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Removal of oxidatively generated DNA damage by overlapping repair pathways

Vladimir Shafirovich and **Nicholas E. Geacintov**

Chemistry Department and Radiation and Solid State Laboratory, 31 Washington Place, New York University, New York, New York 10003-5180

Abstract

It is generally believed that the mammalian nucleotide excision repair pathway removes DNA helix-distorting bulky DNA lesions, while small non-bulky lesions are repaired by base excision repair (BER). However, recent work demonstrates that the oxidativly generated guanine oxidation products, spiroimininodihydantoin (Sp), 5-guanidinohydantoin (Gh), and certain intrastrand crosslinked lesions, are good substrates of NER and BER pathways that compete with one another in human cell extracts. The oxidation of guanine by peroxynitrite is known to generate 5 guanidino-4-nitroimidazole (NIm) which is structurally similar to Gh, except that the 4-nitro group in NIm is replaced by a keto group in Gh. However, unlike Gh, NIm is an excellent substrate of BER, but not of NER. These and other related results are reviewed and discussed in this article.

Graphical Abstract

Keywords

Base excision repair; nucleotide excision repair; oxidative stress; DNA damage; reactive oxygen species

1. Introduction – oxidatively generated DNA damage is genotoxic

Environmental factors (infectious agents, asbestos, tobacco, UV light) are known to contribute to the development of chronic inflammation in human tissues [1, 2]. Reactive

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oxygen and nitrogen species (ROS and RNS, respectively) are overproduced at sites of chronic inflammation and induce persistent DNA damage that, if not properly repaired, can ultimately lead to the initiation and promotion of cell proliferation and cancer [3]. Epidemiological and clinical studies suggest that about 25% of all cancer cases worldwide are linked to chronic inflammation. Patients suffering from chronic inflammation are at a much higher risk of developing cancers [4]. A chronic imbalance between DNA damage and repair increases the risk of genomic instability, and it is therefore important to understand the mechanisms of the repair pathways that remove oxidatively generated DNA lesions from the genome. In this contribution, we consider some recent results that indicate that some of these DNA lesions can be excised by different overlapping repair pathways such as base excision, nucleotide incision, and nucleotide excision repair.

2. Mechanisms of DNA repair

2. 1. Base excision repair (BER)

The repair of oxidatively generated lesions is critical for maintaining genomic stability during oxidative stress [5]. Existing paradigms suggest that base excision repair (BER) mechanisms are responsible for the removal of non-bulky oxidatively generated DNA lesions [6]. The mechanisms of BER are highly conserved from bacteria to humans [7, 8] and involve the distinct enzymatic reactions depicted in Figure 1A.

BER proteins recognize damaged nucleobase by first binding to the damaged site and then cleaving the N-glycosyl bond to release the damaged base, thus forming an abasic site as shown in Figure 1A [9]. In the case of monofunctional glycosylases, the abasic site is cleaved by an apurinic (AP) human endonuclease (APE1) to form fragments with 3′-OH and 5′-deoxyribose phosphate (5′-dRP) ends [10]. Polymerase β (Pol β) subsequently adds a nucleotide to the 3′-OH end using the base in the complementary strand as the template. The 5^{\degree -dRP is concurrently removed by the AP lyase activity associated with Pol β (Figure} 1A), and finally the nick is sealed by DNA ligase III/XRCC1 [11]. On the other hand, bifunctional glycosylases in addition possess AP lyase activity, which cleaves the abasic site in DNA resulting in the formation of a single-strand break containing either a phosphate (P) group (β, δ-elimination), or an α,βunsaturated aldehyde (PUA, (β-elimination) at the 3′-end [12, 13]. The 3[']-PUA and 3[']-phosphate groups are further removed by the diesterase activity of APE1 and the phosphatase activity of polynucleotide kinase (PNK) to form the same gapped product as in the case of the monofunctional glycosylase mechanism [14, 15]. This single nucleotide gap is filled by Pol β (Figure 1A), and the nick is sealed by DNA ligase III/XRCC1 as in the case of the monofunctional glycosylases [11].

2. 2. Nucleotide incision repair (NIR)

An alternative nucleotide incision repair pathway involving the AP endonucleases of E. coli Nfo, yeast Apn1 and human APE1, nick DNA on the 5-side of the damaged base, thus generating fragments with 3′-OH ends, as well as a damaged nucleotide on the 5′-end [16, 17] (Fig. 1B). It has been suggested that the NIR pathway can serve as a backup system for BER if the appropriate glycosylase is missing or inefficient. Once the AP endonuclease has

produced the initial incision, the full regeneration and repair of the incised strand can occur as long as the other, subsequent repair factors are also available [18]

2. 3. Nucleotide excision repair (NER)

The mammalian global genomic nucleotide excision repair system (GG-NER) recognizes the distortions in the DNA double helix caused by the DNA lesions, rather than the lesions themselves [19] and the full repair of the DNA damage requires the sequential action of more than 30 proteins [20, 21]. In mammalian GG-NER, the recognition of DNA damage is achieved by the protein heterodimer XPC-RAD23B (Fig. 1C). The resulting XPC-RAD23B – damaged DNA complex recruits the ten-protein factor TFIIH, XPA, XPF and XPG that cooperate to excise the characteristic $\sim 24 - 30$ nucleotide (nt) dual incision products that contain the lesion and are the hallmarks of successful NER [22, 23]. By contrast, transcription coupled nucleotide excision repair (TC-NER) is initiated when human RNA polymerase II (hRNAPII) is stalled by DNA lesions. The stalled polymerase serves as the signal for recruiting the NER factor (TFIIH, etc.) and other NER factors that lead to the NER double incisions and, ultimately, the filling of the \sim 24–30 nt gap created by the dual incision and the removal of the damage-bearing 24–30 nt fragments. However, TC-NER removes DNA lesions only from the transcribed strand of active genes [24], and thus repairs a smaller, but critical fraction of cellular DNA damage.

3. Guanine is the major target of reactive oxygen and nitrogen species

The primary target of oxidatively generated damage in DNA is guanine [25], the most easily oxidizable nucleic acid base in DNA [26]. The oxidation of guanine is typically initiated either by one-electron abstraction or by the addition of hydroxyl radicals (Fig. 2) [27].

The radical intermediates formed are highly reactive and rapidly transform to stable endproducts. The most abundant and best known oxidatively generated guanine lesion is 8 oxoG that is ubiquitous in cellular DNA [25, 28]. Other oxidation products include the diastereomeric 5,8′-cyclo-2′-deoxypurine lesions [29–31]. In gamma irradiated and aerated aqueous nucleoside solutions these lesions are formed at \sim 40 times lower concentrations than 8-oxoG; however, the levels of cdG and cdA were found to increase by factor of 10 – 20 as the oxygen concentration was diminished [32]. Alternatively radical intermediates can transform to 2,6-diamino-4-hydroxy-5-formamidopyrimidine (FapyG) [25, 27, 33]. Formation of FapyG has been detected upon exposure of DNA in aerated aqueous solutions to either hydroxyl radicals or one-electron oxidants [34, 35]. Furthermore, FapyG is produced in two-fold higher yield than 8-oxoG in gamma irradiated cellular DNA [36]. Radicals derived from the one-electron oxidation of guanine remain strong electrophiles and readily add to neighboring thymines to form guanine(C8)-thymine(N3) crosslinks $(G[*]-T[*])$ in air-equilibrated solutions (Fig. 2) [37]. Other forms of cross-linked DNA lesions include G[C8-5m]T and G[8–5]C lesions [29, 30, 38–42]. Guanine radicals readily combine with oxyl radicals to form stable end-products [43], while combination with nitrogen dioxide radicals leads to the formation of 5-guanidino-4-nitroimidazole (NIm) [44, 45]. NIm was found among a number of other products of guanine oxidation by peroxynitrite [46, 47] and serves as a marker of inflammation-related oxidation mechanisms [48].

It is well established that 8-oxoG is more easily oxidized than the parent guanine base [49]. Its further oxidation by diverse oxyl radicals $(CO_3^{\bullet-}, \text{'}NO_2, SO_4^{\bullet-}, RO^{\bullet})$ [45, 50–53] and peroxynitrite [47], can lead to the formation of the diastereomeric spiroiminodihyadantoin (Sp) and 5-guanidinohydantoin (Gh) lesions [54–61]. The Sp and Gh lesions have been detected in mice with infection-induced colitis at concentration levels of about one percent, relative to the more abundant 8-oxoG levels [62]. Due to the presence of chiral carbon atoms, the Sp and Gh nucleobases exist as R and S diastereomers. Oligonucleotides containing single, site-specifically inserted S-Sp and R-Sp lesions can be isolated by anionexchange HPLC [63]. In aqueous solutions, the Gh diastereomers are easily interconvertible, and can isomerize to iminoallantoin (Ia) (Fig. 2) [55]. In DNA, the isomerization of Gh to Ia occurs in basic solutions ($pH > 8.2$) [64]. The Sp and Gh lesions are products of fourelectron oxidation mechanisms of guanine (in green color in Fig. 2).

4. BER of oxidatively modified guanine bases

A number of oxidatively modified guanine oxidation products are recognized by DNA glycosylases, which belong to the Nth (or Endonuclease III) and/or Fpg/Nei (or Endonuclease VIII) proteins [65]. The bifunctional human glycosylase NTH1 repairs oxidized pyrimidines and formamidopyrimidines by β-elimination mechanisms (Fig. 1A). NTH1 is a member of the helix-hairpin-helix (HhH) superfamily of DNA glycosylases that are highly conserved from bacteria to humans [66]. The 8-oxoG and FapyG lesions opposite cytosine in the complementary strand are recognized and removed by the human bifunctional glycosylase hOGG1 [67]. The latter also belongs to the HhH superfamily and removes the damaged bases also by the β-elimination mechanism. However, DNA replication past 8-oxoG occurs frequently in an error-prone manner by incorporating adenine across this lesion [68]. The DNA glycosylase MUTYH (also a member of the HhH superfamily) removes adenine paired with 8-oxoG or FapyG in the opposite strand [69].

The prokaryotic Fpg protein, referred also as MutM, which is known to repair 8oxoG and FapyG [70] belongs to the Fpg/Nei family of DNA glycosylases [65]. However, the eukaryotic Fpg homolog NEIL1 does not excise 8-oxoG, but recognizes and processes its oxidation products Sp and Gh [71, 72]. NEIL1 also recognizes oxidized pyrimidines and formamidopyrimidines [73–76] and removes these lesions by the β,δ-elimination mechanism (Fig. 1A). NEIL2 repairs the same lesions also by β ,δ-elimination, but preferably in single-stranded rather than double-stranded DNA [77, 78]. NEIL3 excises the hydantoins Sp and Gh, as well as oxidized pyrimidines (with lower efficiencies) and cleaves the remaining AP site via β-elimination [79, 80].

5. NER of diastereomeric 5′**,8-cyclopurines**

The presently accepted DNA repair paradigms are based on the concept that small, nonbulky, oxidatively generated DNA lesions are repaired by base excision repair pathways, whereas bulky DNA lesions are recognized and removed by GG-NER or TC-NER mechanisms. While the mechanisms of lesion recognition are different in GG-NER and TC-NER, the resulting $24 - 30$ nt dual incision products are common to both repair pathways.

A well known exception to the BER/NER paradigm, are the diastereomeric set of non-bulky, oxidatively generated $5'R$ and $5'S 5', 8-cycle-2'-deoxyguanosine (cdG)$ and $5', 8-cycle-2'$ deoxyadenosine (cdA) lesions. The cdG and cdA DNA lesions are characterized by a covalent C-C bond between the purine C8 and the 2′-deoxyribose C5′ atoms within the same nucleoside. The N-glycosidic bond of the 5['], 8-cyclopurine lesions is resistant to acid/ base-catalyzed hydrolysis [81, 82], and is also resistant to base excision repair in mammalian cell extracts [83, 84], as well as to purified NEIL1, NEIL2, Fpg, OGG1, Endo III, and Endo VIII BER proteins [85]. However, the 5′,8-cyclopurines cause significant local distortions to the DNA double helix [86] and are therefore good substrates of mammalian [83, 84] and prokaryotic E. coli nucleotide excision repair systems [87]. The NER dual incision efficiencies of the diastereomeric cdA lesions are about four times greater in the case of the $(5'R)$ - than the $(5'S)$ -cdA lesion incorporated into plasmid DNA [83]. In linear 135-mer DNA duplexes, the $5^{'R}$ cdG stereoisomer is incised \sim 1.5 more efficiently than the 5′S cdA lesion in 135-mer DNA duplexes in HeLa cell extracts [85]. More recently, the relative NER efficiencies of all four 5′R and 5′S diastereomeric 5′,8-cyclopurines were compared in human HeLa cell extracts [86] and the results are summarized in Table 1.

In these experiments, The 5′R diastereomers of both the cdA or cdG lesions are recognized ~two-fold better than the respective $5'S$ lesions (Table 1), and the $5'R$ –cdG lesions is a somewhat better NER substrate than the 5[']R cdA lesion. These results are qualitatively consistent with the observations of Kuraoka et al. [83] who reported a higher $(5'R–cdA)/$ (5′S–cdA) NER efficiency in plasmid DNA, and Pande et al. [85] who obtained similar 5^{\prime} S–cdG/5^{\prime}S–cdA excision ratios of ~1.3–1.5 as in Table 1 in linear DNA. The quantitative differences between these published values and those reported here are most likely attributable to base sequence context effects since the effects of base sequence have been observed in the case of the benzo[a]pyrene diol epoxide-derived guanine adducts [89, 90].

Detailed molecular modeling and molecular dynamic simulation studies indicate that there are differences in the local perturbations and dynamics of the DNA backbone imposed by the cross-linked 5′,8 bonds and their absolute configurations. The absolute configurations of the 5′R cdA and 5′R cdG lesions give rise to a greater distortion and a more pronounced weakening of the local base stacking interactions in the case of the diastereomeric 5[']R lesions [86]. These stereochemical effects are correlated with the observed higher NER dual incision efficiencies in the case of the $5'R$ cdA and $5'R$ cdG lesions than the stereoisomeric 5′S lesions, respectively.

6. Interplay between BER and NER pathways in the repair of oxidatively generated lesions

We have recently identified a set of non-bulky DNA lesions that are oxidatively generated by free radical mechanisms, and that are substrates of overlapping BER and NER mechanisms.

6.1. Intrastrand guanine(C8) – thymine(N3) crosslinked DNA lesions

Oxidatively generated DNA lesions with covalent bonds between neighboring nucleobases include interstrand and intrastrand crosslinked nucleotides. The interstrand cross-linked

(ICL) lesions are characterized by covalent bonds between two nucleotides positioned on opposite DNA strands, whereas the coupling of two nucleotides on the same strand give rise to intrastrand cross-linked (IntraCL) lesions. ICL lesions generated by a variety of bifunctional agents such as cisplatin [91], are difficult to remove by DNA repair mechanisms and are therefore highly genotoxic [42, 92]. Well-known examples of IntraCL lesions are the UV radiation-induced cyclobutane pyrimidine dimers and the pyrimidine (6–4) pyrimidone photoproducts [23, 93] that are genotoxic if not removed by repair mechanisms.

Oxidatively generated IntraCL lesions with covalent linkages between the C8-atom of guanine and the methyl group of an adjacent thymine (G[8–5m]T) on its $3'$ -side [38], and the analogous G[8–5]C [39], and G[8–5m]C [94] intrastrand tandem lesions are formed in DNA solutions exposed to γ-radiation or under the action of Fenton reagents. These IntraCL lesions are known to be repaired by prokaryotic NER pathways [95–97] and evidence has been presented that these IntraCL lesions may be substrates of NER in mammalian tissues [98].

The more recently discovered guanine(C8)-thymine(N3) lesions (Fig. 2) identified in vitro [37, 47], have also been detected in human HeLa cells by isotope dilution LC-MS/MS methods [99]. There are two types of G*–T* lesions: in one case, the cross-linked guanine and thymine bases are either adjacent to one another (G*T*) or separated by one intervening cytosine (G^*CT^*) [37]. We have shown that both types of lesions are good substrates of NER in human HeLa cell extract experiments, with the G*T* lesion being removed less efficiently than the G*CT* lesion [100]. Thermal DNA melting studies reveal that both lesions significantly destabilize duplex DNA, and that the destabilization induced by the G*CT* cross-link is considerably greater [100]. Computational and modeling studies have also shown that both lesions dynamically distort and destabilize DNA duplexes by distorting normal Watson–Crick base-pairing and base-stacking interactions, and by causing the untwisting of base pairs accompanied by an opening of the minor groove [100]. These structural perturbations are much more pronounced in the G*CT* than in the G*T* crosslinked lesions, and are correlated with the differences in the NER activities of these two substrates in HeLa cell extracts.

In contrast to $5'$, 8-cyclopurine lesions, the G^{*}CT^{*} and G^{*}T^{*} IntraCL lesions are incised in human HeLa cell extracts by BER as well as by NER mechanisms [101]. Detailed studies with purified repair proteins have shown that the bacterial, yeast, and human bifunctional DNA glycosylases (Nei, NEIL1, Nth, NTH1), as well as AP endonucleases (Nfo, Apn1 and APE1) cleave the strands adjacent to the G^*CT^* and G^*T^* IntraCL lesions (Fig. 3) embedded in site-specifically modified oligonucleotide duplexes.

Analysis of the cleavage products by denaturing polyacrylamide gel electrophoresis (Fig. 3), in combination with MALDI-TOF/MS methods, showed that the DNA glycosylases/AP lyases excise the cross-linked guanine and cleave the resulting abasic sites via β- and β,δelimination mechanisms. In turn, the AP endonucleases of E. coli, Nfo, yeast Apn1 and human APE1 cleave the duplex DNA containing G*CT* and G*T* lesions on the 5[']-side of the cross-linked guanine, and are thus capable of initiating the nucleotide incision repair pathway [101]. These experiments were performed with purified proteins in vitro and clearly

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show that the G^*T^* and G^*CT^* intrastrand crosslinks are efficiently incised by BER and NIR pathways at the sites of these lesions.

In HeLa cell extracts both G^*CT^* and G^*T^* lesions are also removed by NER mechanisms [100]. It is interesting to note, that the yields of NER products are higher $($ \sim 14%) than of BER products (\sim 3%) in the very same cell extract experiments in the case of the G^{*}CT^{*} lesion. In contrast, in the case of the G^*T^* lesions, the NER yield is \sim 5 times smaller, while the BER yield is \sim 2 times greater than in the case of G*CT* lesions in the same cell extracts.

6.2. Spiroiminodihyantoin and 5-guanidinohydantoin lesions are substrates of both NER and BER pathways

The Sp and Gh lesions in double-stranded DNA are good substrates of BER enzymes in vitro that include the bifunctional DNA glycosylases E. coli Fpg [102], Nei [103], mammalian NEIL1 and NEIL2 [78], NEIL3 [79, 104–106], human NEIL1 [71, 72], and human NEIL3 [80]. These hydantoins, are also repaired by the prokaryotic NER pathways initiated by UvrABC proteins in vitro [107].

Recently, we found that the Sp and Gh lesions are repaired by competing BER and NER pathways in cell-free extracts derived from human fibroblasts and HeLa cells [108] as demonstrated by the HeLa cell extract experiments shown in Fig. 4.

The autoradiograph of the denaturing polyacrylamide gels clearly shows that incubation of the 135 nt oligonucleotide duplexes containing single S-Sp and Gh lesions in cell free extracts generates two group of products: (1) the characteristic ladders of NER dual incision products of ~20–30 nucleotides in lengths, and (2) the 67-mer BER products with 3′-P and 3′-OH ends (Fig. 1) arising from incisions at the sites of the lesions [108]. The BER products are not observed in the case of the bulky B[a]P-dG adducts, which are exclusively repaired by NER pathways [88, 109]. In contrast to the Sp and Gh DNA lesions, the NIm lesion yields only the BER product of incision, and NER products are absent in this case [46, 108]. Thus, the Sp and Gh lesions are good substrates of both NER and BER pathways, whereas the B[a]P-dG adducts are substrates of NER only, while the NIm lesions are uniquely substrates of BER only.

These conclusions are supported by experiments in cell extracts derived from human cells deficient in the XPC-RAD23B heterodimer, the initial NER sensor of structural distortions caused by DNA lesions, or XPA that plays a critical downstream role in the complex, multistep mammalian NER pathway. In such extracts, the NER pathway is non-functional as shown by the lack of dual incision products when DNA duplexes with $B[a]P-dG$ adducts, Gh, or Sp are incubated in XPC- and XPA-deficient cell extracts. However, when the XPCdeficient cell extracts are complemented with purified XPC-RAD23B, the NER dual incision products reappear [108]. Additional evidence that the dual incision products derived from the Sp- and Gh-containing 135 bp duplexes is indeed due to NER activity, is the observation that the characteristic NER dual incision products disappear in the presence of low concentrations of a monoclonal antibody against XPA. Inhibition of XPA activity by anti-XPA antibodies has been widely used for validating the existence of NER pathways of

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repair [83, 110–112]. For example, the mouse monoclonal anti-XPA [5F12] antibody strongly inhibits NER of oxidatively generated 5′,8-cyclopurine lesions [83], and the 1,3 intrastrand d(GpTpG)-cisplatin cross-linked lesions [111]. Indeed, addition of anti-XPA [5F12] to the cell extracts containing 135 bp Sp-S duplexes selectively inhibits the appearance of the dual incision products, whereas the levels of the 67-mer incision fragments produced by the BER activity remain unaffected

Observation of parallel BER and NER pathways in the repair of the Sp and Gh modified 135 bp oligonucleotide duplexes in cell free extracts from cultured human cells can be explained by competitive binding of the Sp and Gh substrates by NER and BER proteins. Indeed, the addition of exogeneous bifunctional DNA glycosylase NEIL1 enhances the yield of 67 nt BER products, whereas the yield of dual incision products decreases [108]. These results are attributed to a competition between NEIL1 and the initial NER DNA lesion recognition factor XPC-RAD23B for binding to the same DNA lesion that increasingly favors NEIL1 as its concentration is increased.

An interesting question is why the NIm lesion is resistant to NER while the structurally similar Gh lesion is an excellent NER substrate. There are two important structural differences between these two lesions (Fig. 1): (i) the keto group in Gh is replaced by an – NO2 group in NIm, (ii) the 5-membered 5-nitroimidazole ring in NIm is planar, whereas in Gh the hydantoin ring is non-planar. Molecular modeling studies indicate that the NIm lesions adopt flexible and multiple ring-opened structures with the nitro and guanidino groups providing multiple hydrogen bonding possibilities [113]. By contrast, Gh can exist in the forms of two slowly interconverting R and S stereoisomers [55, 114]. On the other hand, the stereoisomeric Sp structures exist as stable, and identifiable R and S stereoisomers [60, 115]. All three lesions, NIm, Gh, and Sp, cause significant thermodynamic destabilization of DNA duplexes [63, 113–120], which is a common feature of DNA substrates that are recognized by the NER machinery. Thus, the Sp and Gh lesions are recognized by the prokaryotic UvrABC nuclease [107], as well as by the eukaryotic NER machinery in human cell extracts as demonstrated here. However, the NER-resistance of NIm appears to be correlated not with a destabilization, but with its conformational flexibility in doublestranded DNA [113].

7. Conclusion

The susceptibility of the oxygen free radical generated 5′,8-cyclodeoxypurine DNA lesions to repair by the nucleotide excision repair pathway, but not the base excision repair pathway, has been known for more than 15 years. Our recent work shows that other oxidatively generated DNA lesions such as spiroiminodihydantoin and guanidinohydantoin, both oxidation products of 8-oxoG, are substrates of overlapping and competing NER and BER pathways in human cell extracts. Under the same conditions, 5-guanidino-4-nitroimidazole (NIm), a lesion derived from the oxidation of guanine in DNA by peroxynitrate, is removed only by a BER pathway, but not the NER mechanism. The recent results reviewed in this article indicate that the range of oxidatively generated DNA lesions that are substrates of the nucleotide excision repair pathway may be much more extensive than previously thought. Understanding the relationships between susceptibility to NER and molecular structure of

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Abbreviations

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- **•** Non-bulky guanine lesions are removed by Nucleotide Excision Repair mechanisms
- **•** DNA Intrastrand cross-linked G[C8-N3]T-thymine lesions are substrates of BER and NER
- **•** DNA hydantoin lesions are repaired by competitive BER and NER pathways
- **•** The DNA guanine lesion 5-guanidino-4-nitroimidazole is repaired by BER but not NER

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Fig. 1.

Excision of damaged nucleobases by (A) BER, (B) NIR (the lesion is not excised in this pathway), and (C) NER mechanisms.

Fig. 2.

Representative two-electron (blue) and four-electron (green) oxidation products of guanine produced by ROS and RNS. Abbreviations: cdG, 5′,8-cyclo-2′-deoxyguanosine; NIm, 5 guanidino-4-nitroimidazole; FapyG, 2,6-diamino-4-hydroxy-5-formamidopyrimidine; 8 oxoG, 8-oxo-7,8-dihydroguanine; G*–T*, intrastrand guanine(C8)-thymine(N3) cross-link; Sp, spiroiminodihydantoin; Gh, 5-guanidinohydantoin; Ia, iminoallantoin.

Fig. 3.

Denaturing polyacrylamide gel electrophoresis analysis of the cleavage patterns generated by DNA glycosylases/AP lyases (BER) and NIR-AP endonucleases (NIR) in duplexes containing G*CT* and G*T* lesions. Panels A and D: duplexes constructed from either $5'$ -3²P-labeled 17 mer G*CT* (A), or G*T* (D) strands hybridized with their natural complementary strands. Panel B: size marker 8-mer oligonucleotide standards with $5'$ -32Plabled 8-mer containing 3′-hydroxyl (3′-OH), or 3′-phosphoaldehyde (3′-PUA), or 3′ phosphate (3′-P) ends are shown in lanes 3, 5, and 7, respectively. These standards were derived from the parent 17-mer strands containing uracil. Panels C and E: duplexes constructed from cordycepin $3'$ - 3^2P -endlabeled 18 mer G*CT* (C) or G*T* (E) strands hybridized with their complementary 17-mer complementary strands. UT indicates untreated oligonucleotide. (Reproduced from Talhaoui et al., J. Biol. Chem. 290 (2015) 4610-14617 [101]).

Fig. 4.

A denaturing polyacrylamide gel showing the appearance of excision (BER) and dual incision (NER) products obtained by incubating, as a function of time, 135-mer duplexes with single Gh, S-Sp, or NIm lesions in HeLa cell extracts. The lesions were positioned at the $67th$ nucleotide counted from the $5'$ -end of the modified strand. The 10R (+)-cis-anti- $B[a]P-N^2-dG$ adducts, a bulky DNA lesion derived from the binding of a diol epoxide metabolite of benzo[a]pyrene, was used as positive control of NER activity in these cell extracts [88, 89]. Lane 1: oligonucleotide size markers. The apparent size range of the NER dual incision products is shown by the dotted lines (red). (Reproduced from Shafirovich et al., J. Biol. Chem. 291 (2016) 5309-5319 [108]).

Table 1

Relative efficiencies of formation of NER dual incision products in human HeLa cell extracts of the diastereomeric cdG and cdA lesions in 135-mer duplexes [86]. The NER dual incision efficiency of a bulky benzo[a]pyrene-derived DNA adduct $((+)$ -cis-B[a]P-N²-dG), known to be an excellent NER substrate [88], is shown as a reference.

