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Roles of UVA Radiation and DNA Damage Responses in Melanoma Pathogenesis

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Abstract

The growing incidence of melanoma is a serious public health issue that merits a thorough understanding of potential causative risk factors, which includes exposure to ultraviolet radiation (UVR). Though UVR has been classified as a complete carcinogen and has long been recognized for its ability to damage genomic DNA through both direct and indirect means, the precise mechanisms by which the UVA and UVB components of UVR contribute to the pathogenesis of melanoma have not been clearly defined. In this review, we therefore highlight recent studies that have addressed roles for UVA radiation in the generation of DNA damage and in modulating the subsequent cellular responses to DNA damage in melanocytes, which are the cell type that gives rise to melanoma. Recent research suggests that UVA not only contributes to the direct formation of DNA lesions but also impairs the removal of UV photoproducts from genomic DNA through oxidation and damage to DNA repair proteins. Moreover, the melanocyte microenvironment within the epidermis of the skin is also expected to impact melanomagenesis, and we therefore discuss several paracrine signaling pathways that have been shown to impact the DNA damage response in UV-irradiated melanocytes. Lastly, we examine how alterations to the immune microenvironment by UVA-associated DNA damage responses may contribute to melanoma development. Thus, there appear to be multiple avenues by which UVA may elevate the risk of melanoma. Protective strategies against excess exposure to UVA wavelengths of light therefore have the potential to decrease the incidence of melanoma.

Keywords

Ultraviolet radiation; Ultraviolet A radiation; Melanoma; Melanocytes; DNA damage; DNA repair; Warburg effect; Nucleotide Excision repair; Immune suppression; DNA damage checkpoints; ATR kinase; DNA damage signaling; Skin Cancer

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1. Introduction

1.1. Melanoma incidence

Cutaneous melanoma is a cancer that often arises from melanocytes located in regions of skin that are frequently exposed to sunlight, such as the face, neck, arms, and hands [Gilchrest et al., 1999]. Melanocytes reside within the basal layer of the epidermis and make contacts with many epidermal keratinocytes, which enables the transfer of the pigment melanin to these cells to protect them from the DNA damaging effects of ultraviolet radiation (UVR) from the sun [Nordlund, 2007; Gilchrest et al., 1996]. Though exposure to UVR from the sun or tanning beds is the most prominent risk factor for developing melanoma, several other factors, including eye color, fair skin, tendency to sunburn, inability to tan, numbers of moles, family history, age, and immunosuppression also contribute to disease risk [Gilchrest et al., 1999]. Melanoma is a major public health concern because of its rapidly growing incidence (at a rate of 3–7% per year for fair-skinned individuals), which is projected to double every 10–20 years [Lens and Dawes, 2004; Leiter and Garbe, 2008; MacKie et al., 2009]. It also has a relatively high rate of lethality in comparison to non-melanoma skin cancers (NMSCs). Indeed, more than 75% of all skin cancer-associated deaths are due to melanoma [Shenenberger, 2012]. In 2016, the National Institute of Health Surveillance, Epidemiology and End Results program (NIH-SEER) reported that there were an estimated 76,380 new cases (4.5% of all new cases of cancer) and 10,130 deaths (1.7% of all cancer deaths) from melanoma. NIH-SEER also reported that in 2013 there were approximately 1,034,460 people living with melanoma of the skin in the United States. The annual treatment cost for melanoma ranged between \$44.9 million among Medicare patients with existing cases to \$932.5 million among all newly diagnosed cases [Guy et al., 2012]. Understanding the factors that contribute to cutaneous melanomagenesis is therefore critical to reducing the burden of this growing disease in people worldwide.

1.2. Ultraviolet radiation

Ultraviolet radiation (UVR) is electromagnetic radiation with wavelengths in the range of 100 nm to 400 nm, which are shorter than visible light but longer than X-rays. The major source of UVR is sunlight, which makes sunlight the most prominent environmental carcinogen to which humans are routinely exposed. UVR can be subdivided into ultraviolet C (UVC; 100–280 nm), ultraviolet B (UVB; 280–320 nm) and ultraviolet A (UVA; 320–400nm) radiation based on the biological effects of the different wavelengths. Some properties of the different forms of UVR are provided in Table 1. Much of our understanding of UVR effects on DNA and cellular DNA damage responses have been derived from studies using a variety of model systems that have utilized UVC light sources. Though the germicidal properties of UVC are well known, the fact that UVC wavelengths of sunlight are effectively blocked by the ozone layer and do not penetrate the skin has led some to question the relevance of studies using UVC to human health. Nonetheless, analyses of mutagenesis in mammalian systems generally support the idea that all UV wavelengths generate similar patterns of mutations in DNA [Brash, 2015], and indeed deep sequencing of genomic DNA from melanoma tumors has revealed a plethora of UV signature mutations [Hodis et al., 2012; Berger et al., 2012; Krauthammer et al., 2012]. Thus, experimental data generated

using UVC light sources provide a valuable resource for understanding fundamental aspects of DNA damage formation and the subsequent cellular responses in human cells.

However, because UVA and UVB wavelengths of sunlight can be absorbed by cells in the different layers of skin by various cellular biomolecules, UVA and UVB are therefore considered to be more relevant to human health. UVA and UVB have several unique properties that are relevant to understanding UVR-induced skin carcinogenesis. UVA comprises 90–95% of terrestrial sunlight UVR and can reach the dermal layer of human skin. In contrast, UVB only affects cells within the epidermal layer of the skin and comprises only a relatively small amount of the UVR from the sun at the surface of the Earth. Nevertheless, UVB is generally thought to be more carcinogenic than UVA because it is more efficiently absorbed by DNA. Although the sun is a natural source of UVA and UVB, it should be noted that there are other UV light sources that humans are sometimes exposed to, including tanning booths, curing lamps (fluorescent lamps, mercury vapor lamps), black light/UV-A lights/ Wood's lamps, high intensity discharge lamps, certain types of light-emitting diodes (LEDs), and lasers [Diffey, 2002]. Thus, within certain patient populations, exposures to these UVR sources may be relevant to understanding disease risk.

1.3. Epidemiological evidence linking UVA and melanoma

According to the International Agency of Research on Cancer of the World Health Organization (WHO), UVR including UVA is carcinogenic to humans. This classification is supported by several lines of evidence, including several epidemiological studies. For example, an association between tanning bed use and melanoma was used to explain an epidemic of melanoma that was observed in Iceland between 1990 and 2006 [Autier et al., 2011b]. Tanning beds primarily emit UVA, though some may emit a small amount of UVB. The UVA fluencies associated with tanning beds are 5 to 15 times greater than direct exposure from the sun. Several other studies have confirmed the association between tanning devices and elevated risk of melanoma [Buckel et al., 2006; Zhang et al., 2012; Le Clair and Cockburn, 2016; Dore and Chignol, 2012].

As will be described in greater detail below, UVA can act on various endogenous and therapeutic photosensitizers to generate reactive oxygen species that damage both DNA and the proteins that repair DNA damage [Brem et al., 2017; Karran and Brem, 2016; Brem and Karran, 2012; Attard and Karran, 2012], which may ultimately promote the mutagenic events that drive skin carcinogenesis [Karagas et al., 2007; Robinson et al., 2013]. For example, the immunosuppressive thiopurine prodrug azathioprine is widely used in organ transplant recipients to prevent rejection and in the management of inflammatory bowel conditions. However, patients treated with azathioprine show a significantly increased risk of skin cancers on parts of the body that are routinely exposed to the sun [Euvrard et al., 2003; Peyrin-Biroulet et al., 2011; Ramiscal and Brewer, 2013]. In addition to possibly preventing the efficient recognition and elimination of mutant pre-cancerous cells by the body's immune system, some immunosuppressive drugs also act as UVA photosensitizers. For example, azathioprine treatment has been shown to sensitize human skin to UVA and to lower the minimal erythemal dose (MED) for UVA and solar simulating radiation [Perrett et al., 2008]. This UVA-dependent photosensitization also generates DNA damage and inhibits

DNA repair protein function [Brem and Karran, 2012; Karran and Brem, 2016; Brem et al., 2017; Attard and Karran, 2012]. Epidemiological evidence has indicated that melanoma is a growing problem in organ transplant recipients receiving immunosuppressive drugs [Fattouh et al., 2017; Dahlke et al., 2014; Green and Olsen, 2015; Zwald et al., 2010], though the mechanism remains unclear. Furthermore, the observation that skin cancers tend to emerge to a greater extent on skin exposed to glass-penetrating UVA wavelengths of light may point to a role for UVA in skin carcinogenesis in organ transplant patients [Atkar et al., 2013].

1.4. UVA and melanoma in animal models

Though UVB wavelengths of light induce both melanoma and non-melanoma skin cancers in various experimental model systems, there has been some controversy regarding the role of UVA alone in causing melanoma. An early study using the *Xiphophorus* hybrid fish model suggested that UVA could cause melanoma [Setlow et al., 1993]. However, this finding was not supported by a follow-up study [Mitchell et al., 2010]. Similarly, though high dose exposure to UVA was thought to induce focal melanocytic hyperplasia in an opossum model of melanoma [Ley, 2001], the effect was found to be much weaker with UVA than with UVB [Robinson et al., 2000]. Moreover, additional studies in mice have shown that although UVA can induce squamous cell carcinoma (SCC), it was unable to directly induce melanoma [de Laat et al., 1997]. Thus, the general consensus from these model systems has been that UVA alone is not able to directly cause melanoma [Robinson et al., 2000; De Fabo et al., 2004; Mitchell and Fernandez, 2012].

However, there are significant differences between the skin of humans and these other model organisms that may impact melanoma susceptibility. In the skin of most animals, melanocytes are restricted to the hair follicle, which is not the case in human skin. The development and use of the hepatocyte growth factor/scatter factor (HGF/SF) transgenic mouse [Takayama et al., 1996; Noonan et al., 2003], which has extra-follicular melanocytes in skin and therefore more closely mimics human skin, has become a useful mouse model of UV-induced melanomagenesis [Recio et al., 2002; De Fabo et al., 2004; Noonan et al., 2001]. Interestingly, a single high dose UVA exposure of neonatal HGF/SF mice (in black C57BL/6 background) was shown to induce the formation of melanoma tumors [Noonan et al., 2012]. However, the same mice in an FVB albino background (which lack the pigment melanin) do not form melanoma after UVA exposure [De Fabo et al., 2004; Noonan et al., 2012]. These findings revealed that UVA may be promoting melanomagenesis in a melanin-dependent manner [Zaidi et al., 2012], which is surprising given that melanin has traditionally been thought to be protective for skin carcinogenesis [Tadokoro et al., 2005]. Furthermore, an elevation in staining for highly mutagenic 8-oxo-guanine (8-oxoG) DNA adducts, which are normally efficiently repaired, was reported in the skin of the UVA-irradiated C57BL/6-HGF mice in comparison to the FVB-HGF mice [Noonan et al., 2012]. Because these adducts represent the major lesion formed in DNA in response to oxidative stress, the authors suggested that these DNA lesions may be responsible for the mutagenesis that drives melanomagenesis. However, recent research showing a UVA- and melanin-dependent mechanism for the induction of non-oxidative, canonical bipyrimidine UV photoproducts [Premi et al., 2015] to be described below has called into question this

interpretation. Nonetheless, these findings show that UVA alone can induce melanoma formation in an experimental mouse model.

1.5. Sunscreens, UVA, and melanoma

Previous studies have suggested that sunscreens provide little to no benefit against melanoma because the sunscreens may be primarily devised to prevent sunburns that are mainly caused by UVB [Autier et al., 1995; Autier et al., 2011a]. It has been proposed that the use of sunscreens that contain only UVB filters may therefore result in greater UVA exposure because the use of the sunscreen allows individuals to remain in the sun for longer periods of time without being burned. This hypothesis, and the current lack of effective UVA filters in many countries including the U.S. [Sargent and Travers, 2016], may provide a cogent explanation for why sunscreen users may experience an elevated risk of melanoma [Autier et al., 2011b; Autier et al., 2011a]. On the other hand, some studies suggest that broad spectrum sunscreens and their long-term monitoring may help to reduce the risk of melanoma [Gallagher et al., 2000]. For example, a long-term Australian study found that sunscreens that contain UVA filters appears to provide protection against malignant melanoma [Green et al., 2011]. Thus, in human patients, limiting the exposure to UVA may help to prevent the development of melanoma.

2. UVA radiation and the DNA damage response

2.1. UVA radiation and the formation of DNA damage

Nucleic acids, proteins, and lipids are all capable of absorbing UV wavelengths of light and thus likely contribute to varying degrees to cutaneous melanomagenesis [Pfeifer and Besaratinia, 2012]. Nonetheless, DNA damage by UVR is the most widely studied and best understood process and will therefore be the primary focus of this review. A variety of forms of DNA damage can be induced by UVR, including bipyrimidine dimers, oxidized bases, protein-DNA crosslinks, and cycloaddition reactions with breakdown products of lipid peroxides [Cadet et al., 2005; Cadet et al., 2015; Cadet et al., 2012]. Furthermore, hydroxyl radicals generated by photooxidative processes can attack DNA to generate single-strand breaks [Dedon, 2008], and double-strand breaks may form in response to aberrant DNA repair intermediates [Wakasugi et al., 2014; Kemp and Sancar, 2016] or as a consequence of replication fork breakage [Quinet et al., 2014; Iyer and Rhind, 2017; Toledo et al., 2013; Elvers et al., 2011; Kaufmann, 2010; Dúngrawala et al., 2015]. Given their relative abundance and the degree to which the lesions have been studied in the context of melanoma, bipyrimidine dimers and oxidized purines will primarily be addressed here. A summary of the major lesions and their mechanisms of repair in human cells is provided in Table 2.

The direct absorption of UV photons of light by DNA induces the formation of photoproducts in genomic DNA, which include cyclobutane pyrimidine dimers (CPDs), pyrimidine (6-4) pyrimidone photoproducts (6-4)PPs, and Dewar isomers [Cadet et al., 2005; Cadet et al., 2015; Cadet et al., 2012]. These photoproducts form between adjacent pyrimidine nucleotides in DNA and include the most commonly recognized “thymine dimers”. In CPDs, a cyclobutane ring forms between the 5,6 bonds of the two pyrimidine

bases. In (6-4)PPs, a stable single bond forms between position 6 and 4 of the two adjacent bases, and upon further irradiation at wavelengths around and above 320 nm, these photoproducts can isomerize to form the Dewar photoproduct [Perdiz et al., 2000; Douki et al., 2003; Douki and Sage, 2016; Douki, 2016]. A variety of factors affect where these photoproducts form in the genome, including DNA sequence context, chromatin architecture, and transcription factor binding [Hu et al., 2017; Bryan et al., 2014; Mao et al., 2016; Sabarinathan et al., 2016; Perera et al., 2016; Poulos et al., 2016; Hu and Adar, 2017]. Thus, the biological consequences of UVR are dependent on not only the amount of UVR absorbed by DNA but also on the distribution and localization of lesions across the genome.

The formation of these UV photoproducts is dependent on the energy of the UV photons, and hence longer wavelengths of UVA are much less able to induce these photoproducts than UVC and UVB. Nonetheless, biologically relevant doses of UVA have been shown to induce CPD formation in both keratinocytes and melanocytes in human skin [Freeman et al., 1989; Young et al., 1998; Mouret et al., 2006]. Moreover, UVA can also facilitate the isomerization of UVB-induced (6-4)PPs into Dewar isomers [Cadet et al., 2005; Douki and Sage, 2016]. Thus, UVA has direct effects on DNA damage formation throughout the genome and may also modulate photoproducts that form in DNA from UVB photons. However, UVA has also long been recognized for its indirect effects on DNA damage formation through the excitation of various cellular photosensitizers, such as flavin, melanin, riboflavin, and porphyrins [Wondrak et al., 2006; Premi et al., 2015]. Along with UVA, these agents result in the production of reactive oxygen species (ROS) that can attack DNA to form single-strand breaks, oxidized pyrimidines, and oxidize purines, of which 7,8-dihydro-8-oxoguanine (8-oxoG) lesions are the most prevalent [Cadet et al., 2005; Cadet et al., 2012]. Though there has been debate about the relative contribution of oxidative stress-induced lesions versus bipyrimidine dimers by UVA on mutagenesis and carcinogenesis, a quantitative HPLC/mass spectrometry study showed that lesions associated with oxidative stress are not the major form of DNA damage induced by UVA in mammalian cells [Douki et al., 2003]. Rather, this study showed that UVA induces CPDs, 8-oxoG, oxidized pyrimidines, and single-strand breaks at a ratio of 10:3:1:1 [Douki et al., 2003; Courdavault et al., 2004]. Thus, CPDs likely represent the most abundant form of DNA damage induced in human skin by UVA wavelengths of light [Mouret et al., 2006]. Interestingly, this situation is slightly different in melanocytes, which exhibit a somewhat higher production of 8-oxoG upon UVA irradiation than keratinocytes [Mouret et al., 2012]. This elevation in 8-oxoG formation may be due in part to the additional ROS that melanocytes are exposed to during the biochemical synthesis of melanin [Denat et al., 2014]. Thus, UVA-induced oxidative stress may play a larger role in melanocyte cancers than keratinocyte cancers.

UVR rapidly induces CPD formation on a timescale of picoseconds, and for decades this process was the only known mechanism by which UVR generates CPDs in DNA. Interestingly, a recent report from Brash and colleagues described an unusual chemical process termed chemiexcitation in which UVA and UVB wavelengths of light can induce CPDs in DNA even hours after UV exposure [Premi et al., 2015; Premi and Brash, 2016] (Figure 1). This “dark CPD” process is particularly relevant to melanocytes and melanoma because it involves the pigment melanin. The exposure of cells to UVR causes the generation of nitric oxide and superoxide through the upregulation of the enzymes iNOS,

NADPH oxidase, and enzymes involved in melanin synthesis. The nitric oxide and superoxide can react to form the oxidant peroxyxynitrite, which is able to degrade polymers of melanin into monomers capable of entering the nucleus. Peroxyxynitrite is also capable of exciting an electron to a triplet state, including within fragments of melanin, to produce an unstable and high energy dioxetane capable of reacting with DNA bases to produce CPDs. This report suggested that the production of dark CPDs is dependent on UVR-mediated ROS (reactive oxygen species) because the use of ROS scavengers, such as vitamin E, resulted in less dark CPD formation. Quantitative analyses of CPD formation in UVA-irradiated melanocytes revealed that more than half of all CPDs may arise after the UV exposure ends. Thus, this chemiexcitation mechanism for CPD formation may be responsible for most of the DNA damage and mutagenic events in UV-irradiated melanocytes and may therefore contribute to melanoma development. These findings may also explain the previous observation that the pigment melanin is apparently required for UVA- but not UVB-induced melanoma induction in the HGF/SF mouse [Noonan et al., 2012]. Interestingly, these dark CPDs were found to be more prominent in melanocytes containing pheomelanin, suggesting that pheomelanin is not only a poorer shield against initial direct CPD formation but is also more prone to form dark CPDs via chemiexcitation. Because much of the work on this novel mode of CPD induction was carried out using mouse skin cells [Premi et al., 2015], it will be important to confirm these findings in human skin.

2.2. DNA damage and mutagenesis

Both bipyrimidine dimers and oxidative photolesions induced by UVR are potentially mutagenic if not repaired, and therefore both forms of damage may be carcinogenic. Whereas cytosine bases are generally quite stable and only slowly undergo spontaneous deamination to form uracil (half-life of 30,000 years) [Frederico et al., 1990], cytosines within CPDs are much less stable (half-life of 2–100 hours) [Barak et al., 1995; Peng and Shaw, 1996; Burger et al., 2003; Tu et al., 1998]. When accurately copied by a DNA polymerase, the replication of these uracils leads to the fixation of C→T/G→A transitions in the DNA. These so-called “UV signature” mutations were first observed in 1964 [Howard and Tessman, 1964] in viral DNA and have since been observed in both naked DNA and DNA isolated from cultured cells and skin following UV exposure and in skin cancers [Brash, 2015; Brash et al., 1991; Sage et al., 2012]. Indeed, of relevance to melanoma, deep DNA sequencing of both gene promoters and exons has revealed a vast preponderance of C→T somatic mutations at bipyrimidines in sun-exposed melanomas [Hodis et al., 2012; Berger et al., 2012; Colebatch et al., 2016; Zhang et al., 2016]. These results have led to the identification of novel melanoma oncogenes and tumor suppressor genes [Krauthammer et al., 2012; Berger et al., 2012] and to the implication that alterations to gene regulatory elements, including in the telomerase (TERT) gene promoter [Lu et al., 2015; Griewank et al., 2014], likely contribute to melanomagenesis.

In addition to bipyrimidine dimers, oxidized bases, such as 8-oxoG, also form in DNA following UV exposure [Cadet et al., 2005; Cadet et al., 2012]. These ROS-dependent DNA lesions are known to generate G→T transversions through mispairing of the oxidized guanine with adenine instead of cytosine [Cooke et al., 2003; Shibutani et al., 1991]. Moreover, oxidation of dNTP pools can result in the misincorporation of 8-oxo-guanine

nucleotide triphosphates into DNA opposite adenines during DNA synthesis to induce T→G mutations [Kamath-Loeb et al., 1997; Drobetsky et al., 1995] that may impact cell fate [Rai, 2010]. The importance of these mutagenic lesions to UVA-induced mutagenesis in skin is unclear however, as 8-oxoGs have been reported to contribute to only 6% of the total UVA mutation spectrum in mouse skin [Ikehata et al., 2008]. Thus, the relatively low level of G→T and T→G changes in melanoma genomic DNA [Hodis et al., 2012; Krauthammer et al., 2012] is consistent with a minor role of these oxidized bases in inducing skin tumors.

In addition to the base adducts described above, strand breaks can also be generated in genomic DNA following UV exposure (Table 2). Single-strand breaks involve the hydrolysis of the phosphodiester backbone in only one strand of DNA and hence are thought to be relatively easy to fix by simple re-ligation via single-strand break repair (SSBR). However, rare, unrepaired single-strand breaks (SSBs) are potentially problematic because an encountering RNA or DNA polymerase can lead to double-strand break (DSB) formation. DSBs breaks are particularly detrimental to cells, and when not lethal, may lead to chromosomal rearrangements that characterize cancer cell genomes [Hanahan and Weinberg, 2011; Bastian et al., 1998; Bauer, 2017]. Precisely how UVR induces double-strand breaks remains unclear. Bipyrimidine dimers are thought to be of greater concern than oxidized bases because they more severely block the progression of canonical replicative DNA polymerases. Thus, the stalling of replicative polymerases at such lesions can lead to the collapse of the replication fork and therefore to DSBs that must be repaired by homologous recombination [Dungrawala et al., 2015; Toledo et al., 2013; Iyer and Rhind, 2017; Quinet et al., 2014; Elvers et al., 2011; Kaufmann, 2010]. However, even in non-replicating cells, there are mechanisms that lead to DSB formation following UV exposure. For example, studies have shown that both DNA DSBs and the activation of DSB break-associated kinase signaling can be observed to take place in a manner dependent on the removal of the UV photoproduct by the nucleotide excision repair machinery [Wakasugi et al., 2014; Kemp and Sancar, 2016]. Depending on the mode of DSB repair, this repair may also introduce mutations or deletions into genomic DNA. Thus, in some circumstances, the repair of a canonical UV bipyrimidine lesion may lead to the aberrant formation of even more problematic DNA lesions.

2.3. Repair of UV-induced DNA damage

Several distinct DNA repair machineries (summarized in Figure 2) are responsible for fixing the DNA damage that is induced by UVR. The repair of bipyrimidine dimers and oxidized guanines in genomic DNA involves two different excision repair pathways that essentially involve the removal, or “excision”, of the damage from the DNA, by either nucleotide excision repair (NER) or base excision repair (BER). The major repair system of importance to UVR and melanoma is nucleotide excision repair (NER), which is a versatile system for removing a wide variety of lesions from DNA, including UV-induced CPDs and (6-4)PPs [Reardon and Sancar, 2005; Scharer, 2013]. In nucleotide excision repair, the lesion is recognized by one of two sub-pathways of NER. In the global genomic NER pathway (GG-NER), XPC (xeroderma pigmentosum group C) assists in the recognition of the lesion and then recruits additional proteins (RPA, replication protein A; TFIIH, transcription factor II-H; and XPA) to unwind the DNA around the lesion so that two nucleases (XPG and XPF)

can make incisions at sites bracketing the lesion to release the damage in the form of a small (~30-nt-long), TFIIH-bound DNA oligonucleotide [Hu et al., 2013; Kemp and Sancar, 2012; Huang et al., 1992; Kemp et al., 2012; Kemp et al., 2014; Choi et al., 2014]. Though not essential for damage recognition or removal in vitro, the product of the XP-E gene, DDB2, may aid in the recognition of UV photoproducts along with XPC [Tang and Chu, 2002; Sugasawa, 2010; Ruthemann et al., 2016]. In transcription-coupled NER (TC-NER), the stalling of RNA polymerase II at the UV photoproduct is recognized by the Cockayne Syndrome (CS) proteins, which ultimately facilitates the recruitment of the other core repair proteins that unwind and incise the DNA. Regardless of the mode of damage recognition, once the damaged oligonucleotide has been removed, the gap that remains in the duplex is then filled in by a DNA polymerase and the remaining nick sealed. The importance of NER to human disease [Marteijn et al., 2014; Cleaver et al., 2009], including UV-induced melanoma, can be observed in patients with the disease xeroderma pigmentosum (XP) [Cleaver, 1968], who have a mutation in one of seven different “XP” genes that prevents NER and elevates melanoma and non-melanoma skin cancer risk by several thousand-fold [Kraemer et al., 1994; Lambert et al., 1995].

The BER pathway is initiated by the action of a glycosylase that removes the damaged nitrogenous base [Boiteux et al., 2017; Baute and Depicker, 2008; Liu and Wilson, 2012]. In the case of 8-oxoG, this is typically carried out by the action of the enzyme 8-oxo-guanine DNA glycosylase (OGG1) [Boiteux et al., 2017]. The loss of OGG1 in mice has been shown to increase the susceptibility to UVB-induced skin cancers [Kunisada et al., 2005]. Glycosylase action generates an apurinic (AP) site in the DNA that is cleaved at the 5' side by the action of AP endonuclease 1 (APE1). To complete repair, DNA polymerase beta (Pol β) removes the 5'-deoxyribose and extends 1 nucleotide from the 3'-hydroxyl. In some cases, the replicative polymerases (pols δ and ϵ) extend 2–12 nucleotides using the intact strand as template. Regardless of the use of either the short or long patch repair mechanisms, a DNA ligase regenerates an intact phosphodiester backbone to restore the DNA duplex.

Because single-strand breaks (SSBs) are an intermediate of BER, the repair of SSBs generated via other means also utilizes some of the same cellular proteins [Abbotts and Wilson, 2017]. DSB repair is more complicated and is affected by several factors, including cell cycle status [Hustedt and Durocher, 2016], such that homologous recombination (HR) is favored during S phase when a homologous DNA template is available for repair. Non-homologous end joining (NHEJ) is the more dominant pathway for repairing double-strand breaks in human cells and involves essentially re-ligating the two broken ends of the DNA back together [Chang et al., 2017]. NHEJ is generally thought to be more mutagenic than HR because nucleolytic processing and error-prone polymerase function at DSB ends may lead to the loss of, or changes to, the genetic information. Nonetheless, the observation that melanomas frequently contain chromosomal translocations [Bastian et al., 1998; Kaufmann et al., 2014] suggests that DSB formation and aberrant repair take place during melanomagenesis.

2.4. UV DNA damage kinase signaling

In addition to direct DNA repair, human cells also possess various kinase-based cell signaling pathways that regulate the cellular response to UV. Classically known as DNA damage checkpoints because of their role in transiently arresting cell cycle progression to allow more time for repair [Sancar et al., 2004; Ciccia and Elledge, 2010; Abraham, 2004], many studies have subsequently revealed numerous functions for these “checkpoint” pathways, including the direct regulation of DNA repair systems, DNA replication, and apoptosis. These pathways are governed by a family of phosphoinositide kinase-like protein kinases (PIKKs) known as ATR, ATM, and DNA-PK [Abraham, 2004; Blackford and Jackson, 2017] that initiate signaling in response to specific DNA damage signals. A schematic of these pathways and their stimuli are shown in Figure 3, and importantly, all three DNA damage kinases have been shown to be activated and to affect cell fate in cells irradiated with UV.

The ATR kinase is traditionally considered to be the major PIKK that is activated following exposure to UVR and primarily within the context of replication stress caused by DNA polymerase stalling at UV photoproducts [Sancar et al., 2004; Cimprich and Cortez, 2008; Nam and Cortez, 2011]. This polymerase stalling uncouples the actions of the replicative DNA helicase from that of the DNA polymerase [Byun et al., 2005] and generates long stretches of single-stranded DNA (ssDNA), which then becomes bound by RPA (the major ssDNA-binding protein in human cells) [Wold, 1997; Fanning et al., 2006; Zou et al., 2006]. RPA-coated ssDNA is thought to be the initial signal that then recruits ATR to the stalled replication fork via a specific interaction with the ATR-interacting protein ATRIP [Zou and Elledge, 2003; Cortez et al., 2001]. However, a number of studies have provided evidence for ATR activation in non-replicating cells as well, via ssDNA gaps generated by NER or APE1 [Vrouwe et al., 2011; Marini et al., 2006; Marti et al., 2006; Matsumoto et al., 2007; Hanasoge and Ljungman, 2007; O'Driscoll et al., 2003; Ray et al., 2016; Kemp et al., 2014] that may be enlarged by Exonuclease 1 [Lindsey-Boltz et al., 2014; Sertic et al., 2011; Giannattasio et al., 2010] or by stalled transcription complexes [Derheimer et al., 2007; Kemp and Sancar, 2016; Kemp, 2017]. Processing of BER intermediates by the enzyme APE2 has also been shown to lead to ATR activation [Willis et al., 2013]. Lastly, *in vitro* biochemical evidence support the notion that ATR and its activator protein TopBP1 may also directly sense UV photoproducts to activate ATR kinase activity independent of any further processing by DNA replication, transcription, or repair [Unsal-Kacmaz et al., 2002; Jiang and Sancar, 2006; Choi et al., 2007; Choi et al., 2009]. In addition to the diverse set of signals for ATR activation, the protein substrates that are targeted for phosphorylation by ATR are numerous and have generally been revealed to play important roles in regulating S phase progression [Cimprich and Cortez, 2008; Nam and Cortez, 2011], including stabilization of the replication fork [Dungrawala et al., 2015], repair of UV photoproducts during S phase events [Auclair et al., 2008], and control of translesion synthesis across UV photoproducts [Andrade-Lima et al., 2015; Gohler et al., 2011]. Nonetheless, recent reports also implicate ATR kinase signaling in the regulation of RNA splicing [Munoz et al., 2017] and in the induction of an apoptotic form of cell death in non-cycling UV-irradiated cells [Kemp and Sancar, 2016; Kemp, 2017].

The related kinase ATM is well-recognized for its activation in response to DNA DSBs, where it is recruited to DSBs by the Mre11-Nbs1-Rad50 (MRN) complex very soon after DSB formation to facilitate HR and delay cell cycle progression [Bakkenist and Kastan, 2004; Kitagawa and Kastan, 2005; Paull, 2015]. However, even in non-cycling cells where HR and cell cycle arrest are not relevant, ATM has been shown to be activated following UV irradiation via NER-dependent and -independent means [Kemp and Sancar, 2016; Tresini et al., 2015; Wakasugi et al., 2014] where it affects RNA splicing [Tresini et al., 2015] and proliferation after cell cycle re-entry [Wakasugi et al., 2014]. Moreover, ATM was shown to be directly activated by DNA containing bulky adducts [Kemp et al., 2011] and by oxidative stress through intermolecular disulfide formation [Paull, 2015; Guo et al., 2010]. Thus, ATM may be a direct sensor of not only DSBs but also reactive oxygen species and/or UV lesions in DNA, which is therefore important to consider in the context of UVA irradiation and melanoma. Proteomic studies have shown that ATM phosphorylates potentially hundreds of proteins in cells containing DNA damage [Matsuoka et al., 2007], including some that regulate mRNA splicing [Tresini et al., 2015]. Its activation in response to oxidative stress facilitates the autophagic degradation of peroxisomes [Zhang et al., 2015]. It should also be noted that there is extensive crosstalk and overlap between ATM and ATR function in cells containing DNA damage [Sancar et al., 2004; Ciccia and Elledge, 2010], and thus it can be difficult to define the particular kinase responsible for substrate phosphorylation following UV irradiation.

In contrast to ATR and ATM, DNA-PK is primarily thought to be activated in response to DSBs that are generated in DNA, and its functions are largely thought to be limited to DSB repair. DNA-PK kinase activity plays an essential role in NHEJ, where it is recruited by its Ku subunits to the breaks to phosphorylate itself and other NHEJ factors that promote DSB repair [Jette and Lees-Miller, 2015; Davis et al., 2014]. However, like ATR [Choi et al., 2007; Choi et al., 2009] and ATM [Kemp et al., 2011], DNA-PK can also be directly activated by bulky DNA adducts [Kemp et al., 2011] that are present in UV-irradiated cells. NHEJ and DNA-PK function are particularly important in non-replicating cells exposed to UV, where the loss of DNA-PK kinase activity results in elevated lethality [Kemp and Sancar, 2016].

3. Regulation of the DNA damage response: UVA and melanocytes

3.1. DNA repair and DNA damage responses in melanocytes and melanoma cells

Because of the importance of DNA repair and DNA damage signaling in the response to UV-induced DNA damage, there has been great interest in determining whether defects in cellular DNA damage responses contribute to melanomagenesis. Using an immunoslot blot method to measure CPD and (6-4)PP removal from genomic DNA, an initial study using UVC-irradiated primary melanocytes and a panel of melanoma cell lines found that both the normal cells and 11 of 12 cancer cell lines repaired the UV photoproducts at similar rates [Gaddameedhi et al., 2010]. However, a more recent study that employed a flow cytometric methodology to study UV photoproduct repair at different cell cycle phases reported that a majority of melanoma cell lines were defective in NER during S phase [Belanger et al., 2014]. This repair deficiency was correlated with a reduced activation of the ATR kinase and

may be explained by altered replicative stress responses caused by an insufficient supply of the protein RPA. Because of its numerous functions in DNA replication, NER, and ATR activation, RPA may become limiting for DNA metabolism under conditions of DNA damage and extensive replication stress [Belanger et al., 2016; Toledo et al., 2013; Guven et al., 2015; Kohler et al., 2016; Tsaalbi-Shtylik et al., 2014]. Interestingly, this finding was supported by additional studies using UVA or UVB light sources (instead of UVC), in which melanoma cells showed a reduced ability to remove UV-induced CPDs from genomic DNA in comparison to normal melanocytes [Murray et al., 2016; Budden et al., 2016]. These latter studies reported the defect to be specific for GG-NER and to involve the reduced expression of the damage sensor protein XPC. Thus, the initiation and/or progression of melanoma may be due in part to an inability to efficiently remove CPDs from genomic DNA.

Another possible factor that may affect how melanocytes recognize and respond to UVR-induced DNA damage is the presence of melanin. Melanin can absorb sunlight and scavenge free radicals, and thus it is generally thought to shield cells from the damaging effects of UVR [Bustamante et al., 1993]. However, the level of reactive oxygen species in melanocytes is likely affected by both the ability of melanin to both scavenge ROS and to inadvertently promote ROS generation [Kipp and Young, 1999; Kvam and Tyrrell, 1999; Kvam and Dahle, 2004]. Using host-cell reactivation assays to monitor the repair of luciferase reporter plasmid DNAs damaged with either hydrogen peroxide or UVC, which yielded oxidative or canonical bipyrimidine UV photoproducts, respectively, one study found that the repair of both types of DNA damage was impaired in pigmented melanocytes in comparison to non-pigmented fibroblasts [Wang et al., 2010]. Using in vitro assays that measured repair protein incision or DNA repair synthesis on DNA templates damaged with UVC or H₂O₂ and incubated in cell-free extracts, the authors went on to show that melanocyte cell-free extracts were partially defective in DNA repair and repair synthesis and that addition of melanin to fibroblast cell-free extract inhibited the repair events. The inhibition of UV photoproduct removal by melanin was supported by another group that used a defined UV photoproduct-containing DNA substrate and cell-free extract in vitro [Gaddameedhi et al., 2010]. However, the authors noted that this inhibition of DNA repair by melanin was non-specific, as melanin also inhibited the ability of bacterial restriction endonucleases to cut DNA at their relevant target sequences. Thus, though melanin may be problematic under certain circumstances, the localization of melanin to cellular compartments outside the nucleus and away from DNA would be expected to limit this form of repair inhibition.

Effective arrest of the cell cycle following DNA damage induction is thought to be important for avoiding mutagenesis and genomic instability by preventing cells with damaged DNA from entering either S phase (where base lesions may be copied in an error-prone manner) or mitosis (where DNA breaks may lead to the loss of genetic information). Thus, G1 and G2 checkpoint responses, which are controlled by the ATR and ATM DNA damage response kinases, may serve as important barriers to tumorigenesis, including in melanoma. Interestingly, a majority of melanoma cell lines were found to display defects in one or both checkpoints following exposure to ionizing radiation [Kaufmann et al., 2008; Carson et al., 2012]. An additional study found a defective G2 checkpoint response to ssDNA gaps produced during the bypass of unrepaired UV photoproducts by the replication fork in

melanoma cells [Wigan et al., 2012]. However, the S-phase checkpoint, which inhibits the firing of new replication origins following DNA damage and likely similarly functions to limit mutagenesis [Ciccia and Elledge, 2010; Sancar et al., 2004; Iyer and Rhind, 2017; Kaufmann, 2010], was found to be normal in UVC-irradiated melanoma cell lines [Cordeiro-Stone et al., 2016]. A recent report further identified a defect in the ATM-dependent cell cycle checkpoint in melanoma cells that was caused by overexpression of PLK1, which negatively regulates ATM signaling [Spoerri et al., 2016]. Because missense mutations in ATR and ATM have been reported in some melanomas [Dombernowsky et al., 2008; Chen et al., 2017], aberrant signaling by mutant kinases may further contribute to melanomagenesis.

3.2. UVA-dependent oxidation of DNA repair proteins

The observation that NER-deficient XP cells are extremely sensitive to UVC and UVB but are not hypersensitive to UVA [Keyse et al., 1983] has indicated that the biological effects of UVA may lay beyond its direct effects in inducing DNA damage. Moreover, CPDs induced by UVA in NER-proficient cells have been reported to take longer to be repaired than CPDs induced by UVB or UVC [Courdavault et al., 2004; Mouret et al., 2006], and indeed CPDs induced by UVB or UVC are moderately less toxic and mutagenic than CPDs induced by UVA [Enninga et al., 1986; Biverstal et al., 2008; Kappes et al., 2006; Runger et al., 2012]. Thus, the biological effects of UVA are likely influenced by it having additional cellular targets, potentially through the well-known induction of reactive oxygen species.

In both bacterial and human cells, exposure to UVA prior to irradiation with UVC or UVB results in increased cell lethality and a slower removal of canonical UV photoproducts [Tyrrell and Webb, 1973; Tyrrell et al., 1984; Smith and Paterson, 1982]. More recently, this phenomenon has been linked to UVA-dependent damage to DNA repair proteins, either alone or in conjunction with photosensitizing drugs [Brem et al., 2017; Karran and Brem, 2016]. A summary of DNA repair proteins that have been reported to undergo oxidation by either UVA or other mechanisms is provided in Table 3, which includes proteins involved in NER [Guyen et al., 2015; Wang et al., 2001; Gueranger et al., 2014; Men et al., 2007; You et al., 2000; Montaner et al., 2007; Kelley et al., 2012; Xanthoudakis et al., 1992; Xanthoudakis and Curran, 1996; Xanthoudakis et al., 1994; Bennett et al., 2009; Andrews et al., 2006; Grosskopf et al., 2010; Zhou et al., 2015; Zhou et al., 2011; Wang et al., 2013; Bravard et al., 2006; Bravard et al., 2010; Morreall et al., 2015; Campalans et al., 2007; Girard et al., 2013; Fribourg et al., 2000; Ding et al., 2009], BER [Guyen et al., 2015; Wang et al., 2001; Gueranger et al., 2014; Men et al., 2007; You et al., 2000; Montaner et al., 2007; Kelley et al., 2012; Xanthoudakis et al., 1992; Xanthoudakis and Curran, 1996; Xanthoudakis et al., 1994; Bennett et al., 2009; Andrews et al., 2006; Grosskopf et al., 2010; Zhou et al., 2015; Zhou et al., 2011; Wang et al., 2013; Bravard et al., 2006; Bravard et al., 2010; Morreall et al., 2015; Campalans et al., 2007; Girard et al., 2013; Fribourg et al., 2000; Ding et al., 2009], and DSB repair [Guyen et al., 2015; Wang et al., 2001; Gueranger et al., 2014; Men et al., 2007; You et al., 2000; Montaner et al., 2007; Kelley et al., 2012; Xanthoudakis et al., 1992; Xanthoudakis and Curran, 1996; Xanthoudakis et al., 1994; Bennett et al., 2009; Andrews et al., 2006; Grosskopf et al., 2010; Zhou et al., 2015; Zhou et

al., 2011; Wang et al., 2013; Bravard et al., 2006; Bravard et al., 2010; Morreall et al., 2015; Campalans et al., 2007; Girard et al., 2013; Fribourg et al., 2000; Ding et al., 2009].

The level of oxidative stress in cells may be exacerbated when UVA interacts with endogenous or exogenous photosensitizers, including 6-thioguanine or fluoroquinolone antibiotics such as ciprofloxacin. Treatment of cultured cells with UVA and photosensitizers has been shown to lead to oxidation of RPA, OGG1, and Ku, and to be associated with inhibition of NER, BER, and NHEJ, respectively [Gueranger et al., 2014; Guven et al., 2015]. Interestingly, RPA plays a particularly important role in multiple aspects of DNA metabolism, including DNA repair, replication, and ATR-dependent DNA damage checkpoint signaling [Wold, 1997; Fanning et al., 2006; Zou et al., 2006]. The depletion of the available pool of RPA protein in cells containing DNA damage and undergoing replication stress has been reported to be responsible for DSB formation [Toledo et al., 2013], and overexpression of RPA partly protects cells from UVA-mediated oxidative stress [Guven et al., 2015]. Thus, several aspects of the cellular response to UV-induced DNA damage may be affected by UVA-dependent oxidation of a single protein, RPA. These issues may be acutely relevant to melanocytes and melanomagenesis because the presence of melanin may exacerbate the effects of UVA on ROS production.

3.3. Regulation of melanocyte DNA damage responses by hormonal signaling

Given that human skin contains diverse cell types in addition to melanocytes, including keratinocytes, fibroblasts, and immune cells, melanocyte responses to UVR are therefore expected to be influenced by interactions with these other cell types through both contact-dependent and -independent means. Research over the past few years has uncovered two major hormonal signaling pathways that act in a paracrine manner to influence melanocyte responses to UV-induced DNA damage [Jarrett and D'Orazio, 2017; Jarrett et al., 2017]. Moreover, additional regulatory systems that have been shown to govern keratinocyte responses to UV and non-melanoma skin cancer risk, including the insulin-like growth factor-1 pathway and the circadian clock, may also be relevant to understanding melanomagenesis and are therefore briefly summarized here. These four systems are outlined in Table 4. It should be noted that most of the work to be described utilized UVB and/or UVC light sources, and thus the role of UVA remains to be fully explored. Moreover, the use of solar simulating light sources that include both UVA and UVB wavelengths will therefore be ideal in future validation studies.

The first known regulatory pathway in melanocytes involves the melanocortin 1 receptor (MC1R), which is a G_s protein-coupled receptor that is present in the melanocyte cell membrane. It is stimulated by α -melanocyte stimulating hormone (α -MSH), which is produced and released by keratinocytes in a p53-dependent manner following UV exposure [Cui et al., 2007; Fell et al., 2014]. The stimulation of MC1R by extracellular α -MSH leads to its cytoplasmic association with adenylyl cyclase and to cAMP production [Garcia-Borron et al., 2014; Garcia-Borron and Olivares, 2014; Swope et al., 2012]. Though a major effector of this signaling is the stimulation of melanin production [Abdel-Malek et al., 2000; D'Orazio et al., 2006], several other important processes are impacted in melanocytes, including a suppression of oxidative stress [Kadekaro et al., 2003; Kadekaro et al., 2012],

the promotion of cell growth [Suzuki et al., 1999], and protection from apoptosis [McGill et al., 2002]. Of particular relevance to the DNA damage response, stimulation of the MC1R has also been shown in a number of studies to affect the efficiency of UV photoproduct removal [Abdel-Malek et al., 2009; Bohm et al., 2005; Hauser et al., 2006; Jarrett et al., 2014; Jarrett et al., 2015; Kadekaro et al., 2010; Song et al., 2009; Swope et al., 2014]. Moreover, recent work has uncovered a rapid response to MC1R signaling in which the activation of Protein Kinase A (PKA) by cAMP leads to the phosphorylation of the DNA damage response kinase ATR on Ser435, which facilitates the localization of XPA to sites of UV photodamage in the nucleus [Jarrett et al., 2014; Jarrett et al., 2016]. ATR is known to regulate NER through several mechanisms, including through the direct phosphorylation of XPA at a site that stabilizes the protein and limits its ubiquitin-mediated proteolysis [Park and Kang, 2016; Lee et al., 2014; Shell et al., 2009; Li et al., 2011; Li et al., 2013]. The MC1R-dependent and non-canonical ATR pathway was shown to facilitate an interaction of XPA with chromatin and to specifically promote the action of the NER endonuclease XPF to make the 5' incision during UV photoproduct removal, which thus promotes NER and limits mutagenesis [Jarrett et al., 2016]. Interestingly, these responses were shown to be defective in cells expressing polymorphic versions of the MC1R that are common to fair-skinned individuals [Valverde et al., 1995; Wolf Horrell et al., 2016], which suggests that the enhanced melanoma risk in fair-skinned individuals may be due in part to this defective MC1R-cAMP-PKA-ATR-XPA signaling pathway [Jarrett et al., 2017; Jarrett et al., 2016].

A second paracrine system that has been shown to regulate melanocyte responses to UV DNA damage is the endothelin signaling pathway. Endothelins are known to affect melanocyte proliferation and pigment production [Yada et al., 1991], and similar to α -MSH, are secreted by UV-irradiated keratinocytes [Imokawa et al., 1992; Yohn et al., 1993]. Endothelins activate the endothelin B receptor (ETBR) on melanocytes, where they regulate melanocyte proliferation, development, and pigmentation [Baynash et al., 1994; Hosoda et al., 1994; Tada et al., 2002]. Of specific relevance to UV irradiation, ETBR signaling has been shown to affect NER and apoptosis in UV-irradiated melanocytes [Kadekaro et al., 2005; von Koschembahr et al., 2015]. Treatment of cultured melanocytes in vitro with endothelin 1 (ET1) reduced UV photoproduct levels and facilitated the activation of the JNK and p38 signaling pathways in a calcium-dependent manner [von Koschembahr et al., 2015]. Facilitation of NER was further correlated with an enhanced turnover of the UV photoproduct damage recognition protein XPC at sites of DNA damage. Thus, the mechanism by which ETBR signaling facilitated NER appears to be distinct from that of MC1R signaling.

Whereas the effect of the MC1R and ETBR pathways on UV responses have been specifically examined in melanocytes and are therefore directly relevant to melanomagenesis, an additional factor that has been investigated in keratinocytes in the context of non-melanoma skin cancer is the insulin-like growth factor-1 (IGF-1) system [Kemp et al., 2017b; Lewis et al., 2009]. In human skin, IGF-1 is primarily supplied to epidermal keratinocytes by dermal fibroblasts [Ando and Jensen, 1993; Barreca et al., 1992; Siddle, 2011], and this production is decreased in the skin of geriatric individuals and is correlated with increased fibroblast senescence [Lewis et al., 2008; Lewis et al., 2010]. In cultured keratinocytes in vitro and basal epidermal skin keratinocytes in vivo, the loss of

IGF-1 receptor (IGF-1R) signaling slows CPD removal [Loesch et al., 2016; Fernandez et al., 2015] and partially abrogates canonical ATR signaling and the suppression of DNA synthesis following UVB exposure [Fernandez et al., 2015; Kemp et al., 2017a]. The association of these defective DNA damage responses with reduced IGF-1 signaling and advanced age may explain the observation that the majority of non-melanoma skin cancers occur in individuals over the age of 60 [Kraemer, 1997]. Though the correlation between patient age and melanoma is much weaker than for non-melanoma skin cancers [Fears et al., 1977; Armstrong and Cust, 2017], the fact that melanocytes express the IGF-1R [Hodak et al., 1996; Rodeck et al., 1987] and the observation that the number of mutations found in melanomas increases with advanced age [Krauthammer et al., 2012] would be consistent with a role for aging and/or the IGF-1 system in the regulation of the DNA damage response in melanocytes. Moreover, because MSH production by UV-irradiated keratinocytes is dependent on p53 [Cui et al., 2007; Fell et al., 2014], and p53 activation has been shown to be disrupted in UVB-irradiated keratinocytes with inactive IGF-1Rs [Lewis et al., 2008], it is possible that altered p53 signaling in IGF-1R-deficient keratinocytes negatively affects MC1R signaling in melanocytes. However, the reported reduction in melanocyte number in older people may serve to limit melanomagenesis in these patient populations by restricting the abundance of the cell type in the skin [Gilchrest et al., 1979]. Further work is therefore necessary to resolve this issue.

One final regulatory system that may influence melanomagenesis is the circadian clock, which controls diverse biochemical, physiological, and behavioral systems in humans and other organisms with a periodicity of approximately 24 h. At the organismal level in mammals, a master clock in the suprachiasmatic nucleus (SCN) in the brain receives external light cues via the optic nerve and then synchronizes peripheral clocks located in tissues throughout the body, including in the skin [Lin et al., 2009; Plikus et al., 2015; Matsui et al., 2016]. At the molecular level, the clock is regulated by a transcription-translation feedback loop that regulates gene expression throughout the course of a 24 h day [Takahashi, 2017] and in recent years has been shown to regulate the cellular response to DNA damage [Sancar et al., 2010; Sancar et al., 2015]. Using lymphocytes isolated from blood at different times of the day from human volunteers, the expression of the BER gene OGG1 was observed to be higher in the morning hours than in the evening hours, and thus lymphocytes accumulated less 8-oxoG at those time points when challenged with oxidative stress [Manzella et al., 2015]. Several studies in mice have investigated circadian regulation of the XPA gene, which is essential for the repair of UV-induced bipyrimidine dimers by the NER pathway. XPA mRNA and protein levels were observed to oscillate with a 24 h periodicity in mouse tissues (including skin), such that XPA mRNA and protein levels were found to be low in the morning and high in the evening [Kang et al., 2009; Kang et al., 2010; Kang et al., 2011; Gaddameedhi et al., 2011; Gaddameedhi et al., 2015; Geyfman et al., 2012; Wang et al., 2017]. This pattern of XPA expression was directly correlated with NER capacity throughout the day in these tissues [Kang et al., 2009; Gaddameedhi et al., 2011]. Moreover, UV skin carcinogenesis studies found that mice irradiated with UVB in the early morning were more susceptible to skin cancer formation, including invasive SCCs, than mice irradiated in the late afternoon/evening [Gaddameedhi et al., 2011]. Additional work also demonstrated that skin inflammation and erythema were similarly affected by the time

of day of UV exposure in mice and were correlated with both low XPA levels and with elevated ATR kinase signaling to its downstream substrates CHK1 and p53 [Gaddameedhi et al., 2015]. Preliminary studies using human skin biopsies indicates that the clock also regulates XPA protein levels in human skin [Guan et al., 2016]. Thus, the interplay between the circadian clock and the cellular DNA damage response likely has important implications for human skin diseases [Dakup and Gaddameedhi, 2017; Sancar et al., 2015]. Because melanocytes also exhibit circadian properties [Hardman et al., 2015; Sandu et al., 2012; Slominski et al., 2015], it is expected that the time of day of UV exposure and the associated level of XPA protein and DNA damage signaling may also impact the risk of melanomagenesis.

3.4. UVA and immunosuppression

The recognition and elimination of mutant, pre-cancerous cells by the body's immune system plays a major role in preventing cancers, including in the skin. UV has been known for decades to have immunosuppressive effects [Gonzalez Maglio et al., 2016; Prasad and Katiyar, 2017], and therefore immunosuppression is considered to be an important risk factor for melanoma. Indeed, organ transplant recipients taking immunosuppressive drugs have been reported to have higher rates of both melanoma and non-melanoma skin cancers [Kubica and Brewer, 2012]. Classical tumor studies in mice showed that whereas the transplantation of UV-induced skin tumors into syngeneic mice resulted in rejection of the tumors, the rejection did not take place if the recipient mice were exposed to UV light [Fisher and Kripke, 1977]. Later work went on to indicate that CPDs in DNA were specifically required to initiate system immunosuppression in the irradiated mice [Kripke et al., 1992]. For that reason, sunlight-induced immunosuppression may be a key factor that plays a role in the pathogenesis of the melanoma. Recent studies report that both UVA and UVB exert immunosuppressive effects [Damian et al., 1999; Damian et al., 2011; Matthews et al., 2010b; Matthews et al., 2010a; Hersey et al., 1987]. Sunscreen studies have confirmed that UVR-induced immune suppression can be prevented by using broad-spectrum sunscreens that provide UVA protection [Hersey et al., 1987]. Contact hypersensitivity studies provide the most compelling evidence of UVA-induced immunosuppression in humans. By using the nickel contact hypersensitivity test in human models, it was reported that there are immunosuppressive effects of UVA (370nm) at doses that corresponded to a 20 min exposure to mid-day summer sunlight [Damian et al., 2011].

The mechanism by which UVR induces immunosuppression remains unclear. Evidence has implicated UV-dependent damage to both lipids and DNA as contributing to the immunosuppression [Kripke et al., 1992; Damiani and Ullrich, 2016; Prasad and Katiyar, 2017]. Nonetheless, through the use of transgenic mice expressing bacterial photolyases that are capable of repairing UV-induced CPDs or (6-4)PPs in whole mouse skin or only the basal keratinocytes, one study showed that the presence of unrepaired CPDs in basal keratinocytes was responsible for systemic immunosuppression [Jans et al., 2006]. Moreover, complete loss of NER activity via mutation of XPA greatly enhances the likelihood of UV-induced systemic immunosuppression in mice [Garssen et al., 2000; Miyauchi-Hashimoto et al., 1996]. Additional studies using mice deficient in either GG-NER or TC-NER suggested that whereas a total NER defect is needed to increase systemic

immunosuppression, a loss of TC-NER is sufficient to enhance local immunosuppression [Kolgen et al., 2003]. Though many studies of immunosuppression have utilized UVB light sources to maximize damage to genomic DNA in epidermal cells, Ngheim and colleagues concluded that UVA (60 kJ/m² or higher) irradiation can also suppress the established immune response in mice [Nghiem et al., 2002]. Moreover, studies have also shown that the application of liposomes containing the bacterial T4N5 enzyme to target CPDs for repair blocked UVR-induced immune suppression [Nghiem et al., 2002; Ullrich et al., 2002; Yarosh, 2004], which further highlights the important role of canonical UV-induced bypyrimidine DNA photoproducts in immunosuppression.

Previous studies linking UV-induced DNA damage to immunosuppression have largely focused on DNA adduct levels and their repair. However, given the major roles for DNA damage kinase signaling in the cellular response to DNA damage described earlier, it is expected that there may be interplay between DNA damage signaling and immunosuppression [Neves-Costa and Moita, 2017]. Consistent with this hypothesis, a recent study uncovered a panel of human melanomas that contain mutations in the ATR kinase that abrogate its canonical signaling functions [Chen et al., 2017]. The loss of ATR function was found to be correlated with both the presence of multiple mutations and with alterations in inflammatory gene expression. A correlation of this phenotype with decreased T cell recruitment and elevated macrophage recruitment suggested that this loss of ATR signaling may facilitate tumor invasion. Thus, an altered immune microenvironment due to loss of UV-induced ATR kinase signaling in some developing melanomas may aid melanoma growth.

4. Summary and conclusions

Previously, there was a misconception that high intensity UVA from artificial tanning devices were safe and not associated with melanoma. However, more recent data from murine experimental studies, and human epidemiological and sunscreen use studies provide compelling evidence for a strong association between UVA and melanoma risk [Autier et al., 2011b; Autier et al., 2011a]. UVA is a complete carcinogen that may play key roles in both the initiation and promotion of melanoma. Consequently, reduced exposure to the sun and other UVA light sources should be employed to minimize the risk of melanomagenesis. Simple protective measures include the avoidance of direct sunlight during peak hours of the day by using hats, proper clothing and seeking shade. Moreover, because sunscreens have been shown to reduce DNA damage formation in UV-irradiated human skin [Olsen et al., 2017], the proper and long-term use of broad-spectrum sunscreens that contain both UVA and UVB filters should also be a part of the strategy to reduce the risk of the melanoma. There is also a clear need for the development of more effective UVA filters in sunscreens [Sargent and Travers, 2016]. Together, these approaches will be expected to limit the amount of unrepaired DNA damage induced by UVA and therefore the mutagenesis and immunosuppression that drive melanomagenesis.

The abundance of UV signature mutation in cutaneous melanomas highlights the relevance of UVR in melanomagenesis. However, the relative contributions of UVA and UVB wavelengths of light and the role of the melanocyte microenvironment in this process have

been enigmatic. Recent research has therefore uncovered novel ways in which UVA may both induce CPD formation in melanocyte DNA and impair the rate of UV photoproduct repair via oxidation of NER proteins. Moreover, alterations to the melanocyte microenvironment by paracrine factors and the immune system may further exacerbate these effects. Defects in DNA repair and the cellular DNA damage response to UVA are expected to ultimately give rise to gene mutations that drive the initiation and promotion of melanomas. Because many of the effects of UVA are thought to be due in great part to its ability to produce ROS, novel strategies should be considered to protect the skin against excessive UVA exposure as well and to ameliorate the effects of ROS generation. Nonetheless, further research is therefore required to provide a more complete understanding behind the pathogenesis of UVA-induced melanoma.

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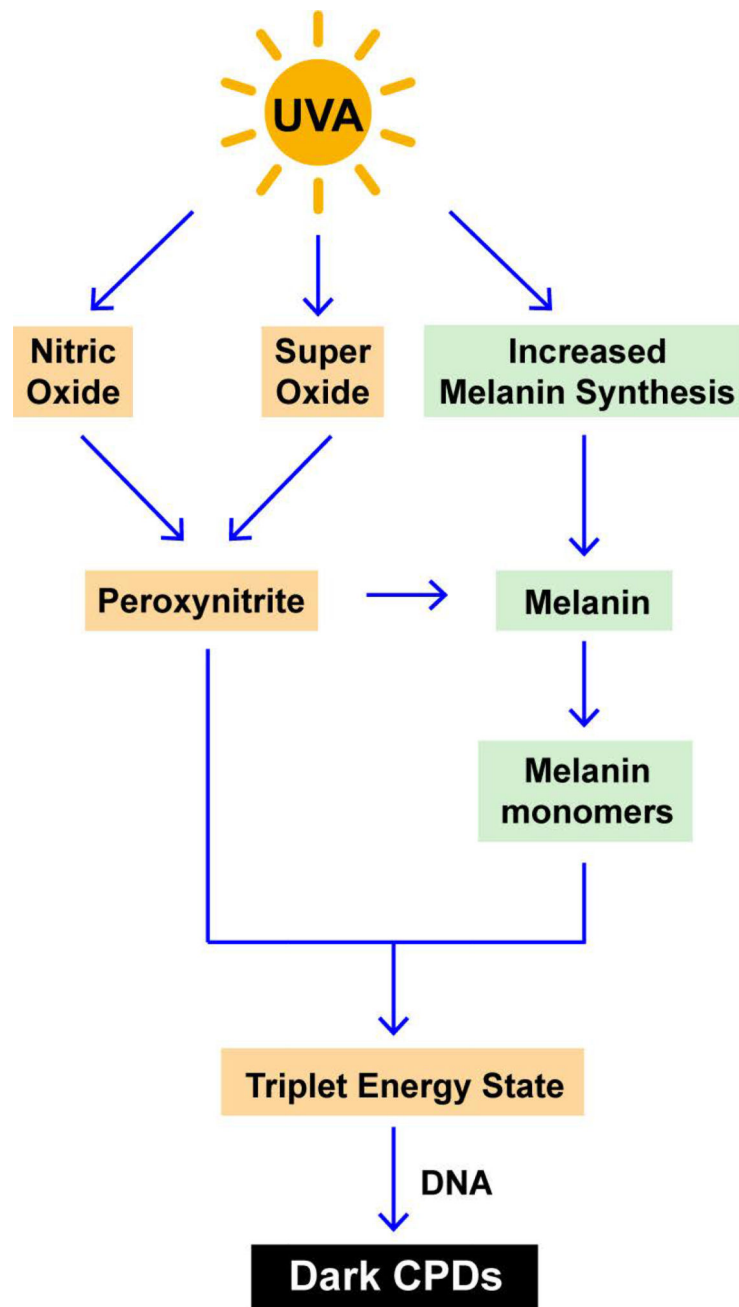


Figure 1. Schematic for the chemiexcitation mechanism of CPD formation by UVA and melanin UVA exposure from the sun or other sources leads to the generation of nitric oxide and superoxide within mammalian cells. These reactive species combine to form peroxyxynitrate, which can then act to degrade melanin (induced by UVA) into monomers and then act on fragments of melanin to produce an unstable but high energy (triplet state) dioxetane that reacts with DNA bases to form CPDs. These CPDs can form hours after UVA exposure and hence are referred to as “Dark CPDs”.

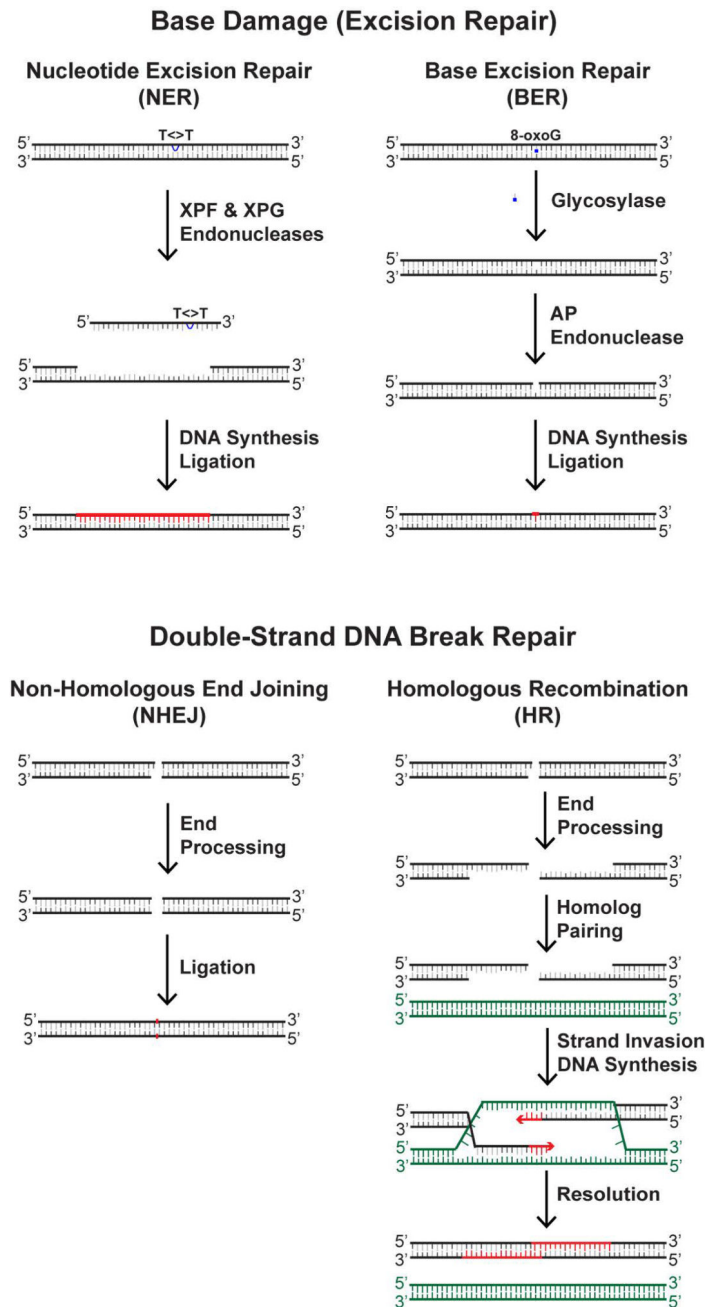


Figure 2. Schematics of major DNA repair systems that are utilized in UV-irradiated cells
 Nucleotide excision repair (NER) system is the major DNA repair pathway that is utilized in UV-irradiated cells because of the high number of bipyrimidine dimers induced by UVR and takes place via a dual incision mechanism (involving the XPF and XPG endonucleases) that removes bipyrimidine dimers (indicated by a thymine dimer T\leftrightarrowT) from DNA in form of a small (~30-nt-long) oligonucleotide. DNA synthesis and ligation complete the repair reaction to restore the duplex to its native state (indicated in red). Base excision repair (BER) is utilized to repair oxidized base damage (such as 8-oxo-guanine [8-oxoG] residues) in UV-irradiated cells. BER involves a glycosylase that first removes the damaged base from

the DNA before the action of AP Endonuclease, which incises the phosphodiester backbone 5' to the apurinic (AP) site. DNA synthesis and ligation then restore the duplex. DNA double-strand breaks also form in UV-irradiated cells and can be repaired by either non-homologous end-joining (NHEJ) or homologous recombination (HR). NHEJ simply involves re-ligating two broken ends to one another without significant end processing. In HR, more extensive end processing and end resection takes place, which allows for strand invasion and pairing to homologous DNA sequence elsewhere in the genome. DNA replication allow for missing sequence to be synthesized before resolution of the HR intermediate and restoration of the DNA duplex.

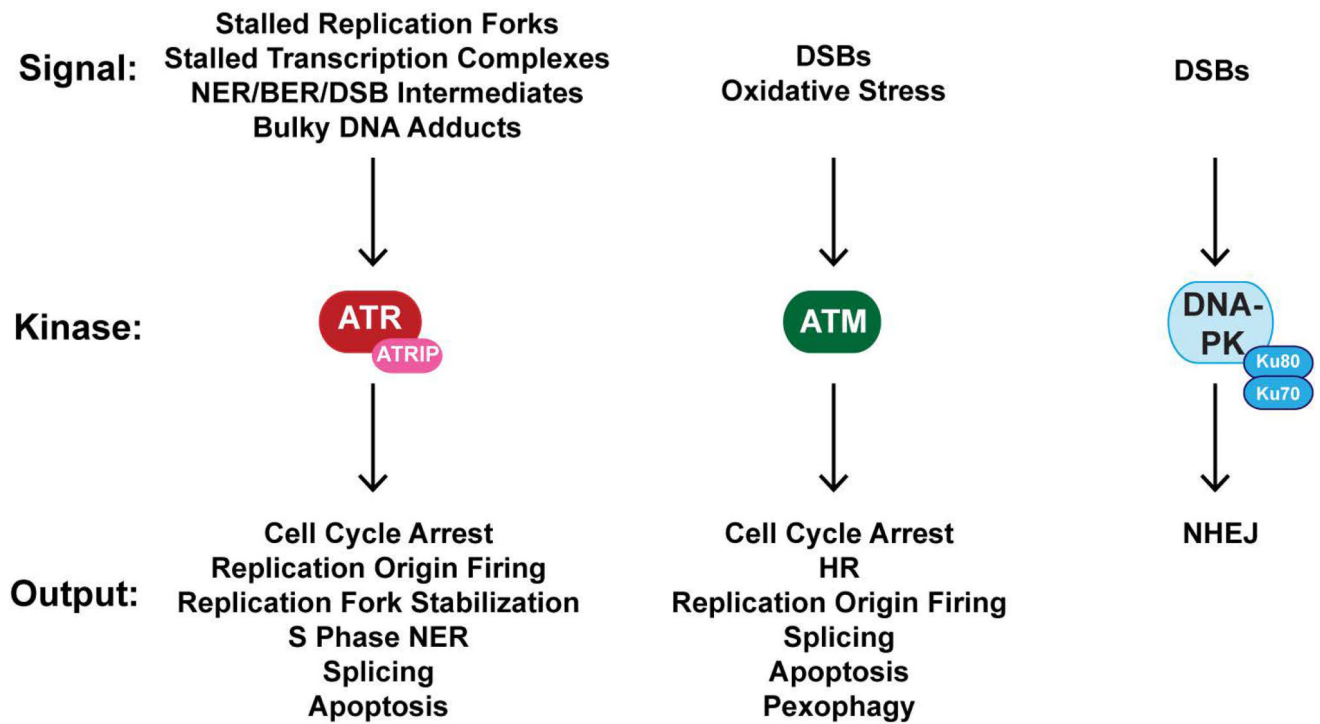


Figure 3. DNA damage response kinases activated in UV-irradiated cells

The ATR, ATM, and DNA-PK protein kinases play pivotal roles in responding to various DNA damage signals in UV-irradiated cells. These kinases then initiate various signaling responses that may result in several different outcomes in the cells, including DNA repair, cell cycle arrest, modulation of DNA replication dynamics, altered gene expression, and cell death.

Table 1
Properties of ultraviolet radiation (UVR)

The common properties of different wavelengths of UVR are provided.

Properties	UVC	UVB	UVA
Wavelength range	100–280 nm	280–320 nm	320–400 nm
% of UVR in terrestrial sunlight	completely blocked by ozone layer	2–10%	90–98%
Penetration through glass	Blocked	Blocked	Passes
Penetration through skin	Reaches top part of epidermis	Only penetrates epidermis	Epidermis and dermis

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Table 2
Forms of DNA damage induced by UVR

The major types of DNA damage induced by UVR are provided along with the principle mechanism of repair and common mutagenic effects.

Type of damage	Repair Mechanism	Mutagenic Effects
Bipyrimidine photoproducts CPDs (6-4)PPs Dewar Isomers	NER	C-to-T transitions Cytosine deamination Error-prone replication
Oxidized purines 8-oxoG	BER	G-to-T transversions
Single-strand breaks (SSBs)	SSBR	DSBs
Double-strand breaks (DSBs)	NHEJ HR	Chromosomal loss or translocations Insertions/deletions Error-prone replication

Table 3
DNA repair proteins reported to undergo oxidation

The indicated DNA repair proteins have been shown to undergo oxidation in mammalian cells. DNA metabolic processes and the functional effects of protein oxidation are provided along with references to the primary literature.

Protein	DNA Metabolic Processes	Effect of Protein Oxidation	References
RPA	NER ATR signaling Replication	Impairs ssDNA binding Inhibits NER	Guyen 2015; Wang 2001; Gueranger 2014; Men 2007; You 2000
PCNA	NER Replication	Unknown	Montaner 2007
APE1	BER Transcription	May block reducing activity towards transcription factors	Kelley 2012; Xanthoudakis 1992, 1994, 1996
Ku	NHEJ	Alters DNA binding Inhibits NHEJ	Gueranger 2014; Bennett 2009; Andrews 2006
XPA	NER	Diminishes DNA binding	Grosskopf 2010; Zhou 2011, 2015
XPE	NER	Reduced gene expression	Grosskop 2010
OGG1	BER	Decreases activity Inhibits 8-oxoG removal Localization to speckles	Gueranger 2014; Bravard 2006; Bravard 2010; Morreall 2015; Camplans 2007
XRCC3	HR	Chromatin re-localization Sensitivity to camptothecin	Girard 2013
TFIIH (p44)	NER	Unknown	Fribourg 2000
PARP	BER SSBR	Inhibits activity Interferes with BER	Zhou 2011, 2015; Wang 2013; Ding 2009
ATM	ATM signaling HR	Activates kinase activity Autophagy of peroxisomes	Guo 2010; Zhang 2015

Table 4
Paracrine regulatory systems that have been reported to affect the DNA damage response and/or skin carcinogenesis

The indicated paracrine system is listed along with known regulatory targets in the DNA damage response.

Regulatory System	Target(s)	References
Melanocortin/MC1R	NER (ATR and XPA)	Abdel-Malek 2009; Bohm 2005; Hauser 2006; Jarrett 2014, 2015; Kadekaro 2010; Song 2009; Swope 2014
Endothelin/ETBR	NER (XPC)	Hosoda 1994; Kadekaro 2005; von Koschembahr 2015
Insulin-like Growth Factor-1/IGF-1R	NER (XPC, XPB, XPF) ATR kinase signaling	Lewis 2010; Loesch 2016; Fernandez 2016; Kemp 2017
Circadian Clock	NER (XPA) BER (OGG1) ATR kinase signaling	Gaddemeedhi 2011, 2015; Geyfman 2012; Wang 2017; Guo 2016; Manzella 2015