Integrated Mechanisms of Ripening and Aroma Formation in Mango Fruit

Abstract

Mango (Mangifera indica), a member of the *Anacardiaceae* family, is one of the most important tropical fruit crops globally, with India being the largest producer. India's extensive mango diversity includes approximately 1,000 cultivars, each characterized by unique attributes such as plant structure, fruit size, skin and pulp colour, taste, and aroma. These traits are critical for consumer acceptance and market value both domestically and internationally. The ripening process in mango is a highly coordinated biological phenomenon involving a complex network of molecular, genetic, and biochemical pathways. This process drives key changes in fruit attributes, including colour development, texture softening, sugar accumulation, and the production of volatile compounds responsible for the characteristic aroma. These transformations significantly enhance the sensory and nutritional quality of the fruit. This review explores the intricate regulatory mechanisms underlying mango ripening, emphasizing the role of hormones such as ethylene and auxins in modulating gene expression. The study also examines the biosynthesis of secondary metabolites, particularly aroma-related compounds, which are vital for consumer appeal. Furthermore, advancements in genomics and proteomics have revealed critical insights into the role of specific enzymes and transcription factors in coordinating these pathways. Understanding the physiological and biochemical changes during mango ripening provides valuable knowledge for improving fruit quality, extending shelf life, and optimizing post-harvest handling. This study highlights recent findings in molecular biology and their implications for breeding and biotechnological interventions aimed at enhancing mango fruit quality.

Keywords: Mango, fruit, ripening, aroma, genes, biochemical pathway.

Introduction

Mango (*Mangifera indica*), a prominent member of the *Anacardiaceae* family, holds a central place in the agriculture and horticulture sectors of tropical and subtropical regions worldwide. Grown in over 87 countries, it ranks as the fifth most produced fruit globally, with an estimated annual output exceeding 34 million tonnes. India, the leading producer, contributes around 50% of this global output, cultivating mangoes across 23 million acres and yielding approximately 18 million tonnes annually (Press Information Bureau, Government of India, Ministry of Commerce and Industry, 2022-2023). The primary mango-producing states in India include Andhra Pradesh, Uttar Pradesh, Bihar, Gujarat, Karnataka, and Maharashtra, reflecting the widespread agricultural significance of this crop (Figure 1). Mangoes are renowned for their rich nutritional profile, being an excellent source of vitamins A and C. They also contain approximately 20% total soluble sugars, with an acidity ranging from 0.2 to 0.5% and about 1% protein content (Fokouo *et al*., 2023; Liu *et al*., 2022). The diverse varieties of mangoes cultivated in India, such as *Alphonso, Dashehari, Kesar, Banganapalli*, and many others, are distinguished by variations in size, shape, color, fiber content, and flavor. These varieties also possess strong, unique aromas and vibrant peel coloration, which make them particularly appealing in the international market (Gautam *et al*., 2023). The diverse aromatic and biochemical profiles of these varieties offer a rich opportunity for studying mango ripening, which involves complex processes such as enzymatic activity, volatile compound production, and changes in texture and color (Liu *et al*., 2022; Yashoda *et al*., 2006).

India's mango diversity offers significant insight into the molecular and biochemical mechanisms that govern ripening and flavor development. The ripening process in mango is a climacteric event, involving numerous physiological, biochemical, and molecular changes. These include the conversion of starches to sugars, changes in fruit texture due to cell wall degradation, and the accumulation of volatile compounds that contribute to the characteristic aroma (Sane *et al*., 2005; Chourasia *et al*., 2008). Understanding these processes not only enhances mango quality and postharvest handling but also holds the potential for improving mango storage and shelf life, making it a crucial area of research in the global fruit trade (Singh *et al*, 2013; Malundo *et al*., 1997).

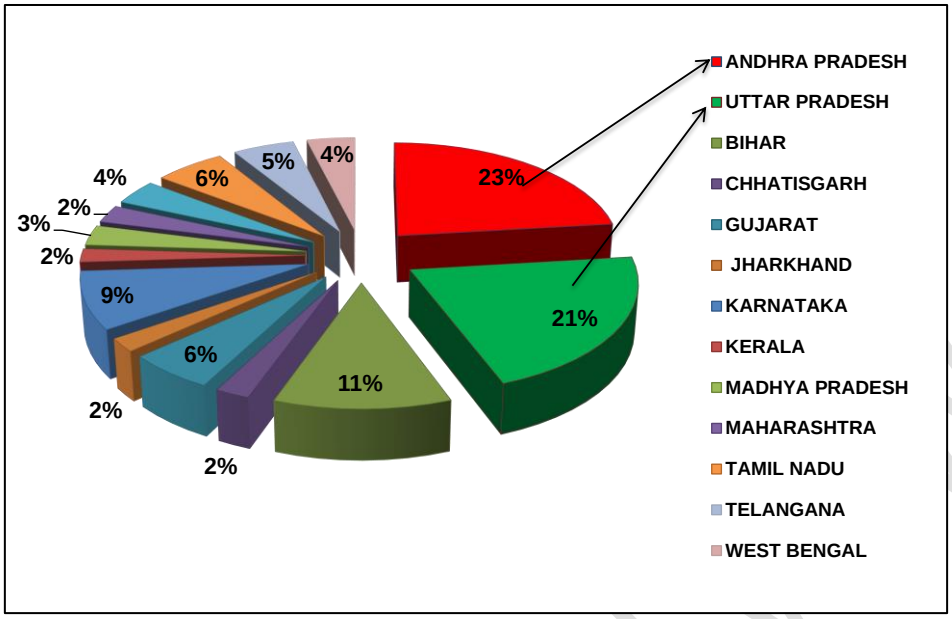

Figure 1: **Major mango producing states in India**. (Press Information Bureau Government of India Ministry of Commerce and Industry 2022-2023)

Studies related to ripening in mango

"Mango is a climacteric fruit characterized by a series of physiological and biochemical changes that occur during ripening initiated by autocatalytic production of ethylene and increase in respiration. Mango is an excellent system to study ripening related changes in climacteric fruits as many varieties exhibit significant changes in various characters that are attributed to climacteric fruit ripening such as softening, acidity, colour, and accumulation of aroma and other secondary metabolites. Gluconeogenesis is mainly active in ripening mango, which is reflected in decreased citrate and succinate levels but increased maleic acid level" (Lazan *et al.*, 1986). "Most of the gluconeogenic enzymes such as Fructose-1-6-diphosphatase (FDPase), Phosphoenolpyruvate carboxykinase (PEPCK), Phosphoenolpyruvate carboxylase (PEPC), Succinate dehydrogenase (SDH), Glucose-6-phosphate (G-6-Pase) and Glucokinase increase significantly during ripening, exhibiting highest activity at the ripe stage, except for malic enzyme, which remains constant throughout" (Yashoda *et al.*,2006).

"The activity of several carbohydrate degrading enzymes correlated with progression of fruit ripening. Different cell wall hydrolases such as PG, PL, Cellulase, Expansins, etc. have been studied at the biochemical and molecular level during mango fruit ripening. Cell wall hydrolases

such as *MiExpA1* and *MiPel1* coding for expansin and pectate lyase respectively have been recognized from *Dashehari* mango, which demonstrates ripening linked expression and associated with mango softening. A rise in Ca^{+2}-dependent PL activity and pectin solubilization correlated with the pectate lyase transcript accumulation during ripening" (Sane *et al.,* 2005; Chourasia *et al.,* 2006). "Cellulase activity increased in several Indian mango cultivars like *Alphonso, Badami, Dashehari, and, Totapuri* etc. during ripening (Kim et al.,2007; Chourasia *et al.,* 2008). *MiCel1,* an endo-β-1, 4-glucanase homologue from mango showed fruit specific and ripening related expression. Its expression was positively correlated with an increase in EGase activity, particularly during the later stages of ripening" (Chourasia *et al.,* 2008). "The β-Galactosidase enzyme has been purified from *Harumanis* mango" (Ali *et al.,* 1995). "It was reported that this enzyme increases during developmental stages of mango fruit" (Rahman *et al.,* 2000). "It was reported that Arabinanase, Galactanase, and Mannanase are very prominent enzymes in mango fruit and their activity peaks at the climacteric stage of ripening" (Bhagyalakshmi *et al.,* 2002; Prabha *et al.,* 2000).

"Genes involved in ethylene biosynthesis, namely ACC synthase and ACC oxidase have been identified in mango" (Gomez- Lim, 1993; Lycett *et al.,* 1997; Deshpande et al., 2017). "The transcripts of these two genes are undetectable in unripe fruit and levels are high in ripe fruit. The expression of ACC oxidase has been shown to precede the transcript of ACC synthase" (Cruz-Hernandez and Gomez- Lim, 1995). Five ripening related cDNAs from two mango cultivars viz., *Alphonso* and *Totapuri* were isolated by Saiprasad and group (2004) using RT-PCR technique. The predicted polypeptides of these five clones were showing similarity to database protein sequences of PRl-1 protein, transcription initiation factor, CCR-4 protein, 18S ribosomal RNA gene, and 23S ribosomal RNA gene.

The information about mango ripening and aroma formation at the molecular level is still in infancy due to unavailability of genomic sequence. The first report about mango transcriptome came in 2014 using *Zill* variety of mango. Later in 2015, Dautt-Castro *et al.* reported transcriptomic study from *Kent* variety of mango using Illumina platform along with trinity software for the *de novo* assembly. Many aroma related genes were found from these transcriptomic studies. Dautt-Castro *et al.,* (2015) have reported six sucrose phosphate synthase genes, two sucrose phosphate phosphatase genes while seven sucrose synthase (SuSy) genes.

Besides these, 29 terpenoid backbone biosynthesis genes and Six LOX genes were identified in the transcriptome. Later on, transcriptomic data for *Dashehari* and *Alphonso* (Srivastava *et al.*, 2016; Deshpande *et al.*, 2017) was established. Fifty-four differentially expressed contigs related to aroma were detected in *Dashehari*. In *Alphonso* transcriptome data, six contigs encoding Monoterpenes synthases, five contigs encoding Sesquiterpene synthase, two furanones were found whereas multiple contigs coding for quinone oxidoreductase and O-methyltransferases were detected. A single contig encoding the hydroperoxide lyase and six contigs encoding 13-lipoxygenase were identified. The group also reported three contigs coding for epoxide hydrolase 2. Mango still faces challenges in tissue culture area, in comparison to other horticultural crops. The difficulties in getting tissue culture raised plant or transgenic are due to associated problems, viz., latent microbial infection, excessive polyphenol exudation, early explants necrosis, etc. In the early nineties, some preliminary reports about genetically transformed mango embryogenic cultures using *Agrobacterium tumefaciens* were published (Pandey *et al.*, 2022; Mathews *et al.*, 1992, 1993; Cruz- Hernandez *et al.*, (1997), however, genetic transformation of mango is still a big challenge.

Chin *et al*. (2019) employed proteomics to clarify the intricate ripening process at both cellular and molecular levels. The study employed 2-dimensional gel electrophoresis (2D-GE) in conjunction with MALDI-TOF/TOF to identify differentially abundant proteins throughout the ripening process of two tropical mango varieties, *Mangifera indica* cv. *Chokanan* and *Mangifera indica* cv. *Golden Phoenix*. The comparative analysis of the ripe and unripe stages of mango fruit mesocarp indicated that the differentially abundant proteins identified can be categorized into three groups: ethylene synthesis and aromatic volatiles, cell wall degradation, and stress-response proteins. An additional category of differential proteins identified from the *Chokanan* variety pertains to energy and carbohydrate metabolism. Among the differential proteins identified, only methionine gamma-lyase was present in both the *Chokanan* and *Golden Phoenix* varieties. Six differential proteins were chosen from each variety for validation through the analysis of their transcript expression via reverse transcription-quantitative PCR (RT-qPCR). The results indicated that two genes, glutathione S-transferase (GST) and alpha-1,4 glucan phosphorylase (AGP), exhibited expression consistent with protein abundance. Cissé *et al*., 2020 examined the impact of calcium carbide on the ripening of *Kent* mango fruit. This research shown that calcium carbide considerably decreases fruit ripening time from 6 days (naturally

ripened fruit) to 3 days (3 g/kg) and 4 days (1 g/kg). The current research also shown that spraying calcium carbide is ineffective in altering mango ripening duration. The physicochemical investigation revealed that CaC_2 may adversely affect some quality indicators, including firmness, pH, acidity, total soluble solids (3 g/kg, CaC_2 per fruit), and vitamin C content. Fruits treated with 1 and 3 g/kg had enhanced skin brightness and yellowness, whereas 1 g/kg resulted in a modest increase in total soluble solids compared to the control. Furthermore, the research determined that the ripening duration and alterations in quality metrics are contingent upon the dosage and manner used. Pathak *et al*. (2022) conducted de novo transcriptome assembly and analysis of *Mangifera indica* (*Dashehari*) using Illumina sequencing. The analysis of transcriptome data resulted in the identification of key genes associated with terpenoid, carotenoid, flavonoid, lactone, lipoxygenase, aromatic amino acid, alkaloid, and phenylpropanoid pathways, which may play a role in aroma biosynthesis. Comparative mRNA expression analysis across five mango varieties (*Dashehari*, *Banganpalli*, *Ratna*, *Mallika*, and *Alphonso*) demonstrated differences related to both variety and ripening stages.

Dong *et al*. (2024) examined the effects of exogenous melatonin on the postharvest ripening of mango (*Mangifera indica* L. cv. *Keitt*). The fruit were immersed in solutions of 0 (control), 100, or 200 μM melatonin for 30 minutes, followed by storage at room temperature (25 ± 1 °C). The findings indicated that melatonin treatments effectively delayed the ripening process, as evidenced by the inhibition of softening, respiration, color change, and chlorophyll degradation in stored fruit. Melatonin treatment at 200 μM significantly delayed the degradation of phosphatidylglycerol (PG) and phosphatidylinositol (PI), while promoting the accumulation of phosphatidylserine (PS) and phosphatidic acid (PA) in membrane phospholipids. Additionally, it inhibited the reduction of the unsaturated fatty acids (IUFA) index and reduced the levels of H_2O_2 and malondialdehyde (MDA) in the fruit exocarp. These effects may collectively enhance membrane integrity and contribute to the delayed ripening process of mango fruit during postharvest storage. The impact of layer-by-layer (LBL) application of chitosan (CH) and carboxymethyl cellulose (CMC) on mangoes during postharvest storage at 15 °C for 20 days was investigated by Ali *et al*. (2024). Mangoes were treated with monolayers of CH (1 % w/v) and CMC (1 % w/v), alongside LBL application of CH and CMC, and these treatments were compared to a control group. The application of CH and CMC-based LBL treatment on mangoes

led to a reduction in decay percentage and weight loss, while also increasing total chlorophyll pigments and inhibiting total carotenoid accumulation.

Studies related to the aroma in mango

In most mango growing countries, the bulk of mango produced is generally consumed as fresh fruit, harvested mostly in the ripened form. Flavour is an important attribute critical to consumer's acceptability. The changes in aroma components found in unripe and ripe fruits indicate that the increase in volatile components is linked to ripening (MacLeod and Snyder, 1985; Gomez-Lim, 1997). There have been several efforts to characterize ripe fruit flavour (Bartley and Schwede, 1987; Engel and Tressl, 1983; Koulibaly *et al., 1992*; MacLeod and Snyder, 1985). Engel and Tressl (1983) recognized monoterpenes as an essential class of volatiles contributing to mango flavour in *Haden, Keitt, Kent, Tommy Atkins*, etc. (Malundo *et al.*,1996, 1997). The only oxygenated volatile compounds found in those varieties were ethanol, acetaldehyde, and hexanal (MacLeod and Snyder, 1985; Malundo *et al.*, 1997). Indian varieties such as *Alphonso, Amrapali, Dashehari, Bombay, Mallika,* etc. have more oxygenated volatile compounds like esters, furanones, and lactones. The terpene hydrocarbons are considered to be essential contributors to the flavour of mango varieties such as *Keitt*, *Kent,* and *Tommy Atkins.* The aroma and volatile composition of mango are affected by various factors including mango species and cultivars difference, fruit maturity at harvest, post-harvest ripening and storage temperature, ripening methods, *etc.*

Kaswija *et al.* performed a comparative study on the effect on sensory attributes and aromatic composition of mango ripened by four different methods *(2006*). The authors kept one cluster of mangoes as a control, i.e., room temperature ripening (25-30ºC). The remaining three groups were given following treatments: (i) Smoked Pit Ripening (SPR), (ii) Untreated Pit Ripening (UPR) and (iii) Ethylene (fruit generated) Pit Ripening (EPR). They showed that the mangoes ripened by EPR and SPR accumulated a more significant number of aromatic compounds. The variation in aromatic volatiles among ripe fruits suggested that it might be due to the changes in the concentration of different aromatic compounds at differing stages of ripening. Vasanthaiah et al. (2007) determined that mangoes harvested at a mature green stage and then matured at temperatures above 15 °C had better flavour than those stored below 15 °C. Controlled

atmospheric storage at 13 °C and softening at 21° C + 1 °C expanded the shelf life of the mango *Kensington pride* without compromising the development of aroma compounds (Nair *et al.,* 2003; Lalel *et al.,* 2004).

Fruit maturity at harvest is one of the critical factors which affect ripening and flavour development in the ripe fruit (Vanoli *et al.,* 1995). Four maturity stages (hard mature, sprung mature green, half-ripe and ripe) were taken and studied during post-harvest ripening for flavour. The fruits harvested at sprung mature green stage exhibited a higher amount of the aroma volatiles, suggesting that sprung green stage should be preferred stage for harvesting (Lalel *et al.,* 2003a). Levels of ethylene were also found to be correlated with the profiles of specific volatiles of the ripening fruits (Lalel *et al.,* 2003b).

Pandit *et al.* (2009) had assessed volatiles blends of 22 Indian and five non-Indian cultivars using solvent extraction and gas chromatography. They reported 84 volatiles belonging to various chemical classes, namely, alcohol, aldehyde, monoterpene hydrocarbon, oxygenated monoterpene, sesquiterpene hydrocarbon, oxygenated sesquiterpene, lactone, ketone, and non-terpene hydrocarbon. 4-Ethoxy ethyl benzoate and an unidentified compound were included in this analysis in the "miscellaneous" category. Although terpene hydrocarbons dominated mango blends, their oxygenated derivatives were also present in mango cultivars and non-Indian varieties such as *Jaffna*, *Willard*, and *Parrot* (Macleod and Pieris, 1984), *Kensington Pride* (Lalel *et al.,* 2003c) and several Colombian cultivars (Quijano *et al.,* 2007). Although many authors have attempted to explore the aroma profiles of cultivated mango, few have studied the volatile composition of its mature raw fruit; no data is available on the chemistry of fruit development and maturation.

Pandit *et al.* (2009) tried to investigate the biochemistry of volatile formation from fruit maturation to ripening in the *Alphonso* variety of mango. A total of 55 volatiles belonging to various chemical classes such as aldehydes, alcohols, mono- and sesquiterpene hydrocarbons, lactones and furanones were identified. Different stages of the *Alphonso* fruit were defined by distinct volatile composition during the transformation from flower to ripe fruit. Ripe fruit was characterized by the *de novo* appearance of lactones and furanones in the blend of monoterpenes. Preethi *et al.* (2014) investigated the aroma blend of *Neelum* and *Bangnapalli*. The aroma

components identified from *Neelum* and *Banganapalli* were 24 and 31, respectively. *Neelam* aroma blend constituted esterase propenal, alkanes, ketones, alcohols, lactone, and acid as associates. In *Banganapalli*, alkanes were the prominent constituent followed by esters, alcohols, ethers, fatty acid, amino acid, triterpene, and sulfur. Sulfur and nitrogen mineral components also contribute to the aroma of mango fruits. Li *et al.,* (2017) explored the aroma profiling of 25 mango cultivars from China, America, Thailand, India, Cuba, Indonesia, and the Philippines. They used headspace solid-phase micro-extraction tandem gas chromatography-mass spectrometer methods to detect the volatile compositions, their related contents, and the inter-varietal differences. A total of 127 volatiles were found in all the cultivars, belonging to different chemical classes. The highest qualitative abundance of volatiles was detected in *Zihua* and lowest in *Mallika* cultivars. Terpene hydrocarbons were the major volatiles. Among them, terpinolene, 3-carene, caryophyllene, and α-Pinene were the dominant components depending on the cultivars. Monoterpenes were primary and most abundant volatile components, whereas aldehydes were least in mango pulp.

Aung *et al*. (2021) conducted combined metabolomics and flavoromic profiling. Fifty-six metabolites and thirty-three taste volatile components were identified in *Nam Dok Mai Si Thong* mango. Palmitic acid had the greatest concentration in the lipid component of mango pulp (28%), followed by linolenic acid (25%) and linoleic acid (23%) at different ripening phases. At day 0 of ripening, β-Sitosterol (3.9%), campesterol (2.4%), and sitostanol (2.4%) exhibited elevated levels. Glycine and leucine peaked at day 4 of ripening, at 3.4% and 3.0%, respectively. The peak sugar concentration (48.7%) was recorded after 8 days of ripening. Ethyl octanoate (6.2–9.5%) and ethyl decanoate (5.4–6.5%) exhibited substantially elevated levels throughout days 4 to 8 of ripening. Datir and Regan (2022) conducted a study on the mango variety *Nam Dok Mai*, recognized for its unique aroma and flavor. An integrative metabolomics and transcriptomics approach identified key volatile organic compounds (VOCs) responsible for the characteristic aroma of mango, including linalool, ethyl butanoate, and hexanal. Simultaneously, transcriptomic analysis indicated the expression profiles of genes associated with VOC biosynthesis, encompassing those related to terpene synthase (TPS), alcohol acyltransferase (AAT), and lipoxygenase (LOX) pathways.

The data integration revealed distinct correlations between volatile organic compounds (VOCs) and their associated biosynthetic genes. The production of linalool correlated with heightened expression of terpene synthase genes, whereas the production of ethyl esters was associated with alcohol acyltransferase activity. The temporal dynamics of aroma development indicate that various compounds reach their peak concentrations at specific ripening stages, with terpenes predominating in the early stages and esters in the later stages.
The findings establish a molecular framework for understanding aroma development in mangoes and identify potential targets for enhancing aroma quality via breeding and postharvest management strategies. Xin *et al*. (2022) investigated the volatile profile of *Tainong* mango, employing metabonomics and transcriptome analyses to examine the production of fragrance components during fruit growth and storage. Total acids, sugar, carotenoids, and enzyme activity were measured in the mango pulp samples. Gas chromatography-mass spectrometry identified volatiles in mango pulp. Real-time polymerase chain reaction was utilized to examine sample RNA sequences. In seven phases, 181 volatiles were extracted and identified from the fruit. Mango samples collected on days 8 and 12 exhibited higher levels of 17 volatile components, predominantly (E,Z)-2,6-nonadienal, while RNA sequencing identified 53,384 transcripts. The differentially expressed genes included activities related to catalysis, transferase functions, adenosine diphosphate binding, transcription factors, and oxidoreductase functions. The concentration of α-Pinene, along with gene expression related to terpenoid metabolism and enzyme activity, increased with fruit maturity, reaching a peak on day 8 of storage. Mangoes deteriorate post-harvest, altering their volatile compounds. Konjac glucomannan phosphate composite film (KGMP), an environmentally friendly polysaccharide-based material, demonstrates excellent film-forming capabilities, stability, antibacterial properties, and water vapor permeability. Li *et al*. (2024) investigate the impact of KGMP on the flavour and aroma of mangoes during storage. Mangoes were treated with KGMP before to and after harvest. The results indicated that KGMP inhibited weight loss, loss of firmness, and loss of colour difference. This postponed accumulation of total soluble solids, heightened titratable acidity, reduced ethylene production, and influenced aroma quality. *JinHwang*, *Keitt*, and *Ivory* had 39, 40, and 31 volatiles, respectively. Altering their contents related to ethylene production. KGMP altered around 70% of mango volatiles while exerting no impact on volatile abundance. The Pre-KGMP treatment had a more pronounced inhibitory effect on volatile abundances; nonetheless,

the increase in significant volatiles such as ethyl acetate, propyl propanoate, and ethyl hexanoate suggests that KGMP treatment might enhance flavor and shelf life. The presence of volatiles such as α-terpinene, diallyl disulfide, and α-phellandrene aids in differentiating mangoes under diverse conditions.

Phosphomevalonate kinase (PMK) is a crucial enzyme in the mevalonic acid (MVA) pathway, which is essential for the biosynthesis of isoprenoids, specifically terpenoids. Pathak *et al*. (2023) investigated two mango cultivars, *Dashehari* and *Banganpalli*, which exhibit contrasting spatio-temporal patterns of ripening polarity, to examine the role of MiPMK in aroma production. MiPMK transcription and enzyme activity exhibited an increase during the ripening process in both varieties. In *Dashehari*, expression in the early-ripening inner zones occurred prior to that in the later-ripening outer zones, whereas in *Banganpalli*, it was more pronounced in the early ripening outer zones. The polypeptide sequences of the two enzymes exhibited variations in several amino acids, which corresponded to differences in kinetic properties, including specific activity and pH optima. The silencing of MiPMK in *Dashehari* fruit via VIGS resulted in the suppression of kinase activity and alterations in the relative contributions of the mevalonic acid (MVA) and methylerythritol 4-phosphate (MEP) pathways. This also modified the fruit metabolite profile, resulting in a reduction or absence of sesquiterpenes, including geranyl geraniol, trans-farnesol, β-caryophyllene, β-pinene, bisabolene, and guaiane, while menthol and d-limonene emerged in silenced fruit. The research indicates that MiPMK levels may regulate downstream metabolite flux within the MVA pathway in mango.

Mangoes deteriorate post-harvest, altering their volatile compounds. Konjac glucomannan phosphate composite film (KGMP), an environmentally friendly polysaccharide-based material, demonstrates excellent film-forming capabilities, stability, antibacterial properties, and water vapor permeability. Li *et al*. (2024) investigate the impact of KGMP on the flavour and aroma of mangoes during storage. Mangoes were treated with KGMP before to and after harvest. The results indicated that KGMP inhibited weight loss, loss of firmness, and loss of colour difference. This postponed accumulation of total soluble solids, heightened titratable acidity, reduced ethylene production, and influenced aroma quality. *JinHwang*, *Keitt*, and *Ivory* had 39, 40, and 31 volatiles, respectively. Altering their contents related to ethylene production. KGMP altered around 70% of mango volatiles while exerting no impact on volatile abundance. The Pre-

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Conclusion and future prospect

During mango fruit ripening, various cell wall hydrolases, including polygalacturonase (PG), pectate lyase (PL), cellulase, and expansins, have been extensively studied at both biochemical and molecular levels. These enzymes play a significant role in the softening process by modifying the fruit's cell wall structure. Additionally, genes involved in ethylene biosynthesis, such as ACC synthase and ACC oxidase, have been identified as key regulators of ripening. Ethylene acts as a primary signaling molecule that modulates the activity of these enzymes either directly or indirectly. However, the precise role of these hydrolases in the softening process remains incompletely understood, requiring further molecular investigations. In terms of aroma, mango fruit is a rich source of volatile organic compounds, with terpenes constituting 51–95% of the total aroma volatiles. Across various mango cultivars, such as *Alphonso*, *Dashehari*, and *Kensington Pride*, a total of 578 volatile compounds have been identified, reflecting a wide diversity in chemical composition. These compounds contribute to the characteristic aroma profiles of different mango varieties, which are important for consumer preference and market value. Despite advancements in identifying and quantifying these metabolites, the molecular mechanisms underlying their biosynthesis, including the genes, enzymes, and regulatory networks involved, remain largely unexplored. While mango ripening has been comprehensively studied at physiological and biochemical levels, molecular studies are relatively sparse. Existing research on mango aroma and volatiles has predominantly focused on the identification and quantification of compounds, without delving into the genetic and enzymatic mechanisms governing their production. There is a critical gap in understanding how specific genes contribute to the biosynthesis of particular classes or groups of aroma compounds and how these processes are regulated during ripening. Addressing these gaps through advanced molecular and genomic approaches could provide insights into the fundamental biology of mango ripening and aroma formation, with implications for improving fruit quality and shelf life.

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