

MICROBIAL REGULATION OF FLORAL SECONDARY METABOLISM IN ORNAMENTAL PLANTS: MOLECULAR MECHANISMS UNDERLYING FLOWER COLOR, FRAGRANCE AND QUALITY

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ABSTRACT

Flower-associated microorganisms have been receiving growing scientific interest in recent years as important constituents of the floral ecosystem. However, possible participation of microorganisms in the specialized metabolism of ornamentals still requires more investigation. Various microbial populations living in nectar, petals, reproductive organs, and other parts of the flower may interact with the hosts by means of microbial metabolites, volatile organic compounds, elicitors, nutrient-dependent effects, and signaling. The interactions might affect the synthesis, accumulation, and composition of floral secondary metabolites connected with traits of flower color, fragrance, and nectar chemical characteristics, among others. The present review considers the current knowledge about the molecular mechanisms of floral specialized metabolism and possible interactions of floral microorganisms with the hosts affecting flower metabolic processes. Special attention is paid to the microbial signaling, calcium and reactive oxygen species signaling, mitogen-activated protein kinase pathways, phytohormone response, transcriptional regulation, and metabolic pathways involved in floral pigmentation and fragrance. Information from ornamental plants, such as chrysanthemum, poinsettia, *Hibiscus mutabilis*, and *Osmanthus fragrans*, is provided. Recent development in various omics technologies, including microbial community profiling together with host transcriptomics, metabolomics, and volatilomics, allows the identification of microbial functions and host pathways responsible for variations in flower metabolic processes. Direct causal links between specific microorganisms or their microbial signaling molecules and host floral biosynthetic genes have not yet been established. Future research will need to include microbial inoculation, multi-omics analysis at the tissue level, synthetic microbial communities, and validation in order to differentiate between microbial synthesis or transformation of floral metabolites and the true modulation of host metabolic pathways.

KEYWORDS: Ornamental plants; Plant–microbe interactions; Secondary metabolism; Floral color; Floral fragrance; Floral microbiome

1. INTRODUCTION

Flowers are highly complex biological systems with multiple components such as colors, odors, nectar quality, and others, whose presence plays an important role in the reproduction process, ecology, and ornamental characteristics of plants. The majority of these factors are associated with the biosynthesis, modification, transport, and accumulation of various metabolites like anthocyanins, other flavonoids, terpenoids, phenylpropanoids, and volatile compounds. The biosynthesis of these metabolites takes place through a series of connected metabolic pathways that are regulated by certain developmental and environmental stimuli (Zhao and Tao, 2015; Mostafa et al., 2022; Pichersky, 2023).

In addition to their own regulatory processes, flowers contain various communities of microorganisms that include bacteria, yeasts, filamentous fungi, and endophytic microorganisms. Microorganisms occupy various niches within flowers, such as nectar, stigmas, petals, pollen, and reproductive organs of flowers and may communicate with the host through chemicals. This highlights the possible participation of microorganisms in the specialized metabolism of ornamentals and shows that microorganisms are another biological component of the floral environment (Rebolledo-Gómez et al., 2019; Vannette, 2020).

Plant–microbe interactions may affect plant metabolism through metabolites and elicitors of microorganisms, nutrient availability changes, phytohormone signaling, Ca²⁺ and reactive oxygen species (ROS) signaling, mitogen-activated protein kinase cascades, and transcriptional regulation. These mechanisms have been studied

extensively in the context of plant defense and general specialized metabolism, thus forming the molecular background for microbial impact on floral metabolism (Zhao et al., 2005; Yuan et al., 2017; Lv et al., 2024). However, the role of these mechanisms in floral tissues and regulation of metabolites involved in ornamental features is still poorly understood.

Evidence from floral systems suggests that microorganisms can impact nectar composition and volatiles and the chemistry of the floral environment (Canto and Herrera, 2012; Vannette and Fukami, 2016; Helletsgruber et al., 2017; Rering et al., 2018). Within ornamental plants, microbial interventions have been linked with changes in pigment development and accumulation of selected flower-associated metabolites such as anthocyanins, flavonoids, and phenols (Zulueta-Rodriguez et al., 2014; Bharti et al., 2021; Sun et al., 2023). However, these findings do not imply that microorganisms regulate the biosynthesis of their hosts' floral chemicals directly. It is thus important to distinguish between microbial synthesis or transformation of chemicals, indirect impacts through plant nutrition and physiology, and actual changes in host gene expression.

Current progress in omics technologies such as transcriptomics and metabolomics creates possibilities for molecular-scale investigations of these processes. Integration of microbial communities with host gene expression and metabolic signatures can help to detect associations between microbial communities, signaling pathways, biosynthetic pathways, and floral characteristics (Mishra et al., 2022; Jain et al., 2024). Recent studies that combine floral microbes and multi-omics analysis further highlight the potential of this approach to investigate dynamic flower color changes and other floral traits (Tang et al., 2026).

Although considerable progress has been made in this area, the molecular basis linking floral-associated microbes and the specialized metabolism of the host is still poorly understood, especially in ornamental plants. With this in mind, this review highlights the possible involvement of microorganisms in the control of secondary metabolism in flowers, focusing on the molecular aspects involved in floral color and fragrance, among other traits. This review also evaluates the information available regarding ornamental plants, differentiates between microbial effects and proposed mechanisms, and considers the possibility of linking the three using an integrated approach.

A conceptual framework illustrating the potential interactions between floral microorganisms, host signaling, specialized metabolism, and floral traits is presented in Figure 1.

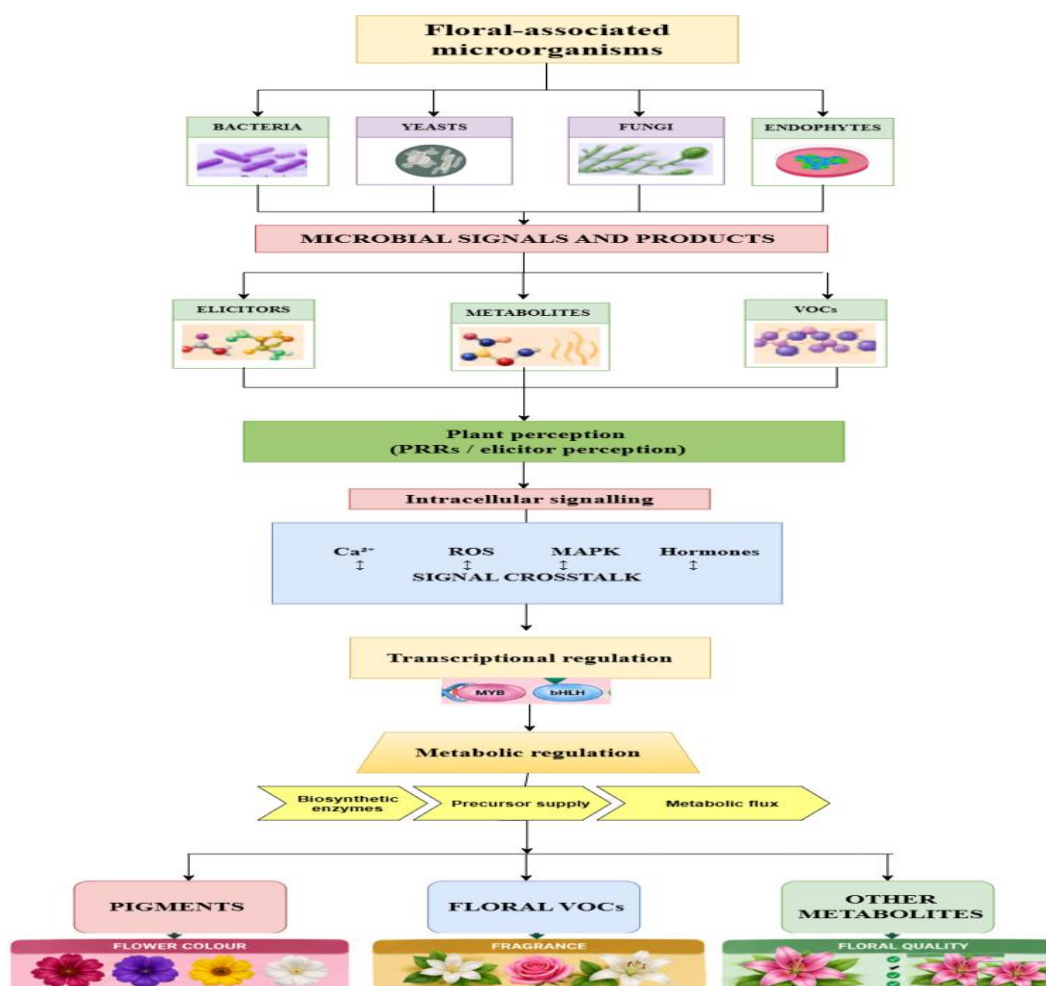


Figure 1. Conceptual framework of microbial interactions with floral signaling, specialized metabolism, and floral traits.

2. MOLECULAR BASIS OF FLORAL SPECIALIZED METABOLISM

Flowers act as complex metabolic systems in which characteristics such as color and fragrance arise from the biosynthesis and accumulation of specific metabolites in particular floral tissues. The main groups that contribute to such characteristics include flavonoids and anthocyanins, carotenoids, betalains, terpenoids, phenylpropanoids, and fatty acid-derived volatile metabolites. Synthesis is developmentally regulated and requires coordinated action of enzymes responsible for biosynthesis, availability of precursors, cellular transport, and transcription (Zhao and Tao, 2015; Mostafa et al., 2022; Pichersky, 2023). While coloration and fragrance have different metabolic origins, these characteristics may be linked biochemically through common precursor metabolism and coordinated regulation (Yeon and Kim, 2021; Shen et al., 2024; Li et al., 2025).

2.1 Floral pigmentation

Flower pigments determine flower coloration according to their type, number, localization, and chemical variations. Anthocyanins represent the main sources of red, violet and blue colors while carotenoids contribute to yellow and orange colors. Betalains contribute to red-violet or yellow colors in plants in which they occur, with a biosynthetic pathway different from that of flavonoids and anthocyanins (Zhao and Tao, 2015; Mekapogu et al., 2020).

Anthocyanin biosynthesis proceeds through the phenylpropanoid and flavonoid pathways. Key structural enzymes include chalcone synthase (CHS), chalcone isomerase (CHI), flavanone 3-hydroxylase (F3H), flavonoid 3'-hydroxylase (F3'H), flavonoid 3',5'-hydroxylase (F3'5'H), dihydroflavonol 4-reductase (DFR), anthocyanidin synthase (ANS), and UDP-glucose:flavonoid 3-O-glucosyltransferase (UGFT). Their coordinated expression determines the formation and modification of anthocyanins and consequently contributes to floral color variation (Mekapogu et al., 2020).

The control of structural genes involved in anthocyanin production is mediated by transcriptional regulation involving R2R3-MYB, bHLH, and WD40 transcription factors. In such cases, regulatory factors may come together to form complexes that are capable of controlling the expression of many structural genes (Zhao and Tao, 2015; Mekapogu et al., 2020).

2.2 Floral fragrance and volatile metabolism

The floral bouquet is formed by a complex blend of volatile organic compounds, usually comprising terpenoids, phenylpropanoid/benzenoid compounds, and fatty acid-derived VOCs. The production and profile of these VOCs depend on the precursor availability, enzyme activity, their transport at intracellular and tissue levels, and developmentally and environmentally regulated biosynthesis (Yeon and Kim, 2021; Mostafa et al., 2022; Pichersky, 2023).

The volatiles belonging to terpenes usually result from methylerythritol phosphate (MEP) and mevalonate (MVA) pathways, which provide precursors for mono- and sesquiterpenes, respectively. Phenylpropanoid/benzenoid volatiles are mostly generated by the metabolism of aromatic amino acids, whereas fatty-acid-based volatiles result from lipid-based pathways. Thus, the bouquet of flower scent involves several metabolic routes and is not just the outcome of one biosynthetic pathway (Mostafa et al., 2022; Pichersky, 2023). New data show that there may be coordination in biosynthesis of floral pigments and volatiles, suggesting that these two major components of flower phenotype have connections at the metabolic and regulatory levels (Shen et al., 2024; Li et al., 2025).

Floral VOC emission is also highly dynamic. Developmental stage, tissue type, circadian regulation, temperature, light, and other environmental factors can alter both the quantity and composition of emitted volatiles. Consequently, changes in floral volatile profiles following microbial exposure must be interpreted carefully because they may reflect direct microbial production or transformation of VOCs, indirect effects on the host, or changes in host volatile biosynthesis (Mostafa et al., 2022; Pichersky, 2023).

2.3 Regulation and metabolic plasticity

Metabolic specialization in flowers is regulated at levels beyond individual biosynthetic enzymes. Transcriptional regulation is involved in coordinating signaling networks, precursor availability, metabolic flux, transport, and responses to the environment, which together determine the final levels of accumulation and release of specialized metabolites. The coordination of pigment and volatile production pathways may lead to the concerted formation of flower color and fragrance (Yeon and Kim, 2021; Shen et al., 2024; Li et al., 2025). Such metabolic flexibility can serve as a potential interface between the plant and its associated microorganisms.

The regulation of plant specialized metabolism by microbes can occur through perception of elicitors, changes in phytohormone signaling, calcium responses, reactive oxygen species, kinase signaling, nutrient acquisition, and regulation of host gene expression (Zhao et al., 2005; Yuan et al., 2017; Lv et al., 2024). These signaling pathways provide a molecular basis for such regulation of floral metabolites. However, the direct link between these general plant-microbe interactions and the particular pathways of pigment and fragrance biosynthesis is still limited.

Therefore, understanding the regulatory processes involved in the modulation of floral secondary metabolism by microbes requires the consideration of all these factors together. The above framework forms the basis for the analysis of the effect that microbes associated with flowers can have on the color and fragrance of flowers in subsequent sections.

3. MICROBIAL SIGNALS AND PLANT MOLECULAR RESPONSES

Microbial partners of flowers interact with host plants by using various microbial stimuli and metabolites, such as elicitors, volatile organic compounds (VOCs), and nutrient-mediated interactions. The detection of such microbial stimuli may lead to changes in intracellular signaling pathways, which result in physiological and metabolic adaptations of the plant. These phenomena have been described in general plant-microbe associations but not specifically in floral specialized metabolism (Zhao et al., 2005; Yuan et al., 2017; Lv et al., 2024).

3.1 Microbial elicitors and host perception

Plant perception of microbe-associated molecular patterns (MAMPs) and microbial elicitors is carried out through host recognition mechanisms. This process is likely to initiate signaling events including changes in calcium ion concentration, ROS production, mitogen-activated protein kinase (MAPK) activation, and regulation of phytohormone pathways (Zhao et al., 2005; Yuan et al., 2017). These could further affect transcriptional events and subsequent metabolic processes.

The application of microbial elicitors can result in the production of plant specialized metabolites through changes in enzyme activity and gene expression. The role of elicitors in the biosynthesis of secondary metabolites has been reported in medicinal and other types of plants, indicating the potential ability of microorganisms or their products to influence host metabolic processes (Chamkhi et al., 2021). However, the direct role of such elicitor response in regulating the synthesis of pigments or fragrances in ornamental flowers has not been sufficiently proven.

3.2 Calcium, ROS and MAPK signaling

The calcium signaling pathway is one of the key elements of the early plant reactions to the perception of microorganisms. Changes in the concentration of free Ca^{2+} ions in the cytosol act as intracellular signals, which activate the calcium-dependent proteins and related signaling cascades. These signaling pathways are involved in the regulation of microbial perception, defense reactions, and other physiological processes in plants (Yuan et al., 2017).

The synthesis of reactive oxygen species (ROS) is another early response in plant-microbe interactions. ROS production acts as a signaling molecule or is part of defense reactions depending on the nature, duration, and cellular context of the interaction. The integration of calcium signaling, ROS production, and MAPK cascades results in the formation of signaling networks, which transmit information about the perception of microorganisms and lead to the activation of cellular reactions and gene expression (Zhao et al., 2005; Yuan et al., 2017).

Nevertheless, possible links may exist between these signaling pathways and specialized metabolism. Direct evidence linking microbial perception through Ca^{2+} –ROS–MAPK signaling to specific floral pigment or fragrance biosynthetic pathways in ornamental plants has not yet been clearly demonstrated.

3.3 Phytohormonal regulation

Microbial interactions can modify plant hormonal signaling, including pathways involving auxins, cytokinins, jasmonates, salicylic acid, ethylene, and other regulatory hormones. Beneficial microorganisms can induce systemic resistance through hormone-associated signaling networks, illustrating the importance of phytohormonal regulation in plant responses to microbial partners (Pieterse et al., 2014).

Changes in hormone signaling may subsequently influence transcriptional regulation and metabolic allocation. Microbe-associated modulation of transcription factors has been documented in plant–microbe interactions, including responses mediated by plant growth-promoting bacteria (Kaleh et al., 2025). Such regulatory effects provide a plausible route through which microorganisms could indirectly influence floral specialized metabolism by altering developmental or stress-responsive transcriptional programs.

Nevertheless, the relationship between microbial hormone modulation and specific floral metabolic pathways remains incompletely resolved. Future studies should determine whether microbial treatments alter hormonal signatures concurrently with expression of floral pigment or fragrance biosynthetic genes and subsequent metabolite accumulation.

3.4 Transcriptional and metabolic responses

Signaling events triggered by microorganisms can ultimately modify host gene expression and metabolic activity. Transcription factors represent an important regulatory level because they coordinate the expression of multiple biosynthetic genes rather than acting on individual metabolic reactions. In floral pigmentation, MYB

and bHLH transcription factors are central components of anthocyanin regulatory networks (Mekapogu et al., 2020).

Microbial interactions may also affect specialized metabolism through changes in nutrient availability, precursor supply, enzyme activity, and metabolic flux. A broad synthesis of plant–microbe interactions indicates that microorganisms can influence secondary metabolism through several interconnected mechanisms rather than through a single regulatory pathway (Lv et al., 2024).

For floral traits, these mechanisms should therefore be considered as components of a potential signaling-to-metabolism continuum:

Microbial signal → host perception → Ca^{2+} /ROS/MAPK and hormonal signaling → transcriptional regulation → biosynthetic activity → metabolite accumulation → floral phenotype.

At present, this sequence represents a mechanistic framework rather than a universally demonstrated pathway for ornamental flowers. Establishing which steps occur in specific floral tissues will be essential for determining whether microorganisms directly regulate host floral secondary metabolism or influence floral traits through indirect physiological effects.

4. MICROBIAL REGULATION OF FLORAL PIGMENTATION

Floral pigmentation is an important ornamental trait determined by the type, concentration, modification, and spatial distribution of pigments within floral tissues. Anthocyanins, carotenoids, and betalains represent major pigment groups contributing to flower color, with anthocyanins being particularly important for red, purple, and blue hues in many ornamental species (Zhao and Tao, 2015; Mekapogu et al., 2020). Because pigment accumulation is controlled by coordinated biosynthetic and transcriptional networks, microbial interactions could potentially influence flower color through several levels of regulation.

4.1 Microbial effects on pigment accumulation

Experimental evidence indicates that microorganisms can influence pigment-related traits in ornamental plants. In poinsettia (*Euphorbia pulcherrima*), inoculation with *Pseudomonas putida* affected anthocyanin pigment accumulation, demonstrating that a plant-associated bacterium can modify the accumulation of a major floral pigment. However, the study did not establish direct regulation of specific anthocyanin biosynthetic genes or transcription factors by the bacterium (Zulueta-Rodriguez et al., 2014).

Microbial amendments have also been associated with pigmentation-related changes in chrysanthemum. Application of *Anabaena torulosa* improved flower quality and was associated with increased pigmentation together with changes in nutrient availability and antioxidant and defense-related responses (Bharti et al., 2021). These observations suggest that microbial treatments may affect pigmentation through broader physiological or nutritional mechanisms, although a direct molecular connection with anthocyanin biosynthesis was not established.

Endophytic microorganisms provide additional evidence for microbial effects on flower-associated specialized metabolites. Sun et al. (2023) characterized endophytic microbial communities among tea chrysanthemum cultivars and evaluated selected bacterial isolates. Inoculation with these isolates was associated with increased concentrations of several flower-associated metabolites, including total flavonoids, chlorogenic acid, luteolin, and 3,5-dicaffeoylquinic acid. These findings support the potential contribution of endophytic bacteria to floral specialized-metabolite accumulation, while the host signaling mechanisms responsible for these responses remain unresolved (Sun et al., 2023).

Together, these studies show that microbial treatments can alter pigment-related and other specialized metabolites in ornamental flowers. The underlying cause, however, remains unresolved, with both host-mediated responses and indirect physiological effects requiring consideration.

4.2 Potential interaction with anthocyanin biosynthesis

The anthocyanin pathway provides a clear molecular framework for investigating potential microbial effects on flower color. Microbial signals may influence host signaling pathways involving Ca^{2+} , ROS, MAPKs, and phytohormones, which could subsequently affect transcriptional regulators and structural genes of the anthocyanin pathway. MYB and bHLH transcription factors are particularly important because they coordinate the expression of multiple structural genes involved in anthocyanin biosynthesis (Mekapogu et al., 2020).

Evidence directly linking a defined floral microorganism or microbial signal to altered expression of specific anthocyanin biosynthetic genes in ornamental plants is still scarce. Consequently, changes in anthocyanin concentration or visible pigmentation alone cannot establish transcriptional regulation of the host pathway.

4.3 Microbial communities and dynamic flower color

Recent multi-omics research has begun to examine microbial communities alongside the molecular processes associated with flower-color variation. In *Hibiscus mutabilis*, integration of metabolomics, transcriptomics, and epiphytic microbial-community analyses revealed spatial and temporal differences in metabolic profiles, host gene expression, and microbial communities during flower-color development (Tang et al., 2026). These findings demonstrate the value of integrating microbiome and host molecular data when investigating floral color dynamics.

The observed relationships remain largely associative. Because microbial communities may change concurrently with flower development, controlled inoculation and functional validation are needed to determine whether particular microorganisms or microbial functions contribute directly to pigment biosynthesis.

4.4 Proposed molecular framework

Taken together, current evidence supports a working model in which microbial signals or microbial-derived products may interact with host perception and signaling pathways, followed by changes in transcriptional regulation, biosynthetic enzyme activity, precursor availability, and pigment accumulation. The resulting changes may contribute to variation in floral pigmentation.

This model represents a working hypothesis rather than an established pathway across ornamental species.

5. MICROBIAL REGULATION OF FLORAL FRAGRANCE

Floral fragrance is produced by complex mixtures of volatile organic compounds (VOCs), including terpenoids, phenylpropanoid/benzenoid compounds, and fatty-acid-derived volatiles. These compounds are synthesized by the plant and released from floral tissues in patterns that vary with developmental stage, tissue type, environmental conditions, and time of day (Mostafa et al., 2022; Pichersky, 2023). In contrast to floral pigmentation, the contribution of microorganisms to floral fragrance is particularly difficult to resolve because microorganisms can both produce and modify volatile compounds and potentially influence host volatile biosynthesis.

5.1 Microbial contribution to the floral volatile pool

Microorganisms inhabiting flowers and nectar can produce volatile metabolites that become components of the local floral odor environment. Nectar-associated microorganisms have been shown to modify nectar volatile composition and consequently influence the attractiveness of flowers to pollinators (Rering et al., 2018). Similarly, epiphytic bacteria can alter floral scent emissions. In *Brassica rapa*, experimental manipulation of epiphytic bacteria demonstrated that bacterial presence can modify the composition and emission of floral scent (Helletsgruber et al., 2017).

These findings indicate that the volatile environment surrounding flowers may represent a combined chemical output of the host plant and its associated microorganisms. Therefore, a change in floral volatile profile following microbial colonization should not automatically be interpreted as altered plant biosynthesis.

5.2 Microbial transformation of floral volatiles

Microorganisms may also influence fragrance through biochemical transformation or degradation of plant-derived compounds. Such activity could modify the abundance or relative composition of individual VOCs without requiring changes in the expression of host biosynthetic genes. Consequently, microbial effects on floral fragrance may arise from processes occurring outside the plant cells as well as from changes in host metabolism. This distinction is important because the measured floral volatile profile represents the final volatile pool rather than a direct measurement of the origin of each compound. Microbial metabolism, therefore, represents a potential intermediate between the compounds released by the plant and the chemical environment experienced by pollinators.

5.3 Reciprocal interactions between floral VOCs and microorganisms

It is possible that the effect of floral VOCs on microbial communities is a two-way process. Floral VOCs have been found to have the ability to manipulate both composition and function of microbial communities. Likewise, floral VOCs can also affect the colonizing microorganisms directly. In *Penstemon digitalis*, for instance, the floral VOC linalool affected the growth of isolated floral bacteria, thus demonstrating that plant-produced floral VOCs can also influence the floral microbiome (Burdon et al., 2018).

For example, genetic differences in floral volatiles were found to alter the floral microbiome in strawberry, suggesting that volatiles can also affect microbial communities through their chemical properties (Wei et al., 2022). Furthermore, floral volatiles were linked to alterations in the composition and function of endophytic fungi in *Osmanthus fragrans* (Shi et al., 2024).

It could be assumed, therefore, that a feedback system exists in which the host floral volatile environment affects microbial colonization and microorganisms, in turn, affect the volatile environment. However, the direction of interaction and its molecular mechanisms might vary depending on plant species, microbial type and floral tissues.

5.4 Potential effects on pollinator behavior

Microbial modification of floral volatiles can have ecological consequences because pollinators use floral chemical cues during flower localization and resource assessment. Nectar-inhabiting microorganisms have been shown to influence volatile composition and pollinator attractiveness, while microbial semiochemicals can also be detected by insects (Rering et al., 2018; Crowley-Gall et al., 2021). Thus, microorganisms may contribute to the chemical signaling environment of flowers and potentially alter pollinator behavioral responses. However, changes in microbial volatile production should be distinguished from genuine regulation of host fragrance biosynthesis.

5.5 Distinguishing microbial production from host regulation

A major challenge in understanding microbial regulation of floral fragrance is determining the origin of individual VOCs. Three non-exclusive mechanisms should be considered:

- (i) Microbial production → microorganisms synthesize VOCs that contribute directly to floral odor;
- (ii) Microbial transformation → microorganisms modify or degrade plant-derived VOCs; and
- (iii) Host metabolic regulation → microbial signals alter plant signaling, gene expression, enzyme activity, or precursor availability, resulting in changes in host VOC biosynthesis.

Current evidence supports microbial effects on floral and nectar volatile profiles, but direct molecular evidence demonstrating that specific floral microorganisms regulate host fragrance biosynthetic genes remains limited. Future studies should therefore combine controlled microbial inoculation with microbiome profiling, quantitative volatilomics, host transcriptomics, enzyme assays, and, where feasible, isotope-tracing approaches. Such integrated experiments would help determine whether microorganisms are producers, transformers, or regulators of the floral volatile pool.

6. MICROBIAL EFFECTS ON OTHER FLORAL QUALITY-RELATED METABOLITES

Along with pigments and volatiles, flowers possess several specialized metabolites responsible for nectar composition, protection, antioxidative activity, nutrition, and other aspects of floral performance. The metabolites include such substances as flavonoids, phenolic acids, alkaloids, and other secondary metabolites. Microbes can affect these metabolites directly by means of biotransformation, through influencing nutrition or signaling from microbes or changing host metabolism (Pang et al., 2021; Lv et al., 2024).

6.1 Microbial effects on nectar chemistry

Nectar acts as an important link between plants, microbes, and pollinators. Nectar chemical composition can change following microbial colonization. Microbes are capable of manipulating the chemical composition of nectar by modifying the sugar content and secondary metabolites thus changing the chemical environment of the nectar that is encountered by pollinators (Canto and Herrera, 2012; Vannette and Fukami, 2016).

Yeasts and bacteria do not always make identical contributions to changes in the chemical nature of the nectar. Their diverse metabolic processes can result in different nectar properties which then contribute to the way that flower-pollinator interactions occur (Vannette and Fukami, 2018). Therefore, microbial contribution to nectar composition can change floral quality without any changes being required in the biosynthetic pathway of the host.

Nectar secondary metabolites also have the potential to affect microbial communities. In a case study conducted recently, it was observed that there was a difference in microbial community richness, diversity, and composition in floral nectar due to variation in pyridine-type alkaloids in the nectar (Aizenberg-Gershtein et al., 2015).

6.2 Phenolic and flavonoid metabolites

Phenols and flavonoids are metabolites involved in antioxidant functions, defense, pigmentation, and numerous other physiological activities in flower tissues. Microorganisms are capable of regulating such metabolites via changes in precursor supply, enzyme activity, signal transduction, and host gene expression (Pang et al., 2021; Lv et al., 2024).

This is supported by evidence from ornamental plants. For example, several selected endophytic bacteria increased the total amount of flavonoids and some phenolic metabolites, such as chlorogenic acid, luteolin, and 3,5-dicaffeoylquinic acid in tea chrysanthemum (Sun et al., 2023). This means that microorganisms could affect the amount of bioactive metabolites in flower tissues. Nevertheless, the mechanisms and signals of these effects have not been identified yet.

These changes could be connected with improved nutrient uptake, the physiological state of the host, microbial elicitation, and other factors.

6.3 Alkaloids and other specialized metabolites

Floral alkaloids can contribute to plant defense and influence interactions with floral microorganisms and pollinators. The composition of these metabolites may affect microbial community assembly within nectar, demonstrating that floral secondary metabolites can act as ecological filters for associated microorganisms (Aizenberg-Gershtein et al., 2015).

More broadly, plant specialized metabolites can influence the composition and function of plant-associated microbiomes, while microorganisms can modify the chemical environment through degradation, transformation, or production of metabolites (Pang et al., 2021; Jacoby et al., 2021). However, compared with pigments and floral VOCs, direct evidence for microbial regulation of alkaloid and other specialized-metabolite pathways specifically in ornamental flowers remains limited.

6.4 Implications for floral quality

Microbial effects on phenolics, flavonoids, nectar metabolites, and other compounds may contribute to broader aspects of floral quality, including antioxidant properties, defense characteristics, nectar chemistry, and

interactions with pollinators. Nevertheless, the biological significance of these changes depends on the specific metabolite, its concentration, its localization within the flower, and whether the change originates from the host plant or from microbial metabolism. Overall, current evidence indicates that microorganisms can modify the chemical environment of flowers and influence selected floral metabolites. However, the molecular mechanisms connecting specific microorganisms with host biosynthetic pathways remain poorly resolved. Future studies should combine tissue-specific microbiome profiling with metabolomics, transcriptomics, enzyme assays, and microbial functional analyses to determine whether observed metabolite changes result from direct microbial metabolism, microbial signaling, or indirect changes in host physiology.

7. OMICS-BASED UNDERSTANDING OF MICROBIAL REGULATION OF FLORAL SECONDARY METABOLISM

The complex relationship between plants and microorganisms makes it difficult to establish a cause-and-effect relationship based on the measurement of individual metabolites or microbial groups alone. Omics techniques provide additional information about the composition of the microbial community, functional capabilities of the microbes, the host's gene expression, and changes in the metabolic pathways, which helps in studying the effect of the microbes on the floral secondary metabolism.

7.1 Microbiome profiling and microbial functional potential

Marker region sequencing through amplicon sequencing methods, such as bacterial 16S rRNA and fungal internal transcribed spacer (ITS) sequences, allows characterization of microbial communities that associate with different floral tissues. The approach helps identify microbes associated with specific developmental stages, floral tissues, or metabolic phenotypes. However, community composition does not provide evidence about the functionality of the associated microbes nor does it prove the contribution of those microbes to a particular floral trait.

Metagenomics provides extra information about the presence of particular microbial genes or microbial functions within the floral microbial community. The metatranscriptomic analysis reveals microbial genes that are transcriptionally active under certain conditions. The information provided by all the mentioned approaches is useful for finding microbial functions possibly responsible for metabolite synthesis, modification, acquisition, or signaling (Mishra et al., 2022; Jain et al., 2024).

7.2 Host transcriptomics

Host transcriptomic analysis can determine whether microbial exposure is accompanied by changes in the expression of genes involved in signaling, transcriptional regulation, and specialized-metabolite biosynthesis. For floral pigmentation, this may include genes encoding enzymes of the flavonoid and anthocyanin pathways together with regulatory MYB and bHLH transcription factors. For fragrance, transcriptomic analysis can target genes involved in terpenoid, phenylpropanoid/benzenoid, and fatty-acid-derived volatile biosynthesis. Comparing transcriptomic profiles between inoculated plants and appropriate controls can therefore help determine whether microbial treatment is associated with transcriptional reprogramming of floral metabolic pathways. However, changes in gene expression should be interpreted together with enzyme activity and metabolite measurements because transcript abundance does not necessarily predict metabolic flux or final metabolite accumulation.

7.3 Metabolomics and volatilomics

Untargeted and targeted metabolomics reveal changes in nonvolatile specialized metabolites such as anthocyanins, flavonoids, phenols, carotenoids, and their related metabolites. Volatilomics provides complementary information about the components and abundance of VOCs emitted by flowers that are essential for floral chemistry and scent (Mostafa et al., 2022). Combining these two sets of data with those of the microbiome and transcriptomics may help uncover relationships between changes in microbial communities, gene expressions in the host, and metabolites. For example, a microbial treatment associated with increased anthocyanin content together with up-regulated expression of genes involved in anthocyanin biosynthesis would provide more convincing evidence of the role of host pathways than measuring the metabolites. However, such relationships need functional confirmation.

7.4 Multi-omics integration and candidate pathway identification

Integration of microbial and host datasets can be used to construct correlation networks and identify candidate microbe–host–metabolite relationships. Microbial taxa or functional genes that consistently correlate with specific host transcripts and metabolites can serve as candidates for subsequent experimental investigation (Mishra et al., 2022; Jain et al., 2024). Recent research in *Hibiscus mutabilis* illustrates the value of integrating epiphytic microbial communities with metabolomic and transcriptomic data to investigate the spatial and temporal dynamics of flower-color development (Tang et al., 2026). Such studies provide a framework for identifying candidate microbial and host pathways associated with floral metabolic variation, although association-based multi-omics analyses alone cannot establish direct microbial control. An integrated multi-omics framework for identifying candidate microbial functions, host pathways, and metabolite associations is presented in Figure 2.

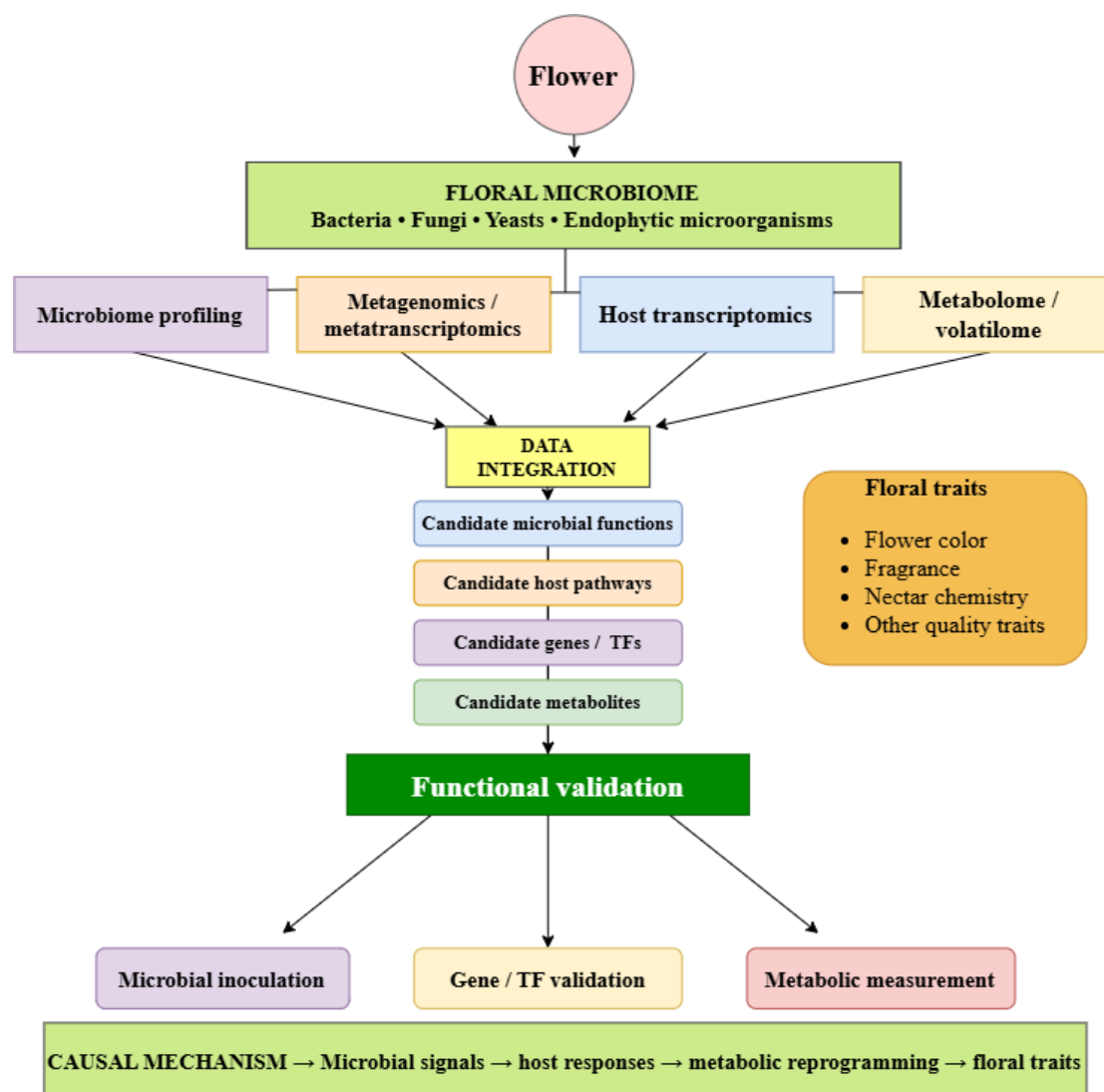


Figure 2. Multi-omics framework for investigating microbial regulation of floral secondary metabolism.

7.5 From candidate associations to functional validation

The major advantage of multi-omics approaches is their ability to generate testable hypotheses rather than simply describe floral microbial communities. Candidate microbial taxa, microbial genes, host transcription factors, biosynthetic enzymes, and metabolites identified through integrated datasets should subsequently be evaluated using controlled inoculation, defined microbial communities, gene-expression analysis, enzyme assays, metabolite quantification, and appropriate genetic or biochemical validation. Thus, a comprehensive multi-omics framework can progress from: Floral microbiome → microbial functional potential/activity → host transcriptional responses → metabolic changes → floral phenotype. Such integration can help distinguish microbial production or transformation of floral compounds from genuine regulation of host specialized metabolism and represents an important step toward establishing causal molecular mechanisms.

8. EVIDENCE FROM ORNAMENTAL CROPS

Evidence linking microorganisms with floral secondary metabolism in ornamental crops is emerging, although the number of mechanistic studies remains limited. Available studies indicate that microbial inoculation or naturally occurring microbial communities can influence floral pigmentation, phenolic and flavonoid metabolites, and other flower-quality traits. These studies provide valuable evidence for microbial effects on floral traits, but the depth of molecular evidence varies considerably among crop systems. Importantly, observed changes in metabolite accumulation or floral phenotype should be distinguished from direct regulation of host biosynthetic pathways.

In poinsettia (*Euphorbia pulcherrima*), inoculation with *Pseudomonas putida* affected anthocyanin pigment accumulation, demonstrating that a plant-associated bacterium can modify a major determinant of floral or bract pigmentation. However, the observed response did not establish a direct effect of the bacterium on specific anthocyanin biosynthetic genes or transcription factors (Zulueta-Rodriguez et al., 2014). Similarly, application of *Anabaena torulosa* to chrysanthemum was associated with improved flower quality and increased

pigmentation, together with changes in nutrient availability and plant antioxidant and defense-related responses. These findings suggest that microbial amendments may influence floral pigmentation through broader physiological and nutritional effects, although the molecular link to pigment biosynthesis remains unresolved (Bharti et al., 2021).

Evidence from endophytic microorganisms provides a stronger connection with floral secondary metabolites. Sun et al. (2023) characterized endophytic microbial communities across tea chrysanthemum cultivars and subsequently evaluated selected bacterial isolates. Microbial inoculation was associated with increases in several flower-associated metabolites, including total flavonoids, chlorogenic acid, luteolin, and 3,5-dicaffeoylquinic acid. This study therefore provides experimental evidence that selected endophytic bacteria can influence the accumulation of bioactive metabolites in chrysanthemum flowers, although the specific host signaling and biosynthetic mechanisms responsible for these changes remain to be resolved.

Microbial treatments have also been investigated in poinsettia for their effects on bract quality. Plant growth-promoting rhizobacteria (PGPR) formulations, alone or in combination with chemical fertilizers, altered physiological traits and bract quality, including characteristics associated with pigmentation (Parlakova Karagöz and Dursun, 2020). Such observations support a role for beneficial microorganisms in modifying ornamental floral quality, but they do not by themselves establish direct transcriptional regulation of pigment biosynthesis.

Recent multi-omics research provides an additional perspective on the relationship between floral microbial communities and flower color. In *Hibiscus mutabilis*, Tang et al. (2026) integrated metabolomics, transcriptomics, and analyses of epiphytic microbial communities to investigate the spatial and temporal dynamics associated with flower-color change. The study identified differences in metabolic and transcriptional profiles together with changes in epiphytic microbial communities across floral tissues and developmental time points. The available evidence remains associative and does not establish direct microbiome control of the host flower-color pathway (Tang et al., 2026).

Overall, evidence from ornamental crops supports the possibility that microorganisms contribute to floral secondary-metabolite accumulation and quality traits, but the available studies remain uneven in mechanistic depth. Future experiments combining controlled microbial inoculation with tissue-specific transcriptomics, metabolomics, enzyme assays, and functional validation of candidate genes will be required to establish causal links between microbial signals and ornamental floral metabolism.

9. KNOWLEDGE GAPS AND FUTURE MOLECULAR APPROACHES

9.1 From association to causation

The central experimental problem is to separate microbial effects from correlations that arise during normal flower development or changes in plant nutrition and physiology. Controlled experiments using single microbial isolates, defined microbial consortia, sterile controls, and re-inoculation approaches are therefore needed to establish causality. Such experiments should also distinguish microbial effects from changes caused indirectly by nutrition, plant growth, or environmental conditions (Rebolleda-Gómez et al., 2019; Vannette, 2020).

9.2 Linking microbial perception with floral metabolic pathways

Plant-microbe interactions can involve calcium signaling, reactive oxygen species, mitogen-activated protein kinase cascades, phytohormones, transcriptional regulation, and changes in nutrient or precursor availability. These mechanisms provide plausible routes through which microorganisms could influence specialized metabolism, but their direct involvement in floral tissues remains insufficiently characterized (Yuan et al., 2017; Lv et al., 2024). A mechanistic test would require linking microbial exposure or microbial-derived signals with changes in floral transcription factors, biosynthetic enzymes, and metabolite accumulation rather than relying on the final phenotype alone.

9.3 Resolving microbial effects on floral fragrance

Floral fragrance represents a particularly complex research gap because changes in floral volatile profiles may result from microbial production of volatile compounds, microbial transformation or degradation of plant-derived compounds, or changes in host volatile biosynthesis. Studies have demonstrated that microorganisms can alter floral or nectar volatile profiles, while floral volatiles can also influence the composition of associated microbial communities (Helletsgruber et al., 2017; Rering et al., 2018; Wei et al., 2022). Therefore, future work should combine microbial community analysis with quantitative volatilomics, host gene-expression analysis, enzyme assays, and, where possible, isotope-tracing approaches. Together, these measurements would allow the microbial contribution to the volatile pool to be separated from changes originating in host fragrance biosynthesis.

9.4 Establishing mechanisms underlying floral pigmentation

Microbial effects on pigmentation have been observed in ornamental plants, but the causal sequence from microbial interaction to pigment accumulation remains incompletely resolved. Future experiments should simultaneously monitor microbial abundance or activity, expression of pigment-pathway genes, transcription factors, enzyme activity, and concentrations of individual anthocyanins, flavonoids, carotenoids, or other relevant pigments. Integrating these measurements would help determine whether microbial treatments influence pigmentation through direct metabolic regulation or indirectly through nutrition, stress signaling, or general plant physiological responses.

9.5 Expanding research beyond nectar

Floral microbiome research has historically concentrated heavily on nectar and, to a lesser extent, stigmas, while petals, pollen, and anthers remain comparatively underexplored. A recent synthesis of floral microbial research confirms this strong organ-level bias and highlights the need for broader investigation across floral tissues (Khan et al., 2026). Tissue-resolved microbiome profiling combined with metabolomics and transcriptomics could determine whether microbial communities differ among petals, anthers, stigmas, pollen, and nectar and whether these differences correspond to tissue-specific metabolic functions.

9.6 Resolving temporal and spatial dynamics

Floral microbial communities and floral metabolites can change with flower development, tissue position, environmental conditions, and time of day. The recent multi-omics analysis of *Hibiscus mutabilis* illustrates the value of examining spatial and temporal variation in flower color together with epiphytic microbial communities (Tang et al., 2026). Longitudinal sampling throughout floral development and diel sampling of volatile emission could therefore provide a more accurate picture of when microbial associations arise and whether they coincide with critical periods of metabolite biosynthesis.

9.7 Integrating multi-omics datasets

The development of a mechanistic framework of floral microbial regulation requires the analysis of several molecular data sets. The microbiome can be profiled to identify the presence of microbial taxa linked to floral traits, while metagenomic and metatranscriptomic data provide insight into microbial functional capabilities and activity. Changes in biosynthesis and signaling pathways may be observed via host transcriptomics, while metabolomics and volatilomics determine the chemical phenotype. Multi-omics approaches have already been employed to understand plant-microbe interactions but not in the context of floral secondary metabolism (Mishra et al., 2022; Jain et al., 2024).

9.8 From individual strains to synthetic communities

Single-strain inoculation experiments provide an important starting point but may not reproduce the interactions occurring within natural floral microbial communities. Future studies should progressively move from individual microbial isolates to defined synthetic communities and, ultimately, naturally assembled microbiomes. Comparing these systems could identify whether particular microbial functions are attributable to individual taxa or emerge from interactions among community members. From an applied perspective, increasing understanding of floral microbial communities may also support microbiome-based management strategies in agricultural and horticultural systems, although such approaches require validation under specific crop and environmental conditions (Burgess and Schaeffer, 2022).

9.9 Functional validation of candidate pathways

The identification of microbial taxa or host genes associated with a floral phenotype should be followed by functional validation. Candidate microbial signals, host receptors, signaling components, transcription factors, and biosynthetic genes should be examined through controlled inoculation, gene-expression analysis, metabolite quantification, enzyme assays, and appropriate genetic or biochemical perturbation. Such approaches would allow the proposed sequence—microbial signal, host perception, intracellular signaling, transcriptional regulation, metabolic change, and floral phenotype to be experimentally tested rather than inferred from correlation alone. Associations identified through microbiome and multi-omics analyses become mechanistically useful only when the corresponding microbial signals, host regulators, and biosynthetic genes are tested experimentally. Establishing this sequence will be essential for determining whether microorganisms are merely associated with floral secondary metabolism or constitute active regulators of ornamental flower traits.

10. CONCLUSIONS

Flower-associated microorganisms represent an underexplored component of ornamental plant biology with the potential to influence flower color, fragrance, nectar chemistry, and other quality-related traits. Evidence from floral microbiome studies and experimental inoculation systems demonstrates that microorganisms can alter floral volatile profiles, nectar composition, pigmentation, and concentrations of selected floral metabolites. However, the strength of evidence differs among traits and plant systems, and direct molecular evidence remains limited in ornamental crops.

The available literature indicates that microbial effects on floral phenotype may arise through several non-exclusive mechanisms, including microbial production or transformation of metabolites, changes in nutrient availability, microbial signaling, and modulation of host metabolic processes. Nevertheless, most studies do not yet establish a complete causal pathway linking microbial perception to specific host transcription factors, biosynthetic enzymes, metabolite accumulation, and the resulting floral phenotype. In particular, direct regulation of host fragrance and pigment biosynthetic pathways by floral microorganisms remains insufficiently demonstrated.

Ornamental crops provide an important opportunity to address these knowledge gaps because flower color, fragrance, nectar chemistry, and other floral characteristics contribute substantially to horticultural and commercial value. Future research integrating controlled microbial inoculation with floral microbiome profiling, transcriptomics, metabolomics, volatilomics, and functional validation should help distinguish direct microbial effects from indirect physiological or nutritional responses. Recent studies combining floral microbial

communities with multi-omics approaches illustrate the potential of this strategy, while also demonstrating that current evidence remains largely associative (Tang et al., 2026). From an applied perspective, improved understanding of floral microbial communities may also support the development of microbiome-based management strategies, although their effectiveness and consistency will require validation across ornamental crops and growing conditions (Burgess and Schaeffer, 2022).

The next step is to move beyond descriptive characterization and determine how microbial communities or their products alter host signaling, metabolic pathways, and floral phenotypes. Linking microbial community composition and activity with host signaling, metabolic pathways, and floral phenotype could provide a molecular framework for understanding the extended floral phenotype and may create new opportunities for sustainable manipulation of ornamental flower quality. The increasing recognition of flowers as microbial hubs, together with the continuing underrepresentation of petals, pollen, and anthers in floral microbiome research, further emphasizes the need for tissue-specific and functionally validated studies (Khan et al., 2026).

Conflict of Interest

The authors declare that there are no conflicts of interest regarding the publication of this review.

Acknowledgements

The authors acknowledge that no external assistance or financial support was received in the preparation of this review.

Data availability statement

No new data were created or analyzed in this study. Data sharing is not applicable to this article.

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