

The orchestrated network of skin photoaging: From intercellular crosstalk to molecular signaling

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SUMMARY: Photoaging is a distinct form of pathological skin aging driven primarily by chronic ultraviolet (UV) radiation, which clinically manifests as wrinkles, dyspigmentation, and loss of elasticity. Although core molecular events induced by UV—such as oxidative stress and DNA damage—are relatively well-understood, there is still a lack of a systematic and integrated understanding of how diverse cell types in the skin collectively drive photoaging through complex interactive networks. This review systematically elaborates the cellular and molecular mechanisms underlying skin photoaging. The key pathways involved are examined, including oxidative stress, apoptosis, dysregulated autophagy, activation of inflammatory cascades, and degradation of the extracellular matrix (ECM). This review further details the pivotal roles of and reciprocal crosstalk among fibroblasts, keratinocytes, melanocytes, and various immune cells. By providing an integrated perspective on these interactions, this review outlines the cellular and molecular mechanism of UV-associated senescence, which uniquely integrates the roles of the immune microenvironment and cellular crosstalk, providing a roadmap for next-generation anti-photoaging strategies.

Keywords: skin photoaging, senescence-associated secretory phenotype (SASP), inflammaging, extracellular matrix remodeling, therapeutic targets

1. Introduction

Photoaging results from chronic and repeated exposure to ultraviolet (UV) radiation—primarily UVA and UVB—along with other environmental factors such as infrared and visible light. Clinically, it is characterized by wrinkles, skin laxity, roughness, dyspigmentation, and telangiectasia. This condition represents a distinct, exogenous form of pathological skin aging. In contrast to intrinsic aging, photoaging is largely confined to areas exposed to the sun including the face, neck, the dorsum of the hands, and the extensors of the forearms. Oxidative stress constitutes the central molecular mechanism underlying its progression.

Chronic sun exposure is a major etiological factor in skin aging, with studies attributing up to 80% of facial skin aging to UV exposure (1). Solar UV radiation (UVR) consists of three wavelength ranges: UVA (320–400 nm), UVB (280–320 nm), and UVC (100–280 nm). Although UVC carries the highest energy, it is predominantly absorbed by the Earth's ozone layer and thus poses minimal risk to human health. The biologically relevant

UVR that reaches the Earth's surface consists mainly of UVB and UVA. UVB, characterized by its short wavelength and high energy, penetrates the skin to a depth of approximately 160–180 μm and is largely absorbed by the epidermis. It induces DNA damage *via* oxidative stress, leading to sunburn, erythema, and skin carcinogenesis. In contrast, UVA constitutes 90–95% of solar UVR and is considered the primary driver of photoaging (2). Despite its lower energy, UVA's longer wavelength enables deeper penetration, penetrating as deep as 1,000 μm into the dermis. Rather than causing direct DNA damage, UVA promotes reactive oxygen species (ROS)-mediated skin aging and pigmentation (3,4).

This review discusses the cellular and molecular mechanisms underlying skin photoaging. Special emphasis is placed on the orchestrating roles of cells—fibroblasts, keratinocytes, melanocytes, and immune cells—as they interact with each other and jointly drive the development of the disease. This work contributes to the systematic understanding of the mechanisms underlying photoaging.

2. The pathogenesis of skin photoaging

2.1. Oxidative stress injury

Oxygen can be enzymatically or non-enzymatically converted into reactive intermediates, collectively termed ROS. Major ROS include the superoxide anion (O_2^-), the hydroxyl radical ($\cdot OH$), and hydrogen peroxide (H_2O_2). The link between ROS and aging is well established and is historically rooted in two influential theories: the free radical theory of aging and the mitochondrial theory of aging (5). Chronic exposure to UV radiation promotes ROS accumulation in skin cells, resulting in oxidative damage, cellular dysfunction, and ultimately, skin photoaging (6-8). Multiple studies have demonstrated that UVR induces ROS and oxygen-derived free radicals in a dose-dependent manner (9-12). In skin keratinocytes and fibroblasts, UV exposure elevates lipid peroxidation, protein carbonylation, and DNA damage (13-15).

A primary defense against this oxidative stress is the Nrf2-Keap1 pathway, which plays a critical role in protecting skin cells from UV-induced damage during photoaging (Figure 1). Under basal conditions, Nrf2 is sequestered in the cytoplasm by its inhibitor Keap1. Oxidative stress triggers the dissociation of Nrf2 from Keap1, allowing Nrf2 to translocate to the nucleus, where it forms a heterodimer with a Maf protein (16). This Nrf2-Maf complex binds to antioxidant response

elements (AREs) in the promoter regions of genes encoding antioxidant and detoxifying enzymes (17), thereby activating their transcription. The subsequent synthesis of these enzymes helps neutralize ROS and mitigate oxidative damage (7,18). In concurrence, molecular analyses have confirmed that UVA irradiation markedly upregulates oxidative stress-responsive genes such as heme oxygenase-1 (HO-1), NAD(P)H:quinone oxidoreductase 1 (NQO1), and the glutamate-cysteine ligase catalytic subunit (GCLC) (19). Beyond the Nrf2 system, peroxisomes also play an essential role in regulating cellular ROS levels, particularly under homeostatic conditions (20).

2.2. Apoptosis

Apoptosis is a genetically programmed, energy-dependent process of controlled cellular self-destruction and represents a key mechanism implicated in skin photoaging (21). UV-induced apoptosis proceeds through two temporally distinct pathways. In the early phase following exposure, UVA1 generates singlet oxygen, which depolarizes mitochondrial membranes and triggers immediate apoptosis. After 24 hours, ROS produced by both UVA and UVB subsequently induce oxidative DNA damage, leading to delayed apoptosis (22,23). The accumulation of DNA lesions activates the p53 pathway, which promotes the transcription of

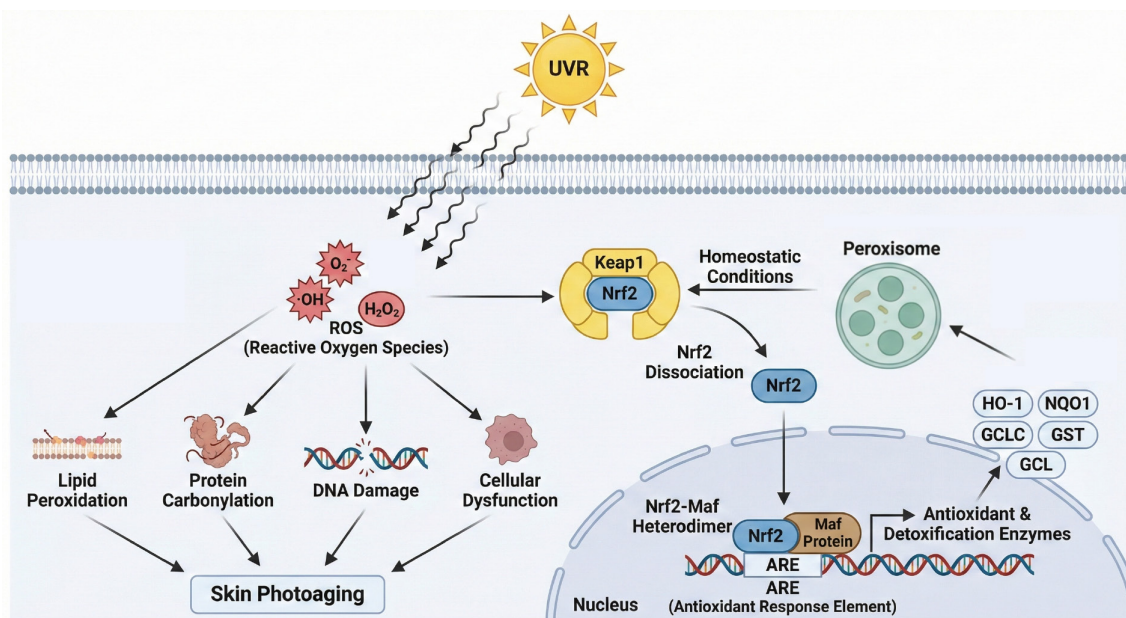


Figure 1. The mechanism of oxidative stress injury. Under ultraviolet (UV) radiation, oxygen is converted into reactive oxygen species (ROS), such as the superoxide anion (O_2^-), the hydroxyl radical ($\cdot OH$), and hydrogen peroxide (H_2O_2). These ROS induce lipid peroxidation, protein carbonylation, DNA damage, and cellular dysfunction. The Nrf2-Keap1 pathway plays a critical role in protecting skin cells from UV-induced damage during photoaging. Under basal conditions, Nrf2 is sequestered in the cytoplasm by Keap1. Upon oxidative stress, Nrf2 dissociates from Keap1 and translocates into the nucleus, where it forms a heterodimer with a Maf protein. This complex binds to antioxidant response elements (AREs) in the promoters of genes encoding antioxidant and detoxifying enzymes, activating their transcription. The resulting enzymes help neutralize ROS and alleviate oxidative damage. Consistent with this mechanism, molecular analyses confirm that UVA irradiation markedly upregulates oxidative stress-responsive genes, including heme oxygenase-1 (HO-1), NAD(P)H:quinone oxidoreductase 1 (NQO1), and the glutamate-cysteine ligase catalytic subunit (GCLC).

autophagy-related genes such as AMP-activated protein kinase (AMPK), Sestrin 2 (SESN2), and Unc-51-like autophagy-activating kinase 1 (ULK1). Activated ULK1, in turn, phosphorylates Beclin-1 to initiate phagophore nucleation (24). The intrinsic (mitochondrial) apoptotic pathway is finely regulated by the balance between anti-apoptotic (e.g., Bcl-2 and Bcl-xL) and pro-apoptotic (e.g., Bax, Bak, and Bid) members of the Bcl-2 protein family, which ultimately determines cellular fate.

2.3. Autophagy

Autophagy is a highly regulated degradation process essential for maintaining cellular homeostasis through the clearance of damaged organelles, misfolded proteins, and other macromolecular debris (Figure 2). It is broadly categorized into macroautophagy, microautophagy, and selective autophagy (25). Based on the specific cellular components targeted for degradation, selective autophagy can be further classified into mitophagy (degrading damaged mitochondria), aggrephagy (degrading protein aggregates), and pexophagy (degrading peroxisomes) (26,27). In skin cells, mitochondria are a primary

source of ROS. Sustained UVR induces mitochondrial DNA mutations and excessive ROS production. Mitophagy acts as a protective mechanism by removing dysfunctional mitochondria, thereby attenuating oxidative stress and genomic damage (28). Similarly, aggrephagy eliminates cytotoxic protein aggregates formed upon UV exposure, while pexophagy degrades impaired peroxisomes that would otherwise exacerbate oxidative stress and accelerate skin aging (29,30).

The autophagic process is orchestrated by a network of signaling pathways and effector molecules. In senescent human dermal fibroblasts, mitochondrial dysfunction is often associated with dysregulation of the PI3K/AKT/mTOR cascade (31). Conversely, AMPK signaling serves as a key positive regulator of autophagy (32,33). Both the inhibition of mTOR and activation of AMPK have protective roles in skin photoaging by promoting the clearance of damaged cellular components and reducing oxidative and DNA damage induced by UVR (34-36).

Central to autophagy are autophagy-related (ATG) proteins. ULK1, a key initiator kinase regulated upstream by mTOR and AMPK, phosphorylates downstream

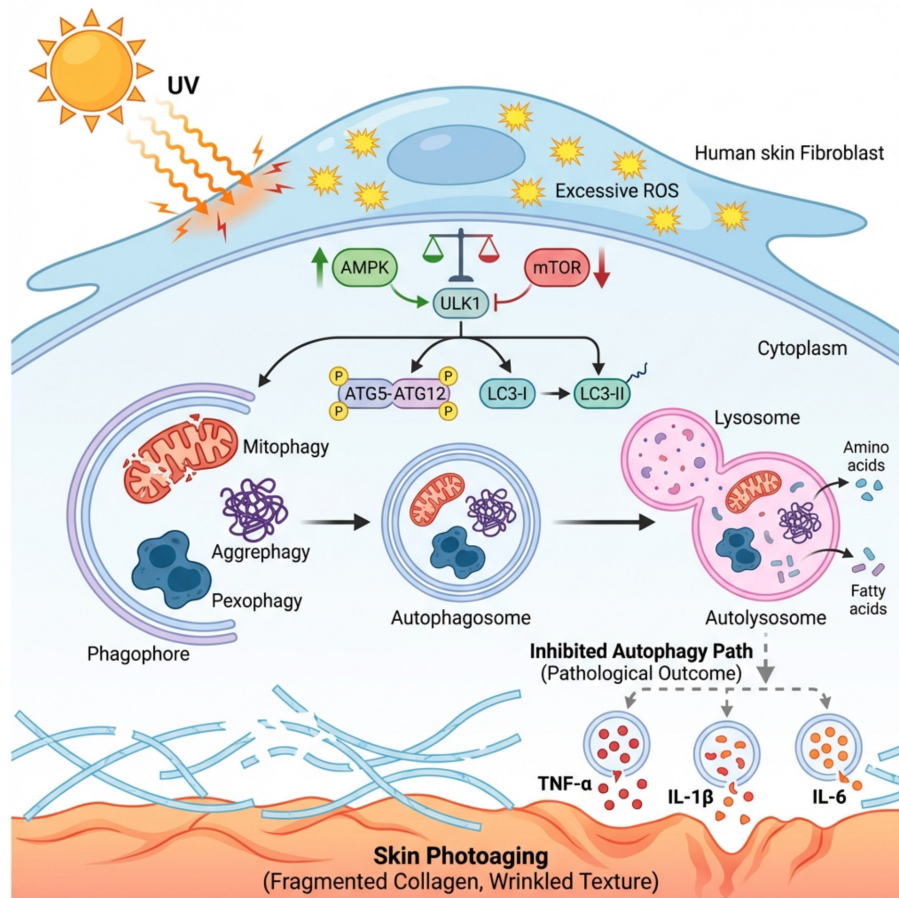


Figure 2. The mechanism of autophagy. Selective autophagy can be classified into mitophagy, aggrephagy, and pexophagy. In senescent human dermal fibroblasts, mitochondrial dysfunction is often accompanied by mTOR inhibition and AMPK activation, which subsequently activates the autophagy-related protein ULK1. ULK1 phosphorylates downstream ATG proteins, such as ATG5, ATG12, and LC3, thereby driving autophagosome formation. This process further promotes the expression of pro-inflammatory mediators, including TNF- α , IL-1 β , and IL-6, collectively exacerbating skin photoaging.

ATG proteins such as ATG5, ATG12, and LC3 to drive autophagosome formation. Importantly, excessive UVR suppresses autophagic flux, leading to the subsequent activation of pro-inflammatory mediators such as tumor necrosis factor- α (TNF α), interleukin 1 β (IL-1 β), and interleukin 6 (IL-6), which collectively exacerbate skin photoaging (37).

2.4. Inflammation-related pathways

The p38 MAPK and NF- κ B signaling pathways are pivotal mediators of the inflammatory response triggered by UVR (38). UV exposure activates multiple members of the MAPK family, including extracellular signal-regulated kinase (ERK), c-Jun N-terminal kinase (JNK), and p38 MAPK. While ERK primarily regulates cell proliferation and survival, its sustained activation upregulates the senescence-associated secretory phenotype (SASP), thereby driving cellular senescence (39,40). Concurrently, NF- κ B is activated under UV stress and promotes the transcription of pro-inflammatory cytokines such as TNF- α , interleukin 1 α (IL-1 α), and IL-1 β . These cytokines recruit immune cells—including monocytes, macrophages, and natural killer (NK) cells—to the site of damage (41,42). Subsequently, these infiltrating immune cells release additional inflammatory chemokines, such as CCL3, CXCL1, CXCL3, and CXCL5 (43). Moreover, MAPK signaling enhances cyclooxygenase-2 (COX-2) production, which exacerbates inflammation and tissue injury during photoaging (44). After the early vasodilatory phase, skin is infiltrated by neutrophils, monocytes, and T cells. These cells not only secrete pro-inflammatory mediators but also induce the release of anti-inflammatory cytokines, including IL-4, IL-10, and transforming growth factor β (TGF- β) (45,46). These regulatory cytokines facilitate the transition from acute inflammation to a prolonged, resolution-phase immunosuppression, a shift that accompanies tissue repair processes at the inflamed site.

2.5. Extracellular matrix (ECM) degradation-related pathways

The degradation of the ECM represents a central hallmark

of skin photoaging. As previously outlined, excessive UVR elicits a robust inflammatory response. This process involves the upregulation of pro-inflammatory cytokines such as IL-1 α and IL-1 β , which in turn stimulate the expression of several matrix metalloproteinases (MMPs)—including MMP-1 (collagenase), MMP-3 (stromelysin), and MMP-9 (gelatinase). These enzymes collectively degrade collagen and other critical ECM components (47,48). Concurrently, UV-induced ERK activation promotes the expression of c-Fos, which forms the transcription factor AP-1 with c-Jun. AP-1 binds to promoter regions of MMP genes, further enhancing their transcription. The resultant overexpression of MMPs leads to extensive collagen breakdown and disruption of the three-dimensional elastin network, ultimately manifesting as skin wrinkling and loss of elasticity (49,50).

3. Roles of cells in skin photoaging

3.1. Fibroblasts

The pathogenesis of dermal fibroblast photoaging is predominantly initiated by chronic UVR, which induces a cascade of intracellular damage (51). Core mechanisms involve the excessive generation of ROS, accumulation of DNA damage, and mitochondrial dysfunction (52,53). Critically, prolonged UV exposure drives cellular senescence, marked by irreversible cell-cycle arrest and the acquisition of an SASP (54). Consequently, photoaged fibroblasts exhibit a profound decline in collagen and elastin production along with elevated expression of matrix-degrading enzymes such as MMPs, collectively leading to ECM disintegration (Table 1) (55).

3.2. Keratinocytes

As the outermost layer of the skin, the epidermis is directly and chronically exposed to solar UVR, rendering it highly susceptible to photoaging (55). In keratinocytes, UVR triggers photoaging through interconnected mechanisms, including oxidative stress with ROS generation, mitochondrial dysfunction, DNA damage, and activation of inflammatory pathways such

Table 1. Key regulators in skin photoaging

Cell type	Upregulated factors	Downregulated factors
Fibroblasts	ROS, SASP, MMPs	Collagen production, elastin production
Keratinocytes	ROS, SASP, MMP-1, MMP-9, IL-1 β , IL-6	Antioxidant defenses
Melanocytes	Melanogenesis, β -catenin signaling	SDF1
Macrophages	MMP-1, MMP-3, MMP-9, Pro-inflammatory factors, M1/M2 ratio	Anti-inflammatory cytokines
Th17/Treg Cells	IL-17A, IL-8, IL-17F, IL-21, IL-22, IL-26, TNF- α , IL-10, TGF- β , SASPs	Immune surveillance
Mast Cells	Serine proteases (tryptase, chymase), Histamine, MMP-9	Not specified

Abbreviation: ROS, reactive oxygen species; SASP, senescence-associated secretory phenotype; MMPs, matrix metalloproteinases; SDF1, stromal cell-derived factor 1.

as NF- κ B and MAPK signaling (5657). These negative factors collectively promote an SASP, characterized by elevated expression of MMPs (e.g., MMP-1 and MMP-9), increased secretion of pro-inflammatory cytokines (e.g., IL-1 β , and IL-6), and a concomitant decline in antioxidant defenses (58,59).

3.3. Melanocytes

Melanocytes, situated primarily within the basal epidermal layer, are responsible for melanin production and proliferate at a low rate. Upon exposure to UVR, keratinocytes release paracrine factors including interleukin 17 (IL-17), endothelin 1 (ET 1), and stem cell factor (SCF) (60). These ligands bind to their respective receptors—MC1R, the endothelin B receptor (ETB), and c Kit—on melanocytes (Figure 3). ET 1 and SCF binding, in particular, activates the ERK1/2 MAPK pathway, thereby promoting melanogenesis (61). Newly synthesized melanin is subsequently transferred to

adjacent keratinocytes, where it functions as a natural photoprotectant by absorbing UVR and mitigating DNA damage (62).

Beyond keratinocytes, senescent dermal fibroblasts also contribute significantly to skin hyperpigmentation (63). Senescent fibroblasts upregulate the secretion of pro-melanogenic growth factors such as hepatocyte growth factor (HGF), keratinocyte growth factor (KGF), and SCF, which directly stimulate melanocytic activity (64-66). Additionally, factors such as secreted frizzled related protein 2 (sFRP2) and growth differentiation factor 15 (GDF15) further enhance melanin synthesis by activating the β -catenin signaling pathway (67). Epigenetic alterations also play a regulatory role, including the downregulation of stromal cell-derived factor 1 (SDF1) and the upregulation of Wnt inhibitory factor 1 (WIF-1), collectively shaping the pigmentary response to chronic UV exposure (68).

3.4. Macrophages

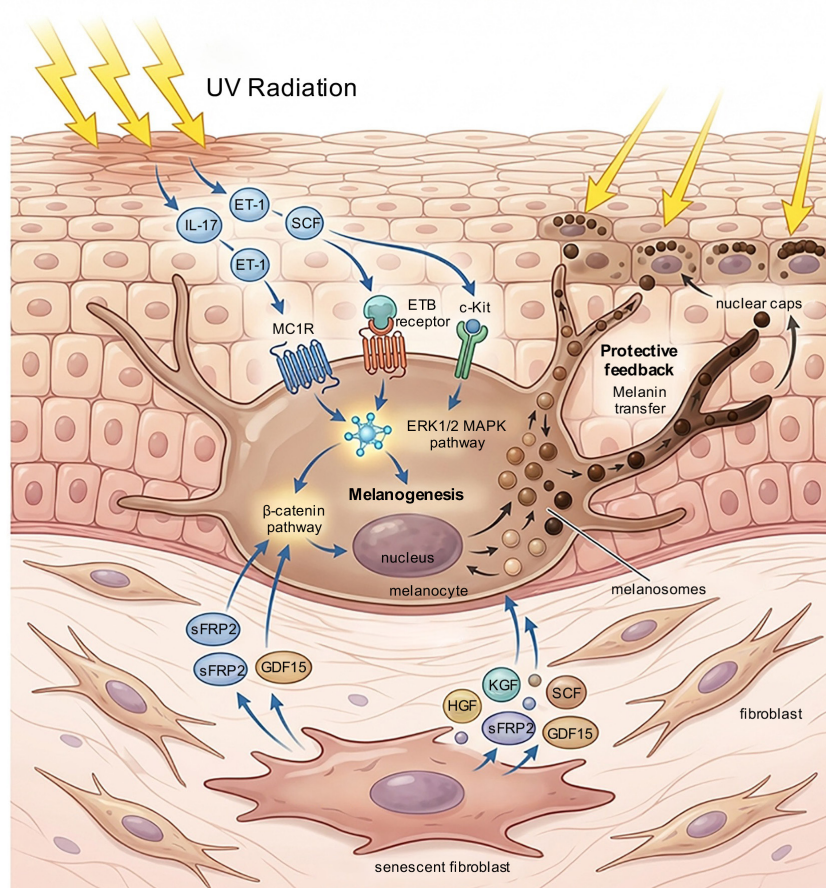


Figure 3. The alteration of melanocytes under UV exposure. Upon UVR, keratinocytes release paracrine factors such as interleukin-17 (IL-17), endothelin-1 (ET-1), and stem cell factor (SCF). These ligands bind to their respective receptors—MC1R, endothelin B receptor (ETB), and c-Kit—on melanocytes. The binding of ET-1 and SCF activates the ERK1/2 MAPK pathway, thereby promoting melanogenesis. In fibroblasts, UV-induced epigenetic alterations downregulate stromal cell-derived factor-1 (SDF1) and upregulate Wnt inhibitory factor-1 (WIF-1), which collectively enhance the secretion of pro-melanogenic factors including hepatocyte growth factor (HGF), keratinocyte growth factor (KGF), SCF, secreted frizzled-related protein 2 (sFRP2), and growth differentiation factor-15 (GDF15). These factors further stimulate melanin synthesis by activating the β -catenin signaling pathway. Newly synthesized melanin is transferred to adjacent keratinocytes, where it acts as a natural photoprotectant by absorbing UVR and reducing DNA damage.

As key components of the innate immune system, macrophages play an important role in maintaining skin homeostasis. In response to various stimuli, macrophages can polarize into two primary subsets: the pro-inflammatory M1 phenotype and the anti-inflammatory M2 phenotype. In response to UVR, M1 macrophages are recruited *via* activation of the p38 MAPK and NF- κ B signaling pathways. They recognize damage-associated molecular patterns (DAMPs) and pathogen-associated molecular patterns (PAMPs) in photodamaged skin through Toll-like receptors (TLRs) and inflammasome signaling, thereby amplifying local inflammation (69). Moreover, they secrete MMPs, including MMP-1, MMP-3, and MMP-9, which are central to the degradation of type I collagen during photoaging (70). In contrast, M2 macrophages, which are polarized by cytokines such as IL-4 and IL-13 *via* the STAT6 pathway (M2a), or by immune complexes and IL-1 receptor antagonists (M2b), or *via* the JAK1/STAT3 pathway in response to IL-10 and TGF- β (M2c), are crucial to tissue repair and remodeling (71). M2 macrophages promote the activation of fibroblasts and ECM deposition by releasing growth factors (*e.g.*, PDGF, VEGF, TGF- β 1, and IGF-1), while downregulating inflammatory markers and MMPs. In photoaged skin, the macrophage balance shifts toward an M1-dominant state, resulting in an elevated M1/M2 ratio (72). This imbalance is significantly correlated with reduced levels of type I, V, and VI collagen in the dermis (73). The sustained inflammatory environment may accelerate fibroblast senescence, which in turn exacerbates collagen dysregulation through the secretion of deleterious factors (74). Notably, the disruption particularly affects type V and VI collagen, which serve as critical bridging molecules that stabilize type I collagen fibrils. Consequently, the altered M1/M2 equilibrium contributes to chronic inflammation, impaired collagen homeostasis, and ultimately to the structural breakdown of the dermal matrix, manifesting as skin laxity and wrinkling (75).

3.5. Th17/Treg cells

T helper 17 (Th17) cells and regulatory T (Treg) cells, as key effector subsets derived from the differentiation of CD4⁺ T cells, play functionally antagonistic roles in immune responses. Th17 cells are characterized by the production of interleukin (IL)-17A and also secrete pro-inflammatory cytokines such as IL-8, IL-17F, IL-21, IL-22, IL-26, and TNF- α , aggravating inflammation-induced skin photoaging (76). In contrast, Tregs, defined by the expression of the transcription factor FoxP3 and surface markers CD25 and CTLA-4, are central to maintaining immune tolerance and homeostasis, largely through the secretion of anti-inflammatory cytokines such as IL-10, IL-35, and TGF- β 1. Beyond accelerating aging, UVR has also been implicated in skin immunosuppression,

this phenomenon is predominantly governed by Tregs (77). Their activation in UV-exposed skin is initiated through two major pathways. Primarily, UVR triggers the migration of Langerhans cells (LC) to regional lymph nodes, where they present antigen and imprint Tregs with skin-homing specificity (78,79). Additionally, UVB acts as a direct photochemical trigger, converting tryptophan into the aryl hydrocarbon receptor (AhR) ligand 6-formylindolo[3,2-b] carbazole (FICZ) and activating the kynurenine pathway, the metabolites of which also serve as AhR agonists (80,81). UVR further stimulates the production of cis-urocanic acid, which results in an inflammatory environment and which promotes the synthesis of prostaglandin E2, collectively establishing a signaling cascade that expands and recruits Tregs to the skin (82,83).

Once localized, Tregs drive photoaging through two synergistic mechanisms that fuel a self-perpetuating cycle of damage. First, through the secretion of IL-10 and TGF- β , Tregs dampen the effector functions of CD4⁺/CD8⁺ T cells, NK cells, and dendritic cells (84-86). This suppression of immunosurveillance compromises the clearance of senescent cells, leading to their accumulation. The senescent cells release SASPs such as ROS, cytokines, and MMPs, exacerbating local inflammation and reinforcing the immunosuppressive microenvironment that sustains Treg activity (87,88). Second, Tregs directly promote tissue degradation. Treg-derived TGF- β inhibits keratinocyte proliferation, upregulates collagen-degrading MMPs, and can induce senescence in resident skin cells (89-91). While IL-10 typically has anti-inflammatory effects, under chronic photo-inflammatory conditions it disrupts proteostasis by suppressing autophagy and antigen presentation. Moreover, ROS released by recruited immune cells activate latent TGF- β , amplifying its tissue-destructive effects (92,93).

3.6. Mast cells

Mast cells are common innate immune cells, recognized as key effector cells in immunoglobulin E (IgE)-mediated allergic inflammation, and play important roles in various physiological and pathological processes (94,95). Mast cells contain a variety of bioactive substances. UV stimulation can promote their activation and degranulation, leading to the release of serine proteases and other mediators, such as tryptase, chymase, histamine, and TNF, which are involved in changes observed in photoaged skin, including solar elastosis, degradation of the ECM, disruption of the basement membrane, and hyperpigmentation (96,97). Tryptase is the most abundant serine protease in mast cells and also functions as a gelatinase. This enzyme is associated with degradation of the basement membrane and the formation of perivascular alterations induced by UVR. Tryptase participates in the degradation of the

dermal ECM by processing MMP precursors into active forms or directly damaging ECM proteins. Repeated UV exposure can also promote the production of mast cell tryptase (98). Mast cell tryptase activates MMP-9 and degrades type IV collagen, thereby promoting wrinkle formation. In summary, tryptase can contribute to ECM damage, disruption of the basement membrane, and solar elastosis in photoaged skin, thereby influencing the progression of photoaging (99-101). Thus, tryptase may serve as a promising therapeutic target for preventing skin photoaging (102).

Histamine is the only recognized amine stored in human mast cells. It can induce MMP-9 production in human primary keratinocytes, promote immune cell migration in the basal layer of the skin, and degrade type IV collagen. Malaviya *et al.* (103) found that under UVR, upregulated histamine release from dermal mast cells in human skin may enhance collagen degradation and promote wrinkle formation. Kim *et al.* (104) treated mice chronically exposed to UV with the antihistamine ketotifen, and they found that ketotifen significantly reduced UV-induced wrinkles and effectively inhibited and delayed skin aging. Besides promoting wrinkle formation in photoaged skin, histamine is also associated with the development of hyperpigmentation. Yoshida *et al.* (105) found that treating human melanocytes with histamine induced morphological changes and increased tyrosinase activity, and they confirmed that histamine activates protein kinase A *via* the H₂ receptor, stimulating

melanogenesis in cultured human melanocytes. Topical application of famotidine (an H₂ antagonist) to UVB-irradiated mouse skin significantly reduced skin pigmentation and the increase in Dopa-positive melanocytes (105).

4. SASP-mediated intercellular crosstalk

In the pathophysiology of skin photoaging, the SASP serves as a central mechanistic hub orchestrating complex intercellular crosstalk among fibroblasts, keratinocytes, melanocytes, and infiltrating immune cells (Figure 4). Chronic UVR initially leads to fibroblast and keratinocyte senescence and SASP accumulation, including MMPs, pro-inflammatory cytokines (*e.g.*, IL-1 β , and IL-6), and growth factors, that not only degrade the ECM but that also have paracrine effects on neighboring cells. Specifically, senescent fibroblast-derived SASP factors such as IGF-1 induce keratinocyte senescence *via* p53/p21 activation, while HGF, KGF, and SCF promote melanogenesis and contribute to hyperpigmentation (Figure 4) (54,106,107). This secretome further recruits and polarizes macrophages toward a pro-inflammatory M1 phenotype, elevating the M1/M2 ratio and perpetuating MMP-mediated collagenolysis. Concurrently, UV-induced Tregs suppress immune surveillance *via* IL-10 and TGF- β , impairing senescent cell clearance and fostering a self-sustaining niche of SASP-producing cells. Mast cells, activated by

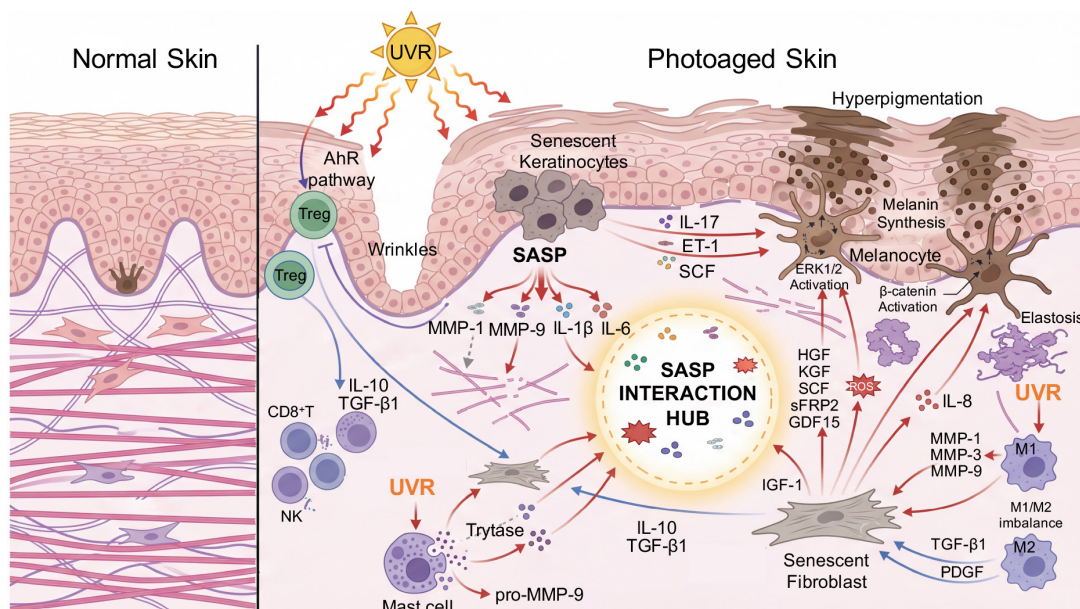


Figure 4. The multicellular SASP network driving skin photoaging. In skin photoaging, the senescence-associated secretory phenotype (SASP) acts as a central hub for intercellular communication. Chronic UV exposure induces senescence in fibroblasts and keratinocytes, leading them to secrete SASP factors (*e.g.*, MMPs, IL-1 β , and IL-6). This secretome degrades the extracellular matrix (ECM) and drives paracrine effects: SASP from fibroblasts promotes senescence in keratinocytes (*via* IGF-1), stimulates melanogenesis (*via* HGF/KGF/SCF), and recruits pro-inflammatory M1 macrophages, which amplify MMP-driven collagen breakdown. Concurrently, UV-induced regulatory T cells (Tregs) suppress immune clearance of senescent cells *via* IL-10/TGF- β , while mast cells release proteases that further degrade the ECM. These interactions form a vicious cycle—immune and epidermal signals exacerbate fibroblast senescence, the SASP of which in turn reinforces inflammation and matrix destruction—leading to the hallmark deterioration of photoaged skin.

UV, release tryptase and histamine, which amplify MMP activity and ECM degradation. The resultant chronic inflammatory microenvironment establishes reciprocal feedback loops—wherein inflammatory signals from immune and epidermal cells exacerbate fibroblast senescence, while SASP from fibroblasts reinforces immune dysregulation and matrix disintegration—collectively driving the progressive structural and functional deterioration characteristic of photoaged skin (51,63).

5. Emerging therapeutic strategies

Current therapeutic strategies targeting skin photoaging focus on antioxidants, ECM metabolism modulators, and senescence-directed interventions (Table 2). In keratinocytes, several natural compounds such as hesperetin and chrysanthemum attenuate senescence by suppressing the MAPK/AP-1 and NF-κB signaling axes, thereby reducing MMP expression (108,109). Nicotinamide (NAM) promotes DNA repair and enhances cellular energy metabolism to delay senescence (110), while mesenchymal stem cell-derived extracellular vesicles (MSC-EVs) deliver tissue inhibitor of metalloproteinase 1 (TIMP1) to inhibit Notch1 signaling, concurrently alleviating inflammation and cellular aging (111). Additional keratinocyte-targeted strategies include pharmacological inhibition of protease-activated receptor 2 (PAR2), enhancement of δ-catenin-mediated DNA repair, and activation of CISD2—a mitochondrial protein that reduces ROS production, suppresses MMP-1 expression, and restores mitochondrial function (112). In parallel, fibroblast-oriented interventions are categorized into antioxidants,

ECM metabolism modulators, and senescence-directed therapies. Numerous phytochemicals, such as resveratrol, salvianolic acid B, galangin, and urolithin A, have antioxidant effects *via* activation of stress-responsive NRF2 and SIRT1 pathways, leading to upregulated antioxidant enzymes (HO-1 and SOD), ROS scavenging, and mitophagy-mediated mitochondrial rejuvenation (113-116). Other agents, including protocatechuic aldehyde, gallic acid, and Scutellaria barbata extracts, primarily remodel ECM homeostasis by inhibiting MMP expression through an AP-1/NF-κB blockade and concurrently enhancing collagen synthesis *via* TGF-β/IGF-1 pathway activation (117,118). As senescence-targeting approaches, chlorogenic acid attenuates fibroblast senescence by inhibiting the glycolytic enzyme ENO1 and suppressing the SASP (119), whereas metformin modulates the PI3K/AKT/mTOR axis and alleviates excessive mitophagy (31). Physical and cell-based approaches, such as low-dose aminolevulinic acid photodynamic therapy (120), microneedling (121), and MSC-based therapies (122,123), represent complementary avenues for restoring dermal homeostasis. Beyond these preclinical and translational efforts, several intervention paradigms have advanced to clinical-stage investigation. For example, 0.5% retinol serums and topical rapamycin provide significant clinical benefits against photoaging, including improved uniformity of skin color, enhanced overall skin tone, increased elasticity, and optimized moisture retention (124,125). Moreover, topical and systemic modulation of the cutaneous microbiome has emerged as a novel strategy to reinforce epidermal barrier function and mitigate low-grade inflammatory drift associated with photoaging (126,127). These evolving

Table 2. Therapeutic strategies for skin photoaging

Therapeutic mechanism	Target/Pathway	Candidate drug/Intervention	Ref.
Antioxidant/Anti-inflammatory	MAPK/AP-1, NF-κB signaling	Hesperetin, chrysanthemum	(108,109)
Antioxidant/Mitochondrial rejuvenation	NRF2, SIRT1 pathways	Resveratrol, salvianolic acid B, galangin, urolithin A	(113-116)
DNA repair	DNA repair	Nicotinamide	(110)
ECM metabolism modulation	AP-1/NF-κB, TGF-β/IGF-1, TIMP1/Notch1	Protocatechuic aldehyde, gallic acid, Scutellaria barbata extracts	(117,118)
Anti-SASP	ENO1, PAR2, PI3K/AKT/mTOR	Chlorogenic acid, metformin	(31,119)
Physical therapy	Photodynamic effect, mechanical stimulation	Aminolevulinic acid photodynamic therapy, microneedling	(120,121)
MSC-based therapy	Skin regeneration	Adipose-derived MSC, MSC-EVs	(122,123)
Clinical stage	Retinoic acid receptor	0.5% retinol serums	(124,125)
Clinical stage	mTOR inhibition	Topical rapamycin	(124,125)
Clinical stage	Cutaneous microbiome modulation	Topical and systemic modulation	(126,127)

therapeutic strategies collectively define a precision-oriented landscape for the clinical management of skin photoaging.

6. Perspective

In the investigation of pathogenesis, single-cell sequencing technologies have provided a revolutionary perspective for understanding the complex mechanisms underlying photoaging. Compared to bulk analysis, this technology has enabled the construction of a high-resolution transcriptomic atlas of human skin aging, revealing distinct changes in cellular composition that differentiate photoaging from chronological aging (128,129). Moreover, single-cell analysis has precisely identified key regulators in photoaging, such as HES1 and KLF6 (130). Furthermore, by integrating analyses of intercellular communication networks, this approach has elucidated the underlying mechanism (129). Epigenetics is another approach that has further revealed the pathogenesis of photoaging. DNA methylation and histone alterations alter the three-dimensional conformation of DNA and subsequent gene expression without altering the underlying genetic sequence, thereby mediating cutaneous photoaging. Given the enduring and heritable nature of these epigenetic modifications, their cumulative effects are considered a key mechanism driving chronic photodamage and the aging process (131).

Over the past few years, rapid progress has been made in artificial intelligence-assisted diagnosis of dermatological conditions. Studies have shown that AI-assisted analysis of reflectance confocal microscopy (RCM) images, which evaluates the morphology (degree of flattening) of the dermal-epidermal junction (DEJ) and classifies dermal collagen fiber types, can intelligently identify photoaging (132).

Therapeutically, exosomes afford a promising strategy to treat photoaging. Derived from stem cells and plants, exosomes have been proven to have regenerative effects on photo-damaged skin. Moreover, as natural extracellular vesicles, exosomes show considerable potential as drug delivery vehicles. Future research could focus on the bioengineering of exosomes—including modification with targeting peptides, cargo optimization (e.g., with specific circRNAs or miRNAs), and the development of novel delivery systems—to achieve efficient and precise delivery (133). Concurrently, investigations into the skin microbiome have revealed that certain probiotic derivatives, such as the supernatant from *Pediococcus acidophilus* LS, have photoprotective and anti-melanogenic effects by inhibiting both the PKA/CREB and MAPK signaling pathways. This offers early evidence for a "microbe-skin axis" in photoaging regulation, although the mechanisms underlying the interaction between microbial metabolites and the host epigenome remain largely unexplored (134).

7. Conclusion

Photoaging is a distinct form of skin aging primarily caused by chronic exposure to UVR (UVA and UVB), clinically manifesting as wrinkles, pigmentation disorders, and loss of elasticity. Its core molecular mechanisms involve oxidative stress, apoptosis, dysregulated autophagy, activation of inflammatory pathways, and degradation of the ECM. Multiple types of skin cells—including fibroblasts, keratinocytes, melanocytes, and immune cells—interact through complex signaling networks to collectively drive disease progression. Recent advances in photoaging research, encompassing the elucidation of pathogenic mechanisms, AI-assisted diagnosis, and therapeutic development, have not only increased our understanding of this process but also expanded the potential for clinical translation. These breakthroughs have laid a robust theoretical foundation for the further development of targeted interventions and precision treatment strategies, holding promise for developing anti-photoaging therapies for more personalized and precision-based approaches.

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