative findings reported in peer-reviewed primary studies and meta-analyses published between 2018 and 2024. The approach is appropriate where the goal is to detect cross-study patterns in a heterogeneous but rapidly growing literature and to organise them into an ecological framework.

3.1 Data Sources and Search Strategy

Peer-reviewed articles were identified through bibliographic and full-text databases using combinations of the terms "microbial volatile organic compounds", "plant VOC emission", "PGPR", "induced systemic resistance", "arbuscular mycorrhizal fungi", "endophyte", "herbivore-induced plant volatiles" and "soil microbial diversity". Priority was given to studies reporting directional or percentage changes in emission or metabolite content, to review articles consolidating mechanisms, and to quantitative meta-analyses providing pooled effect sizes suitable for tabulation.

3.2 Inclusion Criteria and Data Extraction

Studies were retained if they (i) addressed a plant-associated microorganism or microbial community, (ii) reported an effect on plant or soil VOC emission, metabolite content, or a downstream ecological outcome, and (iii) fell within or were consolidated during the 2018–2024 window. From each source, the microbial agent, host plant, affected volatiles, direction and magnitude of change, mechanism and ecological consequence were extracted. Because emission was quantified by diverse methods—headspace GC–MS, solid-phase microextraction, leaf-cuvette sampling and volatilomic profiling—effects are reported here as standardised directions and representative magnitudes rather than pooled statistical estimates, and Tables 1–5 present the synthesised secondary data underlying the discussion.

3.3 Analytical Framework and Limitations

The extracted evidence was organised along two axes: the microbial agent (bacterial, fungal, community) and the ecological level of impact (plant physiology, herbivore, third trophic level, microbial community, atmosphere). This framework structures the results and discussion. Two limitations should be noted. First, methodological heterogeneity across studies limits strict quantitative comparability, so magnitudes are indicative. Second, publication and taxonomic biases—toward cultivable bacteria, model plants and beneficial

outcomes—mean the synthesised picture may over-represent positive and well-studied interactions. These constraints are revisited in the conclusion.

4. Results

The synthesised secondary data are presented in five tables. Table 1 summarises the direction and magnitude of VOC change induced by major microbial agents. Table 2 details representative bacterial inoculants and the ISR pathways they engage. Table 3 consolidates quantitative AMF effects on volatile and secondary-metabolite pools. Table 4 maps community-level and soil-diversity effects. Table 5 organises the multi-trophic ecological consequences. Together they support the interpretive synthesis that follows.

Table 1. Direction and representative magnitude of microbial effects on plant/soil VOC emission (secondary data, 2018–2024).

Microbial agent	Host / system	VOC classes affected	Direction & magnitude
PGPR (Bacillus, Pseudomonas)	Multiple crops	GLVs, terpenoids, indole, MeSA	Increase; blend enrichment
Paenibacillus polymyxa E681	Arabidopsis	Long-chain VOCs (tridecane)	Novel emission; ISR priming
AMF – Funneliformis mosseae	Grapevine (Vitis)	Aldehydes, terpenes, MeSA	Leaf VOC pool +~85%
AMF (meta-analysis, 233 obs.)	Medicinal plants	Terpenoids; flavonoids	Terpenoids +~53%; overall +27%
Glomus spp.	Sorghum roots	Alkanes, terpenes (44 VOCs)	Quantity & identity altered
Reduced soil diversity	Bulk soil	Total mVOC flux	Total flux up; richness down
Soil inoculum	Invasive lupin	Green-leaf volatiles	GLV emission increased

GLVs = green-leaf volatiles; MeSA = methyl salicylate; ISR = induced systemic resistance; obs. = paired observations. Magnitudes are representative values drawn from cited primary and meta-analytic sources.

Table 2. Representative bacterial inoculants, elicitor volatiles and defence signalling pathways engaged.

Bacterial strain / group	Elicitor / key volatile	Signalling pathway	Reported outcome
Bacillus subtilis GB03	2,3-butanediol, acetoin	ISR (JA/ET)	Growth promotion + ISR
Paenibacillus polymyxa E681	Tridecane (C13)	SA, JA, ET markers	PR1/VSP2 induction
Bacillus amyloliquefaciens FZB42	Blend / priming	JA-linked priming	Reduced aphid reproduction
Pseudomonas / Serratia spp.	Inhibitory VOC blend	Direct antimicrobial	Pathogen growth inhibition
Bacillus altitudinis (maize)	HIPV modulation	Genotype-dependent	Effect driven by cultivar
Mixed PGPR consortia	Multiple determinants	SA + JA/ET synergy	Enhanced ISR efficacy

JA = jasmonic acid; SA = salicylic acid; ET = ethylene; HIPV = herbivore-induced plant volatile; PR1/VSP2 = defence marker genes.

Table 3. Quantitative arbuscular mycorrhizal fungi (AMF) effects on plant volatile and secondary-metabolite pools.

AMF species	Host	Metabolite / VOC group	Reported change
Funneliformis mosseae IMA1	Grapevine	Total leaf VOCs	+~85%
AMF (pooled meta-analysis)	Medicinal plants	Terpenoids	+~53%
AMF (pooled meta-analysis)	Medicinal plants	Flavonoids	+~68%
AMF (pooled meta-analysis)	Belowground organs	Active ingredients	+~32%
AMF (pooled meta-analysis)	Aboveground organs	Active ingredients	+~18%
R. clarus / C. etunicatum	Black pepper	Sesquiterpene hydrocarbons	54–79% (increase)
Glomus intraradices/mosseae	Sorghum roots	Root VOC profile	Species-specific shift

Values are representative magnitudes reported in the cited studies and meta-analyses; sampling methods (HS–SPME, leaf-cuvette GC–MS) differ across sources.

Table 4. Community-level and soil-diversity effects on VOC emission and function.

Community factor	Observed effect on VOCs	Producer / consumer taxa	Functional implication
Reduced microbial diversity	Total flux increases	Producers dominate	Loss of consumer sink
Reduced microbial diversity	Compound richness declines	Fewer distinct emitters	Narrower signalling
High-diversity balanced soil	Moderated net flux	Proteobacteria, Bacteroidetes, fungi (+)	Producer–consumer balance
Soil inoculum transfer	Foliar GLV emission rises	Whole-community effect	Altered herbivore resistance
mVOC-based monitoring	Flux as activity proxy	Community-wide	Volatilomics diagnostic

GLV = green-leaf volatile; (+) indicates positive correlation with emission. Several prokaryotic phyla act as net consumers of soil VOCs.

Table 5. Multi-trophic ecological consequences of microbially altered VOC blends.

Trophic / ecological level	Mechanism	Ecological outcome
Plant (1st level)	ISR priming of defence VOCs	Enhanced direct & primed defence
Herbivore (2nd level)	Altered HIPV / plant quality	Reduced herbivore performance
Predators & parasitoids (3rd)	HIPV recruitment signals	Improved biological control
Microbe–microbe	Antimicrobial mVOCs (e.g. DMDS)	Pathogen suppression / biocontrol
Neighbouring plants	Airborne priming	Defence priming in receivers
Atmosphere / ecosystem	Biogenic terpene/isoprene flux	Aerosol & oxidant chemistry

HIPV = herbivore-induced plant volatile; DMDS = dimethyl disulfide; ISR = induced systemic resistance.

4.1 Interpretation of the Synthesised Data

Three patterns emerge from Tables 1–5. First, microbial colonisation predominantly enriches or restructures the volatilome rather than simply scaling it; bacterial inoculants tend to add or amplify defence-associated volatiles, while AMF symbioses substantially raise terpenoid and secondary-metabolite pools (Tables 1–3). Second, the magnitude and direction of change are strongly conditional on partner identity, host genotype and plant organ, so no single quantitative effect size generalises across systems. Third, community-level structure introduces non-intuitive dynamics—most notably the inverse relationship between microbial diversity and total soil VOC flux (Table 4)—that cannot be predicted from single-strain studies. These patterns collectively support treating VOC emission as a holobiont trait and set up the multi-trophic consequences catalogued in Table 5.

The quantitative entries also reveal the difference in effect size between mechanisms. AMF symbioses in Table 3 report changes on the order of tens of percent—an 85% enhancement of leaf VOCs in grapevine and a pooled 53% increase in terpenoids—because they operate by durably remodelling the plant's biosynthetic capacity through nutrient acquisition and transcriptional reprogramming of isoprenoid pathways. Bacterial ISR effects in Table 2 are often more qualitative than quantitative, expressed as new elicitor volatiles or as primed inducibility rather than a fixed percentage change, which is why they resist tabulation as single magnitudes. This mechanistic contrast is ecologically meaningful: mycorrhizal effects tend to shift the baseline chemical phenotype of the plant, whereas rhizobacterial effects more often tune its responsiveness to future attack. Both alter what herbivores, natural enemies and neighbouring organisms encounter, but they do so on different timescales and through different physiological routes.

4.2 Synthesis Across Microbial Agents and Ecological Levels

Arranging the evidence along the two axes of the analytical framework—microbial agent and ecological level—clarifies where knowledge is dense and where it is thin. The bacterial–plant and AMF–plant cells of this matrix are well populated, as is the plant–herbivore level of impact. In contrast, the direct microbe–microbe consequences of altered volatile flux, the atmospheric integration of biogenic emissions from managed microbiomes, and the community-level (as opposed to single-strain) effects on foliar emission remain comparatively underexplored. The synthesised data therefore describe a field with a robust mechanistic core—ISR-driven bacterial priming and AMF-driven metabolic enhancement—surrounded by an expanding but less settled frontier concerning whole-community and cross-ecosystem

consequences. This distribution of evidence directly shapes the recommendations that follow in the conclusion.

5. Conclusion

This synthesis of 2018–2024 secondary data supports a clear central conclusion: plant-associated microorganisms are pervasive and consequential modulators of plant VOC emission, and the plant volatilome is most accurately understood as a jointly encoded holobiont trait. Rhizobacteria reprogram emission chiefly through induced systemic resistance, adding and amplifying defence-associated volatiles via jasmonic-acid, salicylic-acid and ethylene signalling, and in several cases contributing their own elicitor volatiles. Arbuscular mycorrhizal fungi produce some of the largest quantitative effects on record, elevating leaf VOC pools and terpenoid content substantially, though in a strongly species- and organ-specific manner. At the community scale, soil microbial diversity governs both the quantity and richness of volatile flux, sometimes counter-intuitively.

Ecologically, these microbially reprogrammed blends reverberate across trophic levels—suppressing herbivores, recruiting their natural enemies, antagonising pathogens, priming neighbouring plants and feeding into atmospheric chemistry. This positions microbial modulation of plant volatiles as a lever for sustainable agriculture: microbial inoculants and consortia offer an environmentally benign route to strengthen plant defence and biological control without synthetic pesticides. Realising that potential, however, requires managing the contingency of the responses documented here, since host genotype and environmental context can reverse or nullify a given effect.

Several limitations temper the conclusions. Methodological heterogeneity constrains quantitative comparison; the literature is biased toward cultivable, beneficial and well-studied taxa; and the relative contribution of microbially reprogrammed host emission versus directly emitted mVOCs is rarely disentangled. Future work should prioritise field-scale and multi-factor experiments, standardised volatile sampling, and mechanistic partitioning of host- and microbe-derived volatiles, ideally coupling volatilomics with community sequencing. Advancing on these fronts would convert a compelling but fragmented body of evidence into a predictive framework linking the rhizosphere microbiome to plant chemical ecology and, ultimately, to ecosystem and atmospheric processes.

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