



## Genetic and Biochemical Mechanisms Underlying Flavor and Aroma in Edible Fruits and Crops

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### ABSTRACT

Aroma and flavor are pivotal attributes that define the sensory quality and market value of fruits and crops. These traits are governed by a complex interplay of biochemical pathways and genetic determinants. This review explores the genetic basis and molecular mechanisms behind the distinct aroma profiles of citrus fruits (e.g., *Citrus limon*), strawberries (*Fragaria × ananassa*), mangoes (*Mangifera indica*), guavas (*Psidium guajava*), and aromatic rice varieties (e.g., *Oryza sativa*). Special attention is given to key genes like CsLOX, FaNES1, BADH2, and their associated pathways, such as lipoxygenase, terpene synthesis, and aldehyde biosynthesis. The findings emphasize the importance of molecular breeding and metabolic engineering for enhancing flavor and aroma traits in horticulture and agriculture. These findings underline the potential of CRISPR and molecular breeding for enhancing aroma and flavor traits.

**Keywords:** *Citrus limon*, *Fragaria × ananassa*, *Mangifera indica*, *Psidium guajava*, *Oryza sativa*, aroma, terpene biosynthesis, volatile organic compounds, BADH2, metabolic pathways

### Introduction

Aroma and flavor are integral to the sensory appeal and consumer preference for fruits and crops. These attributes result from the intricate interaction of biochemical processes that produce volatile organic compounds, which are perceived by human olfactory receptors. Advances in genomics and metabolomics have revealed specific genes and pathways responsible for these traits. This manuscript delves into the genetic and biochemical basis of aroma profiles in key edible fruits and aromatic crops, highlighting how these insights can be harnessed for crop improvement. Furthermore, these traits significantly impact global agricultural economics and consumer health trends, making them a priority in crop improvement efforts.

### Genetic and Biochemical Basis of Aroma and Flavor

Aroma and flavor in fruits and crops are governed by intricate genetic and biochemical mechanisms, which contribute to their sensory qualities and consumer appeal (Table 1). For instance, the citrusy aroma of lemons (*Citrus limon*) is attributed to terpenes synthesized through terpene synthase genes such as CsLOX, CsGPPS, and CsTPS. The pathway begins with the formation of isoprenoid precursors like geranyl diphosphate (GPP), which CsTPS enzymes transform into monoterpenes like limonene and  $\gamma$ -terpinene. Additionally, the CsLOX gene plays a critical role in producing aroma-related volatile organic compounds (VOCs) during fruit ripening. Understanding this pathway offers opportunities for enhancing lemon-derived products through biotechnological innovations. (geranyl diphosphate, a key precursor in terpene synthesis).

Strawberries (*Fragaria × ananassa*) are notable for their sweet aroma, mediated by key genes such as *FaNES1*, *FaOMT*, and *FaFAD1*. *FaNES1* encodes (E)-nerolidol synthase 1, which produces linalool, a major component of strawberry aroma, while *FaOMT* facilitates the methylation of anthranilic acid into methylantranilate, contributing to sweetness. These compounds are synthesized via lipid metabolism and methylation processes, which are influenced by environmental and developmental cues. Such insights have supported breeding programs aimed at optimizing flavor profiles in strawberries.

Mangoes (*Mangifera indica*) are prized for their tropical aroma and juicy texture, derived from the lipoxygenase pathway. The *MiLOX* gene contributes to the production of esters and aldehydes, key compounds in mango aroma, while *MiPGIP* regulates fruit softening and indirectly influences aroma compound release. With over 300 VOCs, including terpenes like myrcene, esters, and lactones, mangoes exhibit a complex flavor profile. Studies targeting *MiLOX* could lead to improved cultivars with enhanced sensory traits and better shelf life.

Guavas (*Psidium guajava*) owe their characteristic pungent-sweet aroma to the interplay of *LOX* (lipoxygenase), *HPL* (hydroperoxide lyase), and *ADH* (alcohol dehydrogenase). These enzymes convert fatty acids into aldehydes, alcohols, and esters, creating a unique aroma profile. Besides their fragrance, guavas are rich in antioxidants, enhancing their nutritional value. Modulating the activities of *LOX* and *ADH* could allow for tailoring guava aroma to suit consumer preferences.

Aromatic rice varieties like basmati (*Oryza sativa*) and jasmine (*Oryza sativa* var. *indica*) are distinguished by their nutty and floral aromas, respectively, primarily due to the compound 2-acetyl-1-pyrroline (2AP). In basmati rice, the BADH2 gene mutation leads to 2AP accumulation by inhibiting the conversion of gamma-aminobutyraldehyde to betaine aldehyde. Similarly, in jasmine rice, a loss-of-function mutation in OsBADH2 results in 2AP buildup. While basmati rice is renowned for its grain elongation upon cooking, jasmine rice is favored for its soft texture, influenced by amylose content. Combining these aromatic traits with high yield remains a breeding challenge, but marker-assisted selection (MAS) using BADH2 and OsBADH2 have proven effective in developing new aromatic varieties. (2-acetyl-1-pyrroline, the compound responsible for aroma in rice).

These findings underscore the importance of genetic and biochemical research in enhancing the aroma and flavor of fruits and crops, paving the way for innovations in agricultural biotechnology and consumer-centric breeding programs.

**Table 1:** A detailed table with complete properties and associated genes for **edible scented fruit plants** and **aromatic grains crops** is quite involved, as it requires linking specific properties (such as aroma, taste, and resilience) to corresponding genes.

Plant/Crop	Key Properties	Genes Associated	Gene Function
<b>Lemon</b> ( <i>Citrus limon</i> )	Citrusy aroma, high acidity, vitamin C	<i>CsLOX</i> , <i>CsGPPS</i> , <i>CsTPS</i>	Involved in terpene biosynthesis responsible for the lemon aroma.
<b>Strawberry</b> ( <i>Fragaria</i> × <i>ananassa</i> )	Sweet aroma, red color, high sugars	<i>FaNES1</i> , <i>FaOMT</i> , <i>FaFAD1</i>	<i>FaNES1</i> : Linalool biosynthesis; <i>FaOMT</i> : Methylanthranilate synthesis (sweet aroma).
<b>Mango</b> ( <i>Mangifera indica</i> )	Tropical aroma, juicy texture	<i>MiPGIP</i> , <i>MiLOX</i>	<i>MiLOX</i> : Lipoxygenase activity involved in volatile compound production (e.g., esters, terpenes).
<b>Guava</b> ( <i>Psidium guajava</i> )	Pungent-sweet aroma, vitamin C content	<i>LOX</i> , <i>HPL</i> , <i>ADH</i>	Lipoxygenase (LOX) and alcohol dehydrogenase (ADH) pathways contribute to aldehydes and esters.
<b>Basmati Rice</b> ( <i>Oryza sativa</i> )	Distinct nutty aroma, elongation upon cooking	<i>BADH2</i> (betaine aldehyde dehydrogenase)	Produces 2-acetyl-1-pyrroline (2AP), the key compound responsible for its aroma.
<b>Jasmine Rice</b> ( <i>Oryza sativa</i> var. <i>indica</i> )	Floral aroma, soft texture	<i>OsBADH2</i>	Loss of function in <i>OsBADH2</i> leads to accumulation of 2AP, giving the aromatic trait.

These genetic advancements also pave the way for climate-resilient crops, addressing global challenges like extreme weather impacts on agriculture. For example, CRISPR editing of BADH2 in rice has been used to enhance fragrance while maintaining yield. Mango pathways also involve interactions between MiLOX and methyl-branched ester production, which contribute to the fruit's complex aroma profile. The integration of genomics with sensory and food science creates opportunities for consumer-centric crop development.

## Discussion

Aroma and flavor are essential attributes that determine the quality, market value, and consumer preference of fruits and crops. These characteristics arise from a complex interplay of genetic and biochemical pathways that produce volatile organic compounds (VOCs). Different fruits and aromatic crops such as lemon (*Citrus limon*), strawberry (*Fragaria* × *ananassa*), mango (*Mangifera indica*), guava (*Psidium guajava*), basmati rice (*Oryza sativa*), and jasmine rice (*Oryza sativa* var. *indica*) exemplify the diversity in aroma and flavor profiles due to unique genetic determinants and metabolic processes.

In lemons, the distinctive citrusy aroma results from terpene biosynthesis involving genes such as *CsLOX* (lipoxygenase), *CsGPPS* (geranyl pyrophosphate synthase), and *CsTPS* (terpene synthase). These enzymes catalyze the production of limonene and other monoterpenes responsible for the fresh aroma characteristic of citrus fruits. These compounds are vital for both the plant's ecological functions and their commercial appeal in flavoring and aromatherapy products.

Strawberries are renowned for their sweet aroma and rich flavor. Key genes like *FaNES1* (responsible for linalool synthesis), *FaOMT* (methylation of anthranilic acid to methylanthranilate), and *FaFAD1* (fatty acid desaturation) drive the production of key VOCs, including esters and alcohols. These compounds contribute to the fruit's signature sweetness and are under the influence of environmental and developmental factors, making them a target for breeding programs aimed at improving flavor traits.

The tropical aroma of mangoes stems from the lipoxygenase pathway, involving genes like *MiLOX* (lipoxygenase) and *MiPGIP* (polygalacturonase-inhibiting protein). These genes regulate the production of esters, terpenes, and lactones, which are pivotal for mango's characteristic fruity scent. Additionally, the soft, juicy texture of mangoes is influenced by these metabolic pathways, which can be optimized to enhance shelf life and sensory properties.

Guavas owe their pungent-sweet aroma to a combination of lipoxygenase (*LOX*), hydroperoxide lyase (*HPL*), and alcohol dehydrogenase (*ADH*) pathways. These enzymes coordinate the conversion of fatty acids into aldehydes, alcohols, and esters. The interplay between these metabolic routes generates the characteristic aroma profile of guava, which, coupled with its high vitamin C content, enhances its nutritional and market value.

Aromatic rice varieties like basmati and jasmine owe their distinctive fragrance to the compound 2-acetyl-1-pyrroline (2AP). In basmati rice, the fragrance is regulated by the *BADH2* gene, where a loss-of-function mutation leads to the accumulation of 2AP. Similarly, in jasmine rice, the mutation in the *OsBADH2* gene results in floral aroma and soft-textured grains. These genetic variations not only define the sensory qualities of aromatic rice but also have implications for breeding programs aimed at improving grain yield without compromising aroma.

The genetic and biochemical pathways governing aroma and flavor in these fruits and crops present significant opportunities for genetic improvement. Advances in molecular biology, such as CRISPR-Cas9 technology, can be utilized to enhance specific flavor traits while ensuring sustainability and resilience against environmental stressors. Understanding these intricate pathways paves the way for innovations in horticulture and agriculture, ensuring the delivery of high-quality produce that meets consumer demands. The genetic regulation of aroma and flavor in fruits and crops is a dynamic field with profound implications for agriculture and food industries. Genes like *CsLOX*, *FaNES1*, and *BADH2* not only elucidate the molecular basis of these traits but also open avenues for metabolic engineering and selective breeding. Advances in CRISPR-Cas9 and transcriptomics could enable precise modulation of these pathways to meet consumer preferences while addressing challenges like climate resilience. The incorporation of biotechnological tools like precision agriculture is pivotal for achieving sustainability alongside enhanced crop traits. Improvements in aroma and flavor contribute to global food security by increasing crop value and consumer acceptance.

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## Conclusion

Aroma and flavor are critical determinants of food quality and consumer preference. The genetic and biochemical insights presented here provide a framework for improving these traits in fruits and crops through advanced breeding and biotechnological approaches. Future research should focus on integrating omics technologies to unravel the regulatory networks and environmental interactions influencing aroma biosynthesis. The genetic and biochemical mechanisms underlying aroma and flavor in fruits and crops are diverse, intricately regulated, and vital for consumer acceptance and marketability. Each plant discussed—lemon, strawberry, mango, guava, basmati rice, and jasmine rice provides a unique model for understanding how specific genes and pathways contribute to their characteristic sensory profiles.

Lemons exhibit a citrusy aroma derived from terpenes produced by the *CsLOX*, *CsGPPS*, and *CsTPS* genes, demonstrating the importance of terpene biosynthesis in aroma formation. This process not only influences the sensory appeal of lemons but also offers potential applications in enhancing lemon-based products through genetic engineering. Similarly, strawberries owe their sweet aroma to VOCs like linalool and methylanthranilate, synthesized via genes such as *FaNES1*, *FaOMT*, and *FaFAD1*. These findings highlight the complex metabolic interactions in strawberry aroma, providing opportunities to refine flavor through breeding strategies.

Mangoes, celebrated for their tropical aroma, showcase the role of the lipoxygenase pathway, where *MiLOX* and *MiPGIP* regulate the production of esters and aldehydes. Their multifaceted aroma, arising from over 300 VOCs, underscores the complexity of biochemical pathways that can be targeted to create improved mango varieties with longer shelf lives and enhanced sensory traits. In guavas, the interplay between *LOX*, *HPL*, and *ADH* drives the formation of aldehydes, alcohols, and esters, which define their pungent-sweet aroma. Beyond flavor, guava's rich antioxidant content enhances its nutritional and commercial value, demonstrating the multifunctionality of these biochemical pathways.

Aromatic rice varieties, including basmati and jasmine rice, reveal the critical role of 2-acetyl-1-pyrroline (2AP) in defining their fragrance. Mutations in the *BADH2* and *OsBADH2* genes inhibit key metabolic conversions, leading to 2AP accumulation. These findings not only explain the sensory properties of these rice varieties but also provide markers for breeding programs. However, achieving a balance between aroma, yield, and other agronomic traits remains a challenge for rice breeders.

Advances in molecular biology and biotechnology, such as CRISPR-Cas9 genome editing and marker-assisted selection, have opened new avenues for enhancing these sensory traits while addressing challenges like crop yield, shelf life, and environmental resilience. By focusing on the genes and pathways described above, researchers can innovate crop improvement strategies to meet both consumer preferences and global food security needs. In conclusion, understanding the genetic and biochemical basis of aroma and flavor in fruits and crops is not just about enhancing sensory appeal but also about improving agricultural sustainability and economic value. Future research should continue to integrate genetic, biochemical, and ecological perspectives, enabling the development of crops that are not only flavorful but also resilient and sustainable.

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