



Review Article

Sunlight damage to cellular DNA: Focus on oxidatively generated lesions[☆]

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ABSTRACT

The routine and often unavoidable exposure to solar ultraviolet (UV) radiation makes it one of the most significant environmental DNA-damaging agents to which humans are exposed. Sunlight, specifically UVB and UVA, triggers various types of DNA damage. Although sunlight, mainly UVB, is necessary for the production of vitamin D, which is necessary for human health, DNA damage may have several deleterious consequences, such as cell death, mutagenesis, photoaging and cancer. UVA and UVB photons can be directly absorbed not only by DNA, which results in lesions, but also by the chromophores that are present in skin cells. This process leads to the formation of reactive oxygen species, which may indirectly cause DNA damage. Despite many decades of investigation, the discrimination among the consequences of these different types of lesions is not clear. However, human cells have complex systems to avoid the deleterious effects of the reactive species produced by sunlight. These systems include antioxidants, that protect DNA, and mechanisms of DNA damage repair and tolerance. Genetic defects in these mechanisms that have clear harmful effects in the exposed skin are found in several human syndromes. The best known of these is xeroderma pigmentosum (XP), whose patients are defective in the nucleotide excision repair (NER) and translesion synthesis (TLS) pathways. These patients are mainly affected due to UV-induced pyrimidine dimers, but there is growing evidence that XP cells are also defective in the protection against other types of lesions, including oxidized DNA bases. This raises a question regarding the relative roles of the various forms of sunlight-induced DNA damage on skin carcinogenesis and photoaging. Therefore, knowledge of what occurs in XP patients may still bring important contributions to the understanding of the biological impact of sunlight-induced deleterious effects on the skin cells.

1. Introduction

Ultraviolet (UV) radiation is part of the spectrum of electromagnetic radiation emitted by the sun and includes the wavelength range from 100 to 400 nm: UVC (100–280 nm), UVB (280–315 nm), and UVA (315–400 nm). The oxygen and ozone in the atmosphere completely absorb the UVC radiation (< 280 nm) and absorb the majority (approximately 90%) of UVB. Thus, the solar UV radiation of relevance to human health and ecosystems consists of UVA and UVB wavelengths [1].

Exposure to UV radiation has both beneficial and adverse effects on

human health. UVB irradiation of the skin is the main source of vitamin D, which plays a critical role in the maintenance of calcium homeostasis in the body and in other important processes [2]. In contrast, excessive UVB exposure causes skin cancer, including cutaneous malignant melanoma and the non-melanoma skin cancers, basal cell carcinoma and squamous cell carcinoma [3]. Once thought to be relatively innocuous, UVA is now known to damage DNA, proteins, and lipids, which can result in harmful consequences, such as carcinogenesis and skin aging. Growing evidence has demonstrated that UVA radiation can induce various types of DNA lesions through direct and indirect mechanisms as well as causing mutations in human skin cells. Thus,

[☆] This article is one of a series of papers on the subject of oxidative DNA damage & repair that have been published as a special issue of Free Radical Biology & Medicine to commemorate the Nobel Prize won by Prof. Tomas Lindahl. A detailed introduction and synopsis of all the articles in the special issue can be found in the following paper by Cadet & Davies [272].

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the participation of UVA in the process of skin cancer induction, including the cutaneous malignant melanoma, and skin photoaging is now accepted, although the specific mechanisms remain unclear [1,3].

In this review, we present an overview of the incidence of solar UV radiation at the Earth's surface and its absorption by DNA and non-DNA chromophores present inside the cells. The direct and indirect mechanisms of DNA damage by UVB and UVA wavelengths are presented, with emphasis in the photosensitized formation of oxidized DNA bases. Complex cellular systems to avoid the deleterious consequences of sunlight exposure and oxidative stress are also discussed. However, the relative consequences of the DNA lesions directly or indirectly induced by sunlight, especially those induced by UVA radiation, on skin carcinogenesis and skin aging are not clear. It should be added that skin photoaging may also be due to photo damaging of other macromolecules, including protein oxidation and extracellular degradation [4], although we will focus this review on the UV-mediated DNA damage. These deleterious effects of sunlight on skin are highly pronounced in the DNA repair-deficient patients with the syndrome xeroderma pigmentosum (XP). Most XP patients have mutations in one of seven genes (XPA through XPG), whose products are involved in the nucleotide excision repair (NER), a mechanism that removes DNA damage induced by UV radiation, as well as many other lesions that cause distortion of the DNA. Additionally, there are also the so-called XP variants, who have normal NER but are defective in translesion synthesis (TLS) after UV-induced DNA damage, as a consequence of mutations in the *POLH* gene that encodes DNA polymerase eta (Pol eta) [5].

Thus, the NER and TLS defects of oxidatively generated DNA lesions receive special attention in this review. In fact, the participation of NER proteins in the removal of oxidized DNA bases suggests a crosstalk between NER and other DNA repair pathways, and Pol eta may also protect cells from the consequences of DNA damage induced by oxidative stress. Thus, although it has been accepted that DNA pyrimidine dimers are the main lesions responsible for the deleterious effects of sunlight, the participation of the cellular oxidative processes that are induced by UVB and mainly UVA radiation in promoting human skin tumors and aging is still an open question that the cells derived from XP patients may help answer.

2. Solar UV radiation incidence on Earth

The intensity of solar UV radiation can be influenced by several environmental factors. For instance, the height of the sun above the horizon (solar zenith angle) influences the incidence angle of UV radiation according to the latitude, time of day and season. At lower elevations, the pathway through the atmosphere is longer, which results in higher absorption and thus a lower UV intensity. UV radiation is more intense in the tropics, near noon and in the summer [6]. Additionally, higher altitudes also have a thinner atmosphere, which results in less attenuation of the sunlight and an increased UV intensity.

As UV radiation penetrates the atmosphere, ozone, clouds and aerosols can modify its intensity. Cloud cover is by far the most important factor that controls UV radiation for any given latitude and altitude. Furthermore, in polluted urban areas, although aerosols and trace gases may provide protection from UV radiation, these constituents can also scatter light, which increases the total exposure to UV radiation in places shaded from direct sunlight [7]. However, in cloud-free and low-aerosol conditions, ozone is the most important factor in controlling the levels of solar UVB incidence and blocking the photochemical reactions of organic molecules [8]. Therefore, the release of ozone-depleting substances catalyzes the breakdown of ozone to molecular oxygen, which does not absorb UVB radiation. Thus, these substances lead to more UVB radiation passing through the stratosphere, which enhances the photochemical reactions and increases the corresponding biological effects [9].

The discovery of the ozone “hole” in the 1980s has led to critical

concern worldwide. Fortunately, the Montreal Protocol continues to be successful in reducing emissions of ozone-depleting substances, and it has been hailed as the most effective environmental treaty ever made [3]. However, ozone-depletion events still continue to occur during the winter and spring over the high latitudes (63–90°) of both hemispheres. Compared to the average total ozone level measured before 1980, the 2010–2013 mean value was lower by ~27% in the southern hemisphere in October and by ~10% in the northern hemisphere in March [10]. Additionally, although the Antarctic ozone hole is located over the polar region, it can also influence the ozone content over southern South America during the spring season, when it increases the UVB incidence at mid-latitudes [11–13]. It has already been demonstrated that polar air masses with a low ozone content can disturb the stratospheric ozone concentration in the South of Brazil [14], where a 1% depletion in ozone content results in an average increase of 1.2% in the UVB intensity [15]. A similar atmospheric phenomenon has already been observed over other mid-latitude regions, such as New Zealand [16] and South Africa [17]. Recently, a dataset containing 35 years of ozone concentration measurements over southern Brazil was analyzed and 72 ozone-depletion events were identified. The average decrease in the ozone content was 9% (± 3.3), and there has been a slight tendency towards a higher frequency of ozone depletion events with time. This is much more apparent from 1997 onwards because the yearly average of events observed from 1979 to 1996 and from 1997 to 2013 increased from 1.1 event per year to 3.1, respectively [18]. Nevertheless, the small ozone values observed in the Arctic can also propagate to mid-latitudes and decrease the ozone content over Western Europe, especially between late March and late April [19].

Regardless of the occurrence of ozone-depletion events in both the Southern and Northern hemispheres, it is important to emphasize that the daily UVA incidence is naturally much higher than the UVB in any given latitude. Latitudinal gradients are stronger for the UVB than for the UVA wavelengths, partly because photons travel a longer path through the atmosphere for the lower solar elevations that prevail at the higher latitudes, which results in a greater absorption of the UVB radiation by the ozone layer [8]. An example of this gradient can be observed in a comparison of the daily UVB and UVA measurements performed at various latitudes in South America [20]. This work demonstrated that the UVB intensity at 5°S is approximately 12-fold higher than at 53°S, whereas the UVA intensity is only approximately 2-fold higher than at the lower latitude. These gradients reflect the different DNA damage profiles induced at different latitudes [20]. A representative example of an environmental measurement of the solar UVB and UVA incidence on a clear sky summer day (2015) at the latitude of 29°S is presented in Fig. 1. These data were obtained using continuous UVB/UVA broadband radiometers (such as the UVB and UVA Radiometers from EKO Instruments Trading, Tokyo, Tokyo-to,

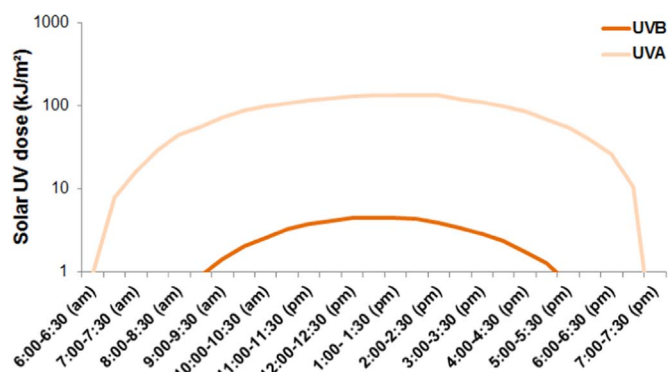


Fig. 1. Illustrative example of an environmental measurement of solar UVB (280–315 nm) and UVA (315–400 nm) incidence in a clear sky summer day (2015) at the latitude of 29°S (Southern Brazil) using continuous UVB/UVA broadband radiometers (EKO Instruments Trading, Tokyo, Tokyo-to, Japan).

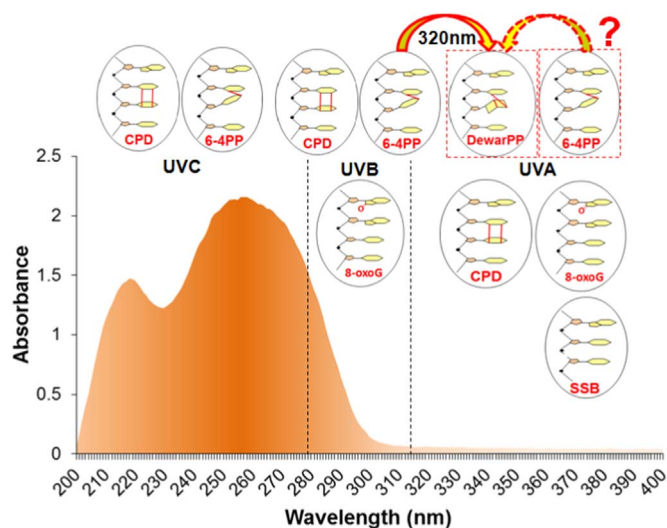


Fig. 2. DNA absorption spectrum and the main types of DNA lesion induced by each UV band. CPD – cyclobutane pyrimidine dimers; 6-4PP – pyrimidine (6-4) pyrimidone photoproducts; DewarPP – Dewar valence isomer; 8-oxoG – 8-oxo-7,8-dihydroguanine; SSB – single-strand breaks.

Japan) that take measurements at 280–315 nm and 315–400 nm, respectively. As expected, Fig. 1 shows that although it is very low early in the morning and late in the afternoon, the intensity of solar UV radiation reached a maximum at midday. The daily UVA dose measured on this day was approximately 39-fold higher than the daily UVB dose, and the percentage of both UVB and UVA wavelengths corresponded to 2.5% and 97.5% of the total UV incidence, respectively.

3. DNA as the main target of UV radiation in living cells

Although nearly all of the UV incidence on the Earth's surface is in the UVA wavelengths, it is well known that UVA radiation is indeed less harmful than UVB. However, UVA is not completely innocuous because it can be absorbed by different cellular chromophores as well as by DNA (Fig. 2).

At the first glance, Fig. 2 indicates that UVC wavelengths are the most effectively absorbed by DNA, followed by UVB, whereas UVA is poorly (almost not) absorbed. But, interestingly, the total absorption of UVA wavelengths by DNA is only 4.2-fold lower than that of UVB wavelengths, while total incidence on Earth's surface is 20-fold higher for UVA. This information indicates that DNA can absorb UVA radiation and suggests that the direct impact of solar UVA radiation on DNA could be even more drastic than previously assumed. In fact, the absorption of UVA wavelengths by DNA was shown long ago. DNA from different sources was shown to differ in its capacity to absorb light for wavelengths over 300 nm, depending on the G:C content [21]. The authors concluded that probably G absorbs these wavelengths more than A and that this may explain at least part of the biological effects of UVA radiation [21].

In addition, several studies have indicated that UVA radiation can directly induce cyclobutane pyrimidine dimers (CPDs) in DNA [22–30], and a few have shown the formation of pyrimidine (6-4) pyrimidone photoproducts (6-4PPs), albeit in much lower quantities than CPD. In fact, although 6-4PPs were not detected by mass spectrometry in UVA-irradiated DNA molecules, these lesions were detected in both purified DNA and DNA repair-deficient human cells by highly sensitive endonucleases, alkaline sensitivity and immunological assays [27]. Moreover, cells that expressed specific photolyases demonstrated that 6-4PPs are responsible, at least partially, for the cell death that is induced by UVA radiation [30]. Importantly, as these DNA photolesions are slowly induced in cellular DNA by UVA, damage removal by repair is continuously occurring, which protects the cells from the conse-

quences of the lesions [27,30].

4. Direct formation of DNA damage by UV radiation

Several efforts have been made to determine the molecular mechanisms by which sunlight induces carcinogenesis and aging. Certainly, the sunlight absorption directly triggers DNA damage, and it is clear from the literature that UVB and UVA wavelengths are responsible for the vast majority of these lesions. Recently, an important review discussed the role of photoexcited states of DNA bases on the direct mechanism of damage formation and demonstrated the existence of “collective” excited states (i.e., excited states delocalized over at least two bases) and the importance of the DNA configuration at the moment of exposure and the dynamics of the functional changes that occur during the excitation that initiates this process [31].

CPDs are formed by two covalent bonds between the C5 and C6 carbon atoms of adjacent nitrogen bases through Frenkel excitons that result in a diastereomeric ring composed of four elements. In the double helix, the *cis-syn* isomer is more abundant than *trans-syn* isomer whereas in single-stranded DNA, the *trans-syn* isomer predominates. 6-4PPs are formed by one covalent bond between the 5'-end C6 and the 3'-end C4 carbon atoms of adjacent pyrimidines via charge-transfer states, and oxetane and azetidine rearrangements (unstable intermediates) occur when the 3'-end is T or C, respectively [31,32]. CPD is a cyclic and rigid 4-carbon ring and less distortive than the non-cyclic 6-4PP [33–35]. The DNA condensation state also affects the formation of these pyrimidine dimers: specifically, CPDs can be formed in both hetero and euchromatin regions, whereas 6-4PPs are uniquely formed in euchromatin [36]. In addition, regions containing telomeres, G-Quadruplex loops, and 5-methylcytosine are prone to CPD formation [37–40].

The conversion of 6-4PPs to Dewar valence isomers results from the intramolecular 4π electrocyclization of the pyrimidone ring after the photon absorption [24,41]. The mechanism that is theoretically predicted involves a photochemical process with an excited state singlet $\pi\pi^*$. In fact, the formation of Dewar isomers requires two photons: the first induces the formation of the 6-4PP and the second is required for the isomerization of this DNA lesion. In this case, the second photon is more likely to come from the UVA range, which is poorly absorbed by normal DNA bases, but it is efficiently absorbed by 6-4PPs; this is essential for its isomerization into the Dewar form. The pyrimidone moiety of 6-4PPs exhibits a specific absorption at approximately 320 nm: more precisely 315 nm for TC 6-4PP and 325 nm for TT 6-4PP. Dewar valence isomers induce an intermediate distortion in DNA structure (21 degrees) compared to CPDs (10 degrees) and 6-4PPs (44 degrees) [35].

The isomerization of 6-4PPs into Dewar isomers has been demonstrated and quantified using mass spectrometry and immunological detection in various studies using bacteria, plants, cultured cells, skin samples and animals [42–45]. Recently, a large-scale study using microorganisms exposed to natural sunlight showed that 20% of the 6-4PPs were converted into Dewar isomers [46]. Concerning the mutagenic properties of pyrimidine dimers, 6-4PPs and Dewar isomers are believed to be more mutagenic than CPDs. 6-4PPs preferentially induce TT to TC transition, whereas Dewar isomers convert TC to TT, and CPDs induce C to T transitions [47].

In fact, the DNA damage that results from UVB and UVA exposure preferentially induces C-T transitions in both *in vitro* and *in vivo* models [48–50]. Furthermore, despite the fact that UVB induces more CPDs than UVA at equimutagenic doses, the DNA photoproducts that are induced by UVA are potentially more mutagenic than those induced by UVB [51]. This could be explained by the less effective cell cycle arrest, weak p53 and p95 activation, and consequently, an ineffective cell cycle checkpoint after UVA irradiation, which can lead to the progression of the replication of the damaged DNA and accumulation of mutations [51]. Deamination of cytosine to uracil, or of methylcytosine

to thymine, within a pyrimidine dimer explains some of these mutations. Replication of a deaminated CPD, for example, by Pol η , will insert an adenine opposite to uracil or thymine, which gives rise to C to T transitions. This model presupposes, however, that the dimer still has some coding capacity during replication. Eventually, mutations arise due to bypass of the DNA damage by an error-prone TLS polymerase. In fact, it has been shown in yeast that Rad30 (a Pol η homolog) performs the non-mutagenic bypass of 6-4PPs containing cytosine, Dewar isomers and 8-oxoG. In the absence of Pol η , another TLS polymerase (Pol ζ) is responsible for performing the bypass, although in this case, the bypass is mutagenic [52]. Recently, it was shown that although Pol η is responsible for CPD bypass, Pol ζ may act preferentially in the gap filling formed during 6-4PP replication in human cells [53].

Finally, DNA single- and double-strand breaks and DNA cross-links can be formed directly or as the result of cellular metabolism after UVA exposure [54–57]. These lesions are very cytotoxic and, if persistent, can cause chromosomal aberrations and tumorigenic transformation of keratinocytes [58]. However, the capacity of UVA radiation to directly induce double-strand breaks has recently been refuted [59], and the presence of this type of lesion may be an indirect result of DNA damage replication [58,60], or, occasionally, due to UVA-induced clusters of single-strand breaks or the repair of close oxidized bases in the DNA [61].

5. Photosensitized formation of oxidatively generated DNA damage

There are extensive literature reports on investigations of the mechanisms by which reactive oxygen species (ROS) are formed after sunlight exposure. A recent review by Cadet and collaborators (2015) details the mechanisms for ROS generation and their reactions with DNA molecules [62]. In fact, both UVA and UVB radiation can induce intracellular redox processes. Both types of radiation reach the basal layer of epidermis, although UVA radiation penetrates the skin more deeply than UVB, which may be relevant for photocarcinogenesis [63].

The ROS generation by UVB radiation has been known for a long time. This reaction can be demonstrated by the use of various techniques that detect the formation of superoxide anion radical ($O_2^{\cdot-}$) and hydrogen peroxide (H_2O_2), among others [64–71]. The delayed generation of ROS and reactive nitrogen species (RNS) by UVB is attributed to the activation of enzymes, such as cyclooxygenase and the NADPH oxidase pathway, or to the activation of inducible NO synthase in response to inflammatory mechanisms [69,72–76]. As a result of these processes, UVB irradiation can also induce bystander effects in non-irradiated neighbor cells [77–80].

Non-DNA chromophores that are present in human skin cells also absorb UVA photons, which lead to the formation of photoexcited states with subsequent generation of ROS and RNS, organic free radicals and other toxic photoproducts [81]. In fact, human skin is an abundant source of numerous chromophores with strong absorption in the UVA and blue visible region. Some examples include porphyrins, heme and bilirubin, melanin and melanin precursors, pterins, flavins and NADPH oxidase, trans-urocanic acid and tryptophan. The mechanisms of photosensitization of these endogenous chromophores have been thoroughly discussed previously [81] and will also be discussed in this issue. The photoexcited state intermediate, most often the triplet state of the sensitizer, can directly interact with substrate molecules to produce large amounts of endogenous ROS via type I and II mechanisms [62,81–83]. The type I reaction involves a complex chain of events that begins with energy transfer from a triplet state energy photosensitizer that give rise to ROS such as the $O_2^{\cdot-}$, H_2O_2 and hydroxyl radical ($\cdot OH$). In contrast, the type II reaction involves a direct energy transfer from the triplet state energy photosensitizer to an oxygen molecule, which results in the formation of singlet oxygen (1O_2) and the subsequent oxidation of biomolecules [82,84,85]. Most frequently, the UVA radia-

tion promotes selective guanine oxidation by 1O_2 , which produces primarily 8-oxo-7,8-dihydroguanine (8-oxoG) [62]. In addition, UVA can also induce ROS through bystander effects and enzymatic activities as described above for UVB [62,76]. Furthermore, a growing body of evidence has suggested that mitochondria, ferritin and NADPH oxidase (Nox-1) participate in the UVA-induced DNA damage [86,87].

Interestingly, recent data have accumulated that show ROS formation after exposure to non-UV wavelengths [88,89]. Specifically, visible light can damage melanocytes through melanin photosensitization and 1O_2 generation [90].

Although many ROS participate in cell signaling mechanisms, the generation of these species at high levels can damage biomolecules that are susceptible to oxidation, thus resulting in several consequences for the cell integrity and function. For instance, lipid peroxidation can destabilize the membrane, which can lead to mutagenesis and cell death. The end-products of such reactions, the unsaturated aldehydes, have the ability to form mutagenic adducts of DNA through base alkylation [91,92]. Moreover, oxidized proteins can lose or gain functions inside the cell or form cross-links with the DNA that block DNA replication and transcription [93–97]. In fact, in model studies, more than one hundred oxidation products of nitrogenous bases and 2-deoxyribose have been demonstrated to be induced in DNA [98]. Many of these DNA lesions that were induced by oxidative processes may be associated with carcinogenesis and aging and are thus relevant for the identification of the consequences of the exposure of human skin to sunlight.

Recently, it was demonstrated that CPDs could also continue to be generated in the skin for more than 3 h after exposure to UVA [99]. The formation of this type of DNA lesion occurs because UVA radiation induces the generation of $O_2^{\cdot-}$ and nitric oxide (NO \cdot). These species cause a sharp increase in the concentration of peroxyntirite, which degrades melanin. In the nucleus, peroxyntirite excites melanin derivatives to a triplet state that has the high energy of a UV photon. These evanescent electronically excited products transfer their triplet energy to DNA, which creates CPDs in the dark [99]. Therefore, this work is a strong indication that the consequences of UVA exposure for the development of melanoma have been underestimated.

The most studied DNA oxidation product is 8-oxoG, which is considered to be the main oxidized DNA base that is detected after UVA exposure, followed by single-strand breaks (SSB) and pyrimidine oxidation products [25,81]. 8-oxoG can be detected unequivocally by HPLC combined with electrochemical detection and mass spectrometry [100,101] or by less quantitative methodologies such as immunochemical detection and the modified comet assay using a specific glycosylase [101–103]. However, immunoassays that are suitable for the detection of bulky adducts such as CPDs are not appropriate for the measurement of oxidized bases due to a lack of antigenicity that leads to cross-reactivity with canonical bases [104]. This oxidized base can be generated by the attack of 1O_2 and $\cdot OH$ as the result of both types II and I photosensitization reactions [101]. 8-oxoG has been detected both immediately after sunlight or UVA and UVB exposure [98] and shortly after UVA irradiation [30,102]. The relative importance of the oxidized DNA bases compared to the pyrimidine dimers in the cellular effects promoted by sunlight exposure is still a matter of debate. According to a recent review, the amount of oxidized DNA lesions is just 1% of total DNA damage induced by UVB [62]. However, the biological role of the redox process induced by UVB is supported by OGG1 knockout mice, which demonstrate an increased susceptibility to skin cancer [103]. In addition, mitochondrial DNA oxidation is also observed during sunlight exposure, and its association with skin aging process is emerging [105].

Although 8-oxoG does not completely block DNA or RNA polymerases and is thus not directly cytotoxic (see below) [106–110], it is known to be highly mutagenic. The oxidation of guanine occurs predominantly by the introduction of an oxo group in the carbon at position 8 in response to 1O_2 attack (type II mechanism), and/or in smaller amounts by one-electron (or hydrogen atom) abstraction (type I

mechanism) [101]. These changes combined with a base twist from the anti to a syn position result in an erroneous pairing with adenine, which leads to a potential G-T transversion [111].

Since 2009, UVA radiation has been recognized as a class I carcinogen [112]. However, the mutagenesis induced by UVA and its contribution to skin cancer development is still unclear, probably due to the uncertainty regarding the relative importance of pyrimidine dimers and oxidized bases in this process [113,114]. According to Ikehata and collaborators (2008), only 6% of the total UVA mutation spectrum in mouse skin is the result of the formation of 8-oxoG [50]. This result can be explained by the high efficiency of Base Excision Repair (BER), which quickly eliminates the oxidized bases up to 6 h after exposure. This contributes to the argument that other DNA lesions play major roles in the mutagenesis induced by sunlight [115–118]. In fact, the low levels of G to T transversions are also consistent with a minor role of 8-oxoG lesions in inducing skin tumors. However, in yeast cells that were defective for 8-oxoG repair, UVA was shown to be highly mutagenic [119]. Thus, new studies on the UVA-induced DNA lesions that are generated in response to redox imbalance (reactive aldehydes, ROS and RNS) need to be carried out to understand the relative role of this environmental agent in human skin carcinogenesis. Evidence for DNA damage as a consequence of redox process after UV exposure is increasing [120–123]. The alpha, beta unsaturated aldehydes (malondialdehyde, hydroxynonenal, crotonaldehyde and trans-trans-2,4-decadienal) are able to penetrate into the nucleus and promote the formation of etheno, propano and open adducts in DNA by Michael additions, the consequences of which must be explored [91,92].

6. Consequences of UV exposure to human health

Many of the deleterious human health effects that result from sunlight exposure are associated with a chain of events that begins with the formation of DNA damage. These lesions can lead to inflammatory and immunosuppressive processes in the epithelial tissue as well as accelerated aging and tumor development. However, UVB absorption by skin cells also triggers the synthesis of pre-vitamin D that is subsequently converted to vitamin D, which has many beneficial consequences. A summary for these effects is illustrated in Fig. 3.

Although DNA lesions are substrates for DNA repair, the accumulation of unrepaired DNA damage increases the frequency of mutations,

contributing to the development of the carcinogenic process. It is well known that mutations induced in the genes that are involved in the maintenance of genomic integrity and in the control of the cell cycle result in a high predisposition to skin cancers [5]. In human cells, DNA damage is initially identified by sensor proteins that transmit the signal and initiate the repair mechanisms. However, unrepaired DNA lesions, such as CPDs and 6-4PPs and some oxidized bases (such as 5',8-cyclo-2'-deoxyribonucleoside), can block the polymerases during the replication and transcription processes [110]. In fact, in human cells, DNA damage initiates many cellular responses (DNA damage responses, DDR), which include the cell cycle arrest (G1/S and S/G2), DNA repair and cell death by apoptosis [30,110,124,125]. In addition to apoptosis, UV exposure can also induce necrosis [30,126] and cellular senescence, a marker of aging process [127–130]. The skin aging that results from the accumulation of UV-induced cellular damage is called photoaging. This damage occurs not only in the genomes of keratinocytes, fibroblasts and melanocytes but also in the genomes of epidermal and mesenchymal stem cells [131]. In addition, UV-generated ROS can damage other important structural components, such as actin and collagen [132], which contributes to the loss of integrity of the dermis and epidermis [128]. Furthermore, UV promotes the up-regulation of Mitogen-Activated Protein Kinase (MAPK), which inhibits the cytokine Transforming Growth Factor (TGF- β), thus resulting in collagen degradation and in its impaired replacement [133,134].

MAPK and TGF- β play important roles in other cellular mechanisms that are involved in the response to sunlight. MAPKs are also activated in response to pro-inflammatory mechanisms via human beta defensin 2 (hBD2) and ROS and RNS generation [135–137]. hBD2 is mainly induced by UVB [138,139], and its transcription is regulated by activator protein 1 (AP-1), which is an inhibitor of collagen synthesis and a participant in the inflammatory and immune responses [140]. AP-1 plays an important role in the inflammatory and immune responses by controlling the expression of c-Jun-N-terminal-kinase (JNK) and p38 proteins. The formation of $^1\text{O}_2$ by UVA activates the JNK and p38 proteins, which contribute to the stabilization and increased levels of COX-2. This protein is responsible for the production of prostaglandins by oxidizing the arachidonic acid in phospholipids and is involved in tumor promotion by inducing increases in interleukin-8 (IL-8) and vascular endothelial growth factor (VEGF) [141]. In fact, the promotion of angiogenesis by the activation of VEGF in normal keratinocytes has been shown after both UVB and UVA irradiation [142,143]. Pro-inflammatory cytokines (Interleukin-1 (IL-1), IL-6, IL-10, IL-12 and TNF- α) are also produced following the production of ROS and DNA damage by UV exposure. These molecules, especially IL-10 and the prostaglandins, have important roles in the immunosuppression induced by UV [144–147]. As a consequence of the redox process, the transcription factor NF- κB pathway is also activated through cytoplasmic I- κB kinase, and this contributes to the formation of cytokines and prostaglandins [148].

Conversely, UVB exposure also promotes vitamin D synthesis through the conversion of 7-dehydrocholesterol, which is present in the plasma membranes of skin cells, to pre-vitamin D₃, which is further isomerized to vitamin D₃ [149]. Vitamin D₃ undergoes two enzymatic oxidation processes, the first in the liver and the second in the kidney, to generate the active form of vitamin D, 1,25-dihydroxyvitamin D [1,25(OH)₂D₃], also known as calcitriol [3,149]. It is important to emphasize that 80–90% of vitamin D in the human body is acquired by the cutaneous synthesis, while the remainder is obtained by the ingestion of food that contains this vitamin [2,150,151]. Therefore, factors such as latitude and season affect the dermal production of vitamin D. During the summer and in low-latitude regions, the skin 7-dehydrocholesterol is more efficiently converted into pre-vitamin D₃, mainly due to higher UVB exposure of the population [152]. However, reduced levels of plasma vitamin D are observed even in sunny countries. Thus, the use of sunscreen, the amount of melanin in the skin, the types of clothing, and high levels of pollution can reduce skin

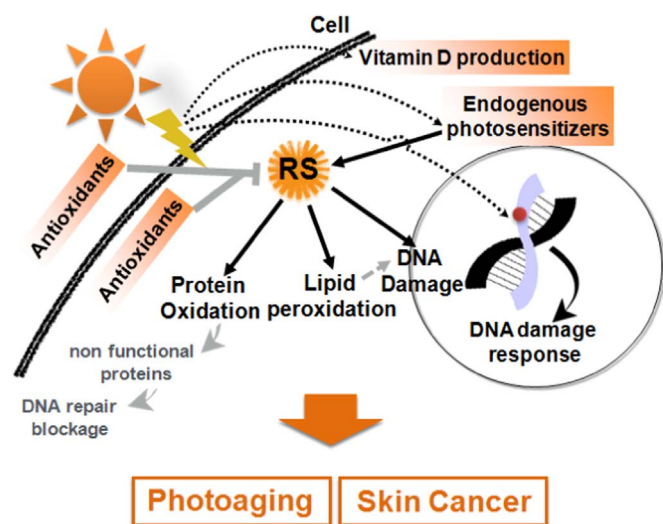


Fig. 3. The solar UV photons are directly absorbed by DNA or by other endogenous sensitizers, which leads to DNA damage and redox process (biomolecule oxidation), respectively. This stimulates numerous cellular consequences, culminating in photoaging and skin cancer. To protect cellular homeostasis, enzymatic and non-enzymatic antioxidants work to suppress the formation and reactions of the reactive oxygen species. The UVB photons are also important for the production of vitamin D.

exposure to UVB and consequently decrease the synthesis of vitamin D [151,153,154].

Vitamin D is a major factor that is required for the development and maintenance of bone tissue and for the calcium and phosphorus homeostasis. In addition, the evidence suggests that this vitamin is involved in many other biological processes, including cell differentiation and proliferation, hormonal secretion, immune system and several chronic diseases [155–158]. For instance, analysis of the data from the Third National Health and Nutrition Examination Survey (NHANES III) revealed an inverse relationship between the serum concentrations of vitamin D and the main cardiovascular risk factors, including hypertension, diabetes mellitus, hypertriglyceridemia and obesity in 15,088 individuals in the United States. The authors observed an odds ratio of 1.24 for cardiovascular events, 2.1 for heart failure, and 1.82 for peripheral arterial diseases in adults in whom the levels of 25-hydroxyvitamin D (25(OH)D) were less than 20 ng/ml [159]. Moreover, recent assessments of the 25(OH)D status concluded that approximately 40% of children and adults in the United States, Canada, Europe, Asia, India, South America and Australia are vitamin D-deficient [2,150]. In addition to musculo-skeletal consequences that include rickets in children and osteomalacia, fractures, muscle weakness and falls in older adults, a growing number of other acute and chronic illnesses have now been indicated by epidemiological, observational and experimental studies to be associated with vitamin D deficiency. These include many types of cancer (breast, colon, etc.), autoimmune diseases (e.g., type 1 diabetes, multiple sclerosis and rheumatoid arthritis), infectious diseases, neurocognitive dysfunction including Alzheimer's disease, type 2 diabetes and cardiovascular disease [2,150]. On the basis that oxidative stress is a common cellular condition shared by many of these disorders, it has recently been demonstrated that vitamin D could have a protective effect against ROS. Although an antioxidant role for vitamin D has not yet been clearly demonstrated, vitamin D supplementation has a protective effect against the oxidative stress-induced damage in vascular endothelial cells, which suggests that it could have a potential application to lower the risk of cardiovascular disease [160].

Table 1 summarizes the most important effects of UV radiation on human health and its biomarkers.

7. Systems that protect cells from sunlight-induced DNA damage

To protect skin cells from the deleterious consequences of sunlight UV, evolution has provided them with numerous systems that either prevent the formation of such damage or remove, repair, or tolerate the DNA lesions. Cells contain a complex system to avoid reactive substances that are formed by sunlight, by either sequestering or removing them from the cell. For example, an antioxidant is a molecule that inhibits or reduces an oxidation process. From the biological point of view, an antioxidant protects biomolecules and cellular structures against the harmful effects of substances that promote oxidation. The endogenous defense system comprises a series of substances that act in different ways to minimize the generation of ROS and their subsequent reactions. Cellular antioxidants include enzymes, non-enzyme sub-

stances (glutathione, ascorbate, tocopherols, carotenoids, albumin and bilirubin), proteins, chelating agents, and phenolic and aromatic molecules.

In contrast, several DNA repair mechanisms constantly survey the genome to remove DNA damage. Eventually, if DNA lesions are not removed, cells may still be able to cope with them, by replicating the damaged DNA because many translesion polymerases allow cells to tolerate DNA damage. The main pathway that is involved in the removal of base damage such as that induced by oxidative stress is BER, but certainly other DNA repair pathways contribute to the cell protection. Among these DNA repair processes, NER proteins can act directly or via interaction with other pathways, and these proteins will be the main focus of this section. Importantly, NER defective human syndromes, including XP, dramatically reveal the importance of this repair pathway on human beings. The increased photoaging and extremely high frequency of skin tumorigenesis of XP patients indicate how sunlight-induced DNA lesions can cause serious damage to the human skin.

8. Antioxidants and mechanisms avoiding DNA damage formation

Antioxidant enzymes, such as catalase (CAT), glutathione peroxidase (GPx), superoxide dismutase (SOD), and peroxiredoxins help control the intracellular concentrations of $O_2^{\cdot-}$, H_2O_2 and organic peroxide. CAT is a heme protein associated with the peroxisomes, which has high activity in the liver [161]. CAT reduces H_2O_2 to H_2O and O_2 , while GPx catalyzes the reduction of hydroperoxides via the oxidation of gamma-L-glutamyl-L-cysteinyl-L-glycine (reduced glutathione - GSH) to form GSSG and H_2O . The product is recycled by glutathione reductase, which converts GSSG into GSH at the expense of NADPH that is derived from the pentose phosphate pathway [162,163]. In addition, several types of SOD are present in the cytosol and in the mitochondria of human cells, where they convert $O_2^{\cdot-}$ into H_2O_2 and molecular oxygen (O_2) [164]. Peroxiredoxins (PRDXs), a ubiquitous family of redox-regulating proteins, are important endogenous antioxidants that protect cells from oxidatively generated damage by reducing H_2O_2 and peroxynitrite and by scavenging thiyl radicals [165].

Other classes of *in vivo* antioxidants are proteins and chelators (such as transferrin and ceruloplasmin) that bind to iron and copper; these can prevent Fenton reactions by blocking the formation of $\cdot OH$, the most reactive ROS [166]. Another important antioxidant is GSH that reacts directly with several ROS, including oxyl radicals ($RO\cdot$), peroxy radicals ($RO_2\cdot$), $\cdot OH$ and 1O_2 . GSH also plays an important role as a cofactor of enzymes (GPx, glyoxylase, and prostaglandin endoperoxide isomerase, as well as serving in ascorbate metabolism) and in communication between cells (gap junctions) [167,168]. Moreover, it participates in the detoxification of many substances including peroxides and xenobiotics through the actions of glutathione-S-transferase and glutathione peroxidase. GSH can also oxidize nonenzymatically in the presence of copper and iron to form the thiol radicals ($GS\cdot$ and $GSS\cdot G$), which are intermediates in the generation of oxidized glutathione and ROS (H_2O_2 , $O_2^{\cdot-}$, $\cdot OH$) [169].

Heme oxygenase 1 (HO-1) also has important roles in the protection

Table 1
Effects of UV radiation on human health and its biomarkers.

| Consequences of UVA and UVB exposure | Biomarkers | References |
|--------------------------------------|--|--------------------------|
| DNA damage | CPD, 6,4PP, oxidized bases, single strand breaks | 22, 25–28, 30–35, 41 |
| Redox process | Biomolecule oxidation | 25, 62, 63, 81–85, 91–96 |
| Inflammation | Cytokines (IL-1, IL-6, IL-10, IL-12 and TNF-alpha) COX-2 | 135–137, 141 |
| Immunosuppression | IL-10, prostaglandins | 144–147 |
| Vitamin D synthesis | 25-hydroxyvitamin D (25(OH)D) in serum | 149, 152 |
| Microenvironment modification | Collagen breakdown | 132, 140 |
| Cell death | Apoptosis and necrosis | 30, 110, 124, 125 |
| Transcription factor induction | AP-1, NF-kB, Nrf-2 | 140, 148, 172, 173 |

against UVA-induced ROS [170,171]. This enzyme is responsible for the heme metabolism to carbon monoxide (CO), ferrous iron and biliverdin. Biliverdin is further reduced to bilirubin by biliverdin reductase. Heme metabolites are also implicated in the anti-inflammatory response through cytokine suppression. The overexpression of HO-1 after UV exposure is controlled by Nrf2 [172], a transcription factor that is involved in the expression of the vast majority of the genes associated with ROS defense, and by the repressor protein Bach1 [173]. Additional effort is needed to completely elucidate the activation and modulation of Nrf2 expression in response to sunlight and to exposure to UVA and UVB separately. Interestingly, although there is evidence that suggests that UVB radiation probably does not activate Nrf2 expression in skin cells, UVA can activate this transcription factor in both fibroblasts and keratinocytes [63,172]. Nrf2 is also modulated by various compounds such as quercetin, ellagic acid, and resveratrol [172], which belong to a class of non-enzymatic antioxidant molecules. Carotenoids are pigments found in the photosynthetic plant tissues and are acquired through the dietary intake of fruits and vegetables. Their antioxidant properties have been studied over the last decades, including their roles in protection from sunlight-induced skin damage [174,175]. In addition, *in vitro* and *in vivo* studies have demonstrated that carotenoids can suppress ROS formation, thus preventing lipid peroxidation, photo-inactivation of antioxidant enzymes, and induction of oxidatively generated DNA damage after UVA and UVB exposure [176–180]. Furthermore, studies conducted in humans supplemented with beta-carotene or with a mix of carotenoids showed that the induction of erythema was less pronounced after UV exposure [181–183].

Ascorbic acid (Vitamin C) and alpha-tocopherol (Vitamin E) are the most abundant antioxidants present in the epidermis and dermis followed by various carotenoids (lycopene, beta-carotene and phytoene) [184]. The protective effect of these dietary compounds has been tested in cultured keratinocytes, animal models and humans. Vitamin C, E and polyphenols are able to scavenge ROS, including H₂O₂, [•]OH and O₂^{•-}, decreasing lipid peroxidation and interleukins levels after UVA and UVB exposure [184–190].

9. DNA repair deficiency and human diseases

Several DNA repair pathways are involved in the removal and/or tolerance of DNA lesions in living cells. These pathways are highly conserved throughout evolution, and for human cells they are involved in the maintenance of genome stability to prevent carcinogenesis and aging. This is dramatically demonstrated by DNA repair hereditary defects that give rise to certain rare genetic syndromes, including ataxia telangiectasia, Nijmegen breakage syndrome, Werner syndrome, Bloom syndrome, Fanconi anemia, xeroderma pigmentosum (XP), Cockayne syndrome (CS), trichothiodystrophy (TTD), UV-sensitive syndrome, and XPF/ERCC1 syndrome (XFE). Although the symptoms differ among these conditions, these human disorders share many clinical features that may include photosensitivity, growth retardation, neurological problems, premature ageing, skin alterations including abnormal pigmentation, telangiectasia, xerosis cutis, and pathological wound healing as well as an increased risk of developing various types of cancer [191]. Deficiencies related to the repair of endogenous DNA lesions, including those generated during oxidative stress, are proposed as the main causes for the symptoms that involve developmental and neurological problems as well as premature aging [5,192].

Although BER is an indispensable mechanism for the repair of oxidized DNA bases, none of the human syndromes cited above is associated with mutations in genes of this DNA repair pathway. It is likely that this could be partially explained on the basis that several distinct paralogues of the BER proteins with overlapping functions are encoded by the genome, and the enzymes have relatively low substrate specificities. For example, the DNA glycosylases have a relatively wide specificity to remove damaged bases from the DNA backbone by hydrolyzing the N-glycosidic bond between the sugar C1' and the base

[193]. However, persistent oxidatively generated DNA damage and BER activity have been implicated in several other human diseases, in particular cancer and inherited and acquired neurological disorders including Alzheimer's disease, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis as well as in aging [194–197]. Another example is *MUTYH*-associated polyposis (MAP) syndrome, in which the patients demonstrate a recessively heritable colorectal polyposis that is linked to an increased risk of colorectal cancer, due to the occurrence of biallelic germline mutations in the *MUTYH* gene [198]. *MUTYH* is a mismatch-repairing glycosylase that scans the newly synthesized daughter strand to locate and remove adenine that is mispaired with 8-oxoG [199], but the absence of this protein is sufficient for the phenotype observed in MAP patients.

BER preferentially repairs non-bulky, non-helix-distorting lesions by removing and repairing damage sustained by deamination, alkylation or oxidation processes, including those induced by sunlight. Briefly, the BER mechanism comprises four minimal steps: (i) base lesion recognition and excision by a DNA glycosylase and cleavage of the resulting apurinic/aprimidinic (AP) site in a concerted reaction by the AP lyase function associated with the DNA glycosylase (bifunctional glycosylases) or by an AP-endonuclease (APE1, for monofunctional glycosylases); (ii) cleaning of 3' blocked termini at the strand break by APE1 and/or polynucleotide kinase 3' phosphatase (PNKP) and 5' blocking phosphodeoxyribose by DNA polymerase β (Polβ); (iii) gap filling by a DNA polymerase; and (iv) nick sealing by DNA ligases to complete repair [200]. There are two major BER sub-pathways in mammalian cells: the long- and short-patch BER (LP-BER, SP-BER, respectively). Short-patch BER replaces excised damage with a single nucleotide using the core proteins: APE1, Polβ, DNA ligase III (LIG3) and X-ray repair cross-complementing protein 1 (XRCC1). In contrast, LP-BER uses APE1 to make a 5' incision at the AP-site and a combination of DNA polymerases β/δ/ε, proliferating cell nuclear antigen (PCNA) and flap endonuclease (FEN1) displaces the strand 3' to the nick producing a flap of 2–10 nucleotides, and then FEN1 endonuclease is responsible for cutting the junction of the single-to-double-strand transition. Pol δ/ε in conjunction with PCNA synthesizes the oligonucleotide to fill the gap, and ligation is performed by Ligase I (LIG1) [195].

In fact, several of the human syndromes listed above are associated with mutations in the genes of NER pathway. NER is a highly versatile and sophisticated DNA repair pathway that counteracts the deleterious effects of numerous structurally unrelated DNA lesions, including lesions that distort the DNA double helix, interfere in base pairing and block DNA duplication and transcription [34]. The first syndrome for which the DNA metabolism defect was described was *xeroderma pigmentosum* (XP; from the Greek, *xero*, dry and *derma*, skin, and the Latin, *pigmentosum*, paint, pigmented) [201,202]. These patients present mainly exacerbated symptoms associated with skin cancer and skin aging. Defective damage removal or tolerance are most likely responsible for the symptoms, and the participation of oxidatively generated DNA damage in these dermal XP symptoms is not completely clear, but they can be related, as illustrated in Fig. 4.

Most XP patients have a defect in NER, which is responsible for the removal of CPD and 6-4PP from the genome, although some XP patients also have defects in the replication of UV-damaged DNA. The main clinical symptom of XP patients is the high frequency of tumors in the sunlight-exposed areas of the skin. Specifically, XP patients under the age of 20 years show a 10,000-fold increase in skin cancer, which demonstrates the substantial importance of DNA repair in cancer prevention in the general population [203–205]. XP patients are also known to have many skin lesions in areas exposed to sunlight, which has a clear parallel with skin photoaging [5]. Twenty to thirty percent of the XP patients also have neurological and or developmental problems that are most likely associated with unrepaired DNA damage [5].

A recently published study analyzed the largest reported cohort of XP patients (89 people; this represents approximately 90% of the XP

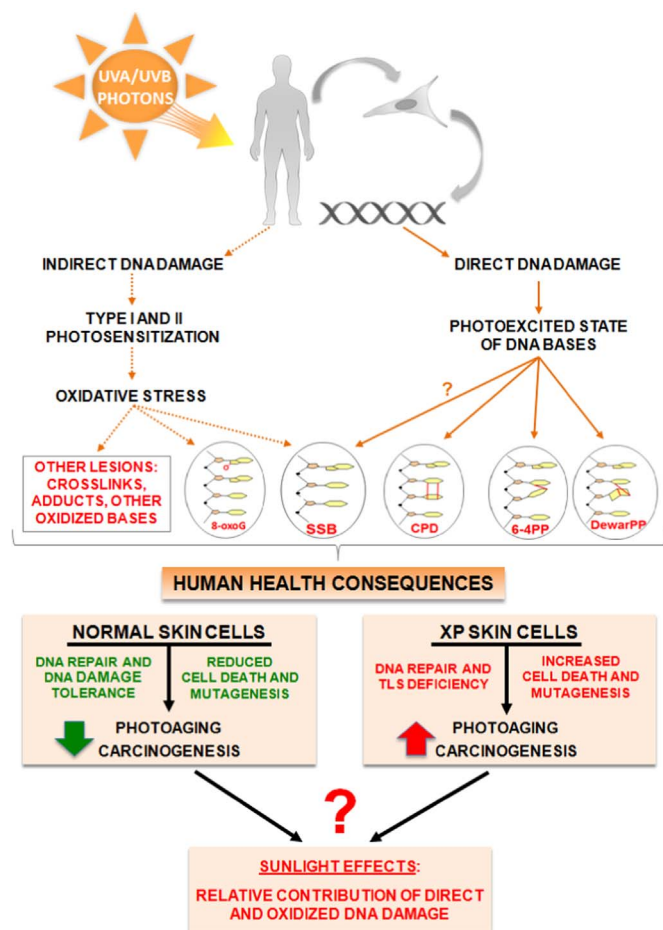


Fig. 4. The DNA damage induced by sunlight has deleterious consequences on human health, such as skin photoaging and carcinogenesis. These consequences are clearly increased in XP patients when compared to the general population. Because these clinical outcomes are increased in XP patients, studies with XP cells may help to better understand the relative contribution of direct and oxidatively generated DNA lesions on these consequences, in both normal individuals and XP patients.

patients in UK) [206]. All participants were examined by the same clinicians using 60 different phenotypical end-points, and in all cases, the observations were correlated with the pathological mutations. The deep phenotyping approach has revealed the heterogeneity of the clinical features between and within complementation groups. The results indicate that skin cancer is most common in XP-C, XP-E, and XP-V patients, which were previously considered to be the milder groups based on cellular analyses. XP-C patients are specifically hypersensitive to ocular damage, and XP-F and XP-G appear to be much less susceptible to skin cancer than other XP groups [206]. However, patients in groups XP-A, XP-D, and XP-G are considered to have the most severe forms of the disease, with early-onset neurological degeneration and abnormally severe sunburn reactions. However, depending on the type and location of the mutation, patients can present milder phenotypes than expected for the gene affected [206].

Curiously, although patients with CS and TTD also have mutations in NER genes, they are cancer-free [207] but generally present developmental defects, neurodegeneration, and accelerated aging [208]. Evidence has shown that NER proteins are involved in repairing oxidatively generated damage [201,209–213]. Recent work using an NER-deficient mouse model provided evidence demonstrating the participation of metabolically induced DNA damage, which, in the absence of repair, blocks gene transcription and results in accelerated aging [214]. In both XP and CS syndromes the severity of the symptoms can be quite variable depending on the complementation group and on

the nature of the mutation. Although the participation of NER in the repair of oxidized DNA damage is well accepted, the effects of these types of lesions induced by sunlight, and especially UVA, on the skin of such patients is usually neglected. Thus, it is possible that several types of UVA-induced DNA damage, not only pyrimidine dimers, could be associated with at least a part of the XP patients' dermal symptoms (including tumors and skin photoaging).

10. Relevance of oxidatively generated DNA damage in NER-deficient cells

NER can be summarized as having four sequential steps to remove DNA damage, including (i) lesion recognition, (ii) unwinding the damaged double helix, (iii) cleavage and excision of the damaged strand and (iv) filling the gap in the molecule by DNA synthesis and final ligation. In all those steps more than 30 proteins act in a sequential and concerted manner to effect repair [5,215].

In summary, NER operates by two distinct pathways: global genome repair (GGR), which removes lesions from the entire genome, and transcription-coupled repair (TCR), which repairs transcriptionally active regions. The GGR sub-pathway involves the recognition of DNA lesions throughout the genome and depends on the XPC/HR23B protein complex as the primary DNA-damage detector. For some types of lesions such as CPDs, the damaged DNA-binding (DDB) complex (composed of two proteins, including XPE) is required to improve the efficiency of the damage recognition and removal. In TCR, the RNA polymerase II (RNAPII) is stalled at the sites of the lesions on the transcribed strand, which plays a role in the recognition step. Transcription arrest, damage recognition and the subsequent repair involve CSA and CSB proteins that are required for ubiquitination of the carboxy-terminal domain of RNAPII [5,215,216].

Subsequently, the repair process follows the same path through the binding of the TFIIH complex via interaction with either XPC or the arrested transcription machinery. TFIIH includes the XPB and XPD proteins, which are 3'–5' and 5'–3' ATP-dependent DNA helicases, respectively. This complex unwinds ~30 bp at the damaged DNA site, which is covered by a single RPA (Replication Protein A) protein and XPA homodimer. These proteins are probably involved in the correct three-dimensional assembly of the NER machinery prior to the endonucleolytic cleavage step. Then, the DNA around the damaged site is cleaved by the XPF-ERCC1 5' and the XPG 3' endonucleases. Once the damaged oligonucleotide is removed, resynthesis is performed by proliferating cell nuclear antigen (PCNA) and replicative DNA polymerases δ and ϵ , which use the 3'-hydroxyl extremity generated by the XPF/ERCC1 incision as a primer to synthesize DNA at the 30-nucleotide-gap. The resulting nick at the 5' end of the gap is sealed by DNA ligase I or III, thus restoring the original DNA molecule in an error-free manner [5,215,216].

The clinical heterogeneity of symptoms presented by patients with NER-associated disorders raises the question of whether defects in this pathway are solely due to impaired repair of helix-distorting DNA lesions, such as the photoproducts CPDs and 6-4PPs. The defects in the roles of the NER proteins in the repair of oxidatively generated DNA damage may be the underlying mechanism behind the accelerated aging and neurodegeneration in CS patients, increased risk for internal cancer development in XPC and neurodegeneration in XPA patients, and the complex phenotypes of XPB, XPD, and XPG patients [201,212,217]. In addition, oxidized DNA bases that are mainly generated by UVA radiation and are different from the classical photoproducts may also affect the skin and induce important symptoms, including cancer. However, little is known about the effect of UVA in NER-deficient cells, and this deserves to be investigated.

CS proteins play critical roles in TC-NER. In addition, CSB can interact with chromatin-bound RNAPII, which suggests that these two proteins are combined in high molecular weight protein complexes [218,219]. Thus, it has been suggested that CSB can stimulate

transcriptional elongation by RNAPII to add one nucleotide to the nascent transcript, which implies a functional interaction between these two proteins [219–221]. CSA is a component of a protein complex that contains also the COP9 signalosome (CSN), a known regulator of cullin-based E3 ubiquitin ligases [216]. In a mechanism that is not well understood, CSA translocates to the stalled RNAPII-CSB complex at the DNA damage site in a CSB-dependent manner [218,222]. The CSA-containing ubiquitin ligase complex has been implicated in the ubiquitination and subsequent degradation of CSB as well as in the termination of the TC-NER process and the restoration of transcription [223]. An integrated model would include the ubiquitination of CSB or the RNAPII large subunit by CSA as a signal for CSB to disassemble the initial TCR complex, leaving the NER complex to finish the job [216].

In addition, the CSA and CSB proteins might have an additional function in the removal of oxidatively generated DNA damage in the nuclei and mitochondria. Studies indicate that human cells deficient in CSB or CSA are more sensitive to H₂O₂ treatment [224] and that primary fibroblasts and keratinocytes from CSA patients are hypersensitive to potassium bromate, a specific inducer of oxidative damage [225]. Furthermore, primary fibroblasts derived from CSA and CSB patients also present an altered redox balance with increased steady-state levels of intracellular ROS as well as basal and induced oxidized DNA [226]. Less information is available for CSA than for CSB, but CSA appears to be involved in the response of oxidatively generated DNA damage in humans [212]. For CSB, it is already known that it can interact with several members of BER pathway, including the strand-break response protein poly(ADP-ribose) polymerase-1 (PARP1), endonuclease VIII-like 1 (NEIL1) DNA glycosylase, and APE1 [227]. In addition, CSB has a regulatory effect on OGG1 expression, and a deficiency in CSB leads to the accumulation of 8-oxoG in DNA [102,228]. Emerging evidence also indicates that CS proteins have additional roles in maintaining mitochondrial DNA (mtDNA) stability, probably by anchoring the BER machinery at lesion sites in mtDNA [229,230]. For instance, after oxidative stress, CSA and CSB proteins are present in mitochondria, where they can directly interact with mtDNA, mtOGG1 and mitochondrial single-stranded DNA-binding protein (mtSSBP-1) [230]. In addition, it has been shown that mtDNA damage accumulates in CSB-defective cells [231].

However, it is important to mention that Brooks (2013) has proposed that although defective TC-NER could explain sun sensitivity in CS patients, a combination of transcription abnormalities that affect RNA polymerases I and II provides an alternative explanation for many aspects of CS-associated neurologic disease and other internal features of CS [232]. Thus, although several lines of evidence support the idea that CS symptoms may be partially explained by the involvement of CSA and CSB in the repair of oxidatively generated DNA lesions and that the accelerated aging may be due to the accumulation of DNA damage in the mitochondria, this is still matter of debate and additional studies are required to gain further insights into the molecular mechanisms that involve the CS proteins in the repair of oxidized DNA bases.

Nevertheless, defects in both XP and CS can occur together in the same patient, which gives rise to a XP/CS phenotype [233]. In these patients, the skin manifestations of XP are observed together with the neurological features of CS, such as calcification of the basal ganglia, demyelination, and cerebellar dysfunction. In general, XP/CS cases are associated with mutations in the *XPB*, *XPD*, or *XPG* genes [234], although mutations on these same genes can also be associated with XP (affecting the skin) only.

The participation of XPG in the repair of oxidized pyrimidines such as 5,6-dihydroxy-5,6-dihydrothymine (thymine glycol) may involve the promotion of binding of the DNA glycosylase-AP lyase hNth1 to the damaged site in human cells [235]. In addition, melanocytes derived from a XPG patient appeared to be deficient in the repair of oxidatively generated DNA damage, which suggested that XPG participates in the repair of these DNA lesions [236]. In fact, fibroblasts from a XPG

patient who presented the XP/CS clinical phenotype were shown to be sensitive to UV radiation as well as to photoactivated methylene blue, which generates ¹O₂ and also reacts with guanine through type I photosensitization mechanism [237], while some XPG mutations (from XP patients with no clinical symptoms related to CS) affect sensitivity to UV radiation but not of oxidatively generated DNA damage [238]. Therefore, mutations in the *XPG* gene support the model that suggests that the development of CS in XPG patients may be related to inefficient excision of endogenous oxidatively generated damage. Clearly, variants of the XPG protein may lead to divergent and complex phenotypes. These observations suggest that the XP phenotype may arise from missense mutations in the *XPG* gene that generally result in a stable XPG protein, whereas XP/CS originates from mutations that result in a truncated and/or unstable XPG protein [238–240].

The helicases must unwind DNA at the right place and time to maintain genomic integrity or gene expression. XPB and XPD are helicases that are present in the human TFIIH complex and catalyze the separation of the DNA duplex by moving along this macromolecule powered by ATP binding and hydrolysis during transcription and repair [241]. In addition to photosensitivity, mutations in the *XPB* and *XPD* genes can also induce premature aging with profound neurological defects as well as increased cancer risk [202]. In DNA repair process, after initial damage recognition and binding of other repair proteins, TFIIH is recruited to the damage opening approximately 27 nucleotides of the excision bubble. Then, the XPD bound to the damaged DNA interacts with XPG and promotes DNA incision. Finally, removal of TFIIH is necessary for re-synthesis of the incised damaged strand. Therefore, mutations on XPB or XPD that destabilize TFIIH generally lead to cell death and tissue degeneration whereas mutations that cause defects in the helicase or ATPase activities disrupt repair and lead to cancer [241]. Despite scarce information regarding the role of either the XPB and XPD helicases in the repair of oxidized DNA bases in the nucleus, it was recently demonstrated that XPD localizes in mitochondria where the helicase activity is critical for the protection of the mtDNA by facilitating the repair of oxidatively generated DNA damage [242].

XPC is one of the key DNA damage-recognition proteins in the GGR and mutations in this gene can increase cancer risk, although neurodegeneration is rarely seen on this group of patients [5,243]. The human XPC forms a heterotrimeric complex that includes the HR23B and centrin-2 proteins. HR23B seems to stabilize XPC, whereas centrin-2 is required to enhance the damage-recognition function of XPC [5,216]. This complex binds to various types of helix-distorting lesions, but it does not bind exactly at the damaged site. XPC protein seems to distinguish between damaged DNA and the native double helix by sensing the single-stranded character of the non-hydrogen-bonded bases in the undamaged strand [241]. In addition to the main role of the XPC complex in the recognition of DNA-distorting lesions, it has been demonstrated that it can functionally interact with several BER proteins, including 3-methyladenine DNA glycosylase, thymine DNA glycosylase (TDG), uracil-DNA glycosylases (UDG), apurinic/apyrimidinic endonuclease 1 (APE1), and 8-oxoguanine DNA glycosylase (OGG1) [244–251]. The proposed mechanism suggests that the XPC complex might bend DNA at the damaged site to facilitate the loading and turnover of the BER glycosylases through protein interaction [244]. A strong indication of this additional function of XPC in the repair of oxidized DNA bases is provided by a mutation that weakens the interaction with OGG1 and, consequently, its cleavage activity. In fact, this mutation was found in one of the rare cases of XPC patients who demonstrate neurological problems [252]. Additionally, studies using human keratinocytes and fibroblasts from XPC patients showed that this protein is important to prevent the accumulation of oxidatively generated DNA damage and its killing effects after exposure to oxidants, such as potassium bromate, X-rays, and methylene blue plus visible light [244,245,253]. However, it is important to mention that the rapid recruitment of XPC to sites of oxidized DNA lesions in living cells occurs

without triggering the recruitment of other GG-NER factors [254].

With regard to the role of XPA in the cellular responses to oxidative stress, it has been shown that fibroblasts that lack functional XPA demonstrate increased genotoxicity and a reduced capacity to repair damage when subjected to oxidative stress [255]. It has been proposed that 5',8-cyclo-2'-deoxyribonucleosides may explain the severe cases of neurodegeneration found in XPA patients because these bulky lesions are exclusively repaired by the NER pathway [256,257]. However, the biological relevance of this type of DNA damage is unclear because they are very rare lesions, due to the very low efficiency of OH-mediated formation [258]. Furthermore, analysis of the autopsied brains of XPA patients revealed increased oxidized DNA and RNA molecules, enhanced lipid peroxidation, and a disturbed expression of Cu/ZnSOD and MnSOD enzymes, which suggested the existence of oxidative stress in the brain cells of these patients [259]. The induction of clusters of oxidized bases might also be the result of oxidative stress with important biological consequences in the cells [260–262]. Interestingly, recent evidence has indicated that oxidatively generated tandem base damage such as two vicinal 8-oxoG modifications, when in the transcribed strand, may increase mutagenesis in cells that lack XPA protein, which indicated that close base damage may depend on NER [217]. This is consistent with the results of a previous study that revealed that the TCR of 8-oxoG is dependent on OGG1, XPA, CSB, UVSSA, and the actively elongating RNA polymerase II, which suggests that there is crosstalk between the DNA repair pathways [213].

Another important, but normally neglected, fact concerning sunlight exposure is that UVA radiation can promote the oxidation of the proteins that are involved in DNA repair, which would impair the removal of the DNA damage. This appears to be particularly relevant with respect to the NER pathway. Recently, it was clearly shown that the oxidative stress generated by UVA promotes oxidation of RPA, which debilitates the ability of the NER to remove photoproducts from human keratinocytes [263]. The susceptibility of the NER proteins to the oxidation generated by UVA or other substances compromises the cell protection against DNA damage, which has clear implications for carcinogenesis [264]. This aspect indicates how protein oxidation can affect the cells' abilities to repair DNA damage, which will be further discussed in another article from this issue.

11. Oxidatively generated DNA damage and translesion synthesis

Some XP patients have a normal capacity to remove DNA lesions from their genome but still demonstrate symptoms associated with sensitivity to sunlight including a high frequency of skin tumors and photoaging. These patients are known as XP variants, and they lack the Pol eta activity [265]. Pol eta is encoded by the *POLH* gene, which has the primary function of properly performing the TLS of damaged DNA, inserting AA in sites that contain TT dimers induced by UV radiation [266,267]. This function contributes to the protection of human cells from the potentially mutagenic effects of UV radiation [268]. In Pol eta-deficient cells, the TT dimers are replicated less efficiently by other DNA polymerases of TLS (usually of Y family), which results in a mutator phenotype that is probably responsible for the high frequency of tumors in these patients [268,269]. As previously noted, UV radiation induces mainly C to T transitions whereas in XP-V cells, the occurrence of T to A transversions, and high levels of G to T and G to C transversions are also observed [265,270]. This raises the question of whether pyrimidine dimers are the only components responsible for this increase in mutagenesis in the XP-V cells or if oxidatively generated DNA damage can also participate in the carcinogenesis process observed in the XP-V patients.

There is evidence that Pol eta performs the bypass of other types of DNA lesions, including O4-methylthymine, O6-methylguanine, and acetylaminofluorene, cisplatin and oxaliplatin adducts. It can also perform the bypass, with moderate efficiency, of 8-oxoG, which has a potentially important role in the suppression of mutations due to this

oxidatively generated DNA lesion in human cells [109,271]. Pol eta can insert A or C opposite a site with 8-oxoG, which may result in a G to T transversion. However, in the absence of Pol eta, other TLS polymerases may be less efficient, which would increase the frequency of this type of mutation. Because UVA radiation may induce oxidized bases, the contribution of these lesions to the process of skin cancer formation in XP-V patients is not known [108,109]. A previously published study in which *Saccharomyces cerevisiae* was exposed to simulated sunlight supports the role of Pol eta in TLS of CPDs and 6-4PPs [52]. Despite growing interest in understanding how mutations contribute to high rates of skin cancer that are due to sunlight exposure, knowledge on the effects of UVA and UVB radiation in human XP-V cells is scarce. Furthermore, these patients have skin lesions that resemble the normal products of photoaging. Thus, studies of the responses of XP-V cells to these wavelengths may help us to understand the origins of the sunlight effects in normal skin.

12. Concluding remarks

Solar UV radiation is a ubiquitous environmental genotoxic agent to which almost everyone is exposed on a daily basis. The effects of UV radiation on human health depend on the amount and type of radiation impinging on the body. Although UVB photons have the highest efficacy to generate the mutagenic and cytotoxic pyrimidine dimers (i.e., CPDs and 6-4PPs), they are also responsible for initiating the synthesis of vitamin D in the skin through the absorption of UVB radiation by 7-dehydrocholesterol. Therefore, exposure to UVB should not be entirely avoided because this would create a huge burden of skeletal disease from vitamin D deficiency. Thus, public health messages regarding safe exposure to the sun are very important to guide people to prefer recurrent shorter periods of exposure to achieve vitamin D production while minimizing the harmful consequences of UV-induced DNA damage due to prolonged exposures.

Sunlight-induced DNA damage is considered to be the main cause for the genetic changes responsible for skin lesions and carcinogenesis including malignant melanoma. However, it is generally accepted that single oxidized DNA bases (i.e., 8-oxoG) are efficiently and quickly (3–6 h) eliminated from the genome by the BER pathway. Nevertheless, oxidizing agents can induce other types of DNA lesions including bulky lesions that block DNA transcription. Thus, these results also raise questions regarding the roles of NER proteins in the repair of DNA damage that is oxidatively generated by sunlight. Similarly, tolerance mechanisms involving the bypass of these lesions may participate in the protection of cells from the deleterious consequences of sunlight. These consequences of sunlight are more evident in XP patients, who are defective in NER or TLS. Thus, what emerges for now is a complex scenario where the mechanisms of additional functions of NER proteins and Pol eta still need to be fully understood, mainly because the range of oxidatively generated DNA lesions induced by sunlight is large. Further studies need to be performed to define the mechanistic basis of the NER and TLS involvement in the cellular consequences of the sunlight-induced oxidation of DNA bases and to address whether this process might be a relevant factor in the development of skin cancer and photoaging.

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