

The Epigenetic Modification in the Pathogenesis of Skin Photoaging

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Abstract

Photoaging is a kind of skin damage induced by long-term exposure to ultraviolet radiation characterized by skin roughness, thickening, relaxation and wrinkles, local pigmentation or telangiectasia, and even tumorigenesis. Admittedly, the mechanisms of photoaging are varied and complicated mainly involving dermal extracellular matrix degradation, cell senescence and epidermal hyperplasia due to a combination of oxidative stress, inflammatory response and epigenetic modification. Epigenetic modifications study reversible and heritable changes in gene function in the absence of nuclear DNA sequence variation. Classic epigenetic events include methylation or hydroxy methylation of DNA dinucleotides, post-translational modifications of amino termini of histone proteins, and non-coding RNA expression. In this review, we introduced the pathological manifestation of skin aging and summarized the possible pathogenesis of photoaging comprehensively. In addition, we focused on the mechanisms of epigenetic contributors to skin aging impacted by UVA and UVB radiation.

Keywords: Epigenetic modification; Photoaging; DNA methylation; Histone modification; Non-coding RNAs

Introduction

Skin aging is a joint action influenced by Ultraviolet (UV) radiation damage (predominantly) combined with Visible Light (VIS) and infrared ray superimposed on so-called intrinsic and programmed aging. And its clinical manifestations include skin roughness, thickening, relaxation and wrinkles, local pigmentation or telangiectasia, and even tumorigenesis [1]. The characteristic histological changes are mainly the degeneration and degradation of dermal collagen and elastic fibers, and parts of them clustered into a mass [2]. Epidermal photoaging is predominantly attributable to UVB (290-315nm) because it's higher in energy than UVA (315-400nm). However, the sunlight radiated on our skin is composed of 90-95% UVA (315-400nm) and 5-10% UVB (280-315nm) [3].

Thus, multiple speculations suggested that UVA had a greater impact on photoaging than UVB. Additionally, VIS (400-700nm) can be divided into red, orange, yellow, green, cyan, blue and purple light, among which red light (605-700nm) can promote cell growth, collagen synthesis and skin homeostasis, while blue light (400-450nm) inhibits cell proliferation and collagen synthesis by promoting ROS production, so blue light exposure is more harmful to the skin than red or green light [4]. Admittedly, excessive exposure to UV rays activates Matrix Metalloproteinases (MMPs), leading to the degradation of existing dermal collagen. An increase of MMPs decreases the synthesis of new collagen via reducing the Extra Cellular Matrix (ECM) exerted tension on fibroblasts attached to collagen fibers [5]. Recent studies showed the pathogenetic mechanisms of photoaging were closely related to DNA breaks [6], oxidative stress damage [7] and immune disorder [8] which referred to multiple signal pathways such as Mitogen Activated Protein Kinase (MAPK) [9], transforming growth factor β 1(TGF β 1) [10], nuclear factor- κ B(NF- κ B) [11] and other non-membrane dependent signaling pathway [12]. Therefore, the induction of fibroblast proliferation and collagen synthesis has become a novel target for many treatments.

Epigenetics is a discipline that does not change underlying DNA sequence while gene expression can be changed genetically, mainly including CpG island DNA methylation and its hydroxy methylation, post-translational modification of histone and non-coding RNA expression [13]. Epigenetic events often occur regularly and naturally while they are

susceptible to various factors including age, environment factors, and disease state [14]. New and ongoing research is constantly uncovering the critical role of epigenetics in a variety of diseases. Recent reports have suggested a critical link between UV (UVA and UVB)-mediated epigenetic modifications and photoaging. Recently, several studies have showed epigenetic modifications are involved in multiple pathways in UV-induced skin injury like inducing expression alterations in PI3K/AKT and NF- κ B cell survival signaling pathways and eventually leading to skin cancer [15-17]. Another study reported sun exposure produced a significant trend towards hypomethylation based on the analysis of a DNA methylation array in sun-exposed and nonexposed skin samples [18]. Moreover, compared with nonexposed skin, it expounded higher global histone H3 acetylation levels in sun-exposed skin by increasing EP300 and decreasing HDAC1 and SIRT1 expression [19]. Further

study found that overexpression of miR-101 and downregulation of its target gene Ezh2 both induced cell senescence in the absence of UVB irradiation [20]. This review comprehensively summarized the underlying mechanisms by which skin aging prevails under repeated exposure to UV radiation, and especially focused on the epigenetic regulation mechanisms of UV radiation impact on skin aging.

Mechanisms of Photoaging

The damage mechanisms of skin photoaging induced by UV irradiation combined with VIS includes oxidative stress, DNA damage, cell apoptosis, MMPs activation, inflammatory response, immunosuppression, the role of Advanced Glycation End Products (AGEs) and epidermal stem cell injury (Figure 1).

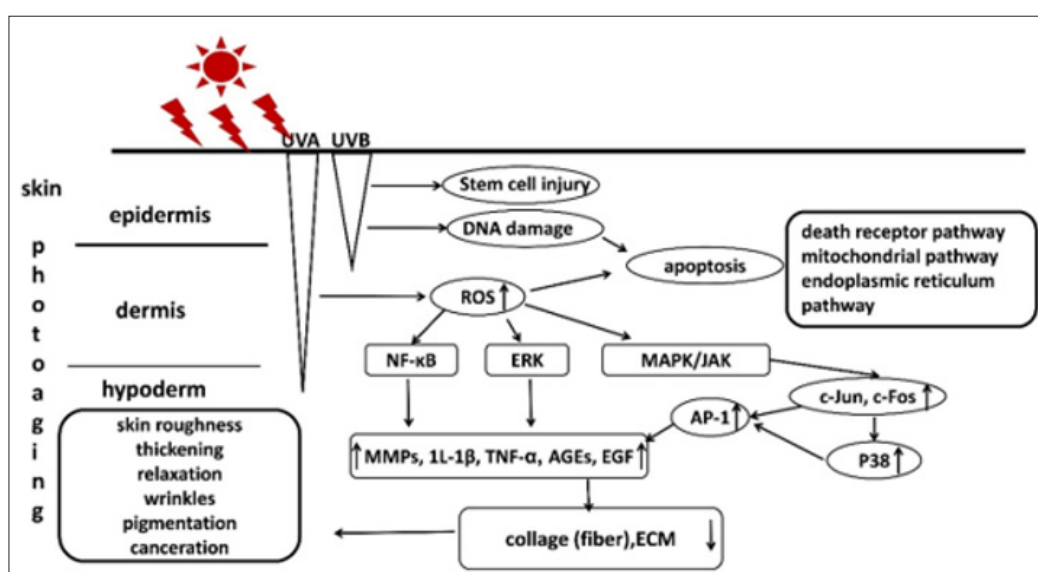


Figure 1: The exact damage mechanisms of skin photoaging induced by UV irradiation.

Oxidative stress

Oxidative stress is a critical cause of skin injury induced by UVA or UVB radiation and blue light which involves an imbalance between the ability of the body to scavenge oxygen free radicals and the production rate of Reactive Oxygen Species (ROS) [21]. Normally, oxygen atoms bind to four electrons in the mitochondrial respiratory chain, but single oxygen atom will carry one electron to escape and form superoxide ions, or ROS, which will be quickly destroyed by the skin's antioxidant defense system. Studies have shown that UV radiation can induce the spawn of ROS including superoxide anion (O_2^-), hydrogen peroxide (H_2O_2), hydroxyl radical ($\cdot OH$) and singlet oxygen (O_1) [22]. When the skin is radiated by UVB, some cell surface receptors will be activated to bind to the corresponding ligands and stimulate the downstream signaling molecules, leading to the activation of reduced Nicotinamide Adenine Dinucleotide Phosphate (NADPH) and the production of ROS [23]. Therefore, intracellular non-enzymatic antioxidant systems (vitamin C, vitamin E, glutathione, trace elements copper, zinc, selenium, etc.) and enzymatic antioxidant systems (superoxide

dismutase, catalase, glutathione peroxidase, etc.) are consumed by excessive ROS, breaking the dynamic balance between oxidation and antioxidant system *in vivo* [24,25]. Abnormal accumulation of ROS in body will break intracellular biological macromolecules (such as nucleic acid, lipids and proteins, etc.), and contribute to abnormal activation of extracellular signal regulated kinase1/2 (ERK1/2) and NF- κ B signaling pathways [26,27]. Also, it will induce DNA damage and cell apoptosis via breaking mitochondrial membrane potential [28].

In addition, it can promote the over-expression of Matrix Metalloproteinases (MMPs) through the Mitogen Activated Protein Kinase (MAPK) signaling pathway, and even abnormally regulate cell differentiation and proliferation to disrupt the inflammatory process, thus leading to the degradation of collagen and the occurrence of skin photoaging [29]. In fact, a recent study reported that fibroblasts exposed in blue light could also promote ROS production, which was equivalent to 25% of the total ROS production of UVA in keratinocytes [30]. Furthermore, another study showed that besides increasing ROS production, blue light

radiation even reduced the expression level of per1 related to cell biological cycle rhythm, so that the repair function of cells cannot be maintained normally, thus aggravating cell damage, aging and even apoptosis [31].

DNA damage

UVB irradiation will directly or indirectly destroy DNA double strand. A variety of DNA damage in keratinocytes occurs by directly absorbing the energy of UVB, such as double-stranded DNA structure destruction, DNA chain breakage, base or base pairs excision or replacement, etc., In melanocytes or keratinocytes containing melanin experiments, UVB irradiation induces the production of Cyclobutene Pyrimidine Dimers (CPD) and pyrimidine-pyrimidone photoproducts, and then these compounds activate the proto-oncogenes while inactivating the tumor suppressor genes, leading to the occurrence of skin tumors [32]. Moreover, as mentioned above, UVA stimulates skin to produce a large amount of ROS, secondary inducing oxidative damage to DNA *in vivo* and develop cyclobutadiazine dimers, especially thymine dimers [33]. All these variations will break single strand DNA fragments and DNA-protein crosslink, thereby hindering DNA replication and transcription, and further enhancing the carcinogenic effect of UVB [34]. In addition, blue light illuminates melanocytes to activate opsin 3 and cause the influx of calcium ions, the latter two reactions activate the ERK and P38 pathways, then activate the MITF transcription factors, which strengthens the tyrosinase activity and increases melanin synthesis, on the one hand, it causes pigment deposition and taches noir formation, on the other hand, excess ROS production induced by UV irradiation can activate the electronic in melanin, then pass the electronic energy to DNA strand to induce DNA damage, and further lead to cell apoptosis [35,36]. From this perspective, blue light also has certain effect to aggravate DNA damage and induce cell apoptosis which will further break the skin barrier function.

Cell apoptosis

UV radiation and its subsequent oxidative or DNA damage can generate mitochondrial dysfunction to induce or promote the occurrence of apoptosis [37]. Generally, the mechanisms of UV-induced apoptosis mainly include death receptor pathway, mitochondrial pathway and endoplasmic reticulum pathway. Firstly, signal transduction mediated by death receptor pathway mainly includes Fas/FasL, Tumor Necrosis Factor Receptor (TNFR) and tumor necrosis factor-related apoptosis inducing ligand signaling pathways. They trigger a series of cascade reactions during apoptosis process via different pathways [38]. Secondly, mitochondrial pathway, also known as endogenous apoptosis pathway, inhibits Bcl-2 while activating Bax, leading to mitochondrial to release cytochrome C. Then, cytochrome C unites with activator protein-1 (AP-1) and Deoxyadenosine Triphosphate (DATP) to form apoptotic complex which activates caspase-9 and cleaves caspase-3. Ultimately, the activated caspase-3 further cleaves different substrates, leading to the amplification of protein cleavage cascades to induce apoptosis [39,40]. Thirdly, endoplasmic reticulum pathway can directly activate different apoptosis signal

junctions such as C/EBP homologous protein pathway, P53 pathway, c-Jun aminoterminal kinase pathway, or its associated caspase pathways [41,42].

MMPs activation

MMPs are a group of zinc ion dependent internal peptidase which can specifically degrade almost all extracellular matrix in the skin. Previous studies have shown that UVA radiation can upregulate the expression of epidermal MMP-1, MMP-3 and MMP-9 [43]. Also, it has been reported that UVB radiation can induce keratinocytes to release cytokines and indirectly promote fibroblast to overexpress MMP-1 by even up to 10 times by way of paracrine [44]. In addition, UVA radiation also increases the expression of transcription factors including c-Jun and c-Fos, activating c-Jun amino terminal kinase pathway and p38 mitogen activated protein kinase pathway. The latter two pathways induce the activation of AP-1 which promotes the expression of MMPs, thus stimulating the production of collagen enzyme which inhibits the synthesis of collagen and promotes its degradation [45]. Study found that infrared ray radiation also increased the expression of c-jun and reduces the production of collagen I and III in cultured human skin fibroblasts, aggravating skin aging [46].

Immunoregulatory effect

Studies have shown that UV radiation can activate the neuroendocrine system to release neuroendocrine mediators which increase the synthesis and secretion of multiple pro-inflammatory cytokines in skin cells, such as histamine, serotonin and kinin [47,48]. As mentioned above, exposure of blue light on fibroblasts can increase ROS production, further causing cellular DNA damage and cell senescence. Ulteriorly, study found that senescent fibroblasts would secrete more vesicles, which were not conducive to maintaining the function of keratinocytes in the epidermis and increased the secretion of IL-6 [49]. These proinflammatory mediators enhance the permeability of capillaries, leading to the extensive infiltration and activation of neutrophils and other phagocytes, thus contributing to skin inflammatory damage and accelerating skin aging [50]. Additionally, UV radiation can induce the release of pro-inflammatory cytokine interleukin 1 beta (IL-1 β) in keratinocytes which activates Epidermal Growth Factor Receptor (EGFR) of fibroblasts and promotes the phosphorylation of extracellular protein kinase pathways to accelerate the degradation of collagen fiber via increasing the expression of MMP-1 in fibroblasts which promotes the occurrence of photoaging [51]. On the other hand, UVB radiation can also stimulate keratinocytes to generate tumor necrosis factor alpha (TNF- α) to mediate inflammatory response [52].

Also, UVB radiation induces the expression of cyclooxygenase 2 and lipoxygenase to increase the synthesis of pro-inflammatory mediators such as prostaglandins and thromboxins [53]. In addition, studies showed that UVB could induce the formation of interleukin 10 (IL-10), TNF- α and other cytokines, reduce the number of Langerhans Cells (LCS), and even affect the function

of it as antigen-presenting cells to cause T cell tolerance and suppress the skin immune system, resulting in a decline in the body's resistance to delayed hypersensitivity ability [54,55]. Also, UVB irradiation induces trans-Urocanic Acid (UCA) to cis-UCA, the latter increases the expression of Galectin-7, thereby upregulating the proportion of apoptotic cells and inhibiting the production of IL-2 derived from T lymphocytes, this principle is widely used in the treatment of atopic dermatitis [56].

Age's function

AGEs can affect the interactions between enzymes and substrates, protein and DNA, even protein and protein, thus altering the biological functions which are rooted in nonenzymatic reaction products among glucose, proteins, lipids, or nucleic acids [57]. Study showed glycation in dermis generally raised after 35 years old, then increased rapidly with intrinsic ageing [58]. Receptors for Advanced Glycation End Product (RAGE) are extensively expressed in the epidermis and dermis such as keratinocytes, fibroblasts, endothelial cells and immune cells (dendritic cells, monocytes). And it can rise when exposed to sun light which may be associated with an increase of proinflammatory cytokine in a time-dependent way [58]. Studies indicated in keratinocytes, AGEs influenced cell differentiation, induced cell aging, decreased the ability of cell vitality and migration, increased the expression of MMPs and enhanced NF- κ B signal pathway.

In Keratinocytes (KCs) culture system, they found the expression of Involucrin (INV) and keratin 10 in normal human KCs treated with AGE-modified collagen I or III was significantly higher than their control group and induced the production of MMP-9 [59]. These results suggested AGE-modified collagens I and III Induce KCs Terminal differentiation. Another study clarified the interaction of S100A8/A9-RAGE was related with the pathogenesis of squamous cell carcinoma in human skin [60] and their interactions aggravated dermal fibrosis via activation of ERK1/2 MAPK and NF-kappa B pathways in mice models [61]. Signal transduction could reduce the proliferation of dermal fibroblasts and induce the activation of caspass-3, caspass-8 and caspass-9 to further lead to the occurrence of apoptosis [62,63]. Interestingly, AGEs were also found to decrease the synthesis of collagen and extracellular matrix as well as induce the expression of the senescence-marker β -galactosidase [64,65]. Also, AGEs can promote the production of ROS and lower the vitality of epidermal keratinocytes and dermal fibroblasts [66].

Epidermal stem cells injury

Epidermal stem cells are the progenitor cells of various epidermal cells. On the one hand, it can migrate downward and differentiate into epidermal basal layer, and then produce hair follicles. On the other hand, it can migrate upward and eventually differentiate into various epidermal cells, which play a critical role in repairing epidermal injury. Research has shown that UVB radiation can damage the epidermal stem cells via damaging the stem cell niche (stem cell storage site, consisting of specific extracellular matrix and niche cells) to influence the survival of epidermal stem cells and by influencing the biological rhythm of

stem cells, thus inhibiting the function of stem cells to repair skin barrier [67,68]. Specifically, study reported melanoma was derived from Melanoma-Competent Melanocyte Stem Cells (MCSCs) upon stimulation by UVB. UVB induces activation and translocation of MCSC through an inflammation-dependent process. In this study, the chromatin-remodeling factor Hmga2 was identified in skin playing a key role in UVB-mediated melanoma formation. These findings delineated the potential function of MCSCs to develop melanoma following UVB stimulation [32]. Another study showed UV-irradiated endothelial cells secreted Stem Cell Factor (SCF) and increased the pigmentation of melanocytes through epithelial-mesenchymal crosstalk depending on SCF/c-KIT signaling pathway during chronic sun exposure [69]. Together these results suggest that epidermal stem cells exposed upon UVB-irradiated to develop various cells to exert multiple potentials.

The Epigenetic Regulation Mechanisms of Photoaging

DNA methylation

There is still a controversial topic that UV-irradiated exposure causes DNA methylation changes. Studies have found that long-term exposure to UVB does not cause substantial genomic DNA methylation changes in keratinocytes experiment *in vitro*, and hypomethylation in skin cancer may be caused by inflammation [70]. A recent study observed large blocks of hypomethylated genome in older (over 60 years old) compared with younger subjects (under 35 years old) in sun-exposed epidermal samples, and the degree of hypomethylation was associated with clinical measures of photoaging [18]. However, word explained that it would emerge gene hypomethylation status when DNA was repairing its damage. Therefore, more ROS production in older needs to remove, resulting in that the body tries to initiate DNA damage repair mechanisms in response to DNA damage and appears hypomethylated level.

However, this conjecture needs more experimental proof. Several items have recently observed widespread distinguishable methylated region across the genome in aging skin [71-73]. And these data were consistent with previous report showing substantial hypomethylation in common skin cancers such as squamous cell carcinoma and basal cell carcinoma [74,75]. Remarkably, the overall level of DNA methylation and the expression level of DNA methyltransferase1(DNMT1) decreased in the process of cellular aging. A recent study found that DNMT1 expression was markedly higher in young Human Skin Fibroblasts (HSFs) than that in passage-aged HSFs, and DNMT1 knockdown significantly induced the senescence phenotype in young HSFs [76]. Nevertheless, the content of DNMT1 and Tet (DNA demethylase) was both decreased in senescent cells, suggesting that the functions of methylation and demethylation were also weakened [70].

Therefore, the reason for the little change of genome-wide promoter methylation level in senescent skin cells may be related to the specificity of gene functions. For senescent cells, some genes such as controlling cell proliferation and differentiation will be weakened, while genes related to cellular stress or immunity may be enhanced [70]. Therefore, we should focus on a specific

gene methylation, so as to objectively evaluate the effect of light radiation on skin aging. The mechanism of light radiation action on skin aging and carcinogenesis is intricate. Interestingly, cumulative evidence identified that various DNA methylation signatures might authenticate cell types according to their developmental potential and possibly provide evidence for their chronological and biological age [77,78]. Another study reported these discrepant methylation patterns also associated with chronologically aged and photoaged skin [79]. These data indicated large scale DNA methylation changes involved in the onset and development of diseases induced by environmental damage with photo-aging.

Histone modification

Histone modification plays a key role in chromatin restructuring and the regulation of gene transcription [80]. Given previously reported normal cellular aging was associated with global histone modification characterized by markers H3K9me3 and H3K27me3 [81]. A recent study carried on by TG Lim et al. [82] showed Caffeic Acid Phenethyl Ester (CAPE) could function as an epigenetic modulator to prevent skin photoaging via targeting Histone Acetyltransferases (HATs), and it also suppressed UV-induced global lysine acetylation of histone H3 in both Human Dermal Fibroblasts (HDFs) and human skin tissues [82]. Previous studies reported that an HAT inhibitor, Anacardic Acid (AA) blocked UV-induced MMP-1 expression and histone modifications in HDF cells through suppressing p300 [19,83]. These studies indicate that epigenetic regulation via inhibition of p300 can be associated with protection from UV-mediated damages of the skin tissue. Furthermore, Ding S et al. [84] observed a higher global histone H3 acetylation level in sun-exposed area compared with sun-protected area, in their ChIP-chip assay, and displayed 227 genes significant hyperacetylation of histone H3 while 81 genes significant hypoacetylation of histone H3 between the two groups. UVB irradiation regulated the histone H3 acetylation levels by increasing EP300 expression and decreasing HDAC1 and SIRT1 expression [19].

In addition, Sirtuin1 (SIRT1) suppressed UVB-induced p53 acetylation and its transcriptional activity, which directly affected the cell cycle arrest. Further study on mouse demonstrated that SIRT1 activation depressed cell senescence under UVB irradiation [84]. Recent studies showed that the acetylated histone H3K9 levels increased at the promoters of several genes such as MMP13, MMP12, MMP3, MMP1 and MMP10. Curiously, these findings

suggested a coordinated transcriptional activation of genes in the MMP cluster at 11q22.3 and that acetylation of histone H3 at lysine 9 played an important role in the UVB-dependent enhancement of transcription of MMP genes in this region [85]. Histone methylation is also a critical modification change catalyzed by EZH2 and MLL1 enzymes [86,87]. In a skin keratinocytes study, it is mentioned that p16INK4a gene expression increased because DNMT and EZH2 binding in its promoter histone H3K27Me3 was decreased, thus promoting cell senescence via inhibiting CDKs expression, interestingly, this effect was dependent on ROS which can regulate the methylation state through JNK-DNMT pathway [88]. In addition, UVB has also been shown to phosphorylate histone H3 through the p38/MSK1 pathway and stimulate COX-2 expression which increases PGE2 level to promote cell proliferation and induce skin cancer [89].

Non-coding RNAs

A study conducted by Greussing et al. [20] Table 1 have identified a network of miRNA-mRNA interactions mediating UVB-induced senescence and observed a parallel activation of the p53/p21/WAF1 and p16INK4a/pRb pathways [20]. Recent findings showed the downregulation of miR-155 expressions in dermal fibroblasts induced by UVA irradiation increased c-Jun protein and mRNA levels. c-Jun is a critical component of transcription factor complex AP-1 which promotes the transcription of matrix metalloproteinases to induce the degradation of extracellular matrix proteins and negatively regulates the collagen synthesis pathway [90]. UV irradiation-induced cellular senescence is one of the manifestations of skin aging. miRNAs screening identified the downregulation of miR-101 by targeting Ezh2 partially blocked the phenotype of UVB-induced senescence [20]. MiR-22 was found to be significantly upregulated when exposed to UVB radiation which promoted cell survival via inhibiting the expression of tumor suppressor gene phosphatase and tensing homolog PTEN expression. Thereby, a long-lasting increasing level of miR-22 induced by UVB radiation has been shown to contribute to tumorigenesis of skin cancers, especially melanoma [91]. Another report found miR-377 induced senescence in human skin fibroblasts by targeting DNA methyltransferase1 [76]. Furthermore, experiments demonstrated that overexpression of miR-23a-depressed autophagy participated in PUVA- and UVB-induced premature senescence. Abnormalities in autophagy are associated with several pathologies, including aging and cancer [92].

Table 1: Some non-coding RNAs action in skin photoaging included.

Name	Target	Function	References
miR-155	c-Jun	collagen synthesis decreased	[90]
miR-101	Ezh2	cell senescence	[20]
miR-22	PTEN	tumorigenesis	[91]
miR-377	DNMT1	cell senescence	[76]
miR-23a	autophagy	cell senescence	[92]
MALAT1	ERK/MAPK	MMP-1 activated	[95]
circCOL3A1-859267	type I collagen	collagen synthesis decreased	[93]

Circular RNAs (circRNAs) are a class of newly identified non-coding RNAs with regulatory potency by sequestering miRNAs like a sponge. A study conducted by Peng et al. [93] identified 29 significantly differentially expressed circRNAs from UVA irradiated and no irradiated HDFs. In brief, the result showed 12 circRNAs were up-regulated and 17 circRNAs were down-regulated. Interestingly, they identified circCOL3A1-859267 regulate type I collagen expression in photoaged human dermal fibroblasts which was the most abundant proteins produced by HDFs in the dermal collagenous extracellular matrix and decreased in photoaged skin [93].

Furthermore, lncRNA expression profile analyzed that 1,494 lncRNAs were upregulated, and 236 lncRNAs downregulated in the UVA-HDF group compared with the control group. Ulteriorly, predicted lncRNA targets by bioinformatic analysis showed correlation to MMP, cathepsin D, mitogen-activated protein kinase and TGF- β signaling pathways [94]. Another study verified overexpression of MALAT1 induced by UVB radiation was independent of ROS generation and might participate in UVB-induced photoaging by regulation of the ERK/mitogen-activated protein kinase signaling pathway [95]. These mechanisms all play a crucial role in human skin photoaging which suggest abnormal expression profiles of long noncoding RNA induced by UV-irradiation may provide novel insight to explain UV-damaging pathology and potential targets for treatment of human skin photoaging.

Conclusion

This review comprehensively summarizes the possible pathogenesis of photoaging and focus on epigenetic modification events occurring in the process of photoaging. Skin photoaging is mainly manifested in the exposed areas of sunlight. Excessive UV radiation will not only affect the appearance of the skin, but also damage human skin and accelerate skin aging. Excessive exposure to UV radiation can even cause genetic mutations and cancer. The mechanisms of photoaging refer to multiple pathways mainly embodying in the overproduction of reactive oxygen species induced by ultraviolet radiation, which result in oxidative damage of cells. Furthermore, UVB induced over-expression of MMPs destroy collagen via regulating the expression of TGF- β and AP-1. Admittedly, as epigenetics era is coming, the transcriptional regulation and posttranslational modification in response to UV radiation has been well studied. There emerged various epigenetic changes in recent years open new horizons in well acknowledged of the molecular mechanism of ultraviolet radiation-induced skin damage. However, seeking for more effective methods to prevent and block skin photoaging is the deficiencies of the current research work, which needs further efforts in future.

Conflict of Interest

The authors declare that they have no competing interests.

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