

# SINGLET OXYGEN INDUCES PREDOMINANTLY G TO T TRANSVERSIONS ON A SINGLE-STRANDED SHUTTLE VECTOR REPLICATED IN MONKEY CELLS

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To elucidate the mechanisms of mutagenesis by singlet oxygen DNA damage in mammalian cells, a SV40-derived single-stranded shuttle vector was exposed to the water soluble endoperoxide 3,3'-(1,4-naphthylidene) dipropionate (NDPO<sub>2</sub>). The damaged vector was transfected into monkey COS7 cells and the plasmid progeny exhibited up to 10 fold increase on the mutation frequency in the *supF* target gene, when compared to untreated vector. The sequence in the *supF* locus of such mutants revealed that singlet oxygen-induced mutagenesis in single-stranded vector is significantly different from spontaneous mutagenesis. Among the base substitutions, most of the mutations involved deoxyguanosines, being G to T transversions the predominant type of change. The data indicate that mutagenesis by singlet oxygen in mammalian cells may be generated by an error prone bypass of damaged deoxyguanosines at the template DNA.

**KEY WORDS:** Singlet oxygen, mutagenesis, DNA damage, 8-hydroxydeoxyguanine, shuttle vector.

## INTRODUCTION

The deleterious effects of the reactive oxygen species are being intensively studied in the last years due to their probable involvement with human ageing, tumor formation and related diseases (1). Among these species, singlet oxygen (<sup>1</sup>O<sub>2</sub>) has been in focus because it has been shown to be generated in several biological systems and it is highly reactive with macromolecules, including nucleic acids and proteins (2,3). Concerning DNA, <sup>1</sup>O<sub>2</sub> induces several different kinds of lesion, with deleterious biological consequences, such as molecule inactivation and mutagenesis (4,5). The high mutagenicity of <sup>1</sup>O<sub>2</sub> is a matter of particular interest. Early work have suggested the involvement of <sup>1</sup>O<sub>2</sub> in the mutagenesis induced by activation of photosensitizers in bacteria (6), yeast (7) and mammalian cells (8). Working with M13 bacteriophage RF DNA treated with photosensitizer, Piette and Van de Vorst (9) and Decuyper-Debergh *et al.* (10) have reported that <sup>1</sup>O<sub>2</sub> DNA lesions were

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carbon (NDP) and molecular oxygen, half in the triplet state and half in the excited

singlet state (12). After treatment, the DNA samples were sterilized and purified with chloroform.

### *Transfection into COS7 Cells and Shuttling into E. coli*

Subconfluent COS7 cells were transfected with treated plasmid DNA (1  $\mu\text{g}$  per 90 mm dish) by the DEAE-dextran technique (21). Three days later the replicated episomal DNA was recovered by a small-scale alkaline lysis procedure adapted from the method described by Birnboim and Doly (22). Then it was shuttled into *E. coli* MBM7070 by the transformation method of Hanahan (23).

### *Mutagenesis Analysis*

Transformant colonies were plated on LB-agar medium in the presence of chloramphenicol (34  $\mu\text{g}/\text{ml}$ ), X-Gal (5-bromo-4-chloro-3-indolyl- $\beta$ -D-galactoside, 0.08 mg/ml) and IPTG (isopropyl- $\beta$ -D-thiogalactoside, 0.1 mM). Colonies bearing plasmids with functional *supF* gene are dark blue, while colonies bearing plasmids with inactivating mutations in this gene are white or light blue. These colonies were restreaked three times on the same medium to confirm the phenotype and the plasmid DNA was extracted by a modified alkaline lysis "mini-prep" method (22). The *supF* locus of these plasmids was then sequenced by the Sanger chain termination method (24) using the Sequenase Version 2.0 kit (United States Biochemical Corporation) and a 17mer oligonucleotide, which hybridizes in a position 5' to the *supF* gene, was used as primer for the sequencing reactions. Only independent mutations are presented: mutants carrying the same modification(s) were considered independent if they were isolated from different transfection experiments in COS7 cells.

## RESULTS

Previous work showed that NDPO<sub>2</sub>-treated single-stranded DNA,  $\pi$ SVPC13FIA vector, yields *supF* mutants after replication in mammalian cells (14). The data presented in Figure 1 show that there is a linear increase up to a factor of 10 in the mutation frequency induced by different NDPO<sub>2</sub> concentrations, in comparison to control DNA, that is, single-stranded DNA submitted to the same experimental conditions without NDPO<sub>2</sub>. As reported before (14,25), the number of lesions induced on single-stranded DNA by NDPO<sub>2</sub> was lower when the reaction was performed in the presence of H<sub>2</sub>O, instead of D<sub>2</sub>O (which prolongs  $^1\text{O}_2$  lifetime), or NaN<sub>3</sub> (an  $^1\text{O}_2$  quencher). No lesions were detected when DNA was treated with NDP, a product of the NDPO<sub>2</sub> thermolysis. Therefore, the damaging action of NDPO<sub>2</sub> is probably due to  $^1\text{O}_2$ . This implies  $^1\text{O}_2$  must also be the agent responsible for the mutagenic effects described here.

In order to characterize the molecular nature of these mutations, the *supF* locus of the mutant plasmids from control and  $^1\text{O}_2$ -treated DNA were sequenced. The results obtained for independent mutants are grouped in Table 1. The mutations induced by NDPO<sub>2</sub>-treatment are mainly single and multiple base substitutions, while, for control DNA, mutations are distributed between gross alterations (deletions) and single base substitutions.

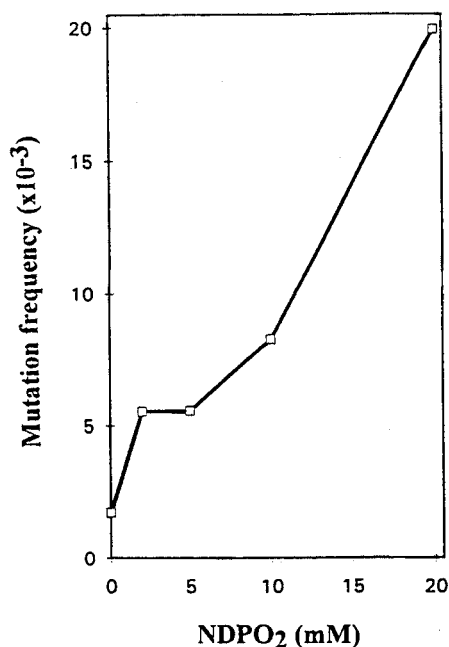


FIGURE 1 Increase in the mutation frequency at the *supF* locus in  $^1\text{O}_2$ -treated single-stranded shuttle vector after replication in monkey COS7 cells. The data are from Ribeiro *et al.* (14).

TABLE 1  
Mutations in control and NDPO<sub>2</sub>-treated single stranded  $\pi$ SVPC13FIA vector replicated in COS7 cells

Types of mutations	Number of mutants	
	Control	NDPO <sub>2</sub> -treated
deletions	7 (38.9%) <sup>a</sup>	1 (8.3%) <sup>a</sup>
frameshift	1 (5.6%) <sup>b</sup>	0
base substitutions		
single	8 (44.4%)	6 (50.0%)
multiple	2 (11.1%) <sup>c</sup>	5 (41.7%) <sup>d</sup>
total	18 (100%)	12 (100%)

<sup>a</sup> Deletions involve from 17 to 183 b, which include the gene itself and the 5' region.

<sup>b</sup> (-1) deletion.

<sup>c</sup> One of them involves 2 adjacent bases (tandem) and, the other, 2 bases separated by an unchanged nucleotide.

<sup>d</sup> Three of them include mutations in tandem.

The types of base substitutions are summarized on Table 2. Among the twenty changes found in mutants originated from  $^1\text{O}_2$ -treated DNA, a significant majority involves dGs: 16 modifications, including 12 G to T substitutions. The latter change is the most frequent type of mutation induced by NDPO<sub>2</sub> treatment. It should be emphasized that the mutations found in untreated DNA were significantly different from those described above. The main difference is the fact that no transversions involving dGs were detected for control DNA.

TABLE 2

Base substitutions in mutants derived from control and NDPO<sub>2</sub>-treated single stranded  $\pi$ SVPC13FIA replicated in COS7 cells

	Number of substitutions	
	Control	NDPO <sub>2</sub> -treated
Transitions	6 (50%)	1 (5%)
C → T	4 (33.4%)	1 (5%)
G → A	2 (16.6%)	0
Transversions	6 (50%)	19 (95%) <sup>a</sup>
C → A	1 (8.3%)	1 (5%)
C → G	4 (33.4%)	2 (10%)
G → C	0	4 (20%)
G → T	0	12 (60%)
A → T	1 (8.3%)	0
Total	12 (100%)	20 (100%)

<sup>a</sup> Spontaneous and NDPO<sub>2</sub>-treated DNA yields different transversion frequencies statistically significant ( $p < 0.01$ , Fisher exact test).

## DISCUSSION

Mutants in the *supF* locus of single-stranded DNA, originated either spontaneously or after  $^1\text{O}_2$ -treatment and replication in monkey COS7 cells, were characterized by DNA sequencing. The *supF* locus is particularly interesting as mutation target gene since it has been extensively used in shuttle vectors and base changes at almost every site of the structural tRNA coding sequence inactivate the suppressor function (26). Although only few independent mutants were found, due to the low recovery of plasmid in the treated samples (14), the data presented here consistently show significant differences between the mutations originated from control and  $^1\text{O}_2$ -damaged vectors. These differences are observed in three levels: (i) types of mutation; (ii) types of base substitutions and (iii) pattern of distribution of mutations along the *supF* locus (not shown). The data concerning spontaneous mutations are in agreement to those reported before for another SV40-derived single-stranded shuttle vector (27): only one transversion out of 30 independent mutations analysed, involving guanine residue, was found. These types of base substitution are the most frequent ones (80%) observed for  $^1\text{O}_2$ -damaged single-stranded vectors (Table 2).

This work confirms and extends the results obtained for a double-stranded shuttle vector treated with NDPO<sub>2</sub> and replicated in mammalian cells (15). In that case, the most frequent base substitution affects G:C base pairs (98%) including G:C to T:A (51%) and G:C to C:G (33%) transversions. In this paper, we observed that 16 of 20 point mutations derived from  $^1\text{O}_2$ -damaged single-stranded vector are targeted to dGs. The use of single-stranded DNA in these experiments eliminates the ambiguity of which strand has been damaged, so that a direct correlation between the types of mutation observed and the site of base damaged can be established (17,28). Moreover, single-stranded DNA is a common structure within the cell (eg. as an intermediate during DNA replication and recombination). Also, the damages in a single-stranded vector cannot be easily repaired. Thus, the data presented here may reflect the consequences of translesion DNA synthesis in the cell nuclei. The mutations clearly occur predominantly opposite to dG templates.

The high frequency of G to T mutations observed in mammalian cells gives clues on the molecular nature of the kind of guanine modifications induced by  $^1\text{O}_2$ . Several lines of evidence indicate that 8-hydroxy-2'-deoxyguanosine (8-oxodG) is an important product of the oxidation of dG in DNA by  $^1\text{O}_2$  (28-31). This base alteration was found to occur about 17-fold more frequently than single strand breaks (29) and about 20-fold more than an imidazole ring-opened purine, 2,6-diamino-4-hydroxy-5-formamidopyrimidine (30) in DNA treated with methylene blue plus light. Devasagayam *et al.* (32) have observed that exposure of free nucleotides to NDPO<sub>2</sub> yields 8-oxodG as the main product of dG oxidation by  $^1\text{O}_2$ . Moreover, *in vitro* experiments indicate that 8-oxodG may miscode for deoxyadenosine during DNA synthesis by several DNA polymerases (33) and NMR structural analysis of a oligonucleotide duplex provide evidence that 8-oxodG stably base pairs deoxyadenosine (34). Three independent studies using vectors containing site-specifically inserted single 8-oxodG residues have shown that G to T transversions are the most frequent mutations arising after *E. coli* transformation (35-37). More recently, Moriya (38) reported that a single 8-oxodG in a single-stranded shuttle vector is mutagenic when replicated in COS7 cells, resulting in G to T transversions. Therefore, 8-oxodG is a strong candidate as the major premutagenic lesion induced by  $^1\text{O}_2$ , yielding G to T transversions in mammalian cells.

Recently, McBride *et al.* (11) have found that, for single-stranded DNA exposed to methylene blue plus light, mutagenesis in *E. coli* is highly dependent on SOS response. The mutations predominantly observed were also base substitutions occurring at template G residues. However, G to C transversions were the most frequent mutations (about 58%), with G to T transversions as the second highest frequent mutations. The G to C transversions were also identified in the system described here and for double-stranded shuttle vectors treated with  $^1\text{O}_2$  (15). This and the other types of mutation observed may be attributed to minor lesions present in  $^1\text{O}_2$ -damaged DNA, such as phosphodiester chain breaks (39,40), alkali and piperidine-labile sites (39) and formamidopyrimidine (30).

The data presented here also reveal that part of the mutants contains multiple base substitutions. This was also verified for double-stranded shuttle vectors with lesions induced by  $^1\text{O}_2$  (15) or other damaging agents (41-44). Seidman *et al.* (43) proposed that multiple mutations arise as result of an error DNA polymerization during excision repair. Excision repair is however unable to act on single-stranded DNA due to the absence of template. Moreover, multiple mutations were also reported for UV-irradiated single-stranded shuttle vectors (27,45). As in this work, these authors have also found that UV mutagenesis is targeted to damaged bases, pyrimidine doublets in that case. Therefore, it seems that at least part of the multiple mutations observed in shuttle vectors may be due to the presence of two or more close lesions on the target gene.

In conclusion, our work using a  $^1\text{O}_2$ -damaged single stranded vector indicates that  $^1\text{O}_2$ -mutagenesis in mammalian cells occur by the miscoding at template modified G residues during DNA replication. The major premutagenic lesion may be 8-oxodG, which mainly generates G to T transversions. The biological importance of mutagenic events presented here is directly related to the occurrence of  $^1\text{O}_2$  within the cell nuclei.

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