

FRAGRANCE ENGINEERING IN FLOWERS: MOLECULAR MECHANISMS, TOOLS & FUTURE PROSPECTS

Rayapu Sai Theja*

Department of Floriculture and Landscaping, College of Horticulture and Forestry, Rani Lakshmi Bai
Central Agricultural University, Jhansi, Uttar Pradesh, India

*Corresponding author email: rayapusais.s@gmail.com

ABSTRACT



Floral fragrance engineering integrates plant molecular biology, genetics, and biotechnology to understand and improve scent in ornamental crops. Floral volatile organic compounds (VOCs), chiefly terpenoids, phenylpropanoids/benzenoids, and fatty-acid derivatives, mediate pollinator attraction, defence, and ecological interactions. Commercial breeding has often prioritized colour, flower size, and vase life, contributing to reduced fragrance in some cultivars. This review summarizes major scent pathways, genes, analytical tools, and improvement strategies, including conventional breeding, genetic engineering, metabolic engineering, and CRISPR-based editing. Recent crop studies illustrate opportunities and ecological considerations for developing fragrant, commercially valuable flowers.

KEYWORDS: Floral fragrance, Volatile organic compounds, Terpenoids, Phenylpropanoids, Genetic engineering, CRISPR-Cas9

INTRODUCTION

Floral fragrance is an important quality trait in ornamental crops, including rose, jasmine, tuberose, carnation, chrysanthemum, petunia and orchid. It contributes to consumer preference, commercial value, essential-oil production and the perfume and cosmetic industries. Ecologically, floral scent attracts pollinators, influences plant–insect interactions and may contribute to reproductive isolation and plant defence (Dudareva et al., 2004).

Fragrance engineering involves improving or modifying floral scent through conventional breeding, molecular genetics and biotechnology. Modern breeding has frequently prioritized flower colour, size and vase life, sometimes at the expense of fragrance. Because floral scent is controlled by complex biosynthetic and regulatory networks, molecular approaches offer opportunities to restore fragrance, enhance desirable compounds and develop novel scent profiles.

MAJOR FLORAL VOLATILE COMPOUNDS AND THEIR FUNCTIONS

Floral fragrance consists of volatile organic compounds (VOCs), generally low-molecular-weight substances that evaporate readily and produce characteristic aromas. These compounds are classified into three principal groups.

1. **Terpenoids:** Terpenoids are derived from five-carbon isoprene units and constitute one of the largest groups of floral volatiles. Important examples include linalool, geraniol, nerol, ocimene and farnesene. They contribute to the characteristic aromas of rose, jasmine, lavender and chrysanthemum. Their emission can attract pollinators and influence interactions between flowers and insects.
2. **Phenylpropanoids and benzenoids:** These compounds are primarily associated with phenylalanine-derived biosynthetic pathways. Examples include eugenol, methyl benzoate, benzyl alcohol and phenethyl alcohol. They contribute to the fragrance of carnation, petunia, snapdragon, orchid and rose. Their production depends on biosynthetic enzymes and regulatory genes controlling precursor conversion and volatile emission.
3. **Fatty-acid derivatives:** Fatty-acid-derived volatiles include aldehydes, alcohols and related compounds that often produce fresh, green or fruity notes. Hexanal and hexanol are representative examples. These compounds may also participate in plant defence and signalling.

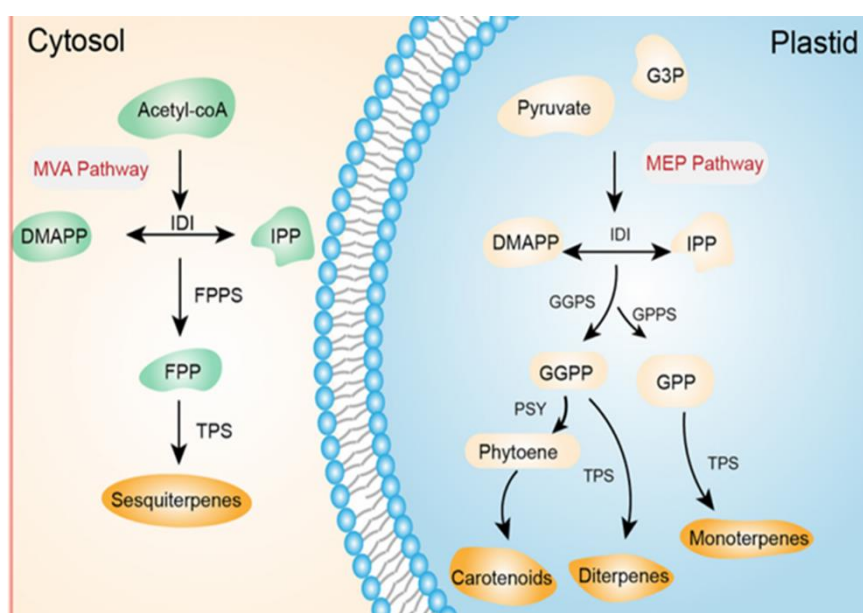


Figure 1. A simplified schematic of terpenoid, biosynthetic pathways with their principal precursors and representative scent compounds

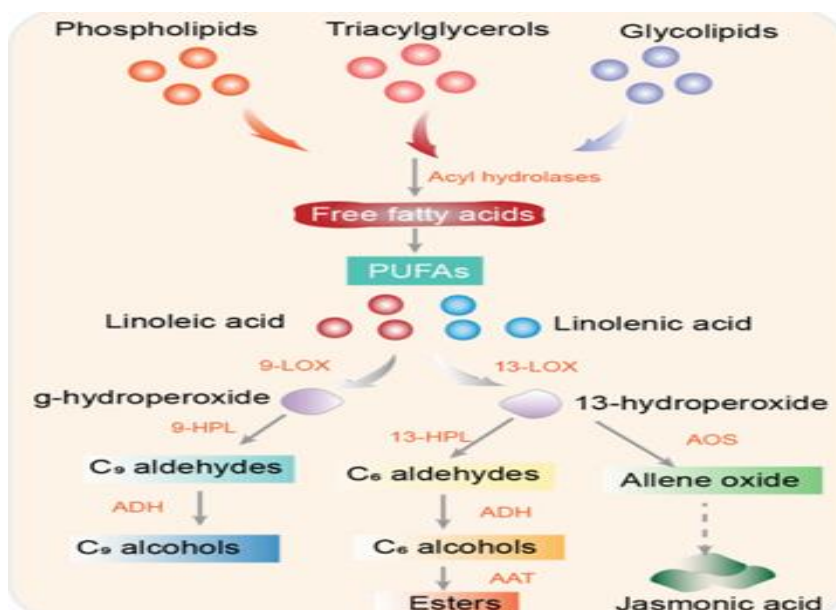


Figure 2. A simplified schematic of the terpenoid phenylpropanoid biosynthetic pathways—with their principal precursors and representative scent compounds

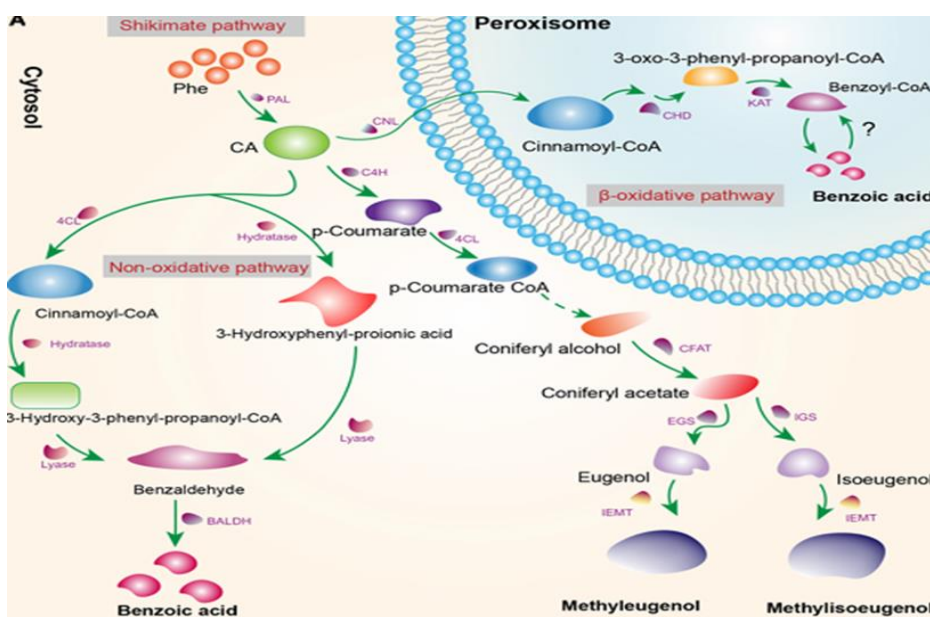


Figure 3. A simplified schematic of the fatty-acid-derived biosynthetic pathways with their principal precursors and representative scent compounds

Floral scent composition varies with species, cultivar, flower-development stage, environmental conditions and time of day. For example, jasmine fragrance includes compounds such as linalool, benzyl acetate, benzyl alcohol and methyl anthranilate, while rose fragrance commonly contains geraniol, citronellol and phenethyl alcohol.

MOLECULAR MECHANISMS AND GENES REGULATING FRAGRANCE

Floral fragrance production involves biosynthetic enzymes, precursor availability, transcription factors and environmental signals. Terpene synthases (TPS) catalyse the formation of several terpenoid compounds, while phenylalanine ammonia-lyase (PAL) contributes to phenylpropanoid metabolism. Other enzymes, including methyltransferases and acyltransferases, help generate specific aromatic compounds.

In petunia, the transcription factor ODORANT1 (ODO1) regulates genes associated with benzenoid production. In rose, fragrance-related genes contribute to the biosynthesis and modification of compounds such as geraniol and citronellol. In orchids, terpene synthase activity is associated with scent production and emission.

Regulation may also depend on developmental and environmental signals. Yeh et al. (2022) demonstrated that CIRCADIAN CLOCK ASSOCIATED 1 (CCA1) regulates terpene synthase expression and daily fragrance emission in *Oncidium* hybrid orchids. This finding highlights the importance of biological rhythms when selecting sampling times and evaluating scent-related traits.

TECHNIQUES FOR FRAGRANCE IMPROVEMENT

1. **Conventional breeding:** Selection, hybridization, backcrossing and recurrent selection can improve fragrance by exploiting existing genetic variation. For example, fragrant wild roses may be crossed with commercial cultivars to restore scent while retaining desirable ornamental characteristics. Similarly, hybridization can combine fragrance with flower colour, form and vase life. However, fragrance is often quantitatively inherited and influenced by multiple genes. Conventional breeding may therefore require several generations and may not produce specific fragrance profiles predictably.
2. **Genetic engineering and genome editing:** Genetic engineering enables targeted modification of fragrance-related genes. Overexpression of biosynthetic genes can increase the production of desired compounds, whereas gene silencing can alter pathways responsible for particular odours. Such modifications must be evaluated for their effects on the overall scent profile and other plant traits. CRISPR-Cas9 offers a more targeted approach to modifying DNA sequences associated with fragrance production. Potential applications include altering negative regulators, modifying biosynthetic enzymes and adjusting the balance of volatile compounds. However, successful improvement depends on understanding gene function, pathway interactions and possible unintended effects.

3. **Metabolic engineering:** Metabolic engineering modifies biochemical pathways to increase the availability of desired fragrance compounds. Strategies include enhancing precursor supply, increasing the expression of key biosynthetic enzymes and reducing competing metabolic routes. For example, changes in terpene synthase activity may influence monoterpene production, while modifications to phenylpropanoid metabolism may alter benzenoid accumulation.

These strategies require careful balancing because a change that increases one volatile may reduce another or affect plant growth and development.

ANALYTICAL AND MOLECULAR TOOLS

Gas chromatography–mass spectrometry (GC–MS) is a central technique for identifying and quantifying floral VOCs. It supports fragrance profiling, cultivar comparison, essential-oil characterization and investigation of changes during flower development, storage and environmental stress. Transcriptomics, particularly RNA sequencing, identifies genes whose expression changes during scent production. Proteomics helps characterize enzymes involved in volatile biosynthesis, while metabolomics measures the chemical compounds accumulating in flowers. Integrating these datasets helps connect gene expression, enzyme activity and fragrance composition. Combining GC–MS with transcriptomic and metabolomic analyses can identify candidate genes and pathways for subsequent functional validation. Quantitative reverse-transcription PCR (qRT-PCR), gene-silencing experiments and overexpression studies can further test the roles of selected genes.

RECENT RESEARCH HIGHLIGHTS

- a. **Carnation:** An integrated transcriptomic and metabolomic investigation of carnation reported that eugenol, β -caryophyllene and cis-3-hexenyl benzoate were important scent constituents, with emissions varying across flower-development stages. Genes associated with phenylpropanoid and terpenoid biosynthesis showed relationships with volatile accumulation. Such findings support the identification of candidate genes for improving carnation fragrance.
- b. **Chrysanthemum:** Wang et al. (2025) investigated the regulation of (E)- β -farnesene biosynthesis in chrysanthemum. Their study identified a regulatory module involving salicylic acid signalling, CmNPR3 and CmWRKY1 that influences the expression of the biosynthetic gene CmE β FS. The findings demonstrate how signalling pathways and transcriptional regulation can affect floral scent production.

- c. ***Oncidium orchid***: Yeh et al. (2022) showed that CCA1 contributes to the daily rhythm of terpene synthase expression and floral scent emission. This research indicates that fragrance improvement should consider not only the amount and composition of VOCs but also when flowers release them.
- d. ***Rhododendron fortune***: Qin et al. (2024) used transcriptomic and metabolomic approaches to investigate genes associated with fragrance-related metabolism in *Rhododendron fortunei*. Their findings highlighted candidate genes involved in aromatic-compound biosynthesis and demonstrated the value of integrated molecular analysis for identifying targets for further research.

CHALLENGES AND FUTURE PROSPECTS

Fragrance engineering faces several challenges. Floral scent is genetically complex, and the functions of many transcription factors, transporters and regulatory elements remain incompletely characterized. Advanced analytical equipment, molecular facilities and skilled personnel may also increase research costs. Ecological safety is equally important. Altering floral scent could change pollinator attraction or other plant–insect interactions. Genetically modified flowers may also raise questions concerning consumer acceptance, regulation and environmental release. Rigorous ecological assessment and transparent communication should accompany the development of engineered cultivars.

Future research should focus on restoring fragrance in modern commercial varieties, developing customized scent profiles and improving fragrance stability under heat, drought and other environmental stresses. Integrating multi-omics, functional genomics and computational modelling may accelerate candidate-gene discovery and improve the precision of fragrance engineering. Sustainable production of valuable floral volatiles could also benefit the floriculture, perfume and cosmetic industries.

CONCLUSION

Fragrance engineering provides opportunities to improve the aesthetic, ecological and commercial value of ornamental flowers. Understanding VOC biosynthesis and its genetic regulation, together with GC–MS, transcriptomics, proteomics and metabolomics, can support the identification of important scent-related genes. Conventional breeding, genetic engineering and genome editing offer complementary approaches to enhancing or restoring fragrance. Future progress will depend on reliable functional validation, balanced improvement of fragrance and flower quality, and careful evaluation of ecological effects.

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