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Article in *Journal of Pineal Research* · August 2024

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## Phytomelatonin: From Intracellular Signaling to Global Horticulture Market

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## ABSTRACT

Melatonin (*N*-acetyl-5-methoxytryptamine), a well-known mammalian hormone, has been having a great relevance in the Plant World in recent years. Many of its physiological actions in plants are leading to possible features of agronomic interest, especially those related to improvements in tolerance to stressors and in the postharvest life of fruits and vegetables. Thus, through the exogenous application of melatonin or by modifying the endogenous biosynthesis of phytomelatonin, some change can be made in the functional levels of melatonin in tissues and their responses. Also, acting in the respective phytomelatonin biosynthesis enzymes, regulating the expression of tryptophan decarboxylase (*TDC*), tryptamine 5-hydroxylase (*T5H*), serotonin *N*-acetyltransferase (*SNAT*), *N*-acetylserotonin *O*-methyltransferase (*ASMT*), and caffeic acid *O*-methyltransferase (*COMT*), and recently the possible action of deacetylases on some intermediates offers promising opportunities for improving fruits and vegetables in postharvest and its marketability. Other regulators/effectors such as different transcription factors, protein kinases, phosphatases, miRNAs, protein–protein interactions, and some gasotransmitters such as nitric oxide or hydrogen sulfide were also considered in an exhaustive vision. Other interesting aspects such as the role of phytomelatonin in autophagic responses, the posttranslational reprogramming by protein-phosphorylation, ubiquitylation, SUMOylation, PARYlation, persulfidation, and nitrosylation described in the phytomelatonin-mediated responses were also discussed, including the relationship of phytomelatonin and several plant hormones, for chilling injury and fungal decay alleviating. The current data about the phytomelatonin receptor in plants (*CAND2*/*PMTR1*), the effect of UV-B light and cold storage on the postharvest damage are presented and discussed. All this on the focus of a possible new action in the preservation of the quality of fruits and vegetables.

**Abbreviations:** 13-LOX, 13-lipoxygenase; 3-OHM, cyclic 3-hydroxy melatonin; 4CL, ligase; 5GT, anthocyanin 5-O-glucosyltransferase; 5-MT, 5-methoxytryptamine; 6PGDH, 6-phosphogluconate dehydrogenase; 9-LOX, 9-lipoxygenase; AA, ascorbic acid; AAO, abscisic aldehyde oxidase; AAT, alcohol acyltransferase; AA/GSH, ascorbate/glutathione; ABA, abscisic acid; ABA1, xanthoxin dehydrogenase; ABF, ABA-responsive element-binding factor; ABTS, 2,2-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid); ACC, 1-aminocyclopropane-1-carboxylic acid; ACO, ACC oxidase; ACS, ACC synthase; ACX, acyl-CoA oxidase; ADC, arginine decarboxylase; ADH, alcohol dehydrogenase; ADP, adenosine diphosphate; ADT, argenase dehydratase; AFB1, aflatoxin B1; H<sub>2</sub>NBH<sub>3</sub>, ammonia borane (ammoniotrihydroborate); AMP, adenosine monophosphate; ANR, anthocyanidin reductase; AnS, anthranilate synthase; AOC, allene oxide cyclase; AOMT, anthocyanidin 3'-methyltransferase; AOS, allene oxide synthase; AOX, alternative oxidase; AP2/ERF, APETALA2/ethylene-responsive element-binding factor; APX, ascorbate peroxidase; APY1, apyrase 1; ARF, auxin response factor; ARG, arginase; ASDAC, *N*-acetylserotonin deacetylase; ASMT, *N*-acetylserotonin methyltransferase; ATG, AuTophagy-related; ATG8-PE, ATG8-phosphatidylethanolamine; ATHB, homeobox-leucine zipper protein; ATP, adenosine triphosphate; ATPase, ATP synthase; ATP-CL, ATP-citrate lyase; AV, acid value; BA, benzoic acid; BA2H, benzoic acid-2-hydroxylase; BRs, brassinosteroids; BSO, L-buthionine-sulfoximine; bZIP, basic leucine zipper; C2H2, cysteine 2/histidine 2; C4H, cinnamic acid 4-hydroxylase; CA, controlled atmosphere; Ca<sup>2+</sup>/CaM, calcium/calmodulin; CaCl<sub>2</sub>, calcium chloride; CAD, cinnamate dehydrogenase; CaMs, calmodulins; CAND2, candidate G protein-coupled receptor 2; CAO, chlorophyll a oxygenase; CAT, catalase; CBB, cassava bacterial blight; CBF1, binding factors; CBLs, calcineurin B-like; CBR, NYC1, chlorophyll b reductase; CCO, cytochrome c oxidase; CCR, cinnamoyl-CoA reductase; CCR, cinnamoyl-CoA reductase; CCT, choline-phosphate cytidylyltransferase; CC-NBS-LRR, coiled-coil nucleotide-binding site leucine-rich repeat; CDPKs or CPKs, calcium-dependent protein kinases; Cel, cellulase; Cer, ceramides; CER1, eceriferum 1; cGMP, guanosine 3'; 5'-cyclic monophosphate; CHI, chalcone isomerase; CHI, chalcone isomerase; Chlase, chlorophyllase; CHS, chalcone synthase; CH-M, chitosan-based melatonin edible coating; CKs, cytokinins; CKX, cytokinin oxidase/dehydrogenase; ClO<sub>2</sub>, chlorine dioxide; CMC-Gel-M, carboxymethyl cellulose-gelatin-melatonin edible coating; CMLLA, chitosan-based melatonin layer-by-layer assembly; CMLs, calcium-binding protein; CMLs, calcium-binding protein; CMV, cassava common mosaic virus; CNGCs, cyclic nucleotide-gated ion channels; CO, carbon monoxide; CoA, 4-coumaric acid:coenzyme A; COLD1, chilling tolerance divergence 1; *COMT*, caffeic acid *O*-methyltransferase; COP1, constitutively photomorphogenic1; CrHYD1, hydrogenase1 gene from *Chlamydomonas reinhardtii*; CRTISO, carotenoid isomerase; CRT/DRE, C-repeat/dehydration-responsive element.

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# 1 | Introduction

Melatonin (*N*-acetyl-5-methoxytryptamine), an indole derivative of tryptophan and a well-known animal hormone, is related to the regulation of different rhythms such as sleep/wakefulness, endocrine, mood, corporal temperature, and others, and also studied in several dysfunctions such as neurological, cancer, and viral therapies [1–8]. Melatonin was discovered in cows in 1958, in humans in 1959 [9, 10], and surprisingly in plants in 1995 by three teams simultaneously [11–13]. Currently, it has been presented as a new plant hormone and as an exciting plant master regulator [14, 15]. In plants, melatonin, so-called phytomelatonin, is a pleiotropic molecule with relevant actions in multiple physiological aspects such as seed germination, stem and root growth, rooting, photosynthesis and stoma regulation, leaf senescence, parthenocarp, fruit set, ripening and senescence of fruits, among others [14–21]. In addition, it plays an essential role in regulating abiotic stress situations (drought, salinity, extreme temperatures, soils contaminated by heavy metals or pesticides, UV radiation, etc.) and biotic stress (mainly bacteria, fungi, and viruses) [22–34]. Phytomelatonin can regulate the redox network in plants, restoring the redox homeostasis state in stressful situations, detoxifying both reactive oxygen species (ROS) and reactive nitrogen species (RNS), activating the ascorbate/glutathione (AA/GSH) cycle and the detoxification enzyme system including GSH-related enzymes [22, 35]. These antioxidant and detoxifying capacities of melatonin are in addition to their regulatory activity as a hormone-regulating hormone in plants. Thus, melatonin can modulate the levels and action of phytohormones such as auxin, gibberellin (GAs), cytokinins (CKs), abscisic acid (ABA), and ethylene, also from jasmonic acid (JA), salicylic acid (SA), and

brassinosteroids (BRs) in stressful situations [21, 36, 37]. All these melatonin-mediated effects imply significant changes at the transcriptional level acting on primary and secondary metabolism elements as described [15, 35].

Owing to health-promoting bioactive phytochemicals exhibiting ROS scavenging potential, horticultural crops exhibit commercial value, nutritional worthiness, and health benefits. Horticultural crop consumption is favorable for ensuring human health by confining chronic diseases such as cancer, cardiovascular, and neurodegenerative diseases in industrial countries [38]. During postharvest life, qualitative and quantitative deterioration of horticultural crops as highly perishable commodities imposes significant economic losses to horticultural industries. Elucidating physiological, biochemical, and molecular regulatory mechanisms governing postharvest storability will enable us to advance strategies for improving horticultural crop marketability. Low-temperature storage has been employed extensively to extend the postharvest life of horticultural crops. However, horticultural crops suffer from chilling injury and fungal decay, which confine low-temperature storage. In addition to conferring tolerance to chilling injury and fungal decay, attempts to introduce safe, eco-friendly strategies for ameliorating stresses, postponing senescence, and preserving horticultural crops' organoleptic and nutritional quality have emerged in recent years [39–41]. In recent years, melatonin has emerged as a universal biostimulator and signaling biomolecule with great potential in the horticultural industry. Insights into physiological, biochemical, and molecular mechanisms employed by exogenous melatonin application will give us a worthy economic

CS, citrate synthase; CTR, constitutive triple response; CuAO, copper binding diamine oxidase; CUPRAC, cupric reducing antioxidant power; CV, chloroplast vesiculation; CYP707A, ABA 8'-hydroxylase; Cyt c, cytochrome c; Cyt c/a, cytochrome c/a; DAO, diamine oxidase; DCD, D-cysteine desulhydrase; DES1, L-cysteine desulhydrase 1; DFR, dihydroflavonol reductase; DG, diacylglycerol; DHA, dehydroascorbate; DHAR, dehydroascorbate reductase; DORN1/P2K1, does not respond to nucleotides 1; DPPH, 2,2-diphenyl picrylhydrazyl; DREB1, dehydration-responsive element-binding protein 1; ED51, enhanced disease susceptibility 1; EGase, endo-1,4-β-glucanase; eIF2, eukaryotic initiation factor 2; eIF4F, eukaryotic initiation factor 4F; EIL5, ethylene insensitive like5; EIN2, ethylene insensitive; EPT, ethanolaminephosphotransferase; ER, endoplasmic reticulum; Er4P, erythrose-4-phosphate; ERF, ethylene response factor; ERL3, ethylene insensitive 3; ETR, ethylene receptor; EXP, expansin; F3H, flavanone 3'-hydroxylase; F3' H, flavonoid 3'-hydroxylase; FAD3 and FAD7, fatty acid desaturase 3 and 7; FK, fructokinase; FLS, flavonol synthase; FRAP, ferric reducing antioxidant power; Fv/Fm, photosynthetic efficiency; G6PDH, glucose-6-phosphate dehydrogenase; GA20ox, GA 20-oxidase; GA2ox, GA 2-oxidase; GABA, γ-aminobutyric acid; GABA-T, γ-aminobutyric acid transaminase; GAD, glutamate decarboxylase; GAs, gibberellin; GC, guanylate cyclase; GDH, glutamate dehydrogenase; GGGT, GDP-L-galactose guanylyltransferase; GLDH, L-galactonol-1,4-lactone dehydrogenase; GME, GDP-D-mannose-3',5'-epimerase; GMPH, mannose-1-phosphate guanylyltransferase; GOGAT, glutamate synthase; GPAT4/8, glycerol-3-phosphate acyltransferase 4/8; GPCR, G protein-coupled receptor; GPP, L-galactose-1-phosphate phosphatase; GPX, glutathione peroxidase; GR, glutathione reductase; GRX, glutaredoxin; GS, glutamine synthetase; GSH, glutathione; GSNOR, S-nitrosogluthathione reductase; GSSG, oxidized glutathione; GST, Glutathione S-transferase; Gt1, rice seed storage protein glutelin; GTs, glycosyltransferases; GWD, α-glucan water dikinase; G/T/M, glutenin/tamarind gum/melatonin bioactive film; G/T-M-E, glutenin/tamarind gum loaded with the binary microemulsion of melatonin/pumello essential oil; Gα; GPA1, heterotrimeric G protein α subunit; H<sub>2</sub>, molecular hydrogen; H<sub>2</sub>O<sub>2</sub>, hydrogen peroxide; H<sub>2</sub>S, hydrogen sulfide; HDA9, histone deacetylase 9; HK, hexokinase; HO1, heme oxygenase 1; HOS1, high expression of osmotically responsive gene1; HPL, hydroperoxide lyase; HRW, hydrogen-rich water; HSE, GAANNTTC, heat shock elements; Hsf20, heat stress transcription factor 20; HSP40, heat shock protein 40 kDa; HY5, elongated hypocotyl 5; HYD, β-carotene hydroxylase; IAA, indole-3 acetic acid; ICDH, isocitrate dehydrogenase; ICE1, inducer of CBF expression 1; ICS, isochorismate synthase; ICS, isochorismate synthase; IDO, indoleamine 2,3-dioxygenase; INS3, inositol 1,4,5-trisphosphate; INV, invertase; IPL, isochorismate pyruvate lyase; JA, jasmonic acid; KAO, ent-kaurenoic acid oxidase; KO, ent-kaurene oxidase; KS, ent-kaurene synthase; LAC, laccase; LacCer, lactosylceramides; LAH, lipolytic acyl hydrolase; LAR, leucoanthocyanidin reductase; LCD, L-cysteine desulhydrase; LD, luzindole; LOG, LONELY GUY; LPA, lysophosphatidic acid; LPC, lysophosphatidylcholine; LPE, lysophosphatidylethanolamine; LPI, lysophosphatidylinositol; LPS, lipase; LUT1/5, lutein-deficient 1/5; M2H, melatonin 2-hydroxylase; M3H, melatonin 3-hydroxylase; MA1, melatonin biosynthesis 1; MAPK, mitogen-activated protein kinase; MDA, malondialdehyde; MDC, SGR/NYE1, Mg-dechelate; MDHAR, monodehydroascorbate reductase; MEJA, methyl jasmonate; MET1, DNA (cytosine-5)-methyltransferase 1; MOF-MEL, melatonin-loaded UiO-66 metal-organic framework nanoparticles; MPTP, mitochondrial permeability transition pores; MSRA/B, methionine sulfoxide reductase; MVK, mevalonate kinase; MYO, myrosinase; NADH-CWP, NADH-dependent cell wall peroxidase; NADK, NAD kinase; NADP-IDH, NADP-dependent isocitrate dehydrogenase; NAS, N-acetylserotonin; NCA, N-carbamoylputrescine amidase; NCED, 9-cis-epoxycarotenoid dioxygenase; NDH, NADH dehydrogenase; NO, nitric oxide; NOA1, NO-associated 1; NOS, nitric oxide synthase; NP, nanoparticles; NR, nitrate reductase; NTR1, NADPH-dependent thioredoxin reductase; N-INV, neutral invertase; O<sub>2</sub><sup>-</sup>, superoxide anion; OAT, ornithine aminotransferase; ODC, ornithine decarboxylase; OGDH, 2-oxoglutarate dehydrogenase; OPDA, oxophytodienoic acid; OPDAR, OPDA reductase; P5CR, pyrroline-5-carboxylate reductase; P5CS, pyrroline 5-carboxylate synthetase; PA, phosphatidic acid; PAL, phenylalanine ammonia-lyase; PaO, pheophorbide a oxygenase; PaO, pheophorbide a oxygenase; PAP, phosphatidate phosphatase; PC, phosphatidylcholine; PCD, programmed cell death; PCM, phase change material; PDC, pyruvate decarboxylase; PDH, pyruvate dehydrogenase; PDS, phytoene desaturase; PE, phosphatidylethanolamine; PEP, phosphoenolpyruvate; PEPC, phosphoenolpyruvate carboxylase; PEPCCK, phosphoenolpyruvate carboxykinase; PG, phosphatidylglycerol; PGI, phosphoglucoisomerase; phyB2, phytochrome B2; PhytoCer, phytoceramides; PI, phosphatidylinositol; PI3K, phosphatidylinositol 3-kinase; PIF4, phytochrome interacting factors; PIP, aquaporins; PIP, aquaporins; PIP2-PLC, phosphatidylinositol 4,5-bisphosphate (PIP2)-dependent phospholipase C; PLA1, phospholipase A1; PLA2, phospholipase A2; PLC, phospholipase C; PLD, phospholipase D; PLP, pyridoxal 5-phosphate; PME, pectin methyltransferase; POD, peroxidase; PP2C12, protein phosphatase 2C 12; PPD, postharvest physiological deterioration; PPH, phytophthasin; PPO, polyphenol oxidase; PRI, pathogenesis-related gene 1; ProDH, proline dehydrogenase; PRPP, 5-phosphoribosyl-1-pyrophosphate; PRX, peroxiredoxin; PS, phosphatidylserine; PsbO, protein 1 PsbO1 in PSII; PSKR1, phytosulfokine receptor 1; PSKA, phytosulfokine α; PSY, phytoene synthase; PTL, pattern-triggered immunity; Put, putrescine; PV, peroxide value; PYL, ABA-receptor protein; p-CPA, p-chlorophenylalanine; RAPTOR1, regulatory-associated protein of TOR; RBOH, respiratory burst oxidase homologs; RBOH, NADPH oxidase, respiratory burst oxidase homologues; RCCR, red chlorophyll catabolite reductase; RGA1, rice G-protein α subunit 1; RNAI, RNA interference; RNS, reactive nitrogen species; ROS, reactive oxygen species; RUP1 and RUP2, UV-B photomorphogenesis 1 and 2; SA, salicylic acid; SAM, S-adenosyl-L-methionine; SAMDC, S-adenosylmethionine decarboxylase; SAMS, S-adenosylmethionine synthase; SAM-MTase, SAM-dependent methyltransferase; SCL, succinate-CoA ligase; SCW, secondary cell wall; SDH, succinate dehydrogenase; SERT, serotonin reuptake transporter; SKDH, shikimate dehydrogenase; SKK, shikimate kinase; SNAT, serotonin N-acetyltransferase; SNO, S-nitrosothiol; SnRK1α/KIN10, SNF1-related protein kinase catalytic subunit alpha KIN10; SnRKs, sucrose nonfermenting-1 (SNF1)-related protein kinases; SOD, superoxide dismutase; SorDH, sorbitol dehydrogenase; SOX, sorbitol oxidase; Spd, spermidine; SPDS, spermidine synthase; Sph, sphingosine; Spm, spermine; SPS, sucrose-phosphate synthase; SSADH, succinic semialdehyde dehydrogenase; STS, stilbene synthase; SuSy, sucrose synthase; SuSy-C, sucrose synthase cleavage; SuSy-S, sucrose synthase synthesis; SUT2, sugar transporter/sucrose carriers; SWEET10, sugars will eventually be exported transporter; TSH, tryptamine 5-hydroxylase; TA, titratable acidity; TAL, tyrosine ammonia lyase; tCA, trans-cinnamic acid; TDC, tryptophan decarboxylase; TEAC, Trolox equivalent antioxidant capacity; TG, triacylglycerols; TGase, transglutaminase; TOR, target of rapamycin; TPP, trehalose-phosphate phosphatase; TPS, trehalose-phosphate synthase; TrpS, tryptophan synthase; Trx2, thioredoxins; TSS, total soluble solids; TyrDC, tyrosine decarboxylase; UCP, mitochondrial uncoupling protein; UFGT, UDP glucose-flavonoid-3-O-glycosyltransferase; unsFA/SFA, unsaturated/saturated fatty acids; UVR8, UV resistance locus 8; VDE, violaxanthin de-epoxidase; WSD1, wax-ester synthase; XET, xyloglucan endotransglucosylase; XTH, xyloglucan endotransglucosylase/hydrolase; YUC, yucca flavin monooxygenase; YUCCA, indole-3-pyruvate monooxygenase; ZAT10, zinc finger protein 10; ZAT7/6/12, zinc finger; ZDS, β-carotene desaturase; ZEP, zeaxanthin epoxidase; β-1,3-Glu, β-1,3-glucanase; β-GAL, β-galactosidase; β-Glu, β-glucosidase; ε-LCY and β-LCY, lycopene cyclase; ΔΨm, mitochondrial membrane potential.

attractive opportunity for ameliorating stresses, postponing senescence, and preserving the organoleptic and nutritional quality of horticultural crops during postharvest life. Recently, considerable research has been invested in improving the postharvest marketability of horticultural crops by exogenous melatonin application or endogenous phytemelatonin accumulation. Owing to environmental and human health risks, exogenous melatonin application as an environmentally friendly strategy or developing plants to extend shelf life by manipulating endogenous phytemelatonin accumulation would be highly economically attractive [16, 42, 43].

In this review, we have elucidated the physiological, biochemical, and molecular mechanisms employed by exogenous melatonin for ameliorating stresses, postponing senescence, and preserving the organoleptic and nutritional quality of horticultural crops as a worthy attractive economic opportunity for improving horticultural crops' marketability. Thus, a detailed analysis of the role of phytemelatonin in postharvest physiology of fruits and vegetables is presented, with emphasis on situations of stress. Thus, the most relevant studies on the biosynthesis of phytemelatonin and its regulation by different transcription factors and protein kinases, among others, the current knowledge about the phytemelatonin receptor in plants, and several studies on melatonin and the effect of UV-B light, the effect of cold storage and the postharvest damage are presented and discussed, including the relationships of melatonin with the plant hormones involved in postharvest physiology. All this on the focus of a possible new action in the preservation of the quality of fruits and vegetables.

## 2 | Phytemelatonin Biosynthesis and Its Genetic and Epigenetic Regulation

### 2.1 | Phytemelatonin Biosynthesis and Its Intracellular Homeostasis

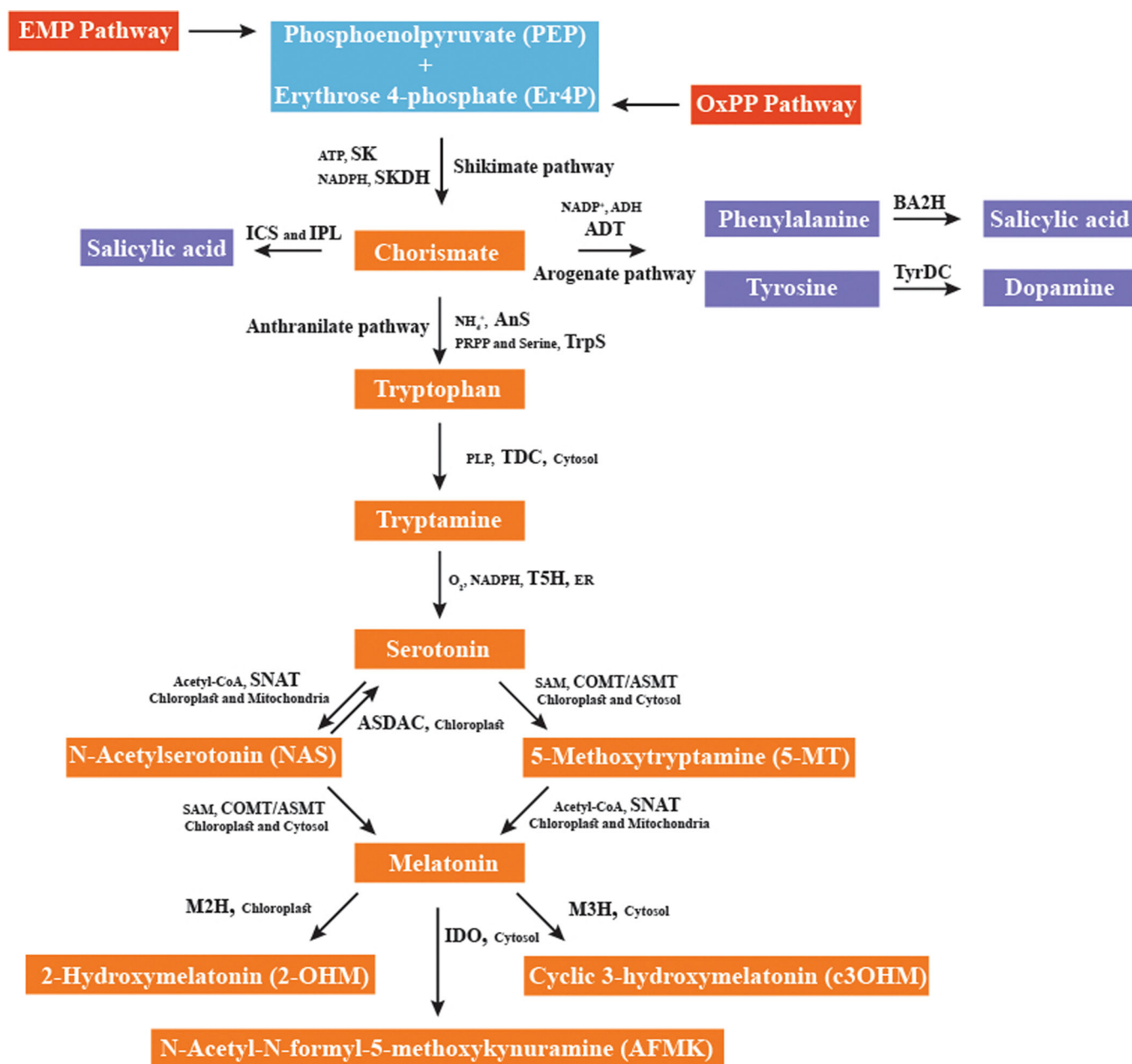
Phosphoenolpyruvate (PEP) provided from the glycolysis (EMP) pathway and erythrose 4-phosphate (Er4P) provided by oxidative pentose phosphate (OxPP) pathway, shikimic acid pathway represented by NADPH-dependent shikimate dehydrogenase (SKDH) and ATP-dependent shikimate kinase (SKK) enzymes are responsible for endogenous tryptophan, tyrosine and phenylalanine biosynthesis [39, 44]. The shikimic acid pathway provides sufficient intracellular tryptophan. In plants, tryptophan decarboxylase (TDC) is accountable for tryptamine biosynthesis from tryptophan in the cytosol, while tryptamine 5-hydroxylase (T5H) is accountable for serotonin biosynthesis from tryptamine in the endoplasmic reticulum. Then, serotonin *N*-acetyltransferase (SNAT) in chloroplast and mitochondria is responsible for *N*-acetylserotonin biosynthesis from serotonin or melatonin biosynthesis from 5-methoxytryptamine (5-MT). *N*-acetylserotonin *O*-methyltransferase (ASMT) or caffeic acid *O*-methyltransferase (COMT) is accountable for melatonin biosynthesis from *N*-acetylserotonin or 5-methoxytryptamine biosynthesis from serotonin in the cytosol, chloroplast and mitochondria [14, 42, 45, 46]. In plants, pyruvate dehydrogenase (PDH) dependent acetyl-CoA supplies prevalent ROS-generating chloroplasts and mitochondria organelles for facilitating SNAT activity for melatonin biosynthesis [47]. In chloroplast, SNAT is

accountable for acetyl-CoA-dependent serotonin acetylation into NAS, while *N*-acetylserotonin deacetylase (ASDAC) in rice (HDAC10) and Arabidopsis (HDAC14) is responsible for *N*-acetylserotonin deacetylating into serotonin (Figure 1). Therefore, SNAT and HDAC activity might be accountable for preserving chloroplast serotonin status for melatonin biosynthesis during senescence and stress [48]. By evolving COMT from ASMT during plant terrestrialization with gene duplication, COMT acquired UV-protective monolignols such as *p*-coumaryl alcohol and coniferyl alcohol biosynthesis capacity, as well as melatonin as a relevant ROS/RNS scavenging molecule [49]. Tsunoda et al. [50] reported that transgenic tomato fruits overexpressing the TDC1 gene displayed higher serotonin biosynthesis. In addition, exogenous serotonin application or endogenous serotonin biosynthesis by TDC1 gene overexpressing is accountable for accelerating fruit ripening by activating colorless non-ripening (SPL-CNR) transcription factor and its downstream ACC oxidase 1 (*ACO1*) and ACC synthase 2/4 (*ACS2/4*) expression [50]. Yang et al. [51] reported that transgenic rice overexpressing *TDC1* gene driven by rice seed storage protein glutelin (Gt1) promoter displayed higher endogenous serotonin biosynthesis in rice endosperm (rice endosperm serotonin fortification), which was accompanied by higher grain quality and promising agronomical traits. Higher endogenous serotonin biosynthesis was associated with higher endogenous lysine accumulation in rice endosperm in transgenic rice overexpressing the *TDC1* gene, which may be favorable for health and nutrition.

Wang et al. [52] reported that transgenic apple and Arabidopsis ectopically overexpressing mouse serotonin reuptake transporter (*MmSERT*) gene displayed higher endogenous phytemelatonin accumulation, which was associated with lower superoxide anion ( $O_2^-$ ) generation and hydrogen peroxide ( $H_2O_2$ ) accumulation, thus protecting membrane integrity, evidenced by lower electrolyte leakage and malondialdehyde (MDA) accumulation, under salinity stress. In plants, plasma membrane-localized *MmSERT* is crucial for reuptakes extracellular serotonin for intracellular phytemelatonin accumulation, which not only is accountable for improving salt resistance of transgenic apple and Arabidopsis by activating the expression of salt-responsive genes but also diminishes the sensitivity of transgenic apple and Arabidopsis to ABA [52]. Indoleamine 2,3-dioxygenase (IDO) activity in plants is accountable for cytosolic AFMK production from melatonin [53]. In the cytosol, melatonin 2-hydroxylase (M2H) activity is responsible for 2-hydroxy melatonin production from melatonin, while melatonin 3-hydroxylase (M3H) activity is accountable for cyclic 3-hydroxy melatonin (3-OHM) production from melatonin in the chloroplast [54–57]. Phytemelatonin biosynthesis genes *TDC*, *T5H*, *SNAT*, *ASMT*, and *COMT* expression regulatory mechanisms have been illustrated in Figure 2.

### 2.2 | Phytemelatonin Biosynthesis Regulation by Histone Deacetylase (HDAs)

During cassava bacterial blight (CBB) development, cassava plants displayed higher histone deacetylase 9 (HDA9) gene expression [58]. Zhao et al. [58] reported that cassava plants overexpressing HDA9 displayed lower tolerance to CBB, which



**FIGURE 1** | Phytomelatonin biosynthesis pathway in plants. TDC, T5H, SNAT, ASMT, and COMT enzymes are responsible for phytomelatonin biosynthesis from shikimate pathway dependent tryptophan in cytosol, chloroplast and mitochondria. In addition, M2H enzyme in chloroplast and M3H and IDO enzymes in cytosol are responsible for melatonin metabolism. SNAT and ASDAC enzymes are responsible for endogenous serotonin homeostasis maintenance.

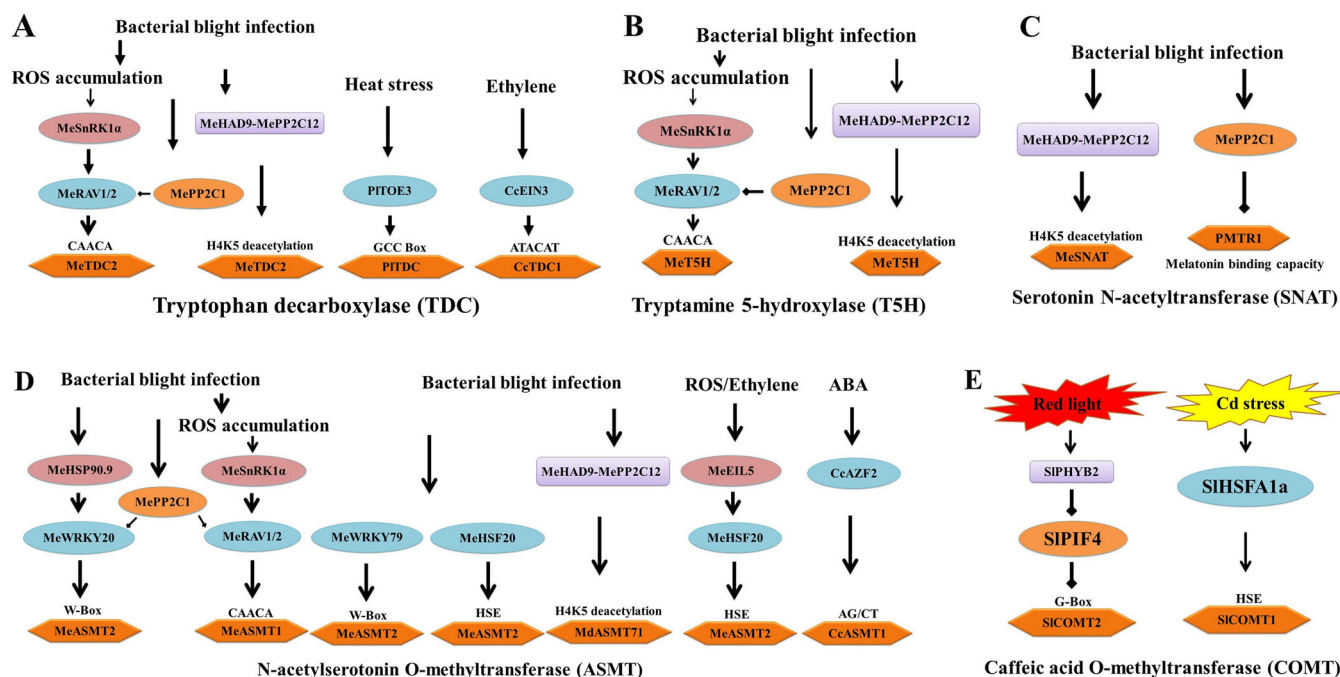
was associated with lower endogenous phytomelatonin biosynthesis by lower *TDC2*, *T5H*, *SNAT*, and *ASMT2* expression, while HDA9 virus-induced gene silencing cassava plants displayed higher tolerance to CBB, which was associated with higher endogenous phytomelatonin biosynthesis by higher *TDC2*, *T5H*, *SNAT*, and *ASMT2* expression. This demonstrates that HDA9 negatively regulates cassava disease resistance. These authors reported that HDA9 binds to the promoters of *TDC2*, *T5H*, *SNAT*, and *ASMT2* and represses their expression via lysine 5 of histone 4 (H4K5) deacetylation, thus suppressing endogenous phytomelatonin biosynthesis. Also, HDA9 physically interacted with protein phosphatase 2C 12 (PP2C12) in vivo and in vitro, and PP2C12 negatively regulates CBB resistance by

interacting with HDA9 through suppressing endogenous phytomelatonin accumulation (Figure 2C).

### 2.3 | Phytomelatonin Biosynthesis Regulation by Transcription Factors (TFs)

By promoting ROS accumulation under bacterial blight infection, RAV1 and RAV2 transcription factors are responsible for conferring cassava resistance front bacterial blight by activating endogenous phytomelatonin biosynthesis. ROS-responsive RAV1 and RAV2 transcription factors directly bind to the CAACA motif in the promoters of *TDC2*, *T5H*, and *ASMT1*,





**FIGURE 2** | Phytomelatonin biosynthesis genes *TDC* (A), *T5H* (B), *SNAT* (C), *ASMT* (D), and *COMT* (E) expression regulatory mechanisms. In plants, SnRK1-RAV1/2, TOE3, and EIN3 transcription factors are responsible for regulating *TDC* gene expression. SnRK1-RAV1/2 transcription factor and histone deacetylase 9 HDA9 are responsible for regulating *T5H* gene expression. In addition, histone deacetylase 9 (HDA9) is responsible for regulating *SNAT* gene expression while protein phosphatase 1 PP2C1 is responsible for PMTR1 melatonin binding capacity. HSP90.9-WRKY20, SnRK1-RAV1/2, WRKY79, HSF20, EIL5-HSF20, and AZF2 transcription factors and HDA9 are responsible for regulating *ASMT* gene expression. HSFA1a and PHYB2-PIF4 transcription factors are responsible for regulating *COMT* gene expression.

thereby activating their expression and boosting endogenous phytomelatonin biosynthesis for enhancing cassava resistance against bacterial blight [59] (Figure 2A,B,D).

In addition to RAV1 and RAV2 transcription factors, the heat-shock factor A1a (HsfA1a) transcription factor regulates plant melatonin biosynthesis. Cai et al. [60] reported that the HsfA1a transcription factor is responsible for conferring cadmium (Cd) stress tolerance to tomato plants by promoting endogenous phytomelatonin biosynthesis. By Cd stress, the HsfA1a transcription factor is responsible for activating *COMT1* expression via direct binding to heat shock elements (HSE, GAANNTTC) in the promoter of *COMT1* and enhancing its expression (Figure 2E). Chen et al. [61] reported that the ethylene-responsive transcription factor EIN3 directly binding to EIN3-binding sites (ATACAT, ATGTAT, ATGTAC, or CTACAT) in the promoter of *TDC1*, triggers *TDC1* expression. Additionally, they reported that the ABA-responsive transcription factor AZF2 directly binds to the A (G/C)T-box in the promoter of *ASMT1* and triggers *ASMT1* expression. These authors found that the transcription factors EIN3 (response to ethylene) and AZF2 (response to abscisic acid) play a role in activating the expression of *TDC1* and *ASMT1*, respectively, which accelerated endogenous phyto-melatonin biosynthesis in hickory nuts. Wei et al. [62] demonstrated that WRKY79 and heat-shock transcription factor 20 (Hsf20) transcription factors directly binding to heat-shock elements (HSE, GAANNTTC) and W-box elements (TTGACC/T) in the promoter of *ASMT2*, respectively, activating *ASMT2* expression, ultimately enhancing tolerance

to CBB through increased endogenous phytomelatonin accumulation. Zhang et al. [63] reported that the APETALA2/ethylene-responsive element-binding factor (AP2/ERF) transcription factor, TOE3, directly binds to the promoter of TDC and activating its expression, enhancing high-temperature stress tolerance by promoting endogenous phytomelatonin biosynthesis in herbaceous peony. By bacterial cassava blight infection, promoting endogenous ROS burst-dependent ethylene biosynthesis and signaling could be responsible for improving immune response. By ethylene signaling, ethylene-responsive transcription factor ethylene insensitive like5 (EIL5) could be accountable for promoting endogenous melatonin biosynthesis by interaction with heat stress transcription factor 20 (Hsf20) in the nucleus and promoting its transcriptional activation activity for activating *ASMT2* expression, thereby promoting endogenous melatonin biosynthesis [64]. EIL5 enhances the transcriptional activation of the melatonin biosynthesis gene *ASMT2* by Hsf20 without binding to its promoter. EIL5 interacts with Hsf20 to promote the expression of *ASMT2* independently of ethylene. In addition, EIL5 could improve the antibacterial activity of pathogen-related gene 3 (PR3) by promoting the physical interaction of Hsf20 and PR3. Hsf20 interacted with PR3 to improve its antibacterial activity. In addition, the antibacterial activity of PR3–Hsf20 was higher than that of PR3 alone, and the antibacterial activity of EIL5–PR3–Hsf20 was higher than that of PR3–Hsf20. These results showed that Hsf20 enhances the antibacterial activity of PR3 and that EIL5 enhances the antibacterial activity of Hsf20 and PR3. Therefore, EIL5 exhibits dual roles in fine-tuning melatonin accumulation and antibacterial activity by employing Hsf20, which illustrates the ethylene-

responsive EIL5 as the integrator of ethylene and melatonin signals in the immune response in cassava [64]. Wei et al. [65] showed that HSP90.9 interacts with WRKY20, which facilitates WRKY20's transcriptional activation on ASMT2 by binding to W-box elements in the ASMT2 promoter and activating *ASMT2* expression to confer tolerance to CBB by increasing endogenous phyto melatonin biosynthesis or suppressing auxin biosynthesis (Figure 2D).

## 2.4 | Phytomelatonin Biosynthesis Regulation by Protein Kinases and Phosphatases

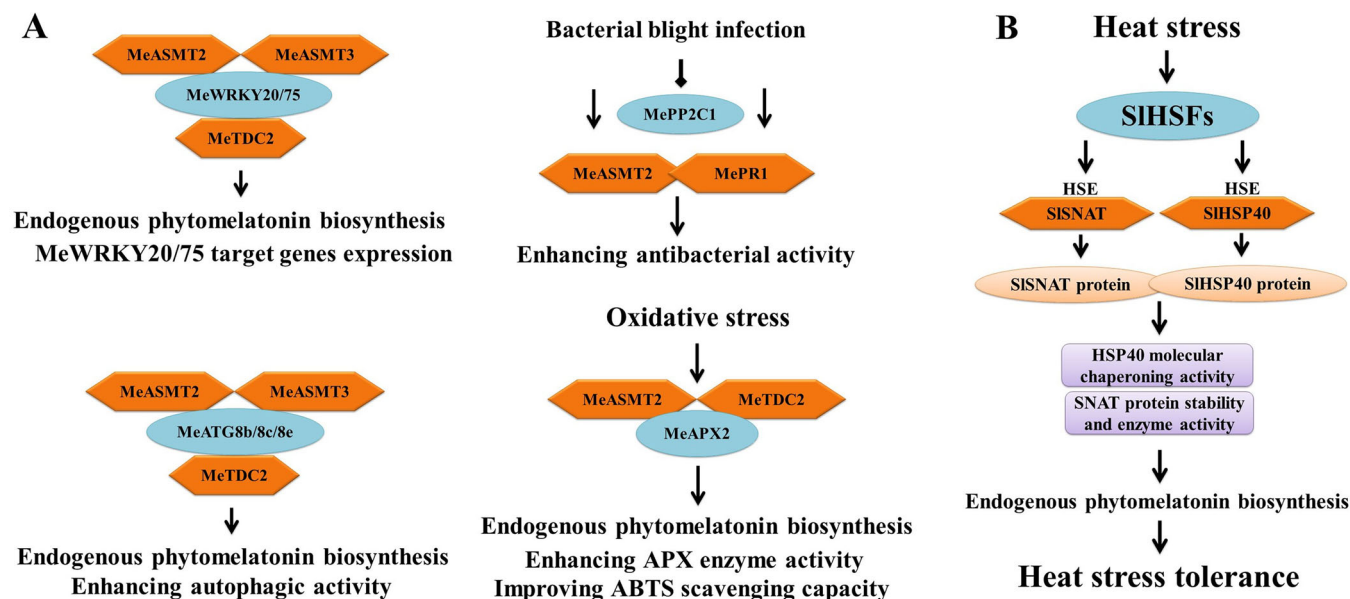
As well as RAV1 and RAV2 transcription factors, ROS-responsive SNF1-related protein kinase catalytic subunit alpha KIN10 (SnRK1 $\alpha$ 1/KIN10) is responsible for physical interaction with and phosphorylation of Serine 45 in RAV1 and Serine 44 in RAV2 which promotes transcriptional activation of *CAT6* and *CAT7* by RAV1/2. Phosphorylation of RAV1/2 by SnRK1 (KIN10) under oxidative stress accelerated the direct binding of RAV1/2 to CACCTG and CAACA motifs in *CAT6* and *CAT7* promoters and activated their expression, which is essential for oxidative stress resistance in cassava as evidenced higher *CAT6* and *CAT7* expression and CAT activity, lower ROS accumulation favorable for preserving membrane integrity [66]. RAV1/2 was located in the nucleus, whereas KIN10 was located in both the nucleus and the cytoplasm. Therefore, cytoplasm into the nucleus translocation of KIN10 might be crucial for the phosphorylation of RAV1/2 during oxidative stress [67]. In addition to activating *CAT6* and *CAT7* expression, phosphorylation of RAV1/2 by SnRK1 (KIN10) under oxidative stress accelerated endogenous phyto melatonin biosynthesis. Wei et al. [68] reported that coat protein is accountable for the pathogenicity determinant of cassava common mosaic virus (CMV) casual of cassava mosaic disease by direct interaction with RAV1/2 transcription factors, which interferes with the interaction of KIN10 with RAV1/2 transcription factors. Wei et al. [68] reported that coat protein inhibits RAV1/2 transcription factors phosphorylation at Serine 45 and Serine 44 by competitively binding to RAV1/2 with KIN10 thereby inhibits transcriptional activation activity of RAV1/2 on melatonin biosynthetic *TDC2*, *T5H*, and *ASMT1* genes along with ROS scavenging *CAT6* and *CAT7* genes. Therefore, coat protein is accountable for attenuating cassava's antiviral responses by suppressing endogenous phyto melatonin biosynthesis and repressing ROS-scavenging CAT activity. KIN10 improves cassava resistance against CMV via interaction with and phosphorylation of RAV1/2 transcription factors at Serine 45 and Serine 44, thereby promoting transcriptional activation activity of RAV1/2 on melatonin biosynthetic *TDC2*, *T5H*, and *ASMT1* genes along with ROS scavenging *CAT6* and *CAT7* genes, which enhances endogenous phyto melatonin biosynthesis along with promotes ROS scavenging CAT activity [68]. Therefore, SnRK1 might be liable for boosting endogenous phyto melatonin biosynthesis and ROS scavenging activity by employing RAV1 and RAV2 transcription factors. In addition to SnRK1 kinase, mitogen-activated protein kinase (MAPK or MAP kinase) also is crucial for regulating endogenous phyto melatonin biosynthesis. Song et al. [69] reported that WRKY17 directly binds to the W-box

cis-element in the ASMT7 promoter, which activates *ASMT7* expression, enhancing endogenous phyto melatonin biosynthesis and conferring drought tolerance in apple plants. Also, ASMT7 is a plasma membrane-localized enzyme accountable for melatonin biosynthesis from NAS. Exogenous melatonin application or biotic/abiotic stressors boosts mitogen-activated protein kinases (MPK3 and MPK6) activity, which might be liable for WRKY17 phosphorylation, which enhances WRKY17 transcription factor binding to the ASMT7 promoter and activates endogenous phyto melatonin biosynthesis by activating *ASMT7* expression. The authors proposed that boosting MPK3 and MPK6 kinase activity by melatonin receptor PMTR1 under melatonin treatment or endogenous phyto melatonin biosynthesis could be crucial for regulating melatonin biosynthesis through the MPK3/6-WRKY17-ASMT7 signaling pathway, which could serve as a promising procedure for producing transgenic melatonin-fortify apples [69]. More research is needed to clarify the role of protein kinases such as calcium-dependent protein kinases (CDPKs) and the target of rapamycin (TOR) in the regulation of phyto melatonin biosynthesis (Figure 2D).

In addition to SnRK1 and MPK3/6, protein phosphatases are also involved in regulating plants' melatonin biosynthesis. In cassava, melatonin biosynthesis 1 (MA1) encodes type 2C protein phosphatase 1 (PP2C1), a negative regulator of endogenous phyto melatonin biosynthesis and signaling. Bai et al. [70] reported that PP2C1 physically interacts with RAV1/2 and WRKY20 in the nucleus. In addition, PP2C1 dephosphorylates RAV1/2 at serine35/34 and WRKY20 at serine176, suppressing RAV1/2 transcriptional activation activity on ASMT1, TDC2, and T5H, as well as WRKY20 transcriptional activation activity on ASMT2 [70]. In addition to suppressing melatonin biosynthesis, PP2C1 interacts with phyto melatonin receptor PMTR1 at the plasma membrane and dephosphorylates phyto melatonin receptor PMTR1 at serine 11, inhibiting melatonin binding and downstream melatonin signaling [70].

## 2.5 | Phytomelatonin Biosynthesis Regulation by Protein-Protein Interactions (PPIs)

PPI reported for melatonin biosynthesis enzymes has been illustrated in Figure 3. Wei et al. [71] reported that WRKY20 and WRKY75 interaction with TDC2, ASMT2, and ASMT3 enzymes not only promotes the transcriptional activity of WRKY20/75 on W-box elements (TTGACC/T) but also triggers endogenous melatonin biosynthesis by enhancing TDC2 and ASMT2/3 activity. Therefore, melatonin biosynthetic TDC2, ASMT2, and ASMT3 enzymes can employ WRKY20/75 transcription factors at the nucleus for promoting endogenous melatonin biosynthesis along with the transcriptional activity of WRKY20/75 on the W-box [71]. Wei et al. [72] reported that TDC2, ASMT2, and ASMT3 interaction with ATG8b/8c/8e promoted endogenous melatonin biosynthesis and enhanced autophagic activity and autophagosome accumulation. In addition, PP2C1 interaction with ASMT2 is responsible for interfering interaction between ASMT2 and PR1. By CBB infection, activating *ASMT2* and *PR1* expression was associated with suppressing



**FIGURE 3** | Protein-protein interaction (PPI) reported for melatonin biosynthesis enzymes. ASMT2/3-WRKY20/75-TDC2 interaction is responsible for promoting endogenous phytomelatonin biosynthesis and WRKY20/75 target expression. ASMT2-PR1 interaction is responsible for enhancing antibacterial activity. ASMT2/3-ATG8b/8c/8e-TDC2 interaction is responsible for promoting endogenous phytomelatonin biosynthesis and enhancing autophagy activity. ASMT2-APX2-TDC2 interaction is responsible for improving ROS scavenging capacity. SNAT-HSP40 interaction is responsible for improving SNAT protein stability and promoting endogenous phytomelatonin biosynthesis.

*PP2C1* expression. By suppressing *PP2C1*, ASMT2 releasing from *PP2C1*, promoted ASMT2 interaction with *PR1*, thereby promoting the antibacterial activity of *PR1* without promoting ASMT2 activity for melatonin biosynthesis, which confers disease resistance [73]. Bai et al. [74] observed that the interaction of ASMT<sub>2</sub>-APX2 and TDC<sub>2</sub>-APX2 promotes APX activity, which is accompanied by endogenous phytomelatonin biosynthesis, thus enhancing 2,2-azino-bis-3-ethylbenzothiazoline-6-sulfonic acid (ABTS) radical scavenging activity (Figure 3A). By functioning as a molecular chaperone, heat shock protein 40 kDa (HSP40) interaction with SNAT in chloroplasts maintains SNAT enzyme stability which supports endogenous phytomelatonin biosynthesis during heat stress, according to Wang et al. [75] (Figure 3B).

## 2.6 | Phytomelatonin Biosynthesis Regulation by Posttranscriptional miRNAs and Posttranslational Persulfidation (H<sub>2</sub>S)

Recently, posttranscriptional regulation of melatonin biosynthesis genes by miRNAs has been reported by Bhowal et al. [76] *TDC5* and *ASMT18* expression in rice seedlings is regulated by miR6249a and miR-1846e, respectively. During light/dark regimes and environmental stress, the opposite expression of osa-miR6249a-OsTDC5 and osa-miR1846e-OsASMT18 pairs has been validated by qRT-PCR [76]. In addition, post-translational persulfidation of melatonin biosynthesis enzymes has been reported by Wang et al. [77]. Exogenous hydrogen sulfide (H<sub>2</sub>S) application conferred osmotic stress resistance in Arabidopsis by activating L-cysteine desulfhydrase 1 (*DES1*) expression, boosting endogenous H<sub>2</sub>S biosynthesis, enhancing

endogenous phytomelatonin biosynthesis resulting from the activation of the expression of *ASMT*, *SNAT*, and *COMT1* genes and S-sulfhydration or persulfidation of ASMT and SNAT proteins.

## 3 | Melatonin, TOR/SnRK1 Signaling and Autophagic Activity

By external environmental stimuli and internal developmental cues, triggering autophagy (AuTophagy; *ATG*) expression is responsible for autophagosome formation and autophagic activity in plants, which serves as a protective strategy for maintaining cellular homeostasis and promoting plant growth or survival. In plants, *ATGs* expression regulation at transcriptional, posttranscriptional, translational, and posttranslational levels have emerged as potential strategies for orchestrating autophagy. In addition, nuclear DNA methylation, histone methylation, and acetylation could be employed for epigenetically regulating *ATGs* expression for cytoplasmic autophagosome formation and autophagy activation in plants. By external environmental stimuli and internal developmental cues, transcriptional factors could be used by ROS and phytohormones signaling pathways for triggering *ATGs* expression, thereby cytoplasmic autophagosome formation and autophagic activation in plants [78]. By external environmental stimuli and internal developmental cues, TOR and SnRK1 could orchestrate autophagy by posttranslational phosphorylation of *ATGs* in plants. By sufficient sugars and energy supply, TOR serves as a negative regulator of cytoplasmic autophagosome formation and autophagic activation by ATG13 phosphorylation, while SnRK1 serves as a positive regulator of cytoplasmic autophagosome formation and autophagic activation under sugars and



energy deficiency by ATG6 phosphorylation [78, 79]. Insufficient intracellular sucrose supply means lower trehalose-6-phosphate biosynthesis could be responsible for SnRK1 activation, thereby promoting autophagy by TOR-dependent or independent pathway [80]. In addition, higher endogenous ABA accumulation under an unfriendly environment could be responsible for promoting autophagy by the SnRK2/TOR signaling pathway. By sufficient intracellular sucrose supply, higher trehalose-6-phosphate biosynthesis could be accountable for SnRK1 inhibition, thereby suppressing autophagy by TOR signaling pathway [81–83].

By activating autophagy under senescence and stresses, fatty acids, amino acids, and sugars supplied from macromolecule degradation could be responsible for intracellular energy and carbon skeletons supplying and avoiding intracellular ROS accumulation. In addition to intracellular energy homeostasis, autophagy activation could be responsible for chloroplast, peroxisome, and mitochondria maintaining and clearance [80, 84–86]. By nutrient or energy deficiency in Arabidopsis, SnRK1 is responsible for autophagy induction by suppressing TOR activity, demonstrating that SnRK1 acts upstream of TOR in the activation of autophagy in Arabidopsis [87]. Recently, Belda-Palazón et al. [88] proposed that promoting growth while suppressing stress response by SnRK2 kinases could be ascribed to nuclear SnRK<sub>2</sub>–PP2C–SnRK1 repressor molecular machinery formation which by enabling TOR kinase activity allow growth during low intracellular ABA accumulation. By higher intracellular ABA accumulation during stresses, ABA binding to PYR1/PYL/RCARs promotes PP2C sequestration, which allows SnRK2 and SnRK1 releasing from SnRK<sub>2</sub>–PP2C–SnRK1 repressor molecular machinery. SnRK2 and SnRK1 trigger stress responses and inhibit growth by accelerating TOR kinase phosphorylation [88, 89]. By ABA accumulation during stress, nuclear to cytoplasm translocation of SnRK1 could be responsible for phosphorylation and suppressing cytoplasmic TOR activity while promoting stress response [90].

In addition to the regulatory function of SnRK1 $\alpha$ 1/KIN10 in endogenous phyto-melatonin biosynthesis, SnRK1 $\alpha$ 1/KIN10 and TOR kinases could be employed by exogenous melatonin application for conferring stress tolerance in plants. Supriya et al. [91] reported that melatonin treatment by seed priming improved drought stress tolerance in cotton seedlings by boosting endogenous phyto-melatonin accumulation accompanied by boosting *SOD*, *CAT*, *APX*, monodehydroascorbate reductase (*MDHAR*), dehydroascorbate reductase (*DHAR*), and *GR* expression and activity along suppressing respiratory burst oxidase homologues D (*RBOHD*; NADPH oxidase) expression, which might be liable for higher endogenous AA and GSH accumulation, lower endogenous O<sub>2</sub><sup>•−</sup> generation and H<sub>2</sub>O<sub>2</sub> accumulation, thereby stabilizing membrane integrity. As well as ROS homeostasis, endogenous phyto-melatonin accumulation was associated with higher glutamine synthetase (*GS*) and glutamate synthase (*GOGAT*) expression and activity (*GS*/*GOGAT* pathway), which might be liable for boosting proline, GSH, and  $\gamma$ -aminobutyric acid (*GABA*) accumulation by endogenous glutamate providing. By endogenous phyto-melatonin biosynthesis, suppressing the *TOR* expression might be liable for boosting autophagy activity by activating *ATG2*, *ATG9*, *ATG18a*, *ATG5*, *ATG12*, *ATG7*, *ATG8c*, and *ATG8i* expression and boosting *ATG8*-phosphatidylethanolamine

(*ATG8*-PE) protein accumulation [91]. Recently, Supriya et al. [92] reported that cotton seeds priming with melatonin conferred drought stress tolerance in cotton plants, which was associated with higher endogenous phyto-melatonin accumulation along with lower endogenous ABA accumulation through suppressing 9-*cis*-epoxycarotenoid dioxygenase (*NCED3*) expression. In addition, lower endogenous glucose accumulation through activating sugars will eventually be exported transporter (*SWEET10*) and sugar transporter/sucrose carriers (*SUT2*) expression was associated with lower endogenous trehalose 6-phosphate accumulation through suppressing trehalose phosphate synthase (*TPS63*) expression along with activating trehalose phosphate phosphatase (*TPP22*) expression. By cotton seeds priming with melatonin, activating *MPK6* expression and promoting *MPK6* protein accumulation in cotton plants under drought stress could be responsible for activating *SnRK2.6* expression along with enhancing *SnRK1* (*KIN10*) expression and protein accumulation. By activating *SnRK2* and *SnRK1* expression, suppressing regulatory-associated protein of TOR (*RAPTOR1*) expression could be responsible for promoting autophagic activity by activating *ATG8c* and *ATG8f* expression along with enhancing *ATG8* lipidation by phospholipid phosphatidylethanolamine (higher *ATG8*-PE accumulation). Therefore, MAPK activation by melatonin could be responsible for ABA-independent *SnRK2*–*SnRK1* signaling pathway activation and TOR signaling pathway inactivation, contributing to drought stress tolerance by promoting autophagy activity [92].

#### 4 | Phyto-melatonin Signaling by CAND2/PMTR1 Receptor

The first melatonin receptor discovered in plants was called AtCAND2/AtPMTR1 by Prof. Qi Chen's group in Arabidopsis [93], which functions as a G protein-coupled receptor boosting its direct interaction with the heterotrimeric G protein  $\alpha$  subunit (G $\alpha$ ; GPA1) leads to enhanced production of ROS by activating NADPH oxidase. This activation boosts Ca<sup>2+</sup> influx and promotes K<sup>+</sup> efflux, ultimately facilitating stomatal closure [93]. Later, in 2021, plasma membrane phyto-melatonin receptor 1 (ZmPMTR1) was also described in maize plants [94], where the stimulation of the ROS scavenging system provides osmotic and drought stress tolerance. Li et al. [95] have shown that Arabidopsis can benefit from drought resistance because of the daily rhythmicity of melatonin generation and signaling. Daytime enhanced expression of the *PMTR1* gene was linked to melatonin signaling, which in turn was mediated by higher melatonin biosynthesis, *ASMT*, *SNAT1*, and *COMT1* expression. Throughout the day, activating stomatal closure at night and transmitting signals in darkness may be attributed to ROS signaling initiated by melatonin through PMTR1. By maintaining ROS dynamics, this rhythmicity helps to reduce water loss and improve water-use efficiency [95].

Exogenous melatonin accelerates stomatal closure via PMTR1, GPA1 melatonin receptor, and signaling-dependent ROS production by NADPH oxidase activation in tobacco plants. As well as melatonin treatment, endogenous phyto-melatonin biosynthesis in guard cells of transgenic tobacco overexpressing

soybean SNAT1 could be responsible for accelerating stomatal closure via PMTR1 and GPA1 melatonin receptor and signaling ROS production by NADPH oxidase activation [96]. Melatonin treatment or endogenous phytemelatonin biosynthesis by overexpressing soybean SNAT1 suppressing phenylalanine ammonia-lyase (*PAL*), chalcone isomerase (*CHI*), chalcone synthase (*CHS1*), flavonol synthase (*FLS2*), and dihydroflavonol reductase (*DFR*) expression might be liable for lower flavonoid biosynthesis leading to higher ROS accumulation in transgenic tobacco guard cells accelerating stomatal closure [96]. In this system, exogenous kaempferol application or boosting endogenous kaempferol biosynthesis by overexpressing *FLS2* might be accountable for suppressing stomatal closure by repressing ROS accumulation; flavonols exhibiting potent ROS scavenging activity that inhibit stomatal closure by impeding ROS signaling. The authors proposed that melatonin biosynthesis and signaling by PMTR1 and GPA1 interfere with flavonol biosynthesis to promote ROS accumulation for accelerating stomatal closure in tobacco plants [96]. Wang et al. [97] reported that PMTR1 is indispensable for endogenous phytemelatonin signaling by the PMTR1-GPA1 pathway for promoting NADPH-dependent ROS accumulation. By ROS accumulation, nitrate reductase (*NR*) and NO-associated 1 (*NOA1*) dependent NO biosynthesis are accountable for accelerating stomatal closure in Arabidopsis.

*Panax notoginseng* and *Arabidopsis thaliana* seedlings displayed higher SNAT1 and COMT1 expression in melatonin treatments, followed by higher *PMTR1* expression. By activating PMTR1-dependent melatonin signaling, promoting MPK3/6 and GPA1-independent signaling pathways might boost stomatal immunity by serving as a plant pattern-triggered immunity (PTI) response [98]. As well as the MPK3/MPK6 signaling pathway, PMTR1 interaction with GPA1 facilitates stomatal closure by activating NADPH oxidase-dependent ROS generation and boosting  $\text{Ca}^{2+}$  signaling independently of the MAPK signaling pathway [98]. By PMTR1/MAPKs and PMTR1/GPA1 signaling pathway, facilitating stomatal closure is crucial for preventing water loss and bacterial infection during nighttime [99, 100].

Zhang et al. [101] reported that transmembrane candidate G protein-coupled receptor 2 (*CAND2*) protein serves as a melatonin receptor in cotton. By melatonin treatment, enhancing *CAND2* expression in cotton plants is accountable for conferring salt tolerance. By melatonin receptor gene *CAND2* silencing using virus-induced gene silencing (VIGS) technology, cotton plants displayed higher salt stress sensitivity as shown by higher  $\text{H}_2\text{O}_2$  accumulation resulting from lower SOD activity. By the melatonin signaling pathway, G protein-coupled receptor *GCR1* as melatonin receptor *CAND2*/PMTR1 interaction with GPA1 might be liable for phosphatidylinositol 4,5-bisphosphate (PIP2)-dependent phospholipase C (PIP2-PLC) activation boosting second messenger inositol 1,4,5-triphosphate (*Ins3P*) accumulation which promotes cytosolic  $\text{Ca}^{2+}$  accumulation [101]. Also, in *CAND2* silencing, cotton plants displayed lower melatonin signal transduction responsible genes *GCR1*, *GPA1*, *PLC*, *ITPK* expression, and lower ROS scavenging activity conferring high salt stress sensitivity [101]. Barman et al. [102] reported that the melatonin receptor of rice, OsPMTR, is a plasma membrane-localized seven-transmembrane protein equivalent to the G-protein coupled receptor. Barman et al. [102]

confirmed the interaction of PMTR with rice G-protein  $\alpha$  subunit 1 (*RGA1*) and chilling tolerance divergence 1 (*COLD1*). By melatonin treatment, rice seedlings displayed higher abiotic stress tolerance responsive interacting proteins partners (*RGA1* and *COLD1*) along with transcription factors (*TGA2.1*, *WRKY90*, *DREB6/ERF60* and *TCP5*) were significantly induced by exogenous melatonin treatment. Phytemelatonin signaling and its possible actions for improving fruits and vegetables quality have been illustrated in Figure 4.

## 5 | Phytemelatonin and Light Signaling Pathways

### 5.1 | UV-B Light Signaling Regulation by Melatonin

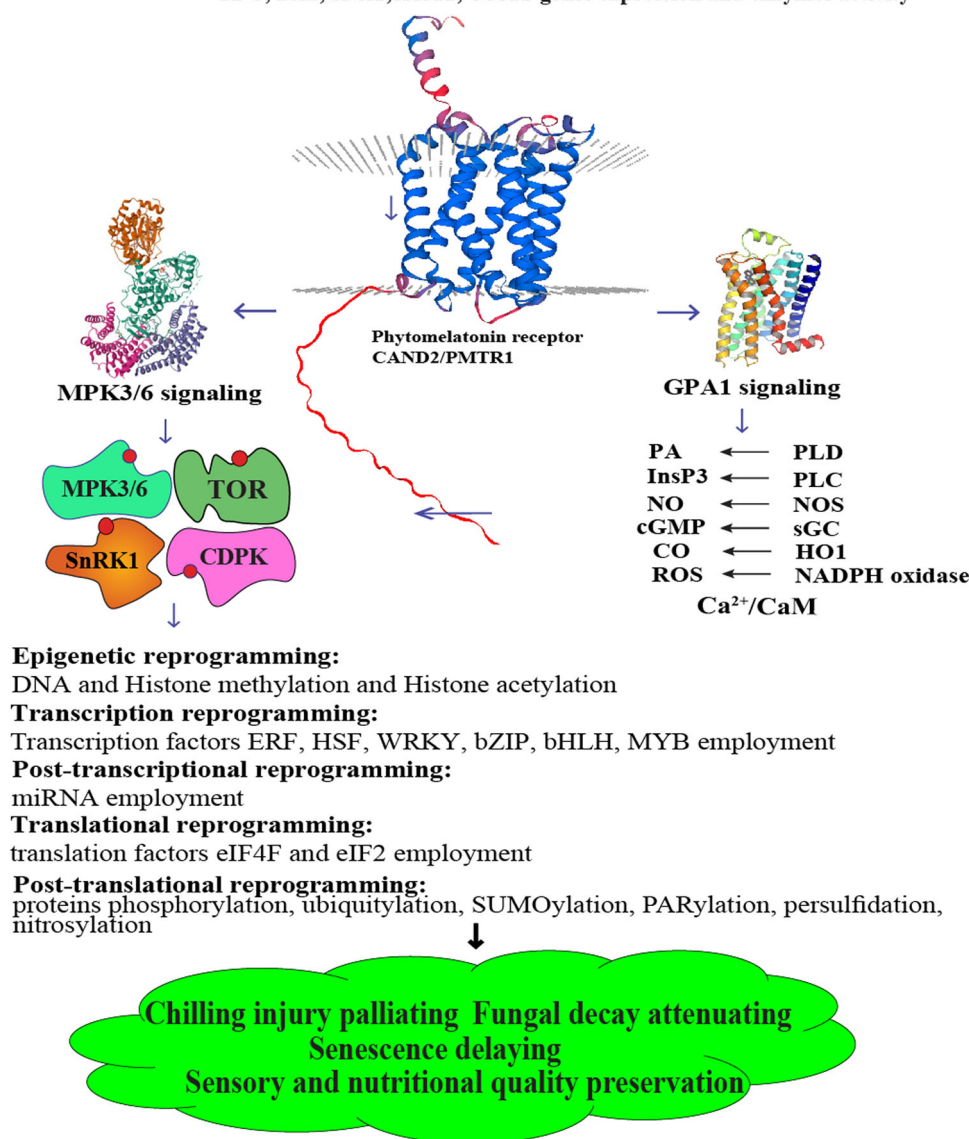
To improve UV-B stress resistance, melatonin as a ROS and RNS scavenger regulates UV resistance locus 8 (*UVR8*)-constitutively photomorphogenic 1 (*COP1*)-elongated hypocotyl 5 (*HY5*) signaling pathway [103]. In Arabidopsis, UV-B light promotes endogenous phytemelatonin biosynthesis by activating *SNAT*, *ASMT*, and *COMT* expression through the *UVR8*-*COP1*-*HY5* signaling pathway. Melatonin treatment conferred oxidative stress tolerance during UV-B light by enhancing *CAT* and *APX* activity and declining  $\text{H}_2\text{O}_2$  and *MDA* accumulation. Exogenous melatonin delays repressor of UV-B photomorphogenesis 1 and 2 (*RUP1* and *RUP2*) expression while boosting *COP1* and *HY5* expression, thereby employing the UV-B signaling pathway for improving antioxidant systems for the stabilizing of Arabidopsis leaves from UV-B stress [33, 103]. Therefore, melatonin employs the UV-B signaling pathway by delaying *RUP1/2* expression for boosting *UVR8*-*COP1*-*HY5* signaling pathway activity. As well as exogenous melatonin, endogenous phytemelatonin biosynthesis by *SNAT* gene overexpression employed the UV-B signaling pathway by boosting *UVR8*-*COP1*-*HY5* transcriptional activity for higher *CAT*, *APX*, and *SOD* expression, lower  $\text{O}_2^-$  generation, and  $\text{H}_2\text{O}_2$  accumulation, and stabilizing membrane integrity [33, 103]. By UV-B application and *UVR8* gene VIGS silencing, Jiang et al. [104] reported that UV-B light signaling by *UVR8* receptor might be liable for palliating chilling injury in tomato fruits by activating *SOD* and *CAT* expression and activity, inhibiting  $\text{O}_2^-$  generation and  $\text{H}_2\text{O}_2$  accumulation, and stabilizing membrane integrity.

Gao et al. [105] reported that melatonin treatment or endogenous phytemelatonin accumulation in apple plants overexpressing *ASMT9* confers tolerance to nitrogen deficiency accompanied by improving photosynthesis efficiency. By quantitative proteomics analysis, Gao et al. [105] reported that apple plants overexpressing *ASMT9* displayed higher glycolysis along with higher *GABA* shunt proteins, which was associated with higher sucrose, glucose and fructose accumulation along with higher arginine, glutamate, histidine, lysine, threonine, and aspartate accumulation. By melatonin treatment or endogenous phytemelatonin accumulation in apple plants overexpressing *ASMT9*, activating *HY5* expression might be liable for directly binding to the nitrate transporters (*NRT2.1* and *NRT2.4*) promoters, thereby activating their expression [105]. By melatonin treatment or increased phytemelatonin accumulation in apple plants overexpressing *ASMT9*, improving photosynthetic efficiency and boosting  $\text{NO}_3^-$

## Exogenous melatonin application

### Endogenous phytomelatonin accumulation

*TDC, T5H, SNAT, ASMT, COMT* genes expression and enzymes activity



**FIGURE 4** | Phytomelatonin signaling and its possible actions for improving fruits and vegetables quality. By exogenous melatonin application and endogenous phytomelatonin biosynthesis, CAND2/PMTR1 dependent MPK3/6 and GPA1 signaling pathways could be responsible for employing SnRKs, TOR, and CDPK signaling cascade for attenuating chilling injury and fungal decay, delaying senescence and preserving organoleptic and nutritional quality of horticultural products by activating epigenetic and genetic mechanisms.

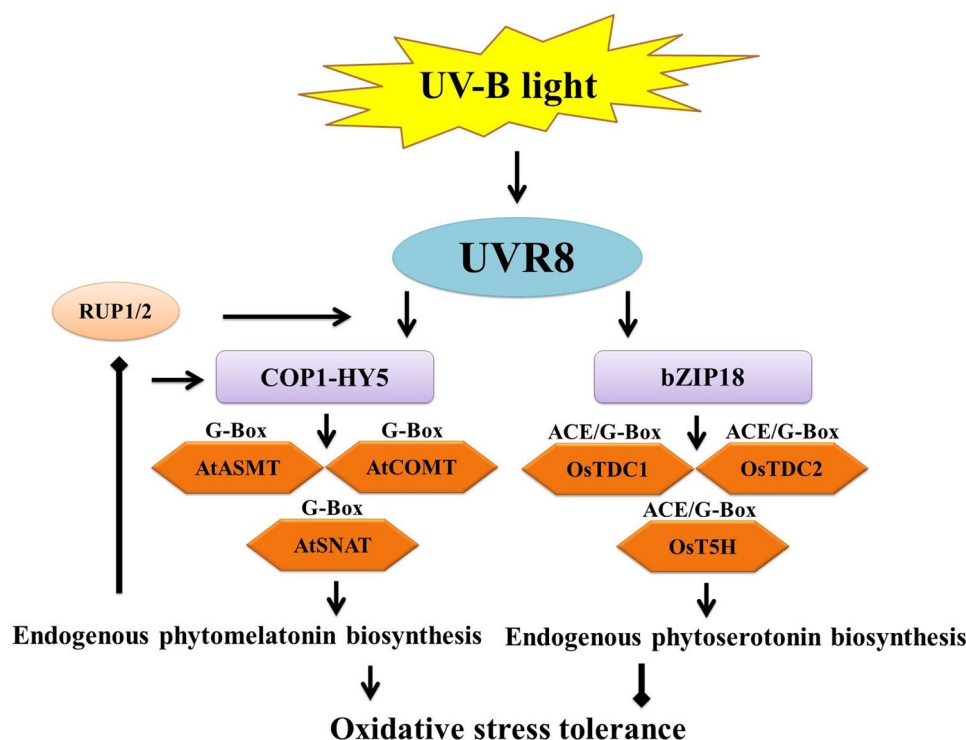
uptake might be liable for enhancing TCA activity, which promotes amino acid metabolism conferring nitrogen deficiency. Gao et al. [105] proposed that the ASMT9-HY5-NRT2.1/NRT2.4 signaling pathway is accountable for conferring tolerance to nitrogen deficiency in apple plants and improving nitrogen use efficiency (NUE) [29].

## 5.2 | Phytomelatonin Biosynthesis Regulation by Light Signaling

By UV-B light, rice basic leucine zipper (bZIP) transcription factor bZIP18 as a functional ortholog of Arabidopsis HY5

might be liable for boosting tryptophan, tryptamine, and serotonin biosynthesis by directly binding to the ACE/G-box *cis*-elements and upregulating rice *TDC1*, *TDC3*, and *T5H* expression (UVR8-COP1-HY5 signaling pathway). By exogenous serotonin application or bZIP18 gene overexpressing, higher  $O_2^-$  generation, and  $H_2O_2$  accumulation in rice seedlings revealed that higher endogenous serotonin accumulation exacerbates UV-B stress [106]. Melatonin interplay with UV-B light signaling in plants has been illustrated in Figure 5.

Rice plants displayed higher endogenous phytomelatonin accumulation, resulting in higher *TDC* and *COMT* expression



**FIGURE 5** | Melatonin interplay with UV-B light signaling in plants. By UV-B light perception and UVR8 activation, COP1-HY5 signaling pathway is responsible for *SNAT*, *ASMT*, and *COMT* expression and promoting endogenous phytomelatonin biosynthesis while COP1-bZIP18 signaling pathway is responsible for *TDC1/2* and *T5H* expression and promoting endogenous phyto serotonin biosynthesis.

by red/blue light application, which is photosynthetically active radiation. Red/blue light perception by phytochromes and cryptochromes boosts PSI and PSII photosystems, and electron transport system activity might be liable for ROS production resulting from electron leakage. Therefore, boosting melatonin biosynthesis in chloroplasts by ROS may be favorable for overcoming oxidative stress [107]. Double chromatic red/blue light in rice seedlings promotes phytomelatonin biosynthesis by activating *TDC* and *COMT* expression [107]. By suppressing *CRY* expression by RNA interference (RNAi), rice plants displayed lower phytomelatonin biosynthesis arising from lower *TDC* expression [108].

Zhang et al. [109] reported that the lower phytomelatonin biosynthesis in leaves and flower buds is crucial for activating flower bud formation in apple trees. Lower phytomelatonin biosynthesis may arise from lower blue and far-red light intensity during spring, leading to lower *ASMT9* and *SNAT5* expression. Blue and far-red light application in apple trees before flowering promotes phytomelatonin biosynthesis by activating *ASMT9* and *SNAT5* expression, suppressing flower bud formation. Also, these authors reported that the melatonin treatment delayed flower bud formation in apple trees by boosting phytomelatonin biosynthesis, resulting in higher *ASMT9* and *SNAT5* expression and protein accumulation. Also, melatonin treatment at 200  $\mu$ M promotes flower bud formation rate, but melatonin treatment at 1000  $\mu$ M represses flower bud formation in apple trees. Delaying flower bud formation in apple trees in response to melatonin treatment may arise from activating gibberellin and vernalization pathways and suppressing autonomous and photoperiod pathways. Therefore,

activating phytochromes and cryptochromes signaling pathway by blue and far-red light application might be liable for boosting the COP1-HY5 transcriptional signaling pathway for activating melatonin biosynthetic *ASMT9* and *SNAT5* expression and protein accumulation in apple plants [109].

Wang et al. [110] reported that the HY5 transcription factor directly binding to the G-box of the promoter of the *SNAT6* gene is accountable for suppressing the *SNAT6* expression and preventing phytomelatonin accumulation. During darkness, COP1 translocation from cytoplasm to nuclear is responsible for boosting HY5 degradation by 26S proteasome. By HY5 degradation, enhancing *SNAT6* expression promoted phytomelatonin accumulation and delayed cotyledon opening in Arabidopsis. Delaying cotyledon opening by transgenic Arabidopsis seedlings overexpressing HY5 and *SNAT6* while boosting cotyledon opening by Arabidopsis seedlings CRISPR/Cas9 silencing HY5 and *SNAT6* demonstrated regulatory roles of HY5 and *SNAT6* in phytomelatonin biosynthesis [110].

Li et al. [111] reported that monochromatic red light promotes phytomelatonin biosynthesis, but monochromatic blue light suppresses phytomelatonin biosynthesis in tomato fruits. In addition, promoting tomato ripening by double chromatic red/blue light (75% red light and 25% blue light) was associated with higher phytomelatonin biosynthesis. By double chromatic red/blue light, phytochromes and cryptochrome signaling pathways synergistically operation could be responsible for promoting phytomelatonin biosynthesis, which promotes tomatoes ripening by enhancing ethylene biosynthesis through upregulating ACC synthase (*ACS2* and *ACS4*) and ACC oxidase (*ACO1*)



expression and accompanying by an increased in lycopene biosynthesis through upregulation of phytoene synthase (*PSY1*) and carotenoid isomerase (*CRTISO*) expressions [111]. Higher phytomelatonin biosynthesis and lower  $H_2O_2$  and MDA accumulation in tomato fruits under double chromatic red/blue light demonstrated that melatonin provides a ROS scavenging mechanism for delaying fruit senescence and accelerating fruit ripening [111]. Recently, Shan et al. [112] reported that accelerating tomato fruit ripening by exogenous melatonin application could be ascribed to regulating DNA methylation of CpG islands (CGIs) of ethylene biosynthesis and signaling genes. By exogenous melatonin application, DNA methylation levels of the CpG island of ACC synthase (*ACS10*) and ethylene response factor 1 (*ERF1*) were decreased, and the DNA methylation level of the CpG island of *CTR1* was increased. In addition, exogenous melatonin application increased *ACS10* and *ERF1* expression and inhibited *CTR1* expression [112].

Zhang et al. [113] reported that *ASMT5* and *COMT2* are responsible for the *N*-acetylserotonin pathway of melatonin biosynthesis, while *ASMT7* is accountable for the 5-methoxytryptamine pathway of melatonin biosynthesis. By red light treatment, tomato fruits displayed higher phytomelatonin levels during fruit ripening, which might be attributed to boosting the *N*-acetylserotonin pathway via upregulating *COMT2* and *ASMT5* expression. Also, phytochrome interacting factors (*PIF4*) transcription factor directly bind to the G-box elements of the *COMT2* promoter, inhibiting *COMT2* expression for suppressing phytomelatonin biosynthesis in tomato fruit. In addition, phytochrome B2 (*phyB2*) interaction with *PIF4* facilitates the degradation of *PIF4* through the 26S proteasome pathway. These authors reported that the *phyB2*–*PIF4*–*COMT2* signaling pathway is accountable for boosting phytomelatonin biosynthesis in tomato fruit during ripening by red light application. *PIF4* ubiquitination-dependent degradation by *phyB2* was confirmed by employing proteasome inhibitor MG132. Enrichment of tomato fruit with exogenous melatonin enhances its agronomic traits and provides health benefits. Therefore, editing the *PIF4* recognition site on *COMT2* by gene-editing strategy CRISPR/Cas9 can be employed for engineering new melatonin-enriched health-boosting tomato fruits [113] (Figure 2E).

## 6 | Phytomelatonin Potential in Postharvest Management of Fruits and Vegetables

### 6.1 | Chilling Injury Alleviating

During cold storage, the cell membrane's physical phase transition from flexible liquid-crystalline to solid-gel structure is accountable for increasing cellular electrolyte leakage. By  $H^+$ -ATPase and  $Ca^{2+}$ -ATPase activity deterioration under cold stress, cytoplasmic acidification is associated with cytosolic  $Ca^{2+}$  accumulation. By  $Ca^{2+}$ /CaM activation, boosting phosphatidylinositol 3-kinase (*PI3K*), phospholipase D (*PLD*), phosphatidate phosphatase (*PAP*), and lipolytic acyl hydrolase (*LAH*) activity is responsible for free linolenic acid releasing for 9-lipoxygenase (9-*LOX*) or ROS-dependent peroxidation during cold stress, which is relevant to membrane integrity deterioration during cold stress. In addition, electron transport elements such as NADH dehydrogenase (*NDH*), succinate dehydrogenase (*SDH*),

cytochrome C reductase (*CCR*), and cytochrome C oxidase (*CCO*), and the deterioration in mitochondria not only is responsible for increasing electron leakage and ROS accumulation but also for hampering intracellular ATP accumulation (*FoF1* ATP synthase). In plants, electrolyte leakage and MDA accumulation have been considered physiological indicators of membrane integrity [39, 40, 114–117].

The results reported by researchers regarding the attenuating chilling injury of horticultural products by exogenous melatonin application during postharvest have been summarized in Table 1. Exogenous melatonin treatments conferring chilling tolerance in horticultural products could be ascribed to promoting signaling  $H_2O_2$  accumulation [120, 125, 158], boosting phytomelatonin accumulation [120, 139, 141], *SlZAT2/6/12*–*CBF1*–arginine pathway activation giving rise to boosting endogenous nitric oxide (*NO*), proline, polyamines and GABA accumulation [119, 121, 124, 129, 130, 133, 138, 141, 146, 147, 152, 158], promoting endogenous polyamines accumulation by activating *MYB44* transcription factor dependent arginine decarboxylase (*ADC*), ornithine decarboxylase (*ODC2*), and spermidine synthase (*SPDS5*) expression [123], sufficient intracellular energy ATP providing [118, 134] along with sufficient intracellular reducing power NADPH providing [126, 140, 146], boosting shikimate pathway activity responsible for sufficient intracellular phenylalanine, tryptophan, and tyrosine providing [126, 146], enhancing phenylpropanoid pathway activity for boosting phenols, flavonoids and anthocyanins accumulation leading to improving ABTS, 2,2-diphenyl picrylhydrazyl (*DPPH*), and ferric reducing antioxidant power (*FRAP*) radical scavenging capacity [120, 131, 141, 146, 148, 158], suppressing polyphenol oxidase (*PPO*) expression and activity by activating *miR528* expression [142] or promoting DNA hypermethylation [127], boosting endogenous SA accumulation while enhancing SA signaling responsive pathogenesis proteins (*PRs*) expression [126, 151], promoting thioredoxins (*Trx*) activation by NADPH-dependent thioredoxin reductase (*NTR*) expression for enhancing oxidized protein repairing methionine sulfoxide reductase (*MSR*) system activity [139, 140], promoting endogenous sucrose accumulation [147], suppressing phospholipase C (*PLC*), phospholipase D (*PLD*) and lipoxygenase (*LOX*) expression and activity accompanying by activating fatty acid desaturases (*FADs*) expression responsible for improving membrane unsaturated/saturated fatty acids (unSFA/SFA) accumulation [118, 143, 145, 148, 154], protecting membrane fluidity and integrity revealed by lower electrolyte leakage and MDA accumulation [119, 134, 135, 154, 158], preserving membrane lipid homeostasis by accelerating membrane lipidome (phospholipids, lysophospholipids, sphingolipids, and glycerides) remodeling by suppressing *PLD*, *PLC*, and *LOX* activity [132], promoting ROS avoiding alternative oxidase (*AOX*) expression and activity accompanying by enhancing ROS scavenging system activity giving rise to lower  $O_2^-$  generation and  $H_2O_2$  accumulation [131, 142, 144, 148, 149, 152] accompanying by higher AA/DHA and GSH/GSSG accumulation [150, 151, 153, 158], improving cell wall structure and stability along with harmonizing cell wall pectin de-esterification and depolymerization [134, 141, 152, 159], promoting GABA shunt pathway activity responsible for sufficient intracellular energy and carbon skeletons providing accompanying by avoiding ROS accumulation [120], promoting endogenous ascorbic acid accumulation by activating ascorbic acid biosynthetic

**TABLE 1** | Chilling injury alleviation by exogenous melatonin application in horticulture products during cold storage.

Plant material	Treatments	Molecular and biochemical effects	References
Tomato fruits ( <i>Solanum lycopersicum</i> )	MEL 100 $\mu$ M	Higher intracellular ATP supplying, higher H <sup>+</sup> -ATPase, Ca <sup>2+</sup> -ATPase, CCO, and SDH activity, higher unSFA/SFA accumulation, higher linoleic (18:2) and linolenic (18:3) acids accumulation, lower palmitic (16:0), stearic (18:0) and oleic (18:1) acids accumulation, higher <i>FAD3</i> and <i>FAD7</i> expression, lower <i>PLD</i> and <i>LOX</i> expression and activity.	[118]
	MEL 100 $\mu$ M	Higher <i>ZAT2/6/12</i> transcription factors expression, higher <i>CBF1</i> transcription factor expression, higher <i>arginase</i> expression and activity, higher endogenous polyamines Put, Spd and Spm accumulation, higher <i>ODC</i> and <i>ADC</i> expression and activity, higher endogenous proline accumulation, higher <i>P5CS</i> and <i>OAT</i> expression and activity, lower <i>ProDH</i> expression and activity, higher endogenous NO accumulation, higher <i>NOS</i> expression and activity, lower electrolyte leakage and MDA accumulation.	[119]
	MEL 100 $\mu$ M	Signaling H <sub>2</sub> O <sub>2</sub> accumulation, higher endogenous phytemelatonin accumulation, higher <i>TDC</i> , <i>T5H</i> , <i>SNAT</i> , and <i>ASMT</i> expression, lower endogenous GABA accumulation, higher GAD, GABA-T, and SSADH activity, higher <i>PAL</i> expression and activity, higher phenols accumulation, higher DPPH scavenging capacity.	[120]
Cucumber fruits ( <i>Cucumis sativus</i> L.)	MEL 100 $\mu$ M	Lower electrolyte leakage, higher chlorophyll accumulation, lower Chlase activity, higher endogenous polyamines Put, Spd and Spm accumulation, higher <i>ADC</i> and <i>ODC</i> expression and activity, higher endogenous proline accumulation, higher <i>P5CS</i> and <i>OAT</i> expression and activity, lower <i>ProDH</i> expression and activity, higher endogenous GABA accumulation, higher <i>GAD</i> and <i>GABA-T</i> expression and activity.	[121]
	MEL 100 $\mu$ M	Lower electrolyte leakage and MDA accumulation, higher endogenous AA accumulation, higher endogenous proline accumulation, lower O <sub>2</sub> <sup>-</sup> generation and H <sub>2</sub> O <sub>2</sub> accumulation, lower weight loss and respiratory intensity.	[122]
	MEL 100 $\mu$ M	Lower electrolyte leakage and MDA accumulation, higher MYB44 transcription factor expression, higher <i>ADC</i> , <i>ODC2</i> and <i>SPDS5</i> expression, higher endogenous polyamines Put, Spd, and Spm accumulation.	[123]
Peach fruits ( <i>Prunus persica</i> )	MEL 100 $\mu$ M	Higher endogenous polyamines Put, Spd and Spm accumulation, higher <i>ADC</i> and <i>ODC</i> expression, higher endogenous proline accumulation, higher <i>P5CS</i> and <i>OAT</i> expression, lower <i>ProDH</i> expression, higher endogenous GABA accumulation, higher <i>GAD</i> and <i>PAO</i> expression.	[124]
	MEL 100 $\mu$ M	Signaling H <sub>2</sub> O <sub>2</sub> accumulation, lower MDA accumulation, higher <i>SOD</i> , <i>CAT</i> , <i>APX</i> , <i>GR</i> , <i>MDHAR</i> , and <i>DHAR</i> expression, higher <i>GMPH</i> , <i>GME</i> , <i>GGGT</i> , <i>GPP</i> , <i>GDH</i> , and <i>GLDH</i> expression, higher AA and GSH accumulation, lower O <sub>2</sub> <sup>-</sup> generation and H <sub>2</sub> O <sub>2</sub> accumulation.	[125]
	MEL 100 $\mu$ M	Lower MDA accumulation, higher unSFA/SFA accumulation, higher linoleic (18:2) and linolenic (18:3) acids accumulation, lower palmitic (16:0), stearic (18:0) and oleic (18:1) acids accumulation, lower <i>LOX</i> activity, higher <i>G6PDH</i> activity, higher <i>SKDH</i> activity, higher phenols accumulation, higher <i>PAL</i> activity, lower <i>PPO</i> activity, higher endogenous SA accumulation.	[126]

(Continues)

TABLE 1 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Mango fruits ( <i>Mangifera indica</i> L.)	MEL 100 $\mu$ M	Higher methylase and demethylase activity, higher chlorogenic acid, neochlorogenic acid, catechin, quercetin-3-glucoside, kaempferol-3-rutinoside and caffeic acid accumulation, lower DNA methylation (CpG methylation) along with higher expression of <i>PAL</i> gene, higher DNA methylation (CpG methylation) along with lower expression of <i>PPO</i> and <i>POD</i> genes.	[127]
	MEL 100 $\mu$ M	Higher SUMO E3 ligase <i>SIZ1</i> expression.	[128]
	MEL 100 $\mu$ M	Lower MDA accumulation, higher endogenous AA accumulation, higher endogenous proline accumulation, higher P5CS and OAT activity, lower ProDH activity, lower ethylene production, weight loss and respiratory intensity.	[129]
	MEL 100 $\mu$ M	Higher endogenous polyamines Put, Spd and Spm accumulation, higher ADC and ODC activity, lower DAO and PAO activity, higher endogenous GABA accumulation, higher GAD activity, lower GABA-T activity.	[130]
	MEL 100 $\mu$ M	Higher endogenous phytemelatonin accumulation, higher PAL and TAL activity, higher phenols and flavonoids accumulation, higher DPPH, TEAC, FRAP and CUPRAC scavenging capacity, higher SOD, CAT, APX, GR and DHAR activity, lower $O_2^-$ generation and $H_2O_2$ accumulation.	[131]
	MEL 500 $\mu$ M	Lower electrolyte leakage and MDA accumulation, lower PLD, PLC and LOX activity, higher PLA2 activity, higher PC, PE, and PI accumulation, lower PA accumulation, higher LPC, LPE and LPI accumulation, lower LPA accumulation, lower Cer, PhytoCer, LacCer and Sph accumulation, lower TG accumulation, higher DG accumulation.	[132]
	MEL 100 $\mu$ M	Higher endogenous proline accumulation, higher <i>P5CS</i> , <i>P5CR</i> , and <i>OAT</i> expression and activity, lower <i>ProDH</i> expression and activity.	[133]
Plum fruits ( <i>Prunus salicina</i> )	MEL 100 $\mu$ M	Higher firmness, lower PG, PME, and EGase activity, lower PLD and LOX activity, lower palmitic and stearic acids accumulation, higher oleic, linoleic, and linolenic acids accumulation, higher unSFA/SFA accumulation, higher ATP and ADP and lower AMP accumulation, higher $H^+$ -ATPase, $Ca^{2+}$ -ATPase, SDH, and CCO activity.	[134]
	MEL 100 $\mu$ M	Higher SAMDC activity, higher endogenous polyamines Spd and Spm accumulation, higher TGase activity, higher plasma membrane covalently enrichment with Put and Spd, higher plasma membrane hydrogen and ionic bonding enrichment with Spd and Spm, lower electrolyte leakage and MDA accumulation, higher membrane proteins sulfhydryl (-SH) accumulation.	[135]
	MEL 1000 $\mu$ M	Lower fresh-reddening, lower ethylene burst, lower phenols and anthocyanins accumulation, lower vanillic acid, caffeic acid, ferulic acid, epicatechin, rutin, dihydroquercetin, kaempferol, and cyanidin-3-glucoside accumulation, higher carotenoids accumulation, higher intracellular ATP supplying, lower <i>PAL</i> , <i>DFR</i> and <i>UFGT</i> expression, higher <i>CRTISO</i> , <i>ZEP</i> , <i>VDE</i> , and <i>ZDS</i> expression, lower <i>PG</i> , $\beta$ - <i>GAL</i> and <i>XET</i> expression, lower <i>ACO</i> , <i>ETR</i> and <i>EFR</i> expression, higher <i>SDH</i> , <i>CCO</i> , and <i>ATPase</i> expression, lower <i>MYB124</i> transcription factor expression.	[136]
	MEL 100 $\mu$ M	Higher SAMDC and TGase activity, higher endogenous polyamines Spd and Spm accumulation, higher plasma	[137]

(Continues)

TABLE 1 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Litchi fruits ( <i>Litchi chinensis</i> )		membrane covalently enrichment with Put and Spd, higher mitochondrial and vacuolar membranes covalently enrichment with Put, higher plasma membrane, mitochondrial and vacuolar membranes hydrogen and ionic bonding enrichment with Spd and Spm, lower electrolyte leakage and MDA accumulation, higher membrane proteins sulfhydryl (-SH) accumulation.	
	MEL 400 $\mu$ M	Lower electrolyte and MDA accumulation, higher anthocyanins accumulation, higher intracellular ATP supplying, higher $H^+$ -ATPase, $Ca^{2+}$ -ATPase, SDH, and CCO activity, higher endogenous proline accumulation, higher P5CS and OAT activity, lower ProDH activity.	[138]
	p-CPA 150 $\mu$ M	Lower endogenous serotonin and melatonin accumulation, lower TDC, T5H, and SNAT expression, higher electrolyte and MDA accumulation, higher $O_2^-$ generation and $H_2O_2$ accumulation, higher LOX activity, lower phenols and anthocyanins accumulation, higher PPO activity, lower SOD, CAT, APX, MDHAR, DHAR and GR activity, lower <i>MsrA1</i> , <i>MsrA2</i> , <i>MsrB1</i> , and <i>MsrB2</i> expression.	[139]
	MEL 500 $\mu$ M	Higher endogenous NO accumulation, higher NR and NOS activity, lower electrolyte and MDA accumulation, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher SOD, CAT, APX, MDHAR, DHAR, and GR activity, higher AA and GSH accumulation, higher intracellular NADPH supplying, higher <i>NTR1</i> and <i>Trx2</i> expression, higher <i>MsrA1</i> , <i>MsrA2</i> , <i>MsrB1</i> , and <i>MsrB2</i> expression.	[140]
Eggplant fruits ( <i>Solanum melongena</i> L.)	MEL 100 $\mu$ M	Higher endogenous phytemelatonin accumulation, higher <i>TDC</i> , <i>T5H</i> , <i>SNAT</i> , <i>ASMT</i> , and <i>COMT</i> expression, higher <i>ZAT2/6/12</i> transcription factors expression, higher <i>CBF1</i> transcription factor expression, higher endogenous polyamines accumulation, higher <i>ODC</i> and <i>ADC</i> expression, higher anthocyanins accumulation, higher <i>PAL</i> , <i>CHS</i> , <i>CHI</i> , <i>DFR</i> , <i>F3H</i> , <i>F3' H</i> , <i>UFGT</i> , and <i>ANS</i> expression, higher SOD and CAT expression, lower $H_2O_2$ accumulation, lower <i>PG</i> , <i>PME</i> and <i>Cel</i> expression and activity, lower electrolyte leakage and MDA accumulation.	[141]
Banana fruits ( <i>Musa acuminata</i> L.)	MEL 200 $\mu$ M	Lower electrolyte leakage and MDA accumulation, higher phospholipids and unSFA accumulation, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher SOD and CAT activity, higher <i>miR528</i> expression, lower <i>PPO1</i> , <i>PPO2</i> , and <i>PPO3</i> expression, lower PPO activity.	[142]
	MEL 200 $\mu$ M	Lower electrolyte leakage and MDA accumulation, higher phenols and flavonoids accumulation, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher CAT activity, lower LOX activity, lower AAO activity, higher endogenous proline accumulation, higher phospholipids and unSFA accumulation, higher <i>omega-3/6 fatty acid desaturase</i> expression.	[143]
Green horn peppers ( <i>Capsicum annuum</i> L.)	MEL 100 $\mu$ M	Lower electrolyte leakage and MDA accumulation, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher SOD, CAT, APX, MDHAR, DHAR and GR activity, higher intracellular ATP supplying, higher AA/DHA and GSH/GSSG accumulation, higher phenols and flavonoids accumulation, higher chlorophyll accumulation, lower weight loss, and respiratory intensity.	[144]
Green bell peppers	MEL 100 $\mu$ M	Lower electrolyte leakage and MDA accumulation, higher endogenous proline accumulation, lower <i>PLD</i> and <i>LOX</i> expression and activity, higher PC and PE accumulation, lower	[145]

(Continues)



TABLE 1 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
( <i>Capsicum annuum</i> L.)		PA accumulation, lower <i>NAC1</i> transcription factor expression, higher <i>SOD</i> , <i>CAT</i> , and <i>APX</i> expression, higher linoleic (18:2) and linolenic (18:3) acids accumulation, lower palmitic (16:0), stearic (18:0) and oleic (18:1) acids accumulation. Higher PC and PE enrichment with unsFA.	
Pear fruits ( <i>Pyrus bretschneideri</i> )	MEL 100 $\mu$ M	Lower electrolyte leakage and MDA accumulation, lower LOX activity, higher endogenous proline accumulation, higher P5CS and OAT activity, lower ProDH activity, higher phenols accumulation, higher 6PGDH activity, higher SKDH activity, higher PAL, C4H, and 4CL activity, lower PPO activity, higher phenols accumulation.	[146]
	MEL 5 mM	Higher endogenous proline accumulation, higher <i>P5CS</i> and <i>OAT</i> expression and activity, lower <i>ProDH</i> expression and activity, higher endogenous GABA accumulation, higher <i>GAD</i> , <i>GABA-T</i> and <i>SSADH</i> expression and activity, higher AA accumulation, higher <i>APX</i> , <i>MDHAR</i> , and <i>DHAR</i> expression and activity, lower <i>AAO</i> expression and activity, higher sucrose accumulation, lower glucose and fructose accumulation, lower <i>NI</i> expression and activity, higher <i>SuSy</i> and <i>SPS</i> expression and activity.	[147]
Pomegranate fruits ( <i>Punica granatum</i> L.)	MEL 100 $\mu$ M	Lower electrolyte leakage and MDA accumulation, higher <i>CAT</i> , <i>SOD</i> , <i>APX</i> and <i>GR</i> activity, lower $H_2O_2$ accumulation, lower <i>PLD</i> and <i>LOX</i> activity, higher phenols accumulation, higher <i>DPPH</i> scavenging capacity, higher <i>PAL</i> activity, lower <i>PPO</i> activity.	[148]
	MEL 100 $\mu$ M	Lower electrolyte leakage, higher phenols accumulation, higher <i>DPPH</i> scavenging capacity, higher <i>PAL</i> activity, lower <i>PPO</i> activity, lower $H_2O_2$ accumulation, higher <i>SOD</i> , <i>CAT</i> , and <i>APX</i> activity.	[149]
Kiwifruits ( <i>Actinidia deliciosa</i> )	MEL 100 $\mu$ M	Lower electrolyte leakage and MDA accumulation, lower lignin accumulation, lower <i>PAL</i> , <i>C4H</i> , and <i>4CL</i> expression and activity, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher <i>SOD</i> , <i>CAT</i> , <i>APX</i> , and <i>GR</i> expression and activity, higher AA and GSH accumulation.	[150]
	MEL 50 $\mu$ M	Lower electrolyte leakage and MDA accumulation, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher <i>SOD</i> , <i>CAT</i> , and <i>APX</i> activity, higher AA and GSH accumulation, higher endogenous phytemelatonin accumulation, higher endogenous SA and tCA accumulation, lower endogenous BA accumulation, higher <i>PAL</i> and <i>BA2H</i> activity, higher <i>PAL</i> and <i>ICS</i> expression, higher <i>PR1</i> expression.	[151]
Zucchini fruits ( <i>Curcubita pepo</i> L.)	MEL 200 $\mu$ M	Lower electrolyte leakage and MDA accumulation, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher <i>SOD</i> , <i>CAT</i> , and <i>APX</i> activity, higher chlorophyll accumulation, higher endogenous glutamate and GABA accumulation, higher <i>GAD</i> activity, lower <i>GABA-T</i> activity, higher endogenous proline accumulation, higher <i>P5CS</i> and <i>OAT</i> activity, lower <i>ProDH</i> activity, lower <i>PG</i> , $\beta$ - <i>GAL</i> , <i>Cel</i> , and <i>PME</i> activity.	[152]
Squash fruits ( <i>Cucurbita pepo</i> )	MEL 200 $\mu$ M	Lower $O_2^-$ generation and $H_2O_2$ accumulation, higher <i>SOD</i> , <i>CAT</i> , <i>APX</i> , <i>MDHAR</i> , <i>DHAR</i> and <i>GR</i> activity, higher AA/DHA and GSH/GSSG accumulation.	[153]
Sapota fruits ( <i>Achras zapota</i> )	MEL 90 $\mu$ M	Lower electrolyte leakage and MDA accumulation, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher <i>SOD</i> and <i>CAT</i> activity, higher endogenous proline accumulation, lower <i>PLD</i> and <i>LOX</i> activity, higher endogenous GABA accumulation.	[154]

(Continues)

TABLE 1 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Apple fruits ( <i>Malus domestica</i> )	MEL 100 $\mu$ M	Higher SAMDC and TGase activity, higher endogenous polyamines Spd and Spm accumulation, higher plasma membrane covalently enrichment with Put and Spd, higher plasma membrane hydrogen and ionic bonding enrichment with Spd and Spm, lower electrolyte leakage and MDA accumulation, higher plasma membrane protein sulfhydryl (-SH) accumulation.	[155]
Apricot fruits ( <i>Prunus armeniaca</i> L.)	MEL 100 $\mu$ M	Higher SAMDC and TGase activity, higher endogenous polyamines Spd and Spm accumulation, higher plasma membrane covalently enrichment with Put and Spd, higher plasma membrane hydrogen and ionic bonding enrichment with Spd and Spm, lower electrolyte leakage and MDA accumulation, higher plasma membrane protein sulfhydryl (-SH) accumulation.	[156]
Loquat fruits ( <i>Eriobotrya japonica</i> )	MEL 50 $\mu$ M	Lower electrolyte leakage and MDA accumulation, higher sucrose accumulation, lower glucose and fructose accumulation, higher chlorogenic acid and neochlorogenic acid accumulation, higher malic acid, oxalic acid, and tartaric acid accumulation, higher ABTS, DPPH, and FRAP scavenging capacity, lower lignin accumulation, lower PAL, 4CL, CAD, and POD activity.	[157]
Cut anthurium flowers ( <i>Anthurium andraeanum</i> )	MEL 100 $\mu$ M	Lower electrolyte leakage and MDA accumulation, higher NADPH oxidase activity, higher signaling $H_2O_2$ accumulation, higher endogenous proline accumulation, higher P5CS and OAT activity, lower ProDH activity, higher phenols accumulation, higher PAL activity, lower PPO activity, higher DPPH scavenging capacity, higher AOX expression, lower damaging $H_2O_2$ accumulation, higher SOD, CAT, APX, and GR activity, higher AA/DHA and GSH/GSSG accumulation.	[158]

L-galactose (Gal) pathway activity [125], accelerating biomembranes enrichment with polyamines for stabilizing corresponding membranes conformations giving rise to lower membrane lipids peroxidation as shown by lower MDA accumulation accompanying by lower membrane proteins peroxidation as shown by lower sulfhydryl accumulation [135, 137, 155, 156], suppressing lignification by lower lignin and cellulose accumulation [150, 157]. As well as epigenetic and genetic mechanisms, melatonin treatment might be liable for palliating chilling injury in fruits and vegetables by boosting proteins posttranslational SUMOylation by SUMO E3 ligase (*SIZ1*) expression and activity and proteins posttranslational S-nitrosylation by NO and persulfidation by  $H_2S$  [128, 140].

## 6.2 | Fungal Decay Attenuating

As well as chilling damage, fungal infection is confining for postharvest management of fresh fruits and vegetables. Fungal elicitors are responsible for plasma membrane receptor-dependent extracellular ROS generation accelerated by NADH-dependent cell wall peroxidase (NADH-CWP). In addition, elicitors-receptor-dependent heterotrimeric G-protein activation might be liable for  $Ca^{2+}$  influx, activating CDPK. CDPK-dependent phosphorylation boosts plasma membrane NADPH oxidase activity and increases extracellular ROS accumulation. By extracellular ROS generation from NADH-CWP and plasma membrane NADPH oxidase activity,

intracellular ROS signaling might be liable for boosting phenylpropanoid pathway responsible for cell wall fortification by phenolics incorporation, as well as hormone signaling such as SA and JA, which are essential for attenuating fungal decay in fruits and vegetables [99, 160, 161].

In recent years, exogenous melatonin has been employed for conferring gray mold decay resistance caused by *Botrytis cinerea* in tomato [162–164], apple [165], grape berries [166, 167], and strawberry fruits [168], blue mold decay by *Penicillium expansum* in apple fruits [169], anthracnose decay by *Colletotrichum musae* in banana fruits [170], anthracnose decay by *Colletotrichum gloeosporioides* and *Colletotrichum brevisporum* in papaya fruits [171], food-borne *Bacillus cereus*, *Bacillus licheniformis*, and *Bacillus subtilis* in cherry tomato fruits [172], ginger rhizome decay by *Fusarium oxysporum* and *Penicillium brevicompactum* [173], *Alternaria alternata*, *B. cinerea*, and *C. gloeosporioides* decay in blueberries fruits [174], *Aspergillus* decay by *Aspergillus flavus* in pistachio fruits [175], soft rot decay by *Botryosphaeria dothidea* in kiwifruits [176], ring rot decay by *B. dothidea* in pear fruits [177] and downy blight caused by *Peronophythora litchii* in litchi fruits [178].

The results reported by researchers regarding the attenuating fungal decay of horticultural products by exogenous melatonin application during postharvest management have been summarized in Table 2. By exogenous melatonin treatments, attenuating fungal decay in fruits and vegetables might be attributed to boosting signaling  $O_2^-$  generation and  $H_2O_2$  accumulation

**TABLE 2** | Fungal decay attenuation by exogenous melatonin application in horticulture products during cold storage.

Plant material	Treatments	Molecular and biochemical effects	References
Papaya fruits ( <i>Carica papaya</i> L.)	MEL 400 $\mu$ M	Lower anthracnose decay caused by <i>Colletotrichum gloeosporioides</i> and <i>Colletotrichum brevisporum</i> , higher NADH oxidase activity, higher signaling $H_2O_2$ accumulation, higher SOD, CAT, APX and GR activity, higher PAL, 4CL and C4H activity, higher phenolic and flavonoid accumulation, lower LPS and LOX activity, lower MDA accumulation, higher CHI and $\beta$ -1,3-Glu activity.	[171]
Table grape fruits ( <i>Vitis vinifera</i> L.)	MEL 200 $\mu$ M	Lower gray mold caused by <i>Botrytis cinerea</i> , higher phenols and flavonoids accumulation, lower electrolyte leakage and MDA accumulation, higher SOD and CAT activity, higher PAL and PPO activity, higher CHI, and $\beta$ -1,3-Glu activity.	[166]
Cherry tomato fruits ( <i>Solanum lycopersicum</i> )	MEL 100 $\mu$ M	Lower gray mold caused by <i>B. cinerea</i> , higher endogenous phytoalexin accumulation, higher signaling $O_2^-$ generation and $H_2O_2$ accumulation, higher endogenous SA accumulation, higher PAL, 4CL, and POD activity, higher phenols, flavonoids and lignin accumulation, higher CHI and $\beta$ -1,3-Glu activity.	[163]
	MEL 100 $\mu$ M	Lower <i>Bacillus cereus</i> , <i>Bacillus licheniformis</i> and <i>Bacillus subtilis</i> incidence, lower <i>FtsZ</i> , <i>FtsA</i> , and <i>divIB</i> expression participating in bacterial cell division, lower <i>FlgB</i> expression participating in bacterial flagellum formation, lower <i>CybB</i> and <i>AtpI</i> expression exhibiting bacterial NADPH oxidase and ATP synthase activity, and lower <i>YikB</i> and <i>YukE</i> expression participating in bacterial ATP-dependent transportation and secretion processes, lower swimming motility and biofilm formation by <i>B. cereus</i> , <i>B. licheniformis</i> and <i>B. subtilis</i> , higher fruit ethylene accumulation and signaling <i>ACO1</i> and <i>ERF6</i> expression, higher fruit nitric oxide biosynthesis and signaling <i>NOS</i> and <i>E3 ubiquitin-protein ligase CSU1</i> expression, lower fruit ROS/ $O_2^-$ accumulation by higher fruit <i>POD18</i> and <i>SOD1</i> expression, higher fruits phenols and flavonoids accumulation, higher fruit ABTS scavenging capacity, higher fruit PRs expression.	[172]
	MEL 100 $\mu$ M	Lower gray mold caused by <i>B. cinerea</i> , higher endogenous phytoalexin accumulation, higher <i>TDC</i> , <i>T5H</i> , <i>SNAT</i> and <i>ASMT</i> expression, lower endogenous NO accumulation, lower <i>NOS</i> expression and activity, higher signaling $O_2^-$ generation and $H_2O_2$ accumulation, higher <i>NADPH oxidase</i> expression and activity, higher endogenous SA accumulation, higher <i>PAL</i> and <i>ICS</i> expression, higher <i>PAL</i> and <i>BA2H</i> activity, higher <i>EDS1</i> and <i>PAD4</i> expression, higher <i>NPR1</i> , <i>TGA2/5</i> and <i>WRKY70</i> expression, higher <i>PR1/2/5</i> expression, higher <i>CHI</i> and $\beta$ -1,3-Glu expression and activity.	[179]
	MEL 100 $\mu$ M	Lower gray mold caused by <i>B. cinerea</i> , higher signaling $O_2^-$ generation and $H_2O_2$ accumulation, higher <i>NADPH oxidase</i> expression and activity, higher <i>CDPK</i> expression, higher endogenous SA accumulation and signaling pathway, higher <i>WRKY70</i> , <i>PAD4</i> , <i>NPR1</i> , <i>TGA5</i> , <i>PR1</i> , <i>PR2</i> and <i>PR5</i> expression, higher <i>CHI</i> and $\beta$ -1,3-Glu expression and activity, higher phenols and lignin accumulation, higher <i>PAL</i> , <i>C4H</i> , <i>4CL</i> and <i>POD</i> activity, higher <i>PAL</i> , <i>C4H</i> , <i>4CL</i> , <i>CCR</i> , <i>CAD</i> and <i>COMT</i> expression.	[164]
Tomato fruits ( <i>Solanum lycopersicum</i> )	MEL 50 $\mu$ M	Lower gray mold caused by <i>B. cinerea</i> , lower $H_2O_2$ accumulation, higher SOD and APX activity, higher <i>CHI</i> , $\beta$ -1,3-Glu, PPO, and <i>PAL</i> activity, higher endogenous MeJA accumulation, higher <i>LOX</i> and <i>AOC</i> expression, lower <i>MYC2</i> and <i>JAZ1</i> expression.	[162]

(Continues)

TABLE 2 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Strawberry fruits ( <i>Fragaria ananassa</i> )	MEL 100 $\mu$ M	Lower gray mold caused by <i>B. cinerea</i> , higher signaling $H_2O_2$ accumulation, higher SOD activity, lower CAT and APX activity, higher PAL activity, higher total phenols and anthocyanins accumulation, higher DPPH scavenging capacity, higher GAD and GABA-T activity, lower endogenous GABA accumulation, higher intracellular ATP supplying, higher acids unSFA/SFA accumulation, lower palmitic (16:0), stearic (18:0) and oleic (18:1) acids accumulation, higher linoleic (18:2) and linolenic (18:3) acids accumulation.	[180]
Jujube fruits ( <i>Zizyphus jujuba</i> )	MEL 200 $\mu$ M	Lower Alternaria rot caused by <i>Alternaria alternata</i> , higher SOD, CAT, and APX activity, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher AA and GSH accumulation, lower electrolyte leakage and MDA accumulation.	[181]
Pistachio fruits ( <i>Pistacia vera</i> )	MEL 1000 $\mu$ M	Lower Aspergillus decay caused by <i>Aspergillus flavus</i> , lower endogenous AFB1 accumulation, higher phenols and flavonoids accumulation, higher DPPH scavenging capacity, higher PAL activity, higher linoleic and linolenic acids accumulation, lower $H_2O_2$ and MDA accumulation, lower LOX activity.	[175]
Blueberry fruits ( <i>Vaccinium corymbosum</i> )	MEL 300 $\mu$ M	Lower <i>Alternaria alternata</i> , <i>B. cinerea</i> , and <i>C. gloeosporioides</i> decay, higher LOX, AOS and AOC expression, higher endogenous JA accumulation and signaling, higher PAL, C4H, 4CL, and CAD expression and activity, higher phenols, flavonoids, anthocyanins, and lignin accumulation, higher CHI and $\beta$ -1,3-Glu expression.	[182]
Litchi fruits ( <i>Litchi chinensis</i> )	MEL 250 $\mu$ M	Lower downy blight caused by <i>Peronophythora litchii</i> , higher PAL, C4H and 4CL activity, higher phenols and flavonoids accumulation, higher G6PDH and 6PGDH activity, higher intracellular NADPH supplying, higher $H^+$ -ATPase, $Ca^{2+}$ -ATPase, SDH and CCO activity, higher intracellular ATP supplying.	[178]
Apple fruits ( <i>Malus domestica</i> )	MEL 100 $\mu$ M	Lower gray mold caused by <i>B. cinerea</i> , higher biocontrol efficacy of <i>Meyerozyma guilliermondii</i> Y-1, higher population growth and colonization of <i>Meyerozyma guilliermondii</i> Y-1, higher PDF1.2 and COI1 expression, higher SOD and CAT activity, higher phenols and lignin accumulation, higher PAL and PPO activity, higher PR1, PR5, $\beta$ -1,3-Glu, and CHI expression.	[165]
	MEL 50 $\mu$ M	Lower blue mold caused by <i>Penicillium expansum</i> , higher PAL, C4H, and 4CL activity, higher LAC and PPO activity, higher PGI and G6PDH activity, higher endogenous phenylalanine, tyrosine, and tryptophan accumulation, higher phenols, flavonoids, and lignin accumulation, higher endogenous caffeic acid, p-coumaric acid, ferulic acid, and erucic acid accumulation.	[169]
Ginger rhizomes ( <i>Zingiber officinale</i> )	MEL 100 $\mu$ M	Lower ginger rhizome decay caused by <i>Fusarium oxysporum</i> and <i>Penicillium brevicompactum</i> , higher $\beta$ -1,3-Glu, PAL, and CC-NBS-LRR expression, higher $\beta$ -1,3-Glu and PAL activity, higher phenols accumulation.	[173]
Guava fruits ( <i>Psidium guajava</i> L.)	MEL 600 $\mu$ M	Lower anthracnose decay caused by <i>C. gloeosporioides</i> , higher phenols and flavonoids accumulation, higher 4CL, C4H and PAL activity, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher AA accumulation, higher CAT, SOD, GR, and APX activity, lower MDA accumulation, lower LPS, PLD and LOX activity, higher CHI and $\beta$ -1,3-Glu activity.	[183]

(Continues)



TABLE 2 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Pear fruits ( <i>Pyrus bretschneideri</i> )	MEL 100 $\mu$ M	Lower ring rot disease caused by <i>Botryosphaeria dothidea</i> , higher endogenous phytemelatonin accumulation, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher AA/DHA and GSH/GSSG accumulation, higher SOD and CAT activity, higher sugars fructose and glucose accumulation, higher organic acids oxalic, quinic, malic, shikimic, and citric acids accumulation, higher autophagosome formation, higher autophagic activity, higher <i>ATG1</i> , <i>ATG5</i> , <i>ATG8c</i> , and <i>ATG10</i> expression.	[177]
Grape berry fruits ( <i>Vitis vinifera</i> L.)	MEL 100 $\mu$ M	Lower gray mold caused by <i>B. cinerea</i> , higher endogenous phytemelatonin accumulation, higher flavonoids accumulation, lower DNA methylation (CpG methylation) along with higher expression of <i>PAL1</i> , <i>STS1</i> , <i>EDS1</i> and <i>CML41</i> , lower <i>MET1</i> and <i>SAM-MTase</i> expression.	[167]
Wax apple fruits ( <i>Syzygium samarangense</i> )	MEL 800 $\mu$ M	Higher endogenous JA and SA accumulation, higher <i>CAT</i> , <i>APX</i> , <i>SOD</i> and <i>GR</i> expression and activity giving, lower $O_2^-$ generation and $H_2O_2$ accumulation, lower <i>LOX</i> expression and activity, lower MDA accumulation, higher <i>GLDH</i> expression, higher AA accumulation, lower <i>PG</i> and <i>Cel</i> expression, higher <i>GAD</i> , <i>GABA-T</i> , and <i>SSADH</i> expression.	[184]

along with activating cytosolic  $Ca^{2+}$  accumulation which is responsible for *CDPK* and *MAPK* expression [163, 164, 171, 179, 180], boosting phytemelatonin accumulation [179], sufficiently intracellular NADPH and erythrose-4-phosphate (Er4P) providing [169, 178], promoting shikimic acid pathway accountable for higher phenylalanine, tyrosine, and tryptophan accumulation [169], boosting phenolic, flavonoid, and anthocyanin accumulation inducing FRAP, ABTS, and DPPH radical scavenging activities [163–166, 169, 171, 173, 175, 178, 182, 183], boosting lignin accumulation [163, 182], boosting endogenous SA accumulation and signaling [163, 179, 184], boosting endogenous JA biosynthesis and signaling [162, 165, 182], boosting endogenous NO accumulation [179], activating coiled-coil nucleotide-binding site leucine-rich repeat (*CC-NBS-LRR*) expression [173] associated with activating PRs such as chitinase (*CHI*) and  $\beta$ -1,3-glucanase ( $\beta$ -1,3-*Glu*) expression [163, 164, 166, 171, 173, 183], sufficiently intracellular ATP providing [178, 180], boosting *SOD*, *CAT*, *APX*, and *GR* expression and activity leading to lower  $O_2^-$  generation and  $H_2O_2$  accumulation favorable for protective membrane integrity [165, 166, 171, 183], boosting GABA shunt pathway activity [180], improving membrane unSFA/SFA accumulation [171, 175, 180, 183] and protective cell wall stability [184].

Wang et al. [177] reported that melatonin treatments confer resistance to ring rot disease caused by *B. dothidea* in pear fruits by boosting phytemelatonin biosynthesis accompanied by lower  $O_2^-$  generation and  $H_2O_2$  accumulation along with higher AA/DHA and GSH/GSSG accumulation resulting from higher SOD and CAT activity, higher fructose and glucose levels, and also in oxalic, quinic, malic, shikimic, and citric acid accumulation. Also, autophagosome formation is boosted by autophagic *ATG1*, *ATG5*, *ATG8c*, and *ATG10* expression. By phytemelatonin biosynthesis, suppressing *TOR* expression or promoting *SnRK1* expression might be liable for boosting autophagy activity by activating *ATG2*, *ATG9*, *ATG18a*, *ATG5*,

*ATG12*, *ATG7*, *ATG8c*, and *ATG8i* expression and boosting *ATG8*-phosphatidylethanolamine (*ATG8-PE*) accumulation [91]. By exogenous melatonin and DNA methylation inhibitor 5-azacytidine (5-azaC) application, Gao et al. [167] reported that lessening DNA methylation by suppressing DNA methyltransferase (*MET1*) expression activating resveratrol biosynthesis, SA biosynthesis,  $Ca^{2+}$  signaling, being MAPK signaling involved in grape berries disease resistance.

Lin et al. [185] reported that the citrus fruits under response to postharvest *Penicillium digitatum* infection exhibit higher  $H_2O_2$  accumulation giving rise to higher endogenous melatonin accumulation. Higher  $H_2O_2$  accumulation in *P. digitatum* in citrus fruits may be crucial for attenuating green mold decay caused by *P. digitatum* infection during postharvest life by promoting cell wall strengthening and triggering defense strategies such as *HSP90* expression. Also, the authors reported that the exogenous melatonin application aggregates green mold decay caused by *P. digitatum* infection in citrus fruits by triggering endogenous melatonin accumulation giving rise to lowering  $H_2O_2$  accumulation by decreasing SOD enzyme activity or scavenging endogenous  $H_2O_2$  accumulation, leading to hampering cell wall strengthening and impeding defense strategies operation such as *HSP90* expression. By green mold decay caused by *P. digitatum* infection, citrus fruits exhibited higher endogenous  $H_2O_2$  accumulation, while exogenous  $H_2O_2$  application attenuated green mold decay caused by *P. digitatum* infection in citrus fruits. In addition, exogenous *N*-acetylcysteine application as a potent ROS scavenger aggregates green mold decay caused by *P. digitatum* infection in citrus fruits. Also, it suggested that signaling  $H_2O_2$  accumulation is responsible for conferring resistance to green mold in citrus fruits via cell wall strengthening and defense genes expression, while exogenous melatonin application conferred susceptibility to green mold by scavenging signaling  $H_2O_2$  in citrus fruits [185].

### 6.3 | Senescence Delaying and Quality Preservation

During postharvest senescence, organoleptic and nutritional quality deterioration of fruits and vegetables restricts their global marketing, which imposes economic loss. This organoleptic and nutritional quality deterioration flows into plant food losses, which impacts global food security, environmental sustainability, and human health [41, 186]. During postharvest management, senescence-associated browning of fresh fruits and vegetables might be attributed to insufficient intracellular energy availability along with ineffective ROS scavenging activity and irrepressible PLD and LOX activities, provoking damage in cell membranes, losing fluidity and integrity evidenced by lower unSFA/SFA ratio. By membrane fluidity and integrity loss, interrupting intracellular compartmentalization might be accountable for accelerating browning arising from PAL-dependent phenolic accumulation in contact with the PPO enzyme [187–189].

During carbon starvation or darkness,  $\alpha$ -glucan water dikinase (GWD) expression is implied in the increased leaf senescence in tomato plants, boosting starch degradation. Consequently, transgenic tomato plants overexpressing GWD promoted leaf senescence by enhancing starch degradation [190]. GWD is a direct target of miR171b, and its overexpression delays leaf senescence by suppressing starch degradation in tomato plants. Melatonin treatments upregulated the *miR171b*-GWD expression, which delayed leaf senescence by suppressing starch degradation and improving energy use efficiency under carbon starvation [190]. In tomato plants, chloroplast vesiculation (CV) is related to boosting leaf senescence by physical interaction with oxygen-evolving enhancer protein 1 PsbO1 in PSII (PsbO) in thylakoids membrane, which its disruption triggers free electrons combination with  $O_2$  and promotes  $O_2^-$  accumulation. In addition, the physical interaction of CV with catalase 3 (CAT3), inhibits CAT3 activity and promotes  $H_2O_2$  accumulation [191]. By *M3H* gene overexpression, lower endogenous phytoalexin accumulation might be liable for increasing leaf senescence in tomato plants. M3H and CV were localized to the cytoplasm and chloroplasts, respectively. Delaying leaf senescence in tomato plants by melatonin treatment or phytoalexin accumulation might be attributed to suppressing CV expression and inhibiting CV physical interaction with PsbO and CAT3, which not only impedes  $O_2^-$  generation in chloroplasts but also promotes  $H_2O_2$  scavenging in peroxisomes, preserving ROS homeostasis. By employing the terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) assay, suppressing CV expression and inhibiting its interaction with PsbO and CAT3 might be advantageous for stabilizing chloroplast integrity and preventing programmed cell death (PCD) in tomato leaves by melatonin treatment or endogenous phytoalexin accumulation via senescence-dependent autophagy and vacuolar-independent pathways [191].

The results reported by researchers regarding the delaying senescence and preserving quality in horticultural products by exogenous melatonin application have been summarized in Table 3. By exogenous melatonin application, delaying senescence and preserving organoleptic and nutritional quality of fruits and vegetables could be attributed to promotion of

signaling  $O_2^-$  generation and  $H_2O_2$  accumulation [272, 282], promotion of endogenous phytoalexin accumulation [236, 241, 245, 246, 272, 292], promoting endogenous NO accumulation [217, 269, 282], promoting endogenous  $H_2S$  accumulation [245], boosting endogenous GABA accumulation [262], inhibiting ethylene accumulation [264, 268, 269, 281], suppressing endogenous ABA accumulation [244, 264], enhancing intracellular ATP supplying [228, 279], ensuring sufficient intracellular NADPH and Er4P supplying [225], boosting SOD, CAT, APX, and GR expression and activity resulting in lower  $O_2^-$  generation and  $H_2O_2$  accumulation imply in fluidity and integrity of membranes [245, 247, 248, 253, 254, 261, 262, 284–286, 288, 289, 302], promotion of endogenous AA accumulation by activating AA biosynthetic L-galactose (Gal) pathway [258, 279], improving membrane unSFA/SFA accumulation [245, 265, 289], enhancing phenylpropanoid pathway activity for boosting phenolic, flavonoid, and anthocyanin accumulation leading to improving ABTS, DPPH, and FRAP radical scavenging capacity [242, 245, 246, 248, 271, 272, 288, 303], upregulating ACS1 expression and ethylene biosynthesis through MYB14 transcription factor and enhancing secondary metabolites, including flavonoids, phenolic acids, stilbenes, and flavonols accumulation [237, 239], enhancing phenylpropanoid accumulation by activating AOX expression which ensures reducing power NADPH and carbon skeletons PEP and Er4P supply by increasing glycolysis, OxPP and shikimate pathways turn-over [225, 304], enhancing oxidized protein repairing systems as MSR activity [227, 230], preserving protein stability by enhancing heat shock proteins (HSPs) expression acting as molecular chaperones [281], suppressing cell wall-degrading genes expression and enzymes activity [240, 250, 251, 257, 264, 268, 274, 302, 305], preventing weight and water loss by enhancing waxes biosynthesis by activating eceriferum 1 (*CER1*) expression along with promoting cutin biosynthesis upregulating glycerol-3-phosphate acyltransferase 4/8 (*GPAT4/8*) expression responsible for cuticle integrity maintenance, suppressing plasma membrane water channels plasma membrane intrinsic protein aquaporins (AQPs) expression for impeding water transport from fruit cuticle, avoiding peel microcracks [244, 249, 251, 252, 306], promoting endogenous sucrose accumulation along with suppressing sorbitol decomposition [238, 259, 280], preserving flavors by regulating citric acid metabolism through enhancing TCA and glyoxylate cycles, GABA shunt, and acetyl-CoA catabolism [283], inhibiting alcoholic off-flavor formation via suppressing ethanol fermentation by lower ethylene responsive factor (*ERF*) transcription factors expression [255], and improving aroma quality by enhancing lactones and esters biosynthesis along with suppressing alcohols and aldehydes biosynthesis [235, 270, 290, 307].

In the horticulture industry, pesticide (fungicide, bactericide, insecticide, etc.) applications have instigated public concerns regarding human, animal, and environmental health. Concerning the pesticide uses in postharvest management, melatonin treatments of jujube fruits exhibited lower endogenous malathion, chlorothalonil, and glyphosate accumulation during postharvest storage. By employing p-chlorophenyl alanine (p-CPA, melatonin biosynthesis inhibitor) and L-buthionine-sulfoximine (BSO, GSH accumulation inhibitor), Deng et al. [275] reported that melatonin treatment promotes endogenous phytoalexin accumulation which enhances GR activity and improves endogenous GSH accumulation, boosting glutathione

**TABLE 3** | Senescence delaying and quality preserving by exogenous melatonin application in horticulture products during cold storage.

Plant material	Treatments	Molecular and biochemical effects	References
Pak choi leaves ( <i>Brassica rapa</i> subsp. <i>chinensis</i> )	MEL 100 $\mu$ M	Delaying leaf yellowing, higher endogenous phytemelatonin accumulation, higher chlorophyll accumulation, higher chlorophyll fluorescence ( $F_v/F_m$ ), lower respiration intensity, lower <i>PGI</i> , <i>SDH</i> and <i>CCO</i> expression and activity, higher <i>6PGDH</i> expression and activity, lower ethylene production, lower <i>ACS</i> and <i>ACO</i> expression and activity.	[192]
	MEL 500 $\mu$ M	Delaying leaf yellowing, higher chlorophyll accumulation, higher chlorophyll fluorescence ( $F_v/F_m$ ), lower <i>Chlase</i> , <i>PPH</i> and <i>MDC</i> , <i>CBR</i> , and <i>CAO</i> expression, lower <i>Chlase</i> , <i>PPH</i> and <i>MDC</i> activity, lower <i>LOX</i> expression and activity, higher <i>SOD</i> , <i>APX</i> and <i>CAT</i> expression and activity, lower $O_2^-$ generation and $H_2O_2$ accumulation, lower weight loss and respiration intensity, higher AA/DHA and GSH/GSSG accumulation, lower electrolyte leakage and MDA accumulation.	[193]
	MEL 100 $\mu$ M	Delaying leaf yellowing, higher chlorophyll accumulation, lower PaO, MDC, and PPH activity, lower <i>CBR</i> , <i>MDC</i> , <i>PPH</i> and <i>PaO</i> expression, higher endogenous IAA accumulation, higher <i>AUX1</i> and <i>PIN3</i> expression, lower endogenous ABA and JA accumulation, lower <i>ABA2</i> , <i>AAO3</i> , and <i>NCED3</i> expression, lower <i>JAR1</i> expression, lower <i>NAC41</i> and <i>NAC87</i> transcription factors expression.	[194]
	MEL 100 $\mu$ M	Delaying leaf yellowing, higher chlorophyll a, chlorophyll b, chlorophyllide a, chlorophyllide b, pheophytin a, and pheophorbide a accumulation, higher cytosolic cGMP accumulation, higher <i>GCI</i> expression and activity, lower <i>CBR</i> , <i>MDC</i> , <i>PPH</i> and <i>PaO</i> expression, lower <i>Chlase</i> , PaO, MDC, and PPH activity.	[195]
Broccoli florets ( <i>Brassica oleracea</i> L. var. <i>italica</i> )	MEL 200 $\mu$ M	Delaying florets yellowing, higher endogenous melatonin, SA, and ABA accumulation, lower endogenous JA accumulation, higher NR, GS, GOGAT, and GDH activity, higher endogenous glutamate supplying, higher chlorophyll accumulation, lower endogenous sucrose supplying, higher SuSy-S and NI activity, lower SuSy-C and SPS activity, lower carotenoids accumulation.	[196]
	MEL 1 $\mu$ M	Delaying florets yellowing, higher chlorophyll accumulation, lower carotenoids accumulation, higher AA and phenols accumulation, higher FRAP scavenging capacity, higher aliphatic glucosinolates glucoraphanin and glucoerucin accumulation, higher indolic glucosinolates glucobrassicin, glucobrassicin, neoglucobrassicin, and 4-methoxy glucobrassicin accumulation, lower aliphatic glucosinolates sinigrin and progoitrin accumulation, higher <i>CYP79F1</i> and <i>CYP79B2</i> expression, higher <i>MYB28</i> and <i>MYB34</i> transcription factors expression.	[197]
	MEL 100 $\mu$ M	Delaying florets yellowing, higher chlorophyll accumulation, higher endogenous phytemelatonin accumulation, higher TDC, T5H, SNAT and ASMT activity, lower carotenoids ( $\beta$ -carotene, $\beta$ -cryptoxanthin, zeaxanthin and lutein) accumulation, lower <i>PSY</i> , <i>PDS</i> , <i>ZDS</i> , <i>CRTISO</i> , $\epsilon$ - <i>LCY</i> and $\beta$ - <i>LCY</i> , <i>VDE</i> , <i>ZEP</i> , <i>LUT1/5</i> , and <i>HYD</i> expression, lower endogenous ABA accumulation, lower <i>NCED</i> expression.	[198]
	LUZ 10 $\mu$ M	Hastening florets yellowing, lower endogenous phytemelatonin accumulation, lower chlorophyll a, chlorophyll b, chlorophyllide a, chlorophyllide b, pheophytin a, and pheophorbide a accumulation, higher <i>Chlase</i> , <i>PPH</i> and <i>MDC</i> activity, higher <i>Chlase</i> and <i>PPH</i> expression, higher ethylene production, higher <i>ACS1</i> , <i>ACS2</i> , <i>ACS3</i> and <i>ACO1</i> , <i>ACO2</i> , and <i>ACO3</i> expression and activity.	[199]

(Continues)

TABLE 3 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Fresh-cut broccoli florets ( <i>Brassica oleracea</i> L. var. <i>italica</i> )	MEL 100 $\mu$ M	Delaying florets yellowing, higher endogenous phyto melatonin accumulation, higher chlorophyll a, chlorophyll b, chlorophyllide a, chlorophyllide b, pheophytin a, and pheophorbide a accumulation, lower Chlase, PPH and MDC activity, lower <i>Chlase</i> and <i>PPH</i> expression, lower ethylene production, lower <i>ACS1</i> , <i>ACS2</i> , <i>ACS3</i> and <i>ACO1</i> , <i>ACO2</i> , and <i>ACO3</i> expression and activity.	[199]
	MEL 100 $\mu$ M	Delaying florets yellowing, higher chlorophyll accumulation, lower Chlase, PPH, PaO and RCCR activity, lower <i>NYC1</i> , <i>NOL</i> , <i>HCAR</i> , <i>Chlase</i> , <i>PPH</i> , <i>PaO</i> , <i>RCCR</i> , and <i>SGR1</i> expression.	[200]
	MEL 80 $\mu$ M	Higher chloroplasts and mitochondria integrity, higher chlorophyll accumulation, lower <i>PPH</i> , <i>PaO</i> and <i>MDC</i> expression, lower mitochondria $O_2^-$ generation and $H_2O_2$ accumulation, higher mitochondrial APX, CAT, and SOD activity, higher mitochondrial membrane permeability, lower mitochondrial MDA accumulation, higher <i>AOX</i> expression and activity, higher <i>CCO</i> expression and activity, lower mPTP opening, higher $\Delta\Psi_m$ , lower mitochondria-cytosol Cyt c translocation, higher mitochondrial Cyt c/a accumulation, delaying PCD.	[201]
	MEL 100 $\mu$ M	Longer shelf life, higher fresh weight, higher hue angle, higher chlorophyll and lower carotenoid accumulation.	[202]
	MEL 100 $\mu$ M	Higher glucoraphanin accumulation, higher <i>Elong</i> , <i>CYP83A1</i> , <i>UGT74B1</i> , and <i>FMOGS-OX1</i> expression, higher MYB28 transcription factor expression, higher <i>MYO</i> expression and activity, lower <i>AOP2</i> expression, higher sulforaphane accumulation.	[203]
	MEL 50 $\mu$ M	Longer shelf life, lower weight loss, higher hue angle, higher chlorophyll and lower carotenoid accumulation, higher phenolic, and flavonoid accumulation, lower MDA accumulation, higher ABTS scavenging capacity.	[204]
Fresh-cut cauliflower ( <i>Brassica oleracea</i> var. <i>botrytis</i> )	MEL 100 $\mu$ M	Delaying florets yellowing, higher endogenous phyto melatonin accumulation, higher alternative electron transporting system activity, higher intracellular ATP supplying, higher chlorophyll, ascorbic acid, phenols, and flavonoids epicatechin, rutin and quercetin accumulation, higher DPPH, ABTS, and FRAP scavenging capacity, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher SOD, CAT and APX activity, lower MDA accumulation.	[205]
	MEL 100 $\mu$ M	Delaying cauliflower floret yellowing, higher endogenous phyto melatonin accumulation, lower <i>PG</i> and <i>LOX</i> expression and activity, higher phenols, ascorbic acid and glucosinolates accumulation, higher DPPH scavenging capacity, lower mitochondria swelling, higher autophagic activity.	[206]
	MEL 100 $\mu$ M	Delaying leaf senescence, higher endogenous phyto melatonin accumulation, higher <i>TDC2</i> , <i>TDC3</i> , <i>TDC4</i> , <i>T5H</i> , <i>ASMT</i> and <i>SNAT</i> expression, lower transcriptional activators <i>ABF1</i> , <i>ABF4</i> , and <i>ABI5</i> expression, lower endogenous ABA accumulation, lower <i>NCED3</i> and <i>AAO3</i> expression, higher chlorophyll accumulation, lower <i>NYC1</i> , <i>NOL</i> , <i>PPH</i> , <i>PaO</i> , <i>RCCR</i> , <i>SGR1</i> , and <i>SGR2</i> expression, lower electrolyte leakage.	[207]
Chinese flowering cabbage ( <i>Brassica rapa</i> ssp. <i>parachinensis</i> )	MEL 100 $\mu$ M	Delaying leaf senescence, lower respiratory intensity, higher intracellular ATP and ADP supplying, lower intracellular AMP supplying, higher ATPase activity, lower ATP synthase expression, lower <i>AOX1/2</i> expression, higher NADK activity, higher	[208]

(Continues)



TABLE 3 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
		intracellular NADP <sup>+</sup> supplying, higher <i>G6PDH</i> and <i>6PGDH</i> expression and activity, higher intracellular NADPH supplying, lower <i>PHI</i> , <i>SDH</i> , <i>CCO</i> , and <i>AAO</i> expression and activity, higher phenols and flavonoids accumulation, higher ascorbic acid accumulation.	
	MEL 100 $\mu$ M	Delaying leaf senescence, lower <i>RBOHB</i> , <i>RBOHC</i> , <i>RBOHD</i> , and <i>RBOHE</i> expression, higher <i>SOD</i> , <i>CAT</i> , <i>APX</i> , <i>GR</i> , <i>MDHAR</i> , and <i>DHAR</i> expression and activity, higher AA/DHA and GSH/GSSG accumulation, lower O <sub>2</sub> generation and H <sub>2</sub> O <sub>2</sub> accumulation, higher O <sub>2</sub> <sup>•−</sup> , OH <sup>•</sup> , and DPPH radicals scavenging capacity, lower MDA accumulation, higher chlorophyll accumulation, lower <i>PaO</i> and <i>MDC</i> expression.	[209]
	MEL 100 $\mu$ M	Delaying leaf senescence, higher chlorophyll accumulation, lower <i>NYC1</i> , <i>NOL</i> , <i>PaO</i> , <i>RCCR</i> , <i>HCAR</i> , <i>MCS</i> , <i>PPH1</i> , <i>PPH2</i> , <i>SGR1</i> , <i>SGR2</i> , and <i>SGR3</i> expression, lower ethylene production, lower <i>SAMS2.1</i> , <i>SAMS2.2</i> , <i>ACS5</i> and <i>ACS10</i> and <i>ACO2</i> and <i>ACO5</i> expression, higher flavonoid accumulation, higher <i>PAL3</i> , <i>C4H</i> , <i>4CL</i> , <i>FLS1</i> , <i>FLS2</i> , <i>FLS3</i> and <i>FLS4</i> expression, lower <i>ERF2</i> and <i>ERF109</i> transcription factor expression.	[210]
	MEL 100 $\mu$ M	Delaying leaf senescence, higher chlorophyll accumulation, lower <i>NYC1</i> , <i>PPH</i> , <i>PaO</i> , and <i>SGR1/2</i> expression, lower endogenous ABA, ethylene, and JA accumulation.	[211]
Spinach leaves ( <i>Spinacia oleracea</i> L.)	MEL 0.20 mg/mL	Delaying leaf yellowing, lower weight loss, higher chlorophyll accumulation, lower MDA accumulation, higher <i>SOD</i> , <i>CAT</i> and <i>POD</i> activity, higher AA accumulation.	[212]
Baby mustard ( <i>Brassica juncea</i> )	MEL 100 $\mu$ M	Buds yellowing delaying, lower weight loss and higher chlorophyll accumulation, higher FRAP and ABTS scavenging capacity, higher phenols and AA accumulation, higher aliphatic glucosinolates sinigrin, gluconapin, progoitrin and glucoiberin accumulation, higher indolic glucosinolates glucobrassicin, neoglucobrassicin, 4-methoxyglucobrassicin and 4-hydroxyglucobrassicin accumulation, higher aromatic glucosinolate gluconasturtiin accumulation.	[213]
White button mushrooms ( <i>Agaricus bisporus</i> )	MEL 100 $\mu$ M	Cap browning alleviating, lower weight loss and higher firmness, higher signaling H <sub>2</sub> O <sub>2</sub> accumulation, higher endogenous phytemelatonin accumulation, higher <i>TDC</i> , <i>T5H</i> , <i>SNAT</i> , and <i>ASMT</i> expression, higher phenols accumulation, higher <i>PAL</i> expression and activity, lower <i>PPO</i> expression and activity, higher AA accumulation, higher DPPH scavenging capacity, lower electrolyte leakage and MDA accumulation.	[214]
	MEL 100 $\mu$ M	Cap browning alleviating, higher hardness, fracturability, chewiness and lower adhesiveness, lower caps opening and off-flavor and higher overall acceptability, lower chitinase and <i>PPO</i> activity, lower mitochondrial electron leakage (O <sub>2</sub> <sup>•−</sup> generating), higher endogenous phytemelatonin accumulation, higher intracellular ATP supplying, higher <i>SOD</i> , <i>CAT</i> , <i>APX</i> and <i>GR</i> activity, higher AA and GSH accumulation, higher <i>NDH</i> and <i>CCR</i> expression and activity, lower mitochondria-cytosol Cyt c translocation, higher mitochondrial Cyt c/a accumulation.	[215]
Lotus seeds ( <i>Nelumbo nucifera</i> )	MEL 100 $\mu$ M	Lotus pods and seeds browning attenuating, higher endogenous phytemelatonin accumulation, higher intracellular ATP and ADP supplying, lower intracellular AMP supplying, higher intracellular NAD <sup>+</sup> and NADH supplying, higher H <sup>+</sup> -ATPase and Ca <sup>2+</sup> -ATPase, <i>SDH</i> and <i>CCO</i> activity, higher oleic, linoleic and linolenic	[216]

(Continues)

TABLE 3 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
		acids accumulation, lower palmitic and stearic acids accumulation, lower LPS, PLD and LOX activity, higher unSFA/SFA accumulation, lower $O_2^-$ generation and $H_2O_2$ accumulation, lower electrolyte leakage and MDA accumulation.	
	LUZ 10 $\mu$ M	Lotus pods and seeds browning acceleration, lower endogenous phytemelatonin accumulation, lower intracellular ATP and ADP supplying, higher intracellular AMP supplying, lower intracellular $NAD^+$ and NADH supplying, lower $H^+$ -ATPase and $Ca^{2+}$ -ATPase, SDH and CCO activity, lower oleic, linoleic and linolenic acids accumulation, higher palmitic and stearic acids accumulation, higher LPS, PLD and LOX activity, lower unSFA/SFA accumulation, higher $O_2^-$ generation and $H_2O_2$ accumulation, higher electrolyte leakage and MDA accumulation.	[216]
	MEL 100 $\mu$ M	Lotus pods and seeds browning attenuating, higher intracellular and mitochondrial NO accumulation, higher intracellular NOS activity, higher $\Delta\Psi_m$ , higher mitochondrial oxygen consumption capacity, lower mitochondrial ROS and MDA accumulation, higher mitochondrial SOD and CAT activity, higher intracellular ATP and ADP supplying, lower intracellular AMP supplying, higher mitochondrial $H^+$ -ATPase, $Ca^{2+}$ -ATPase, SDH, and CCO activity.	[217]
Fresh-cut lotus roots ( <i>Nelumbo nucifera</i> )	MEL 150 $\mu$ M	Fresh-cut lotus root browning attenuating, higher MYB5, MYB6, and MYB308 transcription factors expression, lower PAL, 4CL, C4H, and CHS expression and activity, lower CHI, COMT, HCT and DFR expression, lower PPO expression and activity, lower $H_2O_2$ accumulation, higher SOD, CAT, APX, DHAR and GR activity, lower phenols and flavonoids accumulation, higher DPPH scavenging capacity, lower MDA accumulation.	[218]
Cassava roots ( <i>Manihot esculenta</i> )	MEL 500 mg $L^{-1}$	PPD progression delaying, lower intracellular and mitochondrial $H_2O_2$ accumulation, higher Cu/ZnSOD, CAT1, APX2, DHAR, GR, GPX, POD3, and GST expression, higher SOD, CAT and GR activity.	[219]
	MEL 100 $\mu$ M	PPD progression delaying, lower vascular streaking and vascular discoloration, higher ROS-responsive genes calcium signaling-, phospholipase signaling-, MAPK cascades-, NADPH oxidase-, and WRKY, NAC, ZAT, and HSF transcription factors expression, higher SOD, APX, MDAR, CAT, PRX and GRX expression, lower sucrose synthase, glucose phosphomutase, and ADP-glucose pyrophosphorylase expression, higher starch phosphorylase, $\alpha$ -amylase, and $\beta$ -amylase expression, lower $H_2O_2$ accumulation, higher CAT and APX activity, lower PLC and PLD expression, higher CDPK expression.	[220]
Bamboo shoots ( <i>Bambusa vulgaris</i> )	MEL 1 mM	Bamboo shoot lignification delaying, lower hardening and yellowing, lower lignin and cellulose accumulation, lower PAL and POD activity, higher SOD, CAT and APX activity, lower NAC family SND2 and KNAT7 transcription factors expression, lower MYB family MYB20 and MYB85 transcription factors expression.	[221]
	MEL 500 $\mu$ M	Bamboo shoot lignification delaying, lower lignin and cellulose accumulation, higher phenols and AA accumulation, lower PAL, CAD and POD activity, lower NAC family NAC1, NAC2, NAC3 and NAC4 transcription factors expression, lower MYB family MYB1 and MYB2 transcription factors expression, lower PAL1, PAL2, PAL3, PAL4, CAD1, CAD2 expression.	[222]

(Continues)

TABLE 3 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Fresh-cut bamboo shoots	MEL 500 $\mu$ M	Bamboo shoot lignification delaying, lower lignin and cellulose accumulation, higher $H^+$ -ATPase1/2/3, $Mg^{2+}$ -ATPase1/2/3, $Ca^{2+}$ -ATPase1/2/3, <i>SDH</i> 1/2/3 and <i>CCO</i> 1/2 expression and activity, higher intracellular ATP and ADP supplying, lower intracellular AMP supplying, higher <i>NADK</i> 1/2 expression and activity, higher intracellular $NADP^+$ and $NADPH$ supplying.	[223]
	UV-C + MEL 1 mM	Bamboo shoot lignification delaying, lower cellulose and lignin accumulation, lower PAL, POD, CAD and 4CL activity.	[224]
	MEL 100 $\mu$ M	Higher intracellular $NADPH$ supplying, higher G6PDH and 6PGDH activity, higher AOX expression, higher CAT, APX, SOD and GR activity, lower AAO activity, lower $H_2O_2$ accumulation, higher AA and GSH accumulation, higher phenols, and anthocyanins accumulation, higher DPPH scavenging capacity, higher PAL activity, lower PPO activity.	[225]
Pomegranate fruits ( <i>Punica granatum</i> L.)	MEL 100 $\mu$ M	Lower weight loss, lower PPO activity, higher phenols, anthocyanins and AA accumulation, higher DPPH scavenging capacity, lower bacterial and fungal infections.	[226]
	MEL 400 $\mu$ M	Pericarp browning alleviating, lower $O_2^-$ generation and $H_2O_2$ accumulation, lower electrolyte leakage and MDA accumulation, higher endogenous phytemelatonin accumulation, higher phenols, flavonoids, and anthocyanins accumulation, higher SOD, CAT, APX, and GR activity, lower PPO activity, higher <i>MsrA1</i> , <i>MsrA2</i> , <i>MsrB1</i> , and <i>MsrB2</i> expression.	[227]
	MEL 400 $\mu$ M	Pericarp browning alleviating, lower electrolyte leakage, lower LPS, PLD, and LOX activity, higher PC accumulation, lower PA accumulation, higher unSFA/SFA accumulation, higher oleic, linoleic and linolenic acids accumulation, lower palmitic and stearic acids accumulation, higher intracellular energy supplying, higher $H^+$ -ATPase, $Ca^{2+}$ -ATPase, SDH, and CCO activity.	[228]
	MEL 400 $\mu$ M	Pericarp browning alleviating, higher chromaticity $L^*$ , $a^*$ , and $b^*$ value. Higher endogenous phytemelatonin accumulation, lower endogenous ABA accumulation, higher PUB protein, RING-H2 finger protein, phosphatase 2C, and F-box expression, lower bHLHs transcription factor expression, lower miR858 expression, higher MYB251 and TT2 transcription factors expression, higher <i>PAL</i> , <i>4CL</i> , <i>CHS</i> , <i>CHI</i> , <i>DFR</i> , <i>ANS</i> , and <i>UFGT</i> expression, higher anthocyanins accumulation, lower miR160 expression, higher ARF transcription factor expression, lower <i>XTH</i> , <i>EGase</i> , and <i>EXP</i> expression, higher <i>ZAT10</i> and <i>DREB1</i> expression, higher NAC transcription factor expression, higher AOX expression, lower AAO expression, higher AA accumulation, higher BON association protein 1 expression, lower accelerated cell death 6 and formin protein 18 expression, higher E3 ubiquitin-protein ligase expression, higher <i>PLA1</i> and <i>MYC2</i> expression, higher <i>UCP5</i> expression, higher $H^+$ -ATPase, $Ca^{2+}$ -ATPase, and pyruvate kinase expression, higher <i>NADP-malic enzyme</i> expression, higher 3-ketoacyl-CoA synthase expression, higher <i>GAD1</i> , <i>CaM</i> , and <i>CMLs</i> expression, lower <i>TPP</i> expression.	[229]
	MEL 600 $\mu$ M	Pericarp browning alleviating, higher endogenous phytemelatonin accumulation, lower weight loss, lower $O_2^-$ generation and $H_2O_2$ accumulation, lower electrolyte leakage and MDA accumulation, lower protein carbonyl accumulation, higher phenols, flavonoids and anthocyanins accumulation, higher SOD, CAT and GR activity, lower PPO expression and activity, higher <i>MsrA1</i> , <i>MsrA2</i> , <i>MsrB1</i> , and <i>MsrB2</i> expression.	[230]

(Continues)

TABLE 3 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Table grape fruits ( <i>Vitis vinifera</i> L.)	MEL 500 $\mu$ M	Pericarp browning alleviating, lower weight loss, higher phenols, anthocyanins and AA accumulation, higher CUPRAC scavenging capacity, lower PPO and LAC expression, lower PPO activity, higher DFR and UFGT expression.	[231]
	MEL 200 $\mu$ M	Lower berry abscission and rotten index, lower electrolyte leakage and MDA accumulation, higher endogenous proline, GABA, arginine, Put, Spd, and Spm accumulation, higher N-carbamoyl putrescine amidase, SPDS, and ALDH proteins expression, higher ARG, ODC, ADC, NCA, SPDS, and CuAO expression.	[232]
	MEL 200 $\mu$ M	Higher flavonoids and anthocyanins accumulation, higher 4CL, CHS, F3' H, FLS, and UDPG expression.	[233]
	MEL 100 $\mu$ M	Higher CAT, APX, and SOD activity, lower H <sub>2</sub> O <sub>2</sub> and MDA accumulation, higher AA accumulation, lower DNA methylation, higher DNA demethylase expression.	[234]
	MEL 100 $\mu$ M	Lower rachis browning and berry abscission, lower weight loss rate and respiration intensity, higher phenols, flavonoids and anthocyanins accumulation, higher esters, aldehydes, and alcohols accumulation, lower terpenes accumulation.	[235]
	MEL 200 $\mu$ M	Lower berry abscission and decay incidence, higher endogenous cysteine, methionine, phenylalanine, arginine, tryptophan and GABA accumulation, lower endogenous glutamic acid and proline accumulation, higher TDC2, TDC3, TDC4, T5H1, T5H2, T5H3, T5H4 and T5H5, ASMT1, ASMT2, ASMT3, ASMT4 and SNAT1 and SNAT3 expression, higher endogenous NAS, 5-MT and melatonin accumulation, higher phenols, flavonoids, and anthocyanins accumulation, higher PAL, CHI, F3H1, F3H2, F3' H, LAR, ANR, F3'5' H, 5GT, and AOMT expression.	[236]
	MEL 100 $\mu$ M	Higher phenols, flavonoids, and anthocyanins accumulation, higher chlorogenic acid, gallic acid, epicatechin and malvidin-3,5-glucose accumulation, higher DPPH, ABTS, and FRAP scavenging capacity, higher STS and PAL expression, higher endogenous phytomelatonin accumulation.	[237]
	MEL 100 $\mu$ M	Higher endogenous phytomelatonin accumulation, higher anthocyanins accumulation, higher PAL, CHS, CHI, F3H, F3' H, F3'5' H, DFR, LDOX, and UFGT expression, higher MYBA1 and MYBA2 transcription factors expression, higher sucrose accumulation, higher SPS activity, higher mineral nutrients N, K, Cu, Fe, and Zn absorption and accumulation.	[238]
	MEL 50 $\mu$ M	Higher endogenous phytomelatonin accumulation, higher transcription factor MYB14 expression, higher ACS1 expression, higher ethylene accumulation, higher phenols, flavonoids, stilbenes, and flavonols accumulation, higher STS1, F3'H, LAR2, and DFR expression.	[239]
	MEL 100 $\mu$ M	Lower weight loss and higher TSS, TA, berry adherence strength, and firmness, lower PME and PG activity, lower O <sub>2</sub> - generation and H <sub>2</sub> O <sub>2</sub> accumulation, higher CAT and APX activity.	[240]
Strawberry fruits ( <i>Fragaria ananassa</i> )	MEL 100 $\mu$ M	Higher endogenous phytomelatonin accumulation, higher TDC, T5H, SNAT, and ASMT expression, lower weight loss and higher firmness, higher AA accumulation, lower MDA accumulation, lower H <sub>2</sub> O <sub>2</sub> accumulation, higher phenols and flavonoids accumulation, higher DPPH and ABTS scavenging capacity, higher L* value, higher hue angle.	[241]

(Continues)



TABLE 3 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Sweet cherry fruits ( <i>Prunus avium</i> )	MEL 100 $\mu$ M	Higher endogenous phytemelatonin accumulation, higher anthocyanin accumulation, higher cyanidin 3-glucoside, pelargonidin-3-O-glucopyranoside and pelargonidin-3-malonylglucoside accumulation, higher <i>PAL</i> , <i>C4H</i> , <i>4CL</i> , <i>CHI</i> , <i>CHS</i> , <i>F3H</i> , <i>DFR</i> , <i>ANS</i> , <i>3GT</i> , and <i>UFGT</i> expression.	[242]
	MEL 100 $\mu$ M	Lower respiration intensity, and weight loss, higher firmness, lightness, saturation, hue angle, titratable acidity, and total soluble solids content, lower electrolyte leakage and MDA accumulation, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher endogenous phytemelatonin accumulation, higher SOD, CAT, APX, DHAR, MDHAR, and GR activity, higher AA/DHA and GSH/GSSG accumulation.	[243]
	MEL 100 $\mu$ M	Lower respiration intensity, and ethylene production, higher firmness, higher anthocyanins accumulation, lower MDA accumulation, lower weight and water loss, improving cuticle integrity, higher <i>CER1</i> and <i>GPAT4/8</i> expression, lower water channels <i>PIP1;4</i> and <i>PIP2;7</i> expression, higher endogenous ABA accumulation, higher <i>NCED1</i> expression. Higher <i>Cu/Zn-SOD</i> , <i>Mn-SOD</i> , <i>CAT</i> , <i>APX</i> , <i>MDHAR</i> , <i>DHAR</i> , and <i>GR</i> expression, higher <i>DFR</i> and <i>UFGT</i> expression.	[244]
	MEL 100 $\mu$ M	Lower flesh browning and decay incidence, higher endogenous phytemelatonin accumulation, higher <i>TDC</i> , <i>T5H</i> , <i>SNAT</i> , and <i>ASMT</i> expression, higher endogenous $H_2S$ accumulation, higher <i>LCD</i> and <i>DCD</i> expression and activity, higher phenols, flavonoids and anthocyanins accumulation, higher <i>PAL</i> and <i>CHS</i> activity, lower PPO activity, higher ABTS, DPPH, and FRAP scavenging capacity, higher SOD, CAT, APX and GR activity, lower $H_2O_2$ accumulation, lower PLD and LOX activity, lower MDA accumulation.	[245]
	MEL 100 $\mu$ M	Higher lightness ( $L^*$ ), chromaticity ( $C^*$ ), TSS and TA, lower weight loss, lower electrolyte leakage, higher firmness, higher endogenous phytemelatonin accumulation, higher endogenous phenylalanine, tyrosine, tryptophan, alanine, valine, leucine, glutamine, glutamate, histidine, arginine, GABA, proline, aspartate, asparagine, threonine, isoleucine and methionine accumulation, higher <i>TDC</i> , <i>T5H</i> , <i>SNAT</i> , and <i>ASMT</i> expression, higher anthocyanins, procyanidins and flavonoids accumulation, higher <i>PAL</i> , <i>C4H</i> , <i>4CL</i> , <i>CHS</i> , <i>F3H</i> , <i>F3'H</i> , <i>DFR</i> , <i>ANS</i> , and <i>UFGT</i> expression,	[246]
Blueberry fruits ( <i>Vaccinium corymbosum</i> )	MEL 50 $\mu$ M	Higher firmness, lower decay incidence and weight loss, higher phenols and anthocyanins accumulation, higher <i>PAL</i> expression and activity, higher <i>APX</i> and <i>GST</i> expression and activity, higher ascorbic acid accumulation, lower $O_2^-$ generation and $H_2O_2$ accumulation, lower LOX activity, lower MDA accumulation.	[247]
	MEL 1000 $\mu$ M	Lower flesh browning, higher phenols, flavonoids and anthocyanins accumulation, lower PPO activity, lower $H_2O_2$ and higher AA accumulation, higher SOD, CAT and APX activity, lower LOX activity, lower electrolyte leakage and MDA accumulation.	[248]
	MEL 100 $\mu$ M	Lower water loss, higher cuticular wax accumulation, higher cuticular wax enrichment with diketone, triterpenoid, oleanolic, and hexadecenoic acids.	[249]
	MEL 300 $\mu$ M	Lower electrolyte leakage and MDA accumulation, lower LOX activity, higher anthocyanins and AA accumulation, lower PME, PG, Cel, and $\beta$ -Glu activity, higher protopectin and cellulose accumulation.	[250]

(Continues)

TABLE 3 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Blackberry fruits ( <i>Rubus fruticosus</i> L.)	MEL 50 $\mu$ M	Lower water loss, lower cuticular wax degradation, higher cuticular wax enrichment with triterpenoids ursolic acid, $\alpha$ -amyirin, and $\beta$ -amyirin accumulation, lower cuticular wax saturated fatty acids octadecanoic, eicosanoic, and triacontanoic acid oxidation metabolic degradation, lower PG, $\beta$ -Gal, PME and Cel expression and activity.	[251]
	MEL 100 $\mu$ M	Higher cuticular wax accumulation, higher cuticular wax enrichment with alkanes and triterpenoids $\beta$ -amyirin, $\alpha$ -amyirin, ursolic acid, oleanolic acid, lupeol, and betulinic acid, lower water loss.	[252]
	MEL 100 $\mu$ M	Lower anthocyanin degradation dependent red drupelet reversion, lower PPO activity, higher phenols, flavonoids and anthocyanins accumulation, higher GSH and AA accumulation, higher DPPH scavenging capacity, higher SOD, GR, CAT, MDHAR, DHAR and APX activity, lower H <sub>2</sub> O <sub>2</sub> accumulation, lower MDA accumulation.	[253]
	MEL 200 $\mu$ M	Lower weight loss and disease incidence, higher phenols, flavonoids and anthocyanins accumulation, DPPH scavenging capacity, lower H <sub>2</sub> O <sub>2</sub> accumulation, lower MDA accumulation, lower PPO activity, lower LOX activity, higher AA and GSH accumulation, higher CAT, SOD, APX, DHAR, MDHAR and GR activity.	[254]
	MEL 100 $\mu$ M	Lower ethylene production and respiration intensity, higher firmness, lower <i>ERF4</i> , <i>ERF74</i> , and <i>ERF75</i> expression, lower <i>PDC1</i> and <i>PDC2</i> and <i>ADH1</i> expression and activity, lower endogenous pyruvate accumulation, lower endogenous ethanol and acetaldehyde accumulation, lower alcoholic off-flavor.	[255]
	MEL 100 $\mu$ M	Higher phenols and flavonoids accumulation, higher DPPH, FRAP, and ABTS scavenging capacity, lower MDA accumulation.	[256]
	MEL 100 $\mu$ M	Higher firmness, lower <i>PME</i> , <i>PG</i> , <i>Cel</i> , and $\beta$ - <i>Gal</i> activity, lower MDA accumulation, higher pectin, cellulose, and hemicellulose accumulation, higher ascorbic acid accumulation.	[257]
	MEL 100 $\mu$ M	Higher <i>GME2</i> , <i>GalDH</i> , <i>GalLDH</i> , <i>PMI2</i> , <i>PMM</i> , <i>GMP1</i> , <i>GME1</i> , and <i>GGP1</i> expression, higher <i>APX1</i> , <i>GR</i> , <i>MDHAR1</i> , <i>MDHAR2</i> , and <i>DHAR</i> expression, lower <i>AAO</i> expression, higher endogenous AA accumulation.	[258]
	MEL 100 $\mu$ M	Higher chlorophyll, carotenoid, and AA accumulation, lower softening and weight loss, higher sucrose, glucose, and fructose accumulation, higher starch accumulation, lower amylase activity, higher <i>HK</i> and <i>FK</i> expression, higher <i>AI</i> , <i>NI</i> , <i>SPS</i> and <i>SuSy-S</i> expression and activity.	[259]
	MEL 1.5 mM	Higher TA and AA accumulation, lower TSS and weight loss, higher phenols accumulation, higher DPPH scavenging capacity, higher SOD and CAT activity, lower H <sub>2</sub> O <sub>2</sub> accumulation, lower MDA accumulation.	[260]
Papaya fruits ( <i>Carica papaya</i> L.)			
Peach fruits ( <i>Prunus persica</i> )	MEL 100 $\mu$ M	Lower weight loss, decay incidence and respiration intensity, higher firmness, total soluble solids and AA accumulation, higher SOD, CAT, and APX activity, lower O <sub>2</sub> <sup>-</sup> generation and H <sub>2</sub> O <sub>2</sub> accumulation, lower LOX activity, lower MDA accumulation.	[261]
	MEL 100 $\mu$ M	Lower H <sub>2</sub> O <sub>2</sub> accumulation, lower MDA accumulation, higher DPPH and ABTS scavenging capacity, higher SOD, CAT, and APX activity, higher endogenous glutamate and GABA accumulation, higher <i>GAD1</i> and <i>GAD4</i> expression, lower <i>GABA-T</i> expression.	[262]

(Continues)

TABLE 3 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Mango fruits ( <i>Mangifera indica</i> L.)	MEL 100 $\mu$ M	Lower weight loss and higher firmness, higher phenols and flavonoids accumulation, lower PPO activity, higher AA accumulation, higher CAT activity, higher DPPH scavenging capacity.	[263]
	MEL 500 $\mu$ M	Higher firmness, lower chromaticity b*, lower $\beta$ -carotene accumulation, lower climacteric ethylene production, lower ACS and ACO activity, lower endogenous ACC accumulation, lower endogenous ABA accumulation, lower NCED activity, lower PG, $\beta$ -Gal and PME activity.	[264]
	MEL 100 $\mu$ M	Lower softening, respiration intensity, and chlorophyll degradation, higher PC and PI accumulation, lower PS and PA accumulation, higher unSFA accumulation, lower saturated fatty acids (lauric acid, myristic acid, palmitic acid and stearic acid) accumulation, higher unsaturated fatty acids (linoleic acid and linolenic acid), lower H <sub>2</sub> O <sub>2</sub> accumulation, lower MDA accumulation.	[265]
	MEL 1000 $\mu$ M	Lower weight loss and higher firmness, lower respiration intensity, lower PG, PME, Cel, and $\beta$ -Glu expression and activity, higher AA and GSH accumulation, higher GR activity, lower O <sub>2</sub> - generation and H <sub>2</sub> O <sub>2</sub> accumulation.	[266]
	MEL 1000 $\mu$ M	Lower fungicide prochloraz phytotoxicity, lower endogenous fungicide prochloraz accumulation, lower O <sub>2</sub> - generation and H <sub>2</sub> O <sub>2</sub> accumulation, lower electrolyte leakage and MDA accumulation, higher $\Delta\Psi$ m, lower DNA damage and protein carbonylation, higher SOD, CAT, APX, MDHAR, DHAR and GR activity, higher AA and GSH accumulation, higher cytochrome P450, GST and GT activity.	[267]
Pear fruits ( <i>Pyrus bretschneideri</i> )	MEL 100 $\mu$ M	Lower water soaking and core browning physiological disorders, lower ethylene production, lower ACS1 and ACO1 expression, higher fruit firmness, lower PG1 and Cel expression, higher SOD and DHAR expression and activity, lower LOX expression and activity.	[268]
	MEL 100 $\mu$ M	Lower respiration intensity and ethylene production, higher endogenous NO accumulation, higher NOS expression and activity, lower ACS1, ACO1 and ACO2 expression, fruit firmness, lower PG and Cel expression.	[269]
	MEL 150 $\mu$ M	Lower ethylene production, higher long-chain acyl-CoA synthetase expression, higher ethers, aldehydes and alcohols accumulation, lower ketones accumulation.	[270]
	MEL 200 $\mu$ M	Higher anthocyanin accumulation, higher RBOHF expression, higher signaling O <sub>2</sub> - generation and H <sub>2</sub> O <sub>2</sub> accumulation, higher MYB10 transcription factor expression, higher UFGT expression.	[271]
	MEL 200 $\mu$ M	Higher endogenous phytochrome accumulation, higher TDC, T5H, SNAT and ASMT expression, higher anthocyanin accumulation, higher PAL, CHS, CHI, F3H, ANS, and UFGT expression, higher MYB10, MYB114, bHLH and WD40 transcription factors expression, higher anthocyanins and flavonols accumulation, lower hydroxycinnamate and flavanol accumulation.	[272]
Fresh-cut pear fruits ( <i>Pyrus bretschneideri</i> )	MEL 150 $\mu$ M	Lower enzymatic browning, higher PAL and CHS expression and activity, higher phenols accumulation, higher DPPH and ABTS scavenging capacity, lower PPO1 and PPO5 expression and activity, lower MDA and H <sub>2</sub> O <sub>2</sub> accumulation, higher AA accumulation, lower LOX expressing.	[273]

(Continues)

TABLE 3 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Jujube fruits ( <i>Zizyphus jujuba</i> )	MEL 25 $\mu$ M	Lower respiratory intensity and ethylene production, lower weight loss and higher firmness, higher AA and GSH accumulation, higher APX, MDHAR and GR activity, lower PME, PG, Cel and $\beta$ -Glu activity.	[274]
	MEL 100 $\mu$ M	Lower weight loss and decay incidence, higher firmness, higher endogenous phytemelatonin accumulation, higher GR activity, higher endogenous GSH accumulation, higher GST activity, lower endogenous pesticides chlorothalonil, malathion, and glyphosate accumulation, higher FRAP scavenging capacity, higher phenols and ascorbic acid accumulation.	[275]
	MEL 100 $\mu$ M	Higher endogenous phytemelatonin accumulation, higher <i>PAL</i> , <i>C4H</i> , <i>CHS</i> , <i>CHI</i> , <i>F3H</i> , <i>ANS</i> , <i>DFR</i> , <i>LAR</i> , <i>FLS</i> , and <i>ANR</i> expression, higher caffeic acid, catechin, epicatechin, rutin, ferulic acid, p-hydroxybenzoic acid, and chlorogenic acid accumulation.	[276]
	MEL 100 $\mu$ M	Lower weight loss, higher titratable acid and ascorbic acid accumulation, higher firmness, higher protopectin, cellulose, and hemicellulose accumulation, lower <i>PG</i> , <i>Cel</i> , $\beta$ - <i>Glu</i> , and $\beta$ - <i>Gal</i> , and <i>LOX</i> expression and activity.	[277]
Fresh-cut sweetpotato ( <i>Ipomoea batatas</i> )	MEL 500 $\mu$ M	Lower enzymatic browning, lower $O_2^-$ generation and $H_2O_2$ accumulation, lower MDA accumulation, higher ascorbic acid and $\alpha$ -tocopherol accumulation, lower <i>PAL</i> and <i>PPO</i> activity, higher phenols accumulation, lower <i>LOX</i> expression and activity, higher <i>SOD</i> , <i>CAT</i> , <i>APX</i> , and <i>GR</i> activity, higher <i>SOD1</i> , <i>SOD2</i> , <i>CAT1</i> , <i>APX1</i> , <i>APX3</i> , <i>GR1</i> , <i>GR2</i> and <i>DHAR</i> expression.	[278]
Chestnut rose fruits ( <i>Rosa roxburghii</i> )	MEL 50 $\mu$ M	Higher <i>GME</i> , <i>GGP</i> , <i>GMP</i> , and <i>GalDH</i> expression, higher <i>SOD</i> , <i>CAT</i> , <i>APX</i> , <i>GR</i> , <i>DHAR</i> and <i>MDHAR</i> expression and activity, lower MDA accumulation, lower $H_2O_2$ accumulation, higher AA and GSH accumulation, higher $H^+$ -ATPase, $Ca^{2+}$ -ATPase, <i>SDH</i> and <i>CCO</i> activity, higher intracellular ATP supplying.	[279]
Apple fruits ( <i>Malus domestica</i> )	MEL 50 $\mu$ M	Lower respiratory intensity and ethylene production, higher firmness, soluble sugars, and AA accumulation, lower <i>AI</i> and <i>NI</i> activity, lower <i>SorDH</i> , <i>SOX</i> , and <i>SuSy-C</i> activity, higher <i>SuSy-S</i> and <i>SPS</i> activity.	[280]
	MEL 1 mM	Lower weight loss and physical disorder black necrotic spots incidence, lower ethylene production and signaling, lower <i>ACS1</i> , <i>ACO1</i> , and <i>ACO3</i> , and <i>ERF109</i> expression, lower MDA accumulation, higher <i>SOD</i> and <i>CAT</i> activity, higher <i>HSP11</i> expression.	[281]
Potato tubers ( <i>Solanum tuberosum</i> )	MEL 50 $\mu$ M	Higher tubers wound healing, higher <i>NR</i> and <i>NOS</i> expression, higher endogenous <i>NO</i> accumulation, higher <i>NADPH oxidase</i> expression, higher signaling $O_2^-$ generation and $H_2O_2$ accumulation, higher suberin polyphenol and lignin accumulation, lower weight loss and disease incidence, higher <i>PAL</i> , <i>4CL</i> , and <i>CAD</i> expression and activity, higher <i>POD</i> activity.	[282]
Orange fruits ( <i>Citrus sinensis</i> )	MEL 200 $\mu$ M	Higher <i>PEPC1/2/4</i> and <i>CS1</i> expression, lower endogenous citrate accumulation, higher cytosolic <i>ACO2/3</i> , <i>NADP-IDH2/3</i> , <i>GAD5</i> and <i>GABP</i> expression, higher cytosolic <i>ATP-CL2</i> , <i>PEPCK1</i> and <i>FBPase2</i> expression.	[283]
Navel orange fruits ( <i>Citrus sinensis</i> )	MEL 200 $\mu$ M	Lower respiration intensity and weight loss, higher firmness, TSS, and TA, lower $H_2O_2$ and MDA accumulation, higher <i>CAT</i> , <i>SOD</i> , <i>APX</i> and <i>GR</i> expression and activity, higher AA and GSH accumulation, higher phenols accumulation.	[284]

(Continues)



TABLE 3 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Physalis fruits ( <i>Physalis peruviana</i> )	MEL 200 $\mu$ M	Lower weight loss, higher firmness, lower respiration intensity, higher phenols and carotenoid accumulation, higher CAT, SOD and APX activity, higher DPPH scavenging capacity, higher PAL activity.	[285]
Passion fruits ( <i>Passiflora edulis</i> )	MEL 200 $\mu$ M	Lower shrinkage and browning, lower weight loss, lower ethylene production and respiration intensity, higher firmness, lower electrolyte leakage and MDA accumulation, higher phenols, flavonoids and AA accumulation, higher CAT and SOD activity.	[286]
Hami melon fruits ( <i>Cucumis melo</i> var. <i>saccharinus</i> )	MEL 500 $\mu$ M	Lower softening, weight loss, and respiratory intensity, lower O <sub>2</sub> - generation and H <sub>2</sub> O <sub>2</sub> accumulation, lower MDA accumulation, higher SOD, CAT and APX activity, higher phenols, flavonoids and AA accumulation, higher DPPH and ABTS scavenging capacity, lower LPS, LOX, and PLD activity	[287]
Rambutan fruits ( <i>Nephelium lappaceum</i> )	MEL 125 $\mu$ M	Lower pericarp browning, lower O <sub>2</sub> - generation and H <sub>2</sub> O <sub>2</sub> accumulation, lower electrolytes leakage and MDA accumulation, higher phenols, flavonoids, and anthocyanins accumulation, lower PPO activity, higher SOD, CAT, APX, MDHAR, DHAR and GR activity, higher AA/DHA and GSH/GSSG accumulation.	[288]
Apricot fruits ( <i>Prunus armeniaca</i> L.)	MEL 100 $\mu$ M	Lower pericarp browning, lower softening, decay incidence, and weight loss, higher AA, phenols, and flavonoid accumulation, higher SOD and CAT activity, lower MDA accumulation, lower LOX activity, higher DPPH, ABTS and OH scavenging capacity, lower H <sub>2</sub> O <sub>2</sub> accumulation, lower PPO and higher PAL activity.	[289]
	MEL 2 mM	Higher firmness and TSS, lower ethylene production and respiration intensity, lower LOX, HPL, and ADH activity, lower alcohols and aldehydes accumulation, higher ACX and AAT activity, higher lactones and esters accumulation.	[290]
Plum fruits ( <i>Prunus salicina</i> )	MEL 100 $\mu$ M	Higher firmness, lower respiration intensity and ethylene production, lower weight loss and decay incidence, higher PAL, 4CL, 4CH and POD activity, higher phenols and lignin accumulation.	[291]
Cherry tomato fruits ( <i>Solanum lycopersicum</i> )	MEL 100 $\mu$ M	Higher endogenous phytemelatonin accumulation, higher <i>TDC</i> , <i>T5H</i> , <i>SNAT</i> and <i>ASMT</i> expression, lower weight loss, fruit decay, and TA, higher firmness, TSS as well as TSS/TA, lower electrolyte leakage and MDA accumulation, higher GR, and APX activity, higher AA and GSH accumulation.	[292]
Longan fruits ( <i>Dimocarpus Longan</i> )	MEL 400 $\mu$ M	Lower pericarp browning, higher lightness and h° value, lower a* value, lower electrolyte leakage and MDA accumulation, lower PPO and POD activity, lower O <sub>2</sub> - generation and H <sub>2</sub> O <sub>2</sub> accumulation, higher phenols, flavonoids and GSH accumulation, higher APX and SOD activity.	[293]
Okra fruits ( <i>Abelmoschus esculentus</i> )	MEL 100 $\mu$ M	Higher endogenous phytemelatonin accumulation, higher <i>TDC</i> , <i>T5H1-3</i> , <i>SNAT</i> and <i>COMT1-3</i> expression, higher endogenous IAA and GA accumulation, higher endogenous GABA accumulation, lower endogenous ABA accumulation.	[294]
Pepper fruits ( <i>Capsicum annuum</i> )	MEL 100 $\mu$ M	Lower O <sub>2</sub> - generation and H <sub>2</sub> O <sub>2</sub> accumulation, lower MDA accumulation, higher <i>CAT</i> expression and activity, lower <i>NAC1</i> transcription factor expression, lower <i>PLD</i> and <i>LOX</i> expression, higher AA/DHA and GSH/GSSG accumulation, higher firmness, lower <i>PG</i> and <i>EGases</i> expression.	[295]
Cut peony flowers ( <i>Paeonia lactiflora</i> Pall.)	MEL 500 $\mu$ M	Higher endogenous phytemelatonin accumulation, higher <i>TDC</i> and <i>COMT1</i> expression, higher stems strength, higher S-lignin and G-lignin accumulation (higher S/G lignin accumulation), higher <i>PAL</i> , <i>CCR</i> , <i>CAD</i> , <i>COMT</i> and <i>POD</i> expression.	[296]

(Continues)

TABLE 3 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
Cut rose flowers ( <i>Rosa hybrida</i> )	MEL 200 $\mu$ M	Longer vase life, lower stomatal aperture, higher phenols and GSH accumulation, higher CAT, APX and GR activity, lower H <sub>2</sub> O <sub>2</sub> accumulation, lower electrolyte leakage and MDA accumulation, higher DPPH scavenging capacity.	[297]
Cut tuberose flowers ( <i>Polianthes tuberosa</i> L.)	MEL 100 $\mu$ M	Longer vase life, higher SOD and CAT activity, lower H <sub>2</sub> O <sub>2</sub> and MDA accumulation.	[298]
Cut carnation flowers ( <i>Dianthus caryophyllus</i> L.)	MEL 100 $\mu$ M	Longer vase life, higher fresh weight and water uptake, lower respiration intensity and ethylene production, lower electrolyte leakage, higher chlorophyll and phenols accumulation, higher ABTS scavenging capacity.	[299]
	MEL 1 mg/L	Longer vase life, lower H <sub>2</sub> O <sub>2</sub> and MDA accumulation, higher SOD and POD activity, lower procyanidins, catechin and epicatechin accumulation, lower endogenous SA and ABA accumulation, higher endogenous JA accumulation, higher L-phenylalanine, p-hydroxycinnamic acid, p-coumaric acid, perillyl alcohol, p-coumaryl alcohol, and cinnamic acid accumulation.	[300]
Cut peony flowers ( <i>Paeonia lactiflora</i> Pall.)	MEL 50 $\mu$ M	Delaying senescence and extending vase life, improving stem water balance, lower electrolyte leakage and MDA accumulation, higher SOD and CAT activity.	[301]

S-transferase (GST) activity degrading pesticides, which displays worthy potential to improve healthy food for human consumption. Hu et al. [267] reported that melatonin treatment attenuates fungicide prochloraz phytotoxicity in mango fruits, exhibiting lower endogenous fungicide accumulation, which could be attributed to higher cytochrome P450, GST and glycosyltransferases (GTs) enzyme activities along with higher SOD, CAT, APX, MDHAR, DHAR, and GR antioxidative enzyme activities, with higher endogenous AA and GSH accumulation along with lower O<sub>2</sub><sup>•−</sup> generation, H<sub>2</sub>O<sub>2</sub>, and MDA accumulation, and lower electrolyte leakage, showing higher mitochondrial membrane potential ( $\Delta\Psi_m$ ), and lower DNA damage and protein carbonylation index. Melatonin could be a promising strategy for detoxifying pesticides in fruits and vegetables during postharvest. Therefore, melatonin exhibits great potential to improve food safety for human consumption [267, 275].

By exogenous melatonin application, delaying senescence and preserving organoleptic and nutritional quality of vegetables crops could be attributed to promoting endogenous melatonin accumulation [198, 207], preventing chlorophyll degradation [193, 195, 199, 200, 210, 211], inhibiting ethylene biosynthesis [192, 199, 210], suppressing endogenous ABA accumulation [207], inhibiting carotenoid accumulation [198], promoting cyclic guanosine 3',5'-monophosphate (cGMP) signaling pathway [195], suppressing transcriptional activators ABFs responsive ABA biosynthesis and chlorophyll degradation genes expression [207], suppressing ERF2/ERF109 transcription factors inhibitory on flavonoid biosynthesis [210], promoting glucoraphanin and sulforaphane biosynthesis by enhancing glucoraphanin-sulforaphane system activity [197], suppressing PCD by maintaining mitochondrial biogenesis function [201], intracellular reducing power NADPH and carbon skeletons Er4P supplying [208], enhancing intracellular ATP supplying [208], promoting

endogenous SA and IAA biosynthesis and signaling along with suppressing endogenous JA biosynthesis and signaling [194, 196, 211], enhancing endogenous glutamate supplying by promoting GS and GOGAT activities [196], inhibiting O<sub>2</sub><sup>•−</sup> generation and H<sub>2</sub>O<sub>2</sub> accumulation along with enhancing AA/DHA and GSH/GSSG accumulation responsible for protective membrane integrity [193, 209, 212] and enhancing phenylpropanoid pathway activity for boosting phenols, flavonoids, and anthocyanins accumulation leading to improving ABTS, DPPH, and FRAP radical scavenging capacity [208, 209, 213, 214, 308]. By exogenous melatonin application, alleviating bamboo shoot lignification could be ascribed to suppressing secondary cell wall (SCW) formation by inhibiting cellulose, hemicellulose, and lignin biosynthesis PAL, CAD, and POD expression and activity arising from lower NACs and MYBs transcription factors expression, enhancing intracellular ATP supplying by enhancing H<sup>+</sup>-ATPase, Mg<sup>2+</sup>-ATPase, Ca<sup>2+</sup>-ATPase, SDH, and CCO expression and activity accompanying by enhancing intracellular NADPH supplying by promoting NADK activity [221–223].

In addition, packaging films and edible coatings enrichment with melatonin has been designed in different strategies including chitosan-based melatonin layer-by-layer assembly (CMLLA) [309], melatonin in combination with phase change materials (PCMs) [310], glutenin/tamarind gum/melatonin bioactive film (G/T/M) [311], glutenin/tamarind gum loaded with the binary microemulsion of melatonin/pummelo essential oil (G/T-M-E) [312, 313], melatonin-loaded UiO-66 metal-organic framework nanoparticles (MOF-MEL) [314], carboxymethyl cellulose-gelatin-melatonin edible coating (CMC-Gel-M) [315], and chitosan-based melatonin edible coating (CH-M) [316–318] have been employed with exciting results for alleviating chilling injury and fungal decay, delaying senescence and preserving organoleptic and nutritional quality [43] (Table 4).

**TABLE 4** | Packaging films and edible coatings enrichment with melatonin for improving postharvest storability of fruits and vegetable.

Plant material	Treatments	Molecular and biochemical effects	References
Fresh-cut broccoli florets ( <i>Brassica oleracea</i> L. var. <i>italica</i> )	CMLLA	Higher packaging film DPPH radical scavenging capacity and antibacterial activity, lower weight loss and chlorophyll degradation, higher firmness and sugar/acid ratio.	[309]
White button mushrooms ( <i>Agaricus bisporus</i> )	PCM + MEL	Cap browning attenuating, higher endogenous phytemelatonin accumulation, higher <i>T5H</i> , <i>SNAT</i> , and <i>AMST</i> expression, lower weight loss and higher firmness, lower electrolyte leakage and MDA accumulation, lower $O_2^-$ generation and $H_2O_2$ accumulation, higher phospholipids and unSFA accumulation, higher <i>PAL</i> expression and activity, lower <i>PPO</i> expression and activity, higher phenols accumulation, higher FRAP scavenging capacity, higher intracellular ATP and ADP supplying, lower intracellular AMP supplying, higher $H^+$ -ATPase and $Ca^{2+}$ -ATPase activity, higher SOD, APX and GR activity.	[310]
	G/T/M packaging film	Cap browning attenuating, higher SOD, CAT, APX, GR, DHAR, MDHAR activity, higher AA/DHA and GSH/GSSG accumulation, lower $O_2^-$ generation and $H_2O_2$ accumulation, lower MDA accumulation, lower PPO activity.	[311]
	G/T-M-E packaging film	Cap browning attenuating, higher hardness, fracturability, chewiness and lower adhesiveness, lower caps opening and off-flavor, higher overall acceptability, lower respiration intensity, lower MDA accumulation.	[312]
	G/T-M-E packaging film	Higher firmness, lower cap opening, weight loss, respiration intensity, lower electrolytic leakage, higher SDH and CCO activity, higher intracellular ATP supplying, lower $O_2^-$ generation and $H_2O_2$ accumulation, lower PPO activity, higher SOD and CAT activity.	[313]
Spinach ( <i>Spinacia oleracea</i> L.)	UiO-66 MOF-M packaging film	Delaying leaf yellowing, lower weight loss, higher chlorophyll accumulation, lower MDA accumulation, higher SOD, CAT and POD activity, lower $O_2^-$ generation and $H_2O_2$ accumulation.	[314]
Longkong fruit ( <i>Lansium domesticum</i> )	CMC-Gel-M edible coating	Chilling injury attenuation, lower pericarp browning, weight loss, and respiration intensity, lower PLD and LOX activity, lower electrolyte leakage and MDA accumulation, lower $H_2O_2$ , $OH^-$ , $O_2^-$ accumulation, higher PAL activity, lower PPO activity, higher phenols accumulation, higher DPPH and ABTS scavenging capacity,	[315]
Pomegranate aril ( <i>Punica granatum</i> L.)	CH-M edible coating	Lower aril browning, lower weight loss and respiration intensity, higher AA and anthocyanins accumulation, higher DPPH and FRAP scavenging capacity.	[318]
Sweet cherry fruits ( <i>Prunus avium</i> )	CH-M edible coating	Lower weight loss and respiration intensity, higher firmness, higher AA, phenols and anthocyanins accumulation, higher DPPH scavenging capacity.	[317]
Banana fruits ( <i>Musa acuminata</i> L.)	CH-M edible coating	Lower pericarp browning, lower electrolyte leakage, higher AA, phenols and flavonoids accumulation, lower PPO activity, higher DPPH scavenging capacity, lower PG, $\alpha$ -amylase and xylanase activity, higher firmness.	[316]

## 7 | Plant Hormones and Gas Transmitters Imply Phytomelatonin Biosynthesis

By exogenous ATP application, white mushrooms exhibited higher endogenous phytomelatonin accumulation. Aghdam et al. [319] suggested that the extracellular ATP signaling by does not respond to nucleotides 1 (DORN1/P2K1) could be liable for boosting endogenous phytomelatonin biosynthesis. By boosting endogenous phytomelatonin accumulation resulting from extracellular ATP signaling, activating AOX expression could be liable for avoiding ROS accumulation and ensuring sufficient ATP and carbon skeletons supply, which protect membrane integrity represented by lower MDA accumulation, delays mushroom senescence represented by lower cap browning and preserve white mushroom nutritional quality by boosting higher phenol accumulation and higher DPPH scavenging capacity through phenylpropanoid pathway activity evidenced by enhancing PAL activity along with suppressing PPO activity [319]. By exogenous ATP application, extracellular ATP signaling could be liable for boosting shikimic acid pathway activity, as represented by higher SKDH activity, for sufficient tryptophan supply and support for melatonin accumulation. By serving as an extracellular ATP receptor, plasma membrane purinoreceptor DORN1/P2K1 is responsible for activating NADPH oxidase, activating ROS and  $\text{Ca}^{2+}$  signaling, and boosting NADPH/ $\text{Ca}^{2+}$ -CaM/arginine-dependent NOS/NO system activity [40, 114, 320]. DORN1-dependent NO biosynthesis could be liable for activating soluble guanylate cyclase (sGC) enzyme and cytosolic cGMP accumulation [114]. By silencing mevalonate kinase (MVK) expression using CRISPR/Cas9 technology, Cho et al. [321] revealed that the direct phosphorylation of MVK by DORN1 may be responsible for higher phenylalanine and tryptophan accumulation, reinforcing plant innate immunity [321].

By exogenous phyto-sulfokine  $\alpha$  (PSK $\alpha$ ) application, delaying senescence, attenuating decay, and preserving the nutritional quality of strawberry fruits could be ascribed to activating the endogenous PSK $\alpha$  signaling pathway. By serving as a moonlighting protein, PSK $\alpha$  receptor (PSKR1) exhibited particulate guanylyl cyclase (pGC) activity for producing cGMP. PKG could be liable for target proteins or transcription factors phosphorylation for cytosolic cGMP signaling. In addition to PKG, boosting cytosolic  $\text{Ca}^{2+}$  accumulation by cyclic nucleotide-gated ion channels (CNGCs) opening could be liable for cytosolic cGMP signaling by calcium/calmodulin ( $\text{Ca}^{2+}$ /CaM) or CDPK [40, 114, 322]. By exogenous PSK $\alpha$  application, cytosolic cGMP signaling could be liable for boosting endogenous phytomelatonin accumulation resulting from activating *TDC*, *T5H*, *SNAT*, and *ASMT* expression. By endogenous phytomelatonin accumulation, boosting intracellular ATP supply resulting in higher SDH and CCO activity was accompanied by activating extracellular ATP signaling evidenced by higher extracellular ATP accumulation resulting in lower apyrase 1 (*APY1*) expression, preserving intracellular ATP and ROS homeostasis by regulating TOR/SnRK1 signaling pathways, boosting NADPH oxidase activity and signaling  $\text{H}_2\text{O}_2$  accumulation, activating posttranslational proteins SUMOylation SUMO E3 ligase (*SIZ1*) expression concomitant with suppressing  $\text{NAD}^+$  dissipating poly-ADP-ribose polymerase 1 (*PARP1*) expression, enhancing ROS scavenging system activity, improving OxPP and folate pathways activity for carbon skeletons

and NADPH supplying, and boosting phenols, flavonoids, and anthocyanins accumulation by activating phenylpropanoid pathway [322–331]. According to ROS responsive ERF109 and ERF115 directly binding to phyto-sulfokine 2 (*PSK2*) gene promoter and ERF114 and ERF115 directly binding to *PSK5* gene promoter [332], and brassinosteroid responsive ERF115 directly binding to *PSK5* gene promoter [333], activating *PSKs* expression and signaling by ERFs transcription factors may be responsible for boosting endogenous phytomelatonin accumulation.

By employing EGTA, an endogenous  $\text{Ca}^{2+}$  chelator, Hu et al. [334] reported that exogenous  $\text{CaCl}_2$  application promotes endogenous  $\text{Ca}^{2+}$  accumulation concomitant enhancing endogenous phytomelatonin accumulation by activating *TDC1*, *TDC2*, *T5H*, *ASMT1*, *ASMT2*, *ASMT3*, and *SNAT* expression, which could be responsible for delaying postharvest physiological deterioration (PPD) progression accompanied by promoting ascorbic acid and starch accumulation in cassava storage roots [334]. By exogenous methyl jasmonate (MeJA) and ethanol application, endogenous phytomelatonin accumulation by activating *TDC1*, *TDC2*, *T5H*, *ASMT1*, *ASMT2*, *ASMT3*, and *SNAT* expression could be liable for delaying PPD progression in cassava storage root through boosting endogenous gibberellin and ethylene accumulation accompanying by activating *APX2* and *GR* expression and boosting SOD and CAT activity leading to lower  $\text{O}_2^-$  and  $\text{H}_2\text{O}_2$  accumulation and boosting ABTS scavenging capacity. In addition to delaying PPD, exogenous MeJA, and ethanol application preserves higher ascorbic acid, starch, and carotenoid accumulation and maintains quality in cassava storage roots [335, 336].

Yin et al. [337] reported that exogenous MeJA application promoted endogenous phytomelatonin biosynthesis in mustard sprouts by activating *TDC1*, *TDC2*, *T5H1*, *T5H2*, *SNAT1*, *SNAT2*, *SNAT3*, *SNAT4*, *ASMT1*, *ASMT2*, and *ASMT3* expression. By quantitative iTRAQ proteomic analysis, also, exogenous MeJA application promoted tryptophan biosynthetic pathway proteins expression and supported endogenous phytomelatonin accumulation in mustard sprouts.

Zhou et al. [338] reported that exogenous IAA treatment conferred chilling tolerance in peach fruit by promoting endogenous phytomelatonin biosynthesis arising from activating *TDC1*, *T5H1*, *T5H2*, *SNAT*, and *COMT* expression. By exogenous IAA treatment, higher endogenous phytomelatonin IAA and GABA accumulation was accompanied by lower endogenous GA and ABA accumulation.

Dong et al. [339] reported that hydrogen-rich water (HRW) application delayed senescence in okra fruits by boosting endogenous phytomelatonin biosynthesis resulting from activating *TDC*, *T5H1/2/3*, *SNAT*, and *COMT1/2* expression along with boosting endogenous GA and IAA accumulation accompanying by inhibiting endogenous ABA accumulation. Therefore, boosting melatonin/ABA, GA/ABA and IAA/ABA accumulation could be liable for delaying senescence in okra fruits by HRW application [339]. By employing ammonia borane (ammonio-trihydroborate;  $\text{H}_3\text{NBH}_3$ ) or transgenic tomato and Arabidopsis expressing hydrogenase1 (*CrHYD1*) from *Chlamydomonas reinhardtii* for safe, efficient, stable, long-acting, and lower dosage



H<sub>2</sub> supplying, endogenous molecule hydrogen (H<sub>2</sub>) accumulation is responsible for promoting lateral root branching in tomato and Arabidopsis plants [340]. By endogenous molecule hydrogen (H<sub>2</sub>) accumulation, activating *TDC*, *T5H*, *SNAT*, *ASMT* and *COMT* expression promotes endogenous phyto-melatonin biosynthesis. By pharmacologically inhibiting endogenous phyto-melatonin biosynthesis by employing p-chlorophenylalanine (p-CPA)

application or biotechnological suppressing endogenous phyto-melatonin biosynthesis by *SNAT* and *COMT* genes silencing, Wang et al. [340] reported that endogenous phyto-melatonin biosynthesis is indispensable for promoting lateral root branching in tomato and Arabidopsis by endogenous molecule hydrogen (H<sub>2</sub>) accumulation arising from ammonia borane employing or *CrHYD1* expression (Table 5).

**TABLE 5** | Endogenous phyto-melatonin biosynthesis by employing postharvest technologies for improving postharvest storability of fruits and vegetable.

Plant material	Treatments	Molecular and biochemical effects	References
Fresh walnut fruit ( <i>Juglans regia</i> )	CA + ClO <sub>2</sub>	Higher endogenous phyto-melatonin accumulation, higher POD activity, lower PAL and PPO activity, higher acid value, lower peroxide value and carbonyl value, lower mold incidence.	[341]
Strawberry fruits ( <i>Fragaria ananassa</i> )	PSKα 150 nM	Higher endogenous phyto-melatonin accumulation, higher <i>TDC</i> , <i>T5H</i> , <i>SNAT</i> , and <i>ASMT</i> expression, higher endogenous PSKα accumulation, higher <i>PSK3</i> and <i>PSK6</i> expression, higher <i>PSKR1</i> expression, higher endogenous Ca <sup>2+</sup> accumulation, higher endogenous cGMP accumulation, higher phenols, flavonoids, and anthocyanins accumulation, higher ABTS and DPPH scavenging capacity, higher <i>PAL</i> and <i>CHS</i> expression and activity.	[322]
Table grape ( <i>Vitis vinifera</i> L.)	SA 2 mM	Higher endogenous phyto-melatonin accumulation, lower endogenous histamine and dopamine accumulation. Lower berry drop and decay incidence, higher rutin, cyanidin-3,5-diglucoside and 3-O-glycosidic delphinidin accumulation, higher chlorogenic acid and gallic acid accumulation,	[342]
Okra fruits ( <i>Abelmoschus esculentus</i> )	HRW 220 μM	Higher endogenous phyto-melatonin accumulation, higher <i>TDC</i> , <i>T5H1/2/3</i> , <i>SNAT</i> , and <i>COMT1/2</i> expression, higher endogenous GA accumulation, higher endogenous IAA accumulation, lower endogenous ABA accumulation.	[339]
Mustard sprout ( <i>Brassica juncea</i> )	MeJA 100 mM	Higher endogenous phyto-melatonin accumulation, higher <i>TDC1</i> , <i>TDC2</i> , <i>T5H1</i> , <i>T5H2</i> , <i>SNAT1</i> , <i>SNAT2</i> , <i>SNAT3</i> , <i>SNAT4</i> , <i>ASMT1</i> , <i>ASMT2</i> , and <i>ASMT3</i> expression, higher myrosinase 1, cytosolic sulfotransferase 16, and glutamate-glyoxylate aminotransferase 2 proteins expression.	[337]
Cassava roots ( <i>Manihot esculenta</i> )	CaCl <sub>2</sub> 10 mM	Higher endogenous phyto-melatonin accumulation, higher <i>TDC1</i> , <i>TDC2</i> , <i>T5H</i> , <i>ASMT1</i> , <i>ASMT2</i> , <i>ASMT3</i> , and <i>SNAT</i> expression, PPD progression delaying, higher <i>CaMs</i> , <i>CMLs</i> , <i>CPKs</i> and <i>CBLs</i> expression, higher endogenous Ca <sup>2+</sup> accumulation, higher AA and starch accumulation.	[334]
	MeJA 10 mM	Higher endogenous phyto-melatonin accumulation, higher <i>TDC1</i> , <i>TDC2</i> , <i>T5H</i> , <i>ASMT1</i> , <i>ASMT2</i> , <i>ASMT3</i> , and <i>SNAT</i> expression, PPD progression delaying, higher endogenous GA3 accumulation, higher SOD and CAT activity, lower O <sub>2</sub> <sup>-</sup> generation and H <sub>2</sub> O <sub>2</sub> accumulation, higher ascorbic acid, starch, and carotenoids accumulation.	[335]
	Ethanol 50%	Higher endogenous phyto-melatonin accumulation, higher <i>TDC1</i> , <i>TDC2</i> , <i>T5H</i> , <i>ASMT1</i> , <i>ASMT2</i> , <i>ASMT3</i> , and <i>SNAT</i> expression, PPD progression delaying, higher SOD and CAT activity, lower O <sub>2</sub> <sup>-</sup> generation and H <sub>2</sub> O <sub>2</sub> accumulation, higher ascorbic acid, starch, anthocyanin and carotenoids accumulation, higher ABTS scavenging capacity, higher <i>APX2</i> , <i>GR</i> and <i>Cu/ZnSOD</i> expression, higher endogenous ethylene production.	[336]

(Continues)

TABLE 5 | (Continued)

Plant material	Treatments	Molecular and biochemical effects	References
White button mushrooms ( <i>Agaricus bisporus</i> )	ATP 750 $\mu$ M	Higher endogenous phytemelatonin accumulation, Cap browning attenuating, higher signaling H <sub>2</sub> O <sub>2</sub> accumulation, higher NADPH oxidase activity, higher AOX expression, higher phenol accumulation, higher DPPH scavenging capacity, higher PAL activity, lower PPO activity, higher SKDH activity, lower MDA accumulation.	[319]
Tomato ( <i>Solanum lycopersicum</i> ) and Arabidopsis ( <i>Arabidopsis thaliana</i> )	Ammonia borane or <i>CrHYD1</i> gene overexpressing	Higher endogenous phytemelatonin accumulation, higher <i>TDC</i> , <i>T5H</i> , <i>SNAT</i> , <i>ASMT</i> and <i>COMT</i> expression, higher endogenous H <sub>2</sub> accumulation, higher lateral root branching.	[340]
Peach fruits ( <i>Prunus persica</i> )	IAA 500 $\mu$ M	Higher endogenous phytemelatonin and GABA accumulation, lower endogenous ABA and GA accumulation, higher <i>TDC1</i> , <i>T5H1</i> , <i>T5H2</i> , <i>SNAT</i> , and <i>COMT</i> expression.	[338]

## 8 | Conclusion and Future Perspectives

The different aspects presented in this work point to a spectacular increase in information on phytemelatonin in a few years. It is noteworthy that in the period 2009–2017 there was a number of publications related to melatonin of 33 per year, and in 2018–2020 there was an exponential increase (388 articles, with an average of 130 per year), while in 2023 more than 500 articles were published. Of the aspects analyzed here, we must point out that:

- The biosynthetic pathway of phytemelatonin is well established in higher plants, knowing the enzymes involved and the sites of biosynthesis in the cell. However, some aspects remain unelucidated, such as the detection in many cases of 5-hydroxytryptophan without having detected or identified the enzyme responsible for its formation from tryptophan. Little or nothing is known about the biosynthesis of phytemelatonin in other groups of plants beyond those of agronomic interest.
- We have presented the multiple factors and regulatory elements of the gene expression of phytemelatonin biosynthetic enzymes, being diverse, complex and with aspects of intervention of interest in the postharvest improvement of fruits and vegetables.
- Other aspects analyzed with special interest have been the configuration and mode of action of the plant melatonin receptor (CAND2/PMTR1), less evolved than that of mammals but with common points. And the interesting role of melatonin in autophagic activity, an aspect of maximum interest in melatonin studies in humans and animals.
- Undoubtedly, the improvement in plant tolerance to stressors (resilience) is one of the responses mediated by melatonin of great basic and applied significance. In this work, two of the stressors most directly involved with the postharvest quality of fruits and vegetables have been exposed, such as UV-B light and chilling injury, although multiple examples of water stress and biotic stress (fungal decay) applied to the improvement of postharvest quality and its improvement in the marketing of these products have also been given.

- Possibly one of the aspects that still requires more research is the metabolic, regulatory and signaling interconnections between phytemelatonin and the various plant hormones involved in the ripening and senescence of fruits and vegetables, mainly GAs, ABA, ethylene, SA and JA, as well as auxin and others. The hormonal plant network is clearly modulated by melatonin, which is why it was attributed the role of *plant master regulator*. There is sufficient knowledge to apply it in postharvest improvement that extends the commercial life of agro-products using also the challenges of new materials (new functional packaging, bioactive films) and the globalized refrigerated transport and conservation.

With regard to future perspectives, today, we have enough data and knowledge about the functions of phytemelatonin in higher plants and ways to modulate or alter its endogenous content in tissues to be able to face challenges with direct application in agriculture. Among the most interesting action points where melatonin could play a role in improving physiological processes would be: seed germination, rooting of cuttings, improvement of rhizobiome, vegetative growth, resilience of seedlings against stressors, photosynthesis, CO<sub>2</sub> intake, improvement in primary metabolism, especially in C, N, P and S; improvement of secondary metabolism, regulating the production of polyphenols and terpenoids, mainly; modulation of reproductive processes, affecting flowering, parthenocarpy and ripening, with special emphasis on the postharvest quality of fruits and vegetables. All these possible actions can and should converge in agronomic actions, especially in seedbeds, improving the resilience of seedlings against stress, obtaining seedlings with a better capacity to adapt to the seedbed-field transition, with better rooting capacity, improve plant growth in contaminated soils or in situations of thermal, saline and water stress, among others; improving the quality of functional foods, rich in functional groups such as antioxidants and others, and improving the postharvest of fruit and vegetables, extending their shelf life and ensuring their organoleptic qualities. In addition to preharvest spraying or postharvest dipping, bioactive films and coatings enriched with melatonin-nanoparticles formulations can be considered as promising approaches for improving the postharvest marketability of fruits and vegetables.

## Acknowledgments

Research related to this review was funded by the Ministerio de Ciencia e Innovación (Spain), 'Proyectos de I+D+', Programas Estatales de Generación de Conocimiento y Fortalecimiento Científico y Tecnológico del Sistema de I+D+i y de I+D+i Orientada a los Retos de la Sociedad, del Plan Estatal de Investigación Científica y Técnica y de Innovación 2017–2020 (grant PID2020-113029RBI00 to M.B.A. funded by MCIN/AEI 10.13039/501100011033). More information can be found at the Phytohormones and Plant Development Research Group website (<https://www.um.es/en/web/phytohormones>).

## Conflicts of Interest

The authors declare no conflicts of interest.

## Data Availability Statement

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

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