



Biogenic Volatile Isoprenoid Emission and Levels of Natural Selection

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Abstract | Biogenic volatile isoprenoid emission as a biological process has many worthwhile yet unanswered questions of fundamental scientific and ecological merit. Foremost among them is to understand and quantify the long-term feedback effects of volatile emission on climate and climate-driven macro-evolutionary changes. Moreover, we are now at a stage where our understanding of biogenic isoprenoid emission at the molecular and ecophysiological levels holds the key to the doors of next generation breakthroughs in isoprenoid-dependent applications in synthetic chemistry, human bio-therapeutics and agro-food industries. Like any other living trait/process, biogenic volatile isoprenoid emission has several levels of complex organization. We summarise biophysical, chemical and ecological functions of biogenic volatile isoprenoid emission highlighting aspects of evolution at different levels of natural selection.

Keywords: ecological fitness, evolution, isoprene, isoprenoid biosynthesis, natural selection, photosynthesis, volatile organic compounds

1 Introduction

Constitutive volatile isoprenoid emission by phototrophic living organisms is a process whose biological costs are not trivial while evidence of the (possibly multiple) benefits are still circumstantial, or purely elusive. More than 1000 Tg carbon per year is emitted in the form of volatile isoprenoids, mainly isoprene (C₅H₈) and monoterpenes (C₁₀H₁₆), mainly by terrestrial plants¹ and, as far as we currently know in much lower amount (~10 TgC/yr) by marine phytoplankton.^{2,3} To put this in perspective, this is comparable to the carbon loss caused by global deforestation⁴ (~1200 TgC/yr). The emitted isoprenoids have a prolonged post-emission impact on the climate, especially through oxidation chemistry of ozone in the troposphere, and formation of secondary organic aerosol and precipitation.⁵⁻⁷

Isoprenoids (also called terpenoids) are a large class of versatile macromolecules with great structural diversity despite being all constructed by catenation of five carbon (C5) monomers that are derivatives of isopentenyl pyrophosphate (IPP) and dimethylallyl pyrophosphate (DMAPP). Volatile isoprenoids are small terpenoids whose

conjugated double bounds (dienes) readily react with any atom/molecule with unpaired valence electrons. These are made by one (isoprene), two (monoterpenes) or three (sesquiterpenes) C5 units. Drawing from recent research developments, in this review we examine the phenomenon of biogenic volatile isoprenoid emission from an evolutionary standpoint, at different levels of organization spanning a single living prokaryotic cell to populations of forest trees (Fig. 1, Box 1).

2 A Flexible Structure to Function Relation Among Isoprenoids has Accommodated Long Periods of Neutral Drift in Molecular Evolution

The diversity in isoprenoid emission capacity is a product of interactions between many genes, enzymes and metabolites both within and across interacting pathways. The enzymes involved in isoprenoid biosynthesis belong to a family of closely related terpene synthases (TPSs).⁸ Since there is no significant homology between plant TPS sequences and the known bacterial genomic equivalents, it is inferred that bacterial and plant TPSs do not share a common ancestry⁹ although

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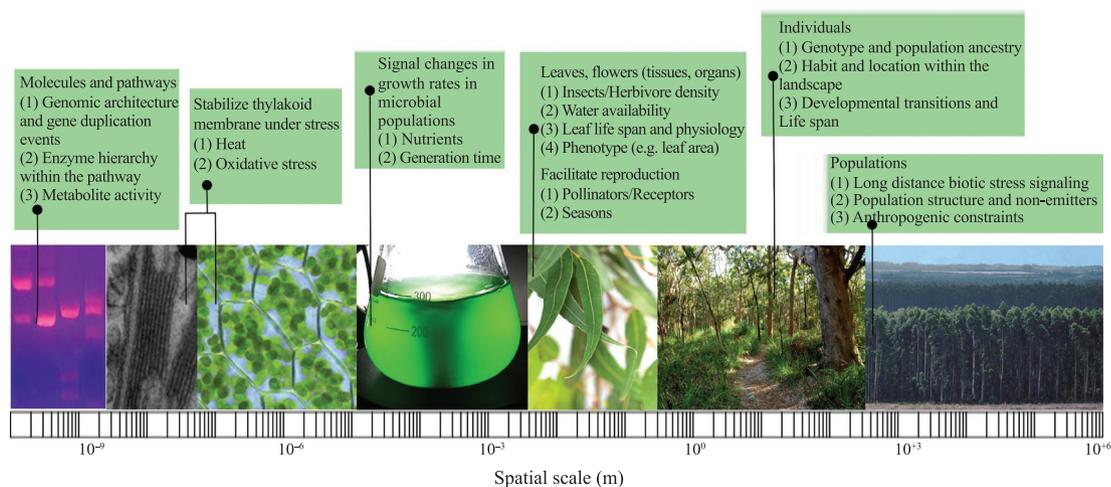


Figure 1: Function of volatile isoprenoids (isoprene and monoterpenes) and means of natural selection.

Box 1 Levels of Natural Selection and the Isoprenoid Emission Trait

Underneath any biological phenomenon, there lies a hierarchy of organization and levels of natural selection that shape and reshape its evolution at different levels from molecules to tissues and from organisms to populations/ecosystems. The debates about the actual unit of natural selection, from the unit being a single gene to a group of organisms, have continued to generate fascinating evolutionary enquiries and polarised disagreements.^{96–98} If there is one thing that is becoming clear then it is the modular nature of the unit of selection. By modularity we mean either a hierarchical or egalitarian network of interacting elements.^{99,100} A module could be a group of genes (elements) co-expressed/co-regulated by similar environmental stimuli. A module could also be a higher order organization that defines tissues and/or organisms. As life organizes itself into intricate interactions, it is of great benefit to strip any trait/behaviour/process of interest into its fundamental components and dissect discrete facets of natural selection at each level of modular organization.

Level 1: Genes (and enzymes) are seen as the site of natural selection in continuous action since genes are the simplest self-replicating and perpetual entities unlike their carrier organisms which undergo life and death^{101,102} (see section 2, Tables 1 and 2).

Level 2: The cell provides a physical framework that facilitates self-correction and selective regulation of a large self-replicating and error-prone chemical regulatory system. Natural selection finds its way through a complex set of cell organelles that share space and resources. The cell membrane concentrates the medium of life within a cell and allows biochemical reactions that are 10 times faster than those in cell-free systems¹⁰³ (see sections 3 and 4).

Level 3: Phenotypic characters such as phyllotaxis, leaf shape and area, canopy architecture, etc., are all products of life history evolution and ‘canalization’, a process in which phenotypes are locked by genotypes and become potentially insensitive to environmental stimuli.¹⁰⁴ Deviation from such set norms constitutes phenotypic plasticity, which is a raw material for natural selection (with or without heritability) especially in long-lived plants^{105,106} (see section 5).

Level 4: When phenotypic variation within a population, with regard to a specific trait or a group of traits, is heritable and its occurrence follows the spatial genetic structure of the population, then such traits of one individual will have differential fitness effects on neighbouring individuals¹⁰⁷ (see section 6).

some enzymes are proposed to be monophyletic at least within major plant clades.^{8,10} Deduced amino acid sequences of large TPS gene families in some gymnosperms and comparative analyses of angiosperm TPSs suggest that modern TPSs

could have evolved from an ancestral diterpene synthase in a eukaryotic ancestor of higher plants, much before specialization of TPS functions and **divergence** of angiosperms and gymnosperms could take place.^{11,12}

Divergence: acquisition of dissimilar characters or traits by related organisms.

Despite an apparently simple chemical structure, a very large number of volatile isoprenoids are present in nature. The idea of “molecular parsimony” suggests that large populations of chemical metabolites (e.g. >60000 terpenoids) with minor differences are synthesized by a relatively small group of enzymes (per organism) because (a) the probability of hitting a chemical conformation of significant potency is always small,¹³ (b) the cost of gene transcription and RNA translation could influence organismal fitness,¹⁴ and (c) promiscuity is the norm in enzyme evolution irrespective of enzyme–substrate specificity.¹⁵ TPSs are known to be promiscuous in that they can act on different versions of related substrates and thus may have been the main contributors to the vast diversity of isoprenoids.¹⁶ Moreover, significant single nucleotide polymorphisms (SNPs) in genes encoding for TPSs are associated with the qualitative and quantitative variation in isoprenoid emission profiles.¹⁷

Minor changes in chemical structures involved in physical/structural function (e.g. membrane lipids, accessory pigments) do not necessarily compromise their functions, and thus are rarely constrained by stringent natural selection.¹⁸ As a result, the same metabolite (e.g. ascorbate¹⁹), with or without minor changes, could acquire novel biochemical functions under different circumstances across divergent clades. The idea of ‘superior biomolecular activity’²⁰ is proposed to explain structural conservatism and functional divergence in chemical molecules. Often, natural selection promotes ‘a chemical blend’ (of various stored aromatics and monoterpenes) rather than a specific structural configuration of a single volatile isoprenoid and such chemical mixtures are more potent than a single molecule in terms of ‘biomolecular activity’.²¹ In this way certain monoterpene blends increase beneficial biological interactions and in some cases are stringently selected to suit interactants in co-evolved biological systems involving flower–pollinator, host–pathogen and plant–herbivore interactions²² (also see section 5).

3 Modes, Mechanisms and Energy Budget of Carbon Reduction Could be the Major Factors Determining Emission Potential of Isoprenoids

Independent prokaryotic origins of plant cell organelles have resulted in multiple biosynthetic pathways with duplicated functions (*sensu lato*) taking place simultaneously within different organelles.^{23,24} Plant isoprenoid biosynthesis occurs through one of the two spatially separated pathways

within a plant cell (Fig. 2). The cyanobacterial pathway takes place in the plastid, and is also referred to as the methyl erythritol phosphate (MEP) pathway; while the archaeal pathway, operating in the cytoplasm, is also referred to as the MVA (mevalonic acid) pathway.^{25–27} The MVA pathway proceeds further into multiple terminal pathways including steroid and hormone biosynthesis. The MEP pathway proceeds further to synthesise stable and structural terpenoids such as carotenoids.

Several models have been proposed to explain the evolutionary events that caused the divergence of archaea and bacteria; however, there is no consensus.²⁸ Sequence similarity and pathway reconstruction analyses show that at least three separate horizontal ‘whole pathway’ transfer events between bacteria and archaea could have taken place²⁹ but the nature of either the original eukaryotic ancestor or the origin of isoprenoid-dependent membrane architecture remains unexplained.³⁰ Both MEP and MVA pathways are almost mutually exclusive among prokaryotes with the exception of *Streptomyces* species, which possess both pathways and it is hypothesized that maintaining both pathways could be beneficial for the bacterium since it allows selective use of resources and specialized functions.^{31,32} It is not clear which pathway appeared first.

Mutual exclusivity of the two pathways also holds among some eukaryotes such as fungi and animals that possess only the MVA pathway.³³ But, the simultaneous occurrence of the two pathways in plants, despite organellar (spatial) separation, creates a complex scenario for natural selection to act on the functionality of this system.²⁴ In fact, (a) all the genomic controls on both the pathways are in the nucleus (the MEP pathway enzymes are nuclear encoded and plastid targeted), and (b) the substrate level cross talk between the two pathways takes place through a selective chloroplast membrane interface through selective transport of IPP from plastid to cytosol.³⁴ The transport of glyceraldehyde-3-phosphate (GAP) from plastid to cytosol, and of phospho-enol-pyruvate (PEP) from cytosol to plastid, suggests ‘an umbilical link’ between the two pathways, as first postulated³⁵ and later confirmed through labelling experiments.³⁶ It was demonstrated that the genetic blocking of either the MVA pathway or the MEP pathway in null mutants, or the complete inhibition of single pathway enzymes in wild-type plants treated with specific inhibitors resulted in a developmental block and a seedling-lethal phenotype. This indicates that the loss of one of the two pathways cannot be compensated by the remaining pathway.³⁷

Parsimony: the minimum number of evolutionary changes to infer phylogenetic relationships between closely related taxa. Parsimony also implies that the simplest hypothesis (among many alternatives) that is sufficient to explain an observation is to be preferred and is most likely to be closest to the reality.

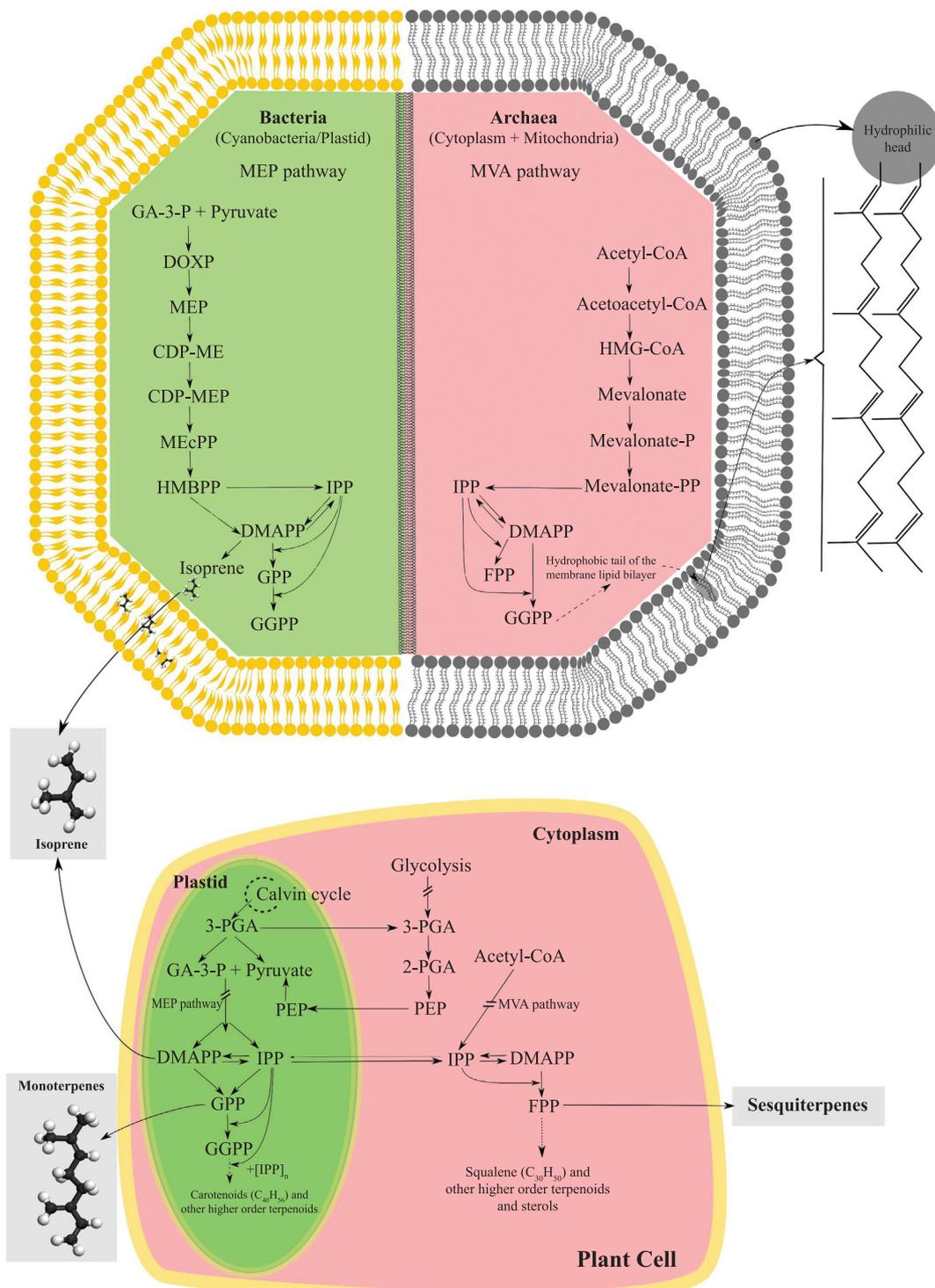


Figure 2: Isoprenoid biosynthetic pathways in bacteria and archaea (top) and in plants (bottom).

Although the MEP pathway contributes to volatile isoprenoid emission in eubacteria as well as in higher plants, surprisingly the MVA pathway outperforms the MEP pathway in *E. coli* engineered for large scale production of isoprenoids.³⁸ Metabolic flux through the MEP pathway

has several bottlenecks and involves allosteric feedback mechanisms.^{39,40} The MEP pathway gene expression is regulated by heat, light and circadian transcriptional factors,^{41,42} which appear to follow hierarchical and modular organization.⁴³ The difficulty of working with the MEP pathway is

due to our lack of understanding of the pathway's evolutionary history. Knowing the two pathways and the selection pressures acting on them (e.g. with reference to gene specific subtleties in codon usage, and oxidative stress sensitivity) will provide important leads in solving problems, especially for large scale microbial production of industrially relevant isoprenoids.

The reasons for differences in productivity and efficiency of these pathways in heterologous expression systems potentially lie in distinct and ancient evolutionary histories of bacteria and archaea, and their ways of acquiring and reducing carbon. While photosynthesis by photoautotrophs (starting with cyanobacteria) is the most influential biological phenomenon in the history of the Earth, it is neither the most ancient nor the most efficient way through which carbon could be reduced for storage and transport. Alternative

autotrophic carbon reduction pathways had evolved much before photosynthesis among early prokaryotes, mostly extremophiles.⁴³ Among those, the chemoautotrophic reduction of carbon to acetyl-CoA is a prominent process that supplies carbon to the MVA pathway in archaea and some bacteria. Comparison between energy demands of alternative autotrophic carbon reduction pathways among extant prokaryotes clearly shows large differences in costs per fixed carbon.^{43,44} The Rubisco-based aerobic CO₂ fixing system is the most expensive among all known autotrophic CO₂-fixing mechanisms. Correspondingly, photoautotrophs have a large energy and reducing power capacity that not only sustains expensive high turn-over of enzymes and their maintenance but also supports constitutive volatile isoprenoid emission via the MEP pathway which also involves several steps of chemical reduction.⁴⁵ It is known

Box 2 Codon Bias and Amino Acid Usage: Contrasting MEP and MVA Pathways in Angiosperms

Table 1: Comparing amino acid frequency in enzymes of two spatially separated isoprenoid biosynthetic pathways in plants.

Amino acid	Frequency of amino acid per 1000 residues/enzyme [†]		P value ($\alpha = 0.05$) t test
	MEP pathway (N = 7 enzymes)* mean \pm 1 SE	MVA pathway (N = 6 enzymes)** mean \pm 1 SE	
Ala	76 \pm 6.9	92 \pm 8.8	0.165
Cys	15 \pm 0.6	21 \pm 0.7	0.000
Asp	59 \pm 2.0	46 \pm 6.1	0.094
Glu	60 \pm 5.4	57 \pm 3.4	0.687
Phe	39 \pm 4.2	35 \pm 2.9	0.514
Gly	72 \pm 4.7	77 \pm 8.1	0.601
His	25 \pm 4.5	20 \pm 2.2	0.377
Ile	60 \pm 2.5	55 \pm 2.8	0.197
Lys	65 \pm 3.7	58 \pm 3.8	0.195
Leu	95 \pm 6.2	100 \pm 9.7	0.677
Met	20 \pm 2.9	26 \pm 2.3	0.159
Asn	35 \pm 3.7	42 \pm 2.0	0.143
Pro	55 \pm 5.0	43 \pm 2.9	0.059
Gln	31 \pm 3.1	33 \pm 2.0	0.691
Arg	46 \pm 4.0	40 \pm 3.1	0.296
Ser	85 \pm 11.0	88 \pm 3.6	0.821
Thr	51 \pm 2.2	50 \pm 3.0	0.811
Val	73 \pm 4.2	74 \pm 4.8	0.912
Trp	9 \pm 1.9	11 \pm 2.7	0.533
Tyr	26 \pm 2.7	26 \pm 6.4	0.949
TOTAL [†]	998	995	

*DXS, DXR, MCT, CMK, MDS, HDS, and HDR; **ACCT, HMGS, HMGR, MVK, PMVK, and PMVDC; [†]Total excludes stop codons (For enzyme names, see Table 2); ^{††}the enzymes responsible for reactions up to the formation of IPP/DMAPP.

Codon bias: the propensity to use a particular triplet codon to specify a particular amino acid.

Box 2 Continued

Codon bias towards optimal/common codons positively correlates with gene expression levels. Abundance of tRNAs influences translational efficiency.^{108–110} Codons coding for rare and structurally critical amino acids possess the least abundant tRNAs, viz. cysteine, tyrosine and tryptophan, which curiously also have the highest probability of mutating into stop codons given the way triplet codons have evolved. Mutations that replace less abundant and structurally important amino acids are always minimised and as a result premature terminal mutations are also minimised by natural selection. Codon usage frequency, calculated for each enzyme in both MVA and MEP pathway using a set of at least three representative sequences from angiosperms of which one sequence within each set was from *Arabidopsis thaliana*, showed no significant difference in overall codon frequency (relative to genome wide codon usage in *Arabidopsis*) between all the genes between and within both pathways with minor exceptions. However, the differences became significant when the pathways were divided into two sections with the top section resulting in IPP/DMAPP biosynthesis and the bottom section involving terpenoid synthases and prenyltransferases. The top section of the MVA pathway comprised significantly more cysteine than the MEP pathway (Table 1). Given adverse factors such as (a) limited availability of tRNA^{Cys}, which is among the least abundant tRNAs in plants¹¹¹ and (b) oxygen sensitivity of the thiol group that puts negative selection pressure on cysteines in cytosolic proteins,¹¹² cysteine richness of MVA pathway enzymes in plants must have ancient phylogenetic constraints. Cysteine richness in the MVA pathway enzymes is perhaps consistent with the pathway's archaeal evolutionary ancestry given that enzymes in thermophilic archaea were rich in disulfide bonds and were selected to remain stable under extreme temperatures.¹¹³ It is also not a coincidence that energetically less expensive (relative to the Calvin cycle) chemoautotrophic CO₂ fixing mechanisms are restricted to anaerobic habitats (e.g. sulphur bacteria and methanogenic archaea; also see section 3), where cysteine richness in MVA pathway was not under negative selection.

Table 2: Genes and enzymes of the MEP and MVA isoprenoid biosynthetic pathways in plants.

Gene	Corresponding enzyme of the MEP pathway	Gene	Corresponding enzyme of the MVA pathway
Top section of the two pathways (reactions leading to the formation of IPP/DMAPP)			
<i>DXS</i>	1-deoxy-D-xylulose 5-phosphate synthase	<i>ACCT</i>	Acetyl-CoA C-acetyltransferase
<i>DXR</i>	1-deoxy-D-xylulose-5-phosphate reductoisomerase (aka: CM synthase)	<i>HMGS</i>	3-Hydroxy-3-methylglutaryl-CoA synthase
<i>MCT</i>	2-C-methyl-D-erythritol 4-phosphate cytidyl transferase	<i>HMGR</i>	3-Hydroxy-3-methylglutaryl-CoA reductase
<i>CMK</i>	4-diphosphocytidyl-2-C-methylerythritol kinase	<i>MVK</i>	Mevalonic acid kinase
<i>MDS</i>	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	<i>PMVK</i>	Phospho-MVA kinase
<i>HDS</i>	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase	<i>PMVDC</i>	Diphospho-MVA decarboxylase
<i>HDR</i>	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase		
Bottom section of the two pathways (reactions leading to the formation of isoprenoids)			
<i>IPI</i>	Isopentenyl diphosphate isomerase		
<i>ISPS</i>	Isoprene synthase	NA	NA
<i>GPS</i>	Geranyl pyrophosphate synthase		
<i>MTS</i>	Monoterpene synthase	NA	NA
<i>GPPS</i>	Geranyl geranyl pyrophosphate synthase		
<i>PS</i>	Phytoene synthase	NA	NA

that both isoprene and monoterpene biosynthesis through the MEP pathway principally utilises carbon fixed *de novo* during photosynthesis.^{46–48} The carbon cost of volatile biosynthesis in plants is around 2% of photosynthesis under stress-free conditions, and increases under abiotic stress, often exceeding 10% of fixed carbon⁴⁹ (both *de novo* and imported from cytosol) with a corresponding increase in energy costs.^{50–52}

Atmospheric CO₂ concentration is a key regulator of photosynthesis and it is also shown to influence volatile isoprenoid emission. Increasing CO₂ concentration increases photosynthesis and decreases isoprene emission, at least during short-term acclimation,^{53–54} but also in plants exposed to life-long high CO₂.⁵⁵ Many have argued a case for CO₂-driven emission changes through geological history.⁵⁶ The high cost on a plant's carbon budget due to emission especially during low CO₂ eras (glaciations), in turn likely constraining photosynthesis, may have exerted a significant negative selection pressure on emission capacity.¹⁰ The same logic does not apply to archaea and the MVA pathway, since none of the known autotrophic archaea employs the **Calvin cycle** to fix carbon. However, the fact that low CO₂ causes increased emission in plants at least over short-term acclimation contradicts the notion of negative selection on emission during glacial periods. The suggestion is confounded by the complex interactive effects of heat and CO₂ on emission, which do not fit any existing **mechanistic theories** of emission behaviour.⁵⁷ There is increasing experimental evidence in favour of a hypothesis proposed in the 1990s that availability of energy (ATPs) controls isoprene synthesis.⁵⁸ ATP and reducing power (NADPHs and equivalents) unused by carbon reduction may explain isoprenoid emission behaviour under varied CO₂ and drought scenarios.^{52,59–61} As put forth earlier, these findings further support the idea that the mechanisms and energy budget of carbon reduction could have been the primary factors through which **natural selection** determined isoprenoid emission capacity and behaviour in prokaryotes and later in plants (also see Box 2).

4 Isoprene Emission is Sensitive to Abiotic Stress Operating at the Level of a Single Cell and Population of Cells

Isoprene emission has distinct and testable physical functions at the level of cells (prokaryotes and unicellular eukaryotes) and multicellular tissues. Hypotheses concerning isoprene-mediated scavenging of free radicals^{62,63} along with possible

membrane stabilization under transient heat stress in higher plants⁶⁴ have strong empirical evidence, and now also some mechanistic understanding.^{65–67} In thermophilic archaea, isoprenoid-linked phospholipids form their cell membranes (Fig. 2), while in bacteria emitted isoprene could simply physically interact with bacterial membrane as proposed in eukaryotes. However, the function of spurts in isoprene emission at different growth phases among some bacteria is still unknown.⁹ The function of isoprene emission among marine phytoplankton such as dinoflagellates and diatoms is also unclear.

Natural selection influences the inter- and intra-specific variation in any heritable characteristic, and the extent of genetic differentiation in certain loci in the genome may reveal the nature of selection.⁶⁸ As mentioned earlier, isoprenoid synthases are promiscuous enzymes with flexible substrate affinities and often evolve through gene duplication events. The newly acquired functions of a duplicated enzyme are normally not efficient and it is hypothesized that hyper-transcription could overcome enzymatic inefficiencies in secondary metabolism.⁶⁹ A gene duplication event could often be followed by selectively neutral mutations in the duplicate gene; thus neofunctionalization is rare and gene redundancy is common.⁷⁰ Therefore, the random emergence of isoprene synthase only in certain limited number of plant phylogenetic clades with altered specificity/efficiency remains unexplained. Two alternative theories have been proposed. One of them posits that the occurrence of isoprene emission capacity in unrelated land plant lineages may be explained by specific environmental conditions that increase **fitness** of emitting species.⁷¹ In an experiment involving isoprene emitting and non-emitting (RNAi mutant) plants acclimated to glacial CO₂ levels (190 ppm), it was found that photosynthesis recovered faster in isoprene emitters than non-emitters after a heat or sun-fleck stress treatment⁷² suggesting that low CO₂ periods during the **Quaternary** could have positively selected for isoprene emission capacity resulting in high emitting plants. However, in most cases, the evolutionary advantage to the isoprene emitting genera is unclear because the trait is often randomly lost. Even if we assume that isoprene emission confers additional fitness to the emitting genus,⁷³ the fact that isoprene synthases have remained very inefficient ($K_m > 2$ mM) compared to other enzymes of the MEP pathway suggests weak selection.⁷⁴ To explain random disappearance and reappearance of isoprene emission in certain limited number of plant lineages we should

Calvin cycle: also known as the photosynthetic carbon reduction cycle. A cyclic pathway used for the fixation of carbon dioxide by photoautotrophic organisms.

Mechanistic theory and modelling: when natural processes are mechanistically determined and the laws of physics and chemistry are sufficient to explain biological phenomena. Mechanistic modelling involves deduction of mathematical relationships between (often) biological variables and it emphasizes the physical, chemical and biochemical principles that explain the observed relationship between variables.

Natural selection: the non-random and differential reproduction of different genotypes acting to preserve favourable variants and to eliminate less favourable variants.

Fitness: the relative competitive ability of a given genotype conferred by adaptive morphological, physiological and behavioural characters. Fitness is often quantified as the average number of surviving progeny of one genotype relative to that of competing genotypes.

Quaternary: period of geological time that covers approximately the last 1.8 million years. The Quaternary is noted for numerous major glacial-interglacial cycles (advancement and receding of polar ice sheets) characterized by significant shifts in global temperature and atmospheric CO₂ concentration.

also account for the roles played by fast growing physiology and long life span in isoprene emitting trees in accumulation of pre-meiotic mutations and tolerance for such mutations in the corresponding loci of their genome.⁷⁵

5 Monoterpenes and Other Aromatics are Under Stringent Selection in Co-Evolved Biological Systems

Plant behaviour, especially in annuals, does not evolve during the course of a plant's lifetime because plants do not have memory in the sense of experience storage within neuronal connections as in animals. Plants “rote-learn” through evolution by natural selection, a very slow process usually operating over many generations at the level of genes, genomes, epigenomes and possibly phenotypic plasticity (which may or may not be determined by genotypes). As a result, several traits may persist in plant populations long after they have lost adaptive relevance. While this might arguably be the case for isoprene emission in long-lived trees (but see⁶⁴), other volatile isoprenoids have well-defined roles in plant defence. For example, induced volatile isoprenoids could be employed effectively to prime intraplant antiherbivory responses.^{76–78} Many metabolites derived from the MVA pathway, primarily sesqui-, di-, and saponin tri-terpenoids, have potent antifungal, antimicrobial, and repellent properties or serve to attract predators or parasitoids.⁷⁹

Less volatile monoterpenes can be stored under most conditions and their induced emission has an important role in maintaining organismal fitness. Constitutive emission of monoterpenes has been shown to defend plant parts that are at high risk of intense herbivore attack, preventing the loss of those parts that might result in substantial fitness costs.²¹ The fact that foliar volatile storing is virtually absent in deciduous trees, which likely are vulnerable to insect attack, suggests a link between monoterpene emission and structural costs of plant parts (also see section 6).

Intraspecific volatile communication mostly involving aromatics and monoterpenes could increase population fitness by benefiting closely related individuals within a large population⁸⁰ (also see Box 1). There is evidence to suggest that interspecific signaling and recognition both in aquatic and terrestrial ecosystems involve volatile isoprenoids.^{81,82} However, high-cost resource mediated communication strategies involving tertiary trophic interactions (e.g. bodyguard insects such as parasitoid wasps or ants) appear to be under more stringent selection than low-cost constitutive or induced information transmission

between plant populations.⁸³ It remains to be seen whether untargeted, constitutive isoprenoid emission of a species is a function of ecosystem heterogeneity.⁸⁴

6 Reconciling Phenotypic, Genetic Diversity and the Sensitivity of Emission Responses in Individuals or Populations of Trees to Environmental Stimuli

Stringent developmental constraints on isoprenoid emission levels (see review⁸⁵) point towards natural selection acting on the whole plant phenotype. Leaf economics and leaf life span have a significant influence on isoprenoid emission profiles.^{53,61} Physical defense strategies involve niche-specific phenotypic adaptations and phenotype constrains chemical defence. For example storing of volatiles is determined by packing efficiency of monoterpene storage glands in leaves, which in turn depends on specific leaf area, distribution and thickness of palisade parenchyma. In addition, natural selection appears not to have favoured a trade-off between chemical and physical defences in most plants,⁸⁶ which could ultimately mean that isoprenoid emission may not show any relationship with the broad trends in plant phenotypic strategies. On the whole, reconciling phenomic variability with genetic diversity and accounting for their cumulative impact on isoprenoid emission profile has not been possible despite significant progress on both fronts. The contradictions between field trials that ignore genetic variation and species-specific controlled experiments that aim to minimize environmental variation have made the challenge more complicated than it ought to be.⁸⁷

The importance of knowing how natural selection is acting on emission behaviour of plant populations is exemplified by the challenges faced by models trying to forecast global isoprenoid emissions given the significant impact of emissions on regional climate and carbon cycles. Most isoprenoid emission models are parameterized based on leaf level isoprenoid emission measurements and there is a large uncertainty in emission variation within **plant functional types (PFTs)**.⁸⁸ There are many local emission discrepancies that are hard to explain,¹ and generalizations are not helped by the fact that emission capacity does not follow consistent phylogenetic patterns.^{72,75,89,90} Vegetation models assume presence or absence of a defined PFT, which ignores the significant impact of fine-scale genetic variations on ecosystem dynamics and their impact on spatial dimensions of emission

Rote-learning: learning or remembering by repetition rather than through developing an association between phenomena.

Plant functional type (PFT): a collection of plant species (vegetation) with similar suits of co-occurring functional traits that exhibit similar responses to external stimuli and have similar effects on ecosystem function. The equivalent of a PFT in the animal kingdom is a ‘guild’.

signature.⁹¹ Ignoring intra-population (fine-scale) variations might work in case of homogeneous clonal plantation emitters, some of which are indeed the most dominant isoprene emitting angiosperms.^{89,92} However, many monoterpene emitters in boreal forests (pines, firs, spruces and oaks) exhibit low domestication and live in large, open-pollinated, native populations. Genetic diversity, gene flow, population heterogeneity and structure (relationship between individuals belonging to a single species) is shown to affect VOC emission profiles⁹³ and such effects are likely magnified in species spread over large geographic areas.⁹⁴ Reassessment of recent literature on plant emission response to changing climate has led to the suggestion that carbon input in the form of isoprenoids into the climate system will increase in future.⁵⁸ Anthropogenic pressure to select suitable agricultural traits might also have contributed to diversify emission in cultivated plants, as found in cork oaks over their cultivation range.⁹⁴

7 Going Forward

Simple chemical derivation (reduction), highly reactive hydrocarbon chemistry, a wide range of ecological benefits, and an unlimited scope for diverse structural configurations have contributed to repeated emergence and functional diversification of biogenic volatile isoprenoid emission in evolutionarily distant and unrelated living systems. It is helpful to remind ourselves that each step during the development of a living organism in some ways represents a cusp of one of the major transitions in the evolution of living complexity.⁹⁵ We are still aiming at discovering metabolic and biophysical aspects of isoprenoid emissions in eubacteria and protists (diatoms and dinoflagellates), and such information is likely needed to further decode the complexity of volatile emissions in higher plants. With every new finding about some aspect of metabolic regulation of isoprenoid emission, it is becoming clearer that emission from living organisms provides a template to investigate other complex biological phenomena with often unclear function and uncertain origins. At the other end of the spatial scale, the consequences of land-use (vegetation) changes and increased temperatures due to unprecedented anthropogenic interference will not only have an impact on air quality and human lifestyle in a rapidly urbanising world, but is also likely to change the isoprenoid emission profiles of emitting and non-emitting living systems.

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