







Table 73. イソフタル酸ジメチルのマトリックス案

| テスト項目 | 必須 DATA | SIPM | SIPE | SIPA |
|---------------------|------------|-----------|------------------|-----------|
| 構造式 | | | | |
| CAS No. | | 3965-55-7 | 24019-46-3 (主成分) | 6362-79-4 |
| 分子量 | | 297 | 357 (主成分) | 269 |
| 物理化学性状 | | | | |
| 融点 | ○ | RA | ○ | RA |
| 沸点 | ○ | RA | ○ | RA |
| 密度 | | | | |
| 蒸気圧 | ○ | | | |
| 分配係数: n-オクタノール/水 | ○ | | | |
| 水溶解度 | ○ | ○ | ○ | ○ |
| 解離定数 | ○ | | | |
| 引火点 | | | | |
| 環境運命と経路 | | | | |
| 安定性 光分解 | ○ | ○ | RA | RA |
| 安定性 水中安定性 | ○ | | | |
| 分配経路を含む媒体間の移動と分配 | ○ | ○ | RA | RA |
| 環境モニタリングデータ | | | | |
| 好気性生分解性 | ○ | ○ | ○ | RA |
| BOD/COD | | | | |
| 生物濃縮 | | | | |
| 生態毒性 | | | | |
| 急性毒性(魚類) | ○ | RA | ○ | ○ |
| 急性毒性(シロコ) | ○ | RA | ○ | ○ |
| 藻類への急性毒性 | ○ | RA | ○ | ○ |
| バクテリア等への急性毒性 | | | | |
| 水生生物への慢性毒性 | | | | |
| 陸生生物への毒性 | | | | |
| ヒト健康毒性 | | | | |
| 急性経口毒性 | ○ | 試験実施 | | |
| 急性吸入毒性 | ○ | | | |
| 急性経皮毒性 | ○ | | | |
| 反復投与毒性 | ○ | RA | ○ | ○ |
| 遺伝毒性in vitro遺伝子突然変異 | ○ | RA | ○ | ○ |
| 遺伝毒性in vitro染色体異常 | ○ | RA | ○ | ○ |
| 遺伝毒性 その他 | | | | |
| 発癌性 | | | | |
| 受胎能 | ○ | 試験実施 | RA | RA |
| 発生毒性 | ○ | 試験実施 | RA | RA |
| 皮膚刺激性/腐食性 | | | | |
| 皮膚感作性 | | | | |
| 人暴露の情報 | | | | |


○:データ取得 RA:リポートアクセス

Table 74. メトキシエチルアクリラートのマトリックス案

| テスト項目 | 必須 DATA | テトラメトキシシラン TMS  | ケイ酸四ナトリウム塩 既存点検物質  | シリケート酸、 sodium salt OECD/SIDS  | メタノール OECD/SIDS CH ₃ -OH | トリメトキシシラン TrMS OECD/SIDS  | テトラエトキシシラン TES OECD/SIDS  |
|---------------------|---------|--|---|---|---|---|---|
| 構造式 | |  | | | | | |
| CAS No. | | 681-84-5 | 13472-30-5 | 6834-92-0 | 67-56-1 | 2487-90-3 | 78-10-4 |
| 分子量 | | 152.25 | | | | | |
| 融点 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 沸点 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 密度 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 蒸気圧 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 分配係数: n-オクタン/水 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 水溶解度 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 解離定数 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 引火点 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 安定性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 光分解 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 水中安定性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 分配経路を含む媒体間の移動と分配 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 環境-生物移行 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 好気性生分解性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| BOD/COD | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 生物濃縮 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 急性毒性(魚類) | ○ | RA | ○ | ○ | ○ | ○ | ○ |
| 急性毒性(シロ) | ○ | RA | 試験中 | ○ | ○ | ○ | ○ |
| 急性毒性(哺乳類) | ○ | RA | 試験中 | ○ | ○ | ○ | ○ |
| 薬理への急性毒性 | ○ | RA | ○ | ○ | ○ | ○ | ○ |
| 8分100毒への急性毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 水生生物への慢性毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 陸生生物への慢性毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 急性経口毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 急性吸入毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 急性経皮毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 反復投与毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 遺伝毒性 in vitro | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 遺伝毒性 in vivo | ○ | RA | ○ | ○ | ○ | ○ | ○ |
| 染色体異常 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 遺伝毒性 in vitro 染色体異常 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 遺伝毒性 in vivo | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 発癌性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 発育阻害 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 発がん性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 皮膚刺激性/腐食性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 皮膚感作性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 人毒害の情報 | ○ | ○ | ○ | ○ | ○ | ○ | ○ |

○:データ取得 RA:リトアニア

Table 75. 脂肪酸クロライドのマトリックス案

| テスト項目 | 必須 DATA | オクタノ酸 (C8脂肪酸) | デカノ酸 (C10脂肪酸) | ラウリン酸 (C12脂肪酸) | ミリスチン酸 (C14脂肪酸) | パルミチン酸 (C16脂肪酸) | ステアリン酸 (C18脂肪酸) | トコサノ酸 (C22脂肪酸) | 塩化水素 |
|------------------|----------|---|---|--|--|--|---|--|------|
| 構造式 | | $\text{CH}_3(\text{CH}_2)_7\text{COOH}$ | $\text{CH}_3(\text{CH}_2)_9\text{COOH}$ | $\text{CH}_3(\text{CH}_2)_{11}\text{COOH}$ | $\text{CH}_3(\text{CH}_2)_{13}\text{COOH}$ | $\text{CH}_3(\text{CH}_2)_{15}\text{COOH}$ | $\text{H}_3\text{C}-\text{CH}_2-\text{CH}=\text{CH}-\text{COOH}$  | $\text{CH}_3(\text{CH}_2)_{20}\text{COOH}$ | HCl |
| CAS No. | 124-07-2 | 334-48-5 | 143-07-7 | 544-83-8 | 57-10-3 | 57-11-4 | 112-85-8 | 7647-01-0 | |
| 分子量 | 144.00 | 172.26 | 200.00 | 228.00 | 256.00 | 284.50 | 340.00 | 36.50 | |
| 融点 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 沸点 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 密度 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 蒸気圧 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 分配係数: n-オクタノール/水 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 水溶解度 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 分解定数 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 引火点 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 安定性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 光分解 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 水中安定性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 分配経路を含む媒体間の移動と分配 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 環境ニマトリックス | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 対気性生分解性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| BOD/COD | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 生物濃縮 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 急性毒性(魚類) | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 急性毒性(シロ) | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 魚類への急性毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| ハチ/77等への急性毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 水生生物への慢性毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 陸生生物への慢性毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 急性経口毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 急性吸入毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 急性経皮毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 反復投与毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 遺伝毒性 in vitro | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 遺伝毒性 in vivo | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 染色体体異常 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 発癌性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 発胎毒性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 皮膚刺激性/腐食性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 皮膚感作性 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |
| 人暴露の情報 | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ | ○ |

○: データ取得

Table 76. p-トルエンスルホン酸のマトリックス案

| テスト項目 | 必須 DATA | p-トルエンスルホン酸・ 水和物 | p-トルエンスルホン酸 | p-トルエンスルホン酸 ナトリウム |
|-------------------------|------------|---------------------|-------------|----------------------|
| | | US チャレンジ | | |
| 構造式 | | | | |
| CAS No. | | 6192-52-5 | 104-15-4 | 657-84-1 |
| 分子量 | | | | |
| 物理化学性状 | | | | |
| 融点 | ○ | ○ | ○ | ○ |
| 沸点 | ○ | ○ | ○ | ○ |
| 密度 | | | | |
| 蒸気圧 | ○ | ○ | ○ | ○ |
| 分配係数: n-オクタンール/水 | ○ | ○ | ○ | ○ |
| 水溶解度 | ○ | ○ | ○ | ○ |
| 解離定数 | ○ | ○ | ○ | ○ |
| 引火点 | | | | |
| 環境運命と経路 | | | | |
| 安定性 光分解 | ○ | ○ | ○ | ○ |
| 安定性 水中安定性 | ○ | | ○ | ○ |
| 分配経路を含む媒体間の 移動と分配 | ○ | ○ | ○ | ○ |
| 環境モニタリングデータ | | | | |
| 好気性生分解性 | ○ | RA | ○ | ○ |
| BOD/COD | | | | |
| 生物濃縮 | | | | ○ |
| 生態毒性 | | | | |
| 急性毒性(魚類) | ○ | RA | ○ | ○ |
| 急性毒性(ミシノ) | ○ | RA | ○ | ○ |
| 藻類への急性毒性 | ○ | RA | ○ | ○ |
| バクテリア等への急性毒性 | | | | |
| 水生生物への慢性毒性 | | | | ○ |
| 陸生生物への毒性 | | | | |
| ヒト健康毒性 | | | | |
| 急性経口毒性 | ○ | RA | ○ | ○ |
| 急性吸入毒性 | ○ | | | |
| 急性経皮毒性 | ○ | | | |
| 反復投与毒性 | ○ | RA | ○ | ○ |
| 遺伝毒性in vitro遺伝子突 然変異 | ○ | RA | ○ | ○ |
| 遺伝毒性in vitro染色体異 常 | ○ | RA | ○ | ○ |
| 遺伝毒性 その他 | | | | |
| 発癌性 | | | | |
| 受胎能 | ○ | RA | | ○ |
| 発生毒性 | ○ | RA | | ○ |
| 皮膚刺激性/腐食性 | | | | |
| 皮膚感受性 | | | | |
| 人暴露の情報 | | | | |

○:データ取得 RA:リードアクロス

F.研究発表

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2. 実用新案登録 (該当なし)
3. その他 (該当なし)

H. 健康危機情報

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Ⅲ. 研究成果の刊行物・別刷



Mutagenic radioadaptation in a human lymphoblastoid cell line

Fumio Yatagai^{a,*}, Yukihiro Umehayashi^a, Masamitsu Honma^b,
Kaoru Sugawara^c, Yuko Takayama^a, Fumio Hanaoka^d

^a Advanced Development and Support Center, The Institute of Physical and Chemical Research (RIKEN), Saitama 351-0198, Japan

^b Division of Genetics and Mutagenesis, National Institute of Health Sciences, Tokyo 158-8501, Japan

^c Genome Damage Response Research Unit, The Institute of Physical and Chemical Research (RIKEN), Saitama 351-0198, Japan

^d Graduate Program, Frontiers in Biosciences, Osaka University, Osaka 565-0871, Japan

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Abstract

We investigated the mutagenic radioadaptive response of human lymphoblastoid TK6 cells by pretreating them with a low dose (5 cGy) of X-rays followed by a high (2 Gy) dose 6 h later. Pretreatment reduced the 2-Gy-induced mutation frequency (MF) of the *thymidine kinase* (*TK*) gene (18.3×10^{-6}) to 62% of the original level (11.4×10^{-6}). A loss of heterozygosity (LOH) detection analysis applied to the isolated *TK*⁻ mutants revealed the mutational events as non-LOH (resulting mostly from a point mutation in the *TK* gene), hemizygous LOH (resulting from a chromosomal deletion), or homozygous LOH (resulting from homologous recombination (HR) between chromosomes). For non-LOH events, pretreatment decreased the frequency to 27% of the original level (from 7.1×10^{-6} to 1.9×10^{-6}). cDNAs prepared from the non-LOH mutants revealed that the decrease was due mainly to the repression of base substitutions. The frequency of hemizygous LOH events, however, was not significantly altered by pretreatment. Mapping analysis of chromosome 17 demonstrated that the distribution and the extent of hemizygous LOH events were also not significantly influenced by pretreatment. For homozygous LOH events, pretreatment reduced the frequency to 61% of the original level (from 5.1×10^{-6} to 3.1×10^{-6}), reflecting an enhancement in HR repair of DNA double-strand breaks. Our findings suggest that the radioadaptive response in TK6 cells follows mainly from mutations at the base-sequence level, not the chromosome level. © 2007 Elsevier B.V. All rights reserved.

Keywords: Adaptive response; TK6 cells; LOH detection system

1. Introduction

An adaptive cellular response occurs when a mild stress applied before a challenging treatment with a DNA-damaging agent decreases the detrimental effects of the challenge. In radioadaptation, as it is usually defined, exposure to a low dose of ionizing radiation

(IR) provides some protection against a high dose. Radioadaptation was first reported by Olivieri et al. [1], who showed that radiation delivered by labeling human lymphocytes with tritiated thymidine causes a decrease in the frequency of chromosomal aberrations induced by subsequent exposure to 15 Gy of IR. That discovery stimulated a series of studies in human lymphocytes and various mammalian cell lines (for review, see refs. [2,3]) and suggested that the adaptive response is an important defense mechanism, especially against low doses of IR. The molecular mechanisms involved, however, remain largely unknown [4–8], and cellular

* Corresponding author. Tel.: +81 48 467 9710;
fax: +81 48 462 1426.

E-mail address: yatagai@postman.riken.go.jp (F. Yatagai).

responses such as the bystander effect, genetic instability and hyper-radiosensitivity seem tightly related to the adaptive response in a specific low-dose region. One of the hot subjects in recent adaptive response studies is the expression of the genes involved in the mechanism [8–10]. Another is the relationship between the adaptive response and the bystander effect [11–15]. In mammalian cells, for example, bystander mutagenesis may be suppressed by an adaptive response [11].

Following the report by Olivieri et al., reduced induction of both micronuclei and sister chromatid exchanges was shown in Chinese hamster V79 cells pre-exposed to low doses of γ -rays or ^3H β -rays [16]. Subsequent studies reported similar radioadaptive responses, such as reduced mutation frequencies in human lymphocytes [17], mouse SR-1 cells [18] and human–hamster hybrid A_L cells [19], an altered mutation spectrum in human–hamster hybrid A_L cells [19], reduced micronucleus frequencies in human lymphocytes [5] and mouse embryo cells [20], and reduced deletions and rearrangements in human lymphoblast cells [21]. The mechanism underlying those radioadaptations may have been the induction of an efficient chromosome repair system by the priming radiation dose, and in fact, the efficiency of DNA double-strand break (DSB) repair in Chinese hamster V79 cells exposed to γ -rays is enhanced by a priming exposure of 5 cGy of γ -rays [22]. Furthermore, DSBs with either blunt or staggered ends, created by restriction enzymes, induce the adaptive response [3].

The human lymphoblastoid TK6 cell line, isolated by Skopek et al. [23], is heterozygous at the *thymidine kinase* (*TK*) locus. Honma's laboratory developed a loss of heterozygosity (LOH) detection system that can be used for molecular analysis of *TK* mutations as well as for detecting alterations at the chromosome level [24,25]. Using that methodology, we were able to detect IR effects at doses as low as 10 cGy [26–28]. Irradiation of TK6 cells with 10 cGy of X-rays clearly demonstrated radiation-specific types of LOH events or interstitial deletions in chromosome 17 [26]. We also observed more efficient induction of such events after 10 cGy irradiation with an accelerated carbon-ion (135 MeV/u) beam [27], and this was apparent in frozen cells exposed to the same carbon-ion beam [28]. These results strongly suggest that the interstitial deletions were the result of end-joining repair of IR-induced DSBs.

Because the radiation-sensitive LOH analysis system in TK6 cells is effective for detecting the fate of radiation-induced DNA double-strand breaks (DSBs),

we use it here to see if the adaptive response could produce measurable changes in IR-induced genetic alterations. The results we obtained were not completely expected, but are interesting.

2. Materials and methods

2.1. Cell culture and adaptive treatment

The methodologies for the detection of *TK*-deficient mutants and the materials and methods used for cell culture and growth have been previously reported [26]. Briefly, TK6 cells were incubated in RPMI1640 medium supplemented with HAT to eliminate pre-existing *TK*⁻ deficient mutants. The cells were then resuspended in fresh normal medium, and 6 ml cell suspension was dispensed into 6-cm diameter Petri dishes. The cells were pretreated ("primed") with 2.5, 5 or 10 cGy of X-rays (250 kVp) at a rate of 10 cGy/min, and placed in a 5% CO_2 humidified incubator. The cell concentration was adjusted to 8×10^5 cells/ml at the end of the post-irradiation incubation period of 1.5, 3, 6, 9 or 12 h. The cells were then challenged with 2 Gy X-rays (250 kVp) at 1 Gy/min. Non-primed irradiated cells treated in the same manner as the primed cells served as controls.

2.2. Survival assay and *TK* mutation assay

To determine the surviving fraction of the challenged cells, we measured the plating efficiency (PE) immediately after irradiation using the limiting dilution method. For mutation expression, we incubated the cells with non-selecting RPMI1640 medium for about 60 h following the X-ray challenge. We measured the PE of incubated cells similarly, determining the *TK* mutation frequency. To select *TK*⁻ mutant clones, we seeded incubated cells into 96-well plates at 4×10^4 cells per well in RPMI1640 medium containing 4 $\mu\text{g}/\text{ml}$ trifluorothymidine (TFT); we harvested the normally growing clones after 2 weeks and the slow growing clones after 4 weeks.

2.3. Determination of optimum irradiation conditions for mutagenic adaptation

To determine the optimum conditions for evoking the mutagenic radioadaptive-response, we tested the MF induced by 2 Gy at 0, 1.5, 3, 6, 9 and 12 h after a priming dose of 10 cGy, selected the optimum interval time, and then tested the MF induced by 2 Gy at that interval time after priming doses of 0, 2.5, 5 and 10 cGy.

2.4. LOH analysis of *TK*⁻ mutants

Fig. 1 illustrates how we classified *TK*⁻ mutants. We first determined *TK* LOH by PCR analysis of exons 4 and 7 [29]. If the PCR products of both were similar to those of the parental *TK* heterozygous cells, we classified the mutant

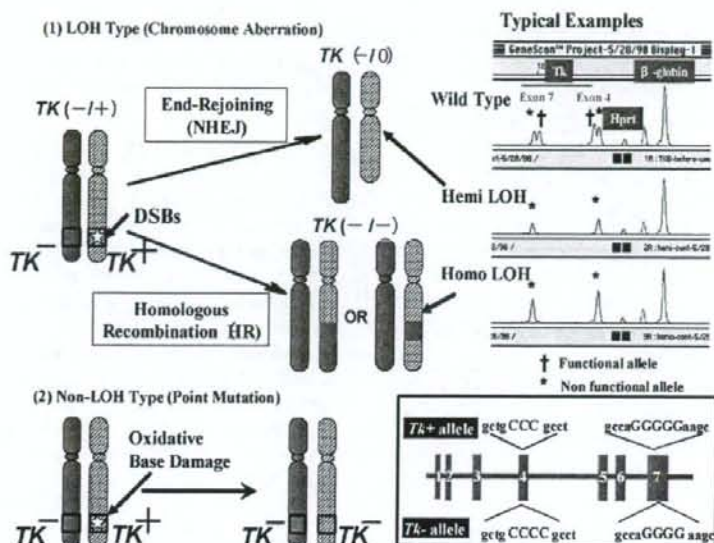


Fig. 1. LOH classifications of TK^- mutants. The first step in the genetic analysis of selected TK^- mutants was to judge whether there was a loss of TK heterozygosity (LOH). This was accomplished by PCR amplification of exons 4 and 7 regions of the TK locus. This step also distinguished between hemizygous LOH (loss of the functional TK allele) and homozygous LOH (replacement of the functional TK allele by a mutated TK^- allele (see ref. [29]).

as a "non-LOH" mutant. We used the same technique to distinguish between hemizygous LOH (in which the functional TK allele is lost) and homozygous LOH (in which the functional TK allele is replaced by TK^-). To determine the extent and size of the deleted or substituted portions of the chromosome involved, we analyzed 11 microsatellite regions (D17S588, D17S1784, D17S785, D17S789, D17S802, D17S807, D17S928, D17S932, D17S1299, D17S1566 and THRA) on chromosome 17 using multiple PCR reactions as described previously [29]. The fine structure of the recovered TK^- LOH mutations was determined by chromosome mapping analysis.

2.5. Base sequencing of non-LOH mutants

For a precise analysis of non-LOH mutants, we extracted RNA using Isogen (Nippon Gene, Japan), and obtained cDNA using a First-Strand cDNA Synthesis Kit, Amersham, USA). Following PCR amplification, the purified 807-bp fragments were sequenced by Takara Bio (Japan). The primers 5'-AGAGTACTCGGGTTCGTGAA-3' and 5'-GCAGCATGCAGGCAGCGTG-3' (forward and reverse, respectively) were used for cDNA synthesis, PCR amplification and base sequencing [30]. To prevent the overestimation of mutational events, we counted identical mutations originating from a single irradiated dish as a single event.

Table 1a

TK mutation frequency (MF) at various time intervals between priming and challenging X-ray exposures (priming dose, 10 cGy; challenging dose, 2 Gy)

| Time interval (h) | 0 | 1.5 | 3 | 6 | 9 | 12 |
|------------------------------|------|------|------|------|------|------|
| TK MF ($\times 10^{-6}$) | 19.8 | 18.1 | 14.4 | 13.5 | 17.8 | 19.7 |

3. Results

3.1. Optimum conditions for mutagenic adaptation

For inducing an adaptive response to X-ray irradiation, the optimum interval between a 10-cGy priming dose and a 2-Gy challenging dose was 6 h (Table 1a), and the optimum priming dose 6 h prior to a 2-Gy challenging dose was 5 cGy (Table 1b). We therefore decided to characterize the induced TK mutants by repeating

Table 1b

TK mutation frequency at various priming X-ray doses (challenging dose, 2 Gy; interval between 2 exposures, 6 h)

| Priming X-ray dose (cGy) | 0 | 2.5 | 5 | 10 |
|------------------------------|------|------|-----|-----|
| TK MF ($\times 10^{-6}$) | 13.3 | 15.8 | 4.5 | 6.3 |

Table 2
Surviving fractions of primed and non-primed TK6 cells following challenge exposure to 2 Gy X-rays

| Experiment | Surviving fraction | |
|-----------------|---------------------|----------------------|
| | Non-primed cells | Primed cells (5 cGy) |
| I | 0.043 | 0.047 |
| II | 0.047 | 0.070 |
| III | 0.049 | 0.040 |
| Mean \pm S.D. | 0.046 \pm 0.0031* | 0.052 \pm 0.016* |

* $P=0.58$; *t*-test.

Table 3
TK mutation frequency in primed and non-primed TK6 cells following challenge exposure to 2 Gy X-rays

| Experiment | TK mutation frequencies ($\times 10^{-6}$) | |
|-----------------|--|----------------------|
| | Non-primed cells | Primed cells (5 cGy) |
| I | 13.3 | 4.5 |
| II | 13.3 | 10.5 |
| III-a | 20.4 | 15.1 |
| III-b | 21.0 | 15.6 |
| Mean \pm S.D. | 18.3 \pm 4.3* | 11.4 \pm 5.1* |

Experiments III-a and III-b were carried out concurrently with survival assay III, but they were independent mutation assays.

* $P=0.020$; *t*-test.

our mutation experiments under those conditions (5 cGy followed 6 h later with 2 Gy).

3.2. Survival assay and TK mutation assay

Table 2 shows the surviving fraction, expressed as PE (2 Gy X-ray irradiated cells)/PE (unirradiated cells) of primed and unprimed cells immediately after the 2-Gy challenge exposure. Irradiation with the priming dose of 5 cGy did not influence the PE of unchallenged cells (data not shown). The effect of priming on survival after 2 Gy X-ray irradiation was 1.1 (0.052/0.046; $P=0.58$, *t*-test). Thus, priming did not significantly affect survival after the challenge exposure.

Table 4
Distribution of mutational classes among the isolated TK mutants

| Mutational class | Number of identified mutants (Exp. I, II, III-a, III-b) [MF $\times 10^{-6}$] | |
|------------------|--|-------------------------------------|
| | Non-primed cells | Primed cells (5 cGy) |
| Non-LOH | 18 (5, 4, 6, 3) [7.1] | 8 (1, 3, 2, 2) [1.9] |
| LOH | | |
| Hemizygous | 15 (3, 3, 7, 2) [6.0] | 27 (8, 7 ^a , 5, 7) [6.4] |
| Homozygous | 13 (3, 4, 3, 3) [5.1] | 13 (2, 3, 5, 3) [3.1] |
| Total | 46 (11, 11, 16, 8) [18.3] | 48 (11, 13, 12, 12) [11.4] |

^a One of the seven mutants was a mixed hemizygous/homozygous type.

On the other hand, priming did affect the TK MF induced by the challenge. Data from 4 independent experiments showed that priming reduced the MF to 62% of the unprimed MF ($P=0.020$, *t*-test) (Table 3).

3.3. LOH analysis of TK⁻ mutants

Table 4 shows the distributions of LOH classes among the isolated TK⁻ mutants as determined by PCR analysis. We isolated non- and "small" LOH mutants (see Sections 3.4 & 3.5) as normal growth mutants in the first selection, except for a few cases. We isolated the remaining LOH mutants as slow growth mutants in the second selection. We estimated the pre-exposure effect from the proportion of each mutational event as follows: (i) 7.1×10^{-6} to 1.9×10^{-6} reduction in corresponding MF of non-LOH events, (ii) 6.4×10^{-6} to 6.1×10^{-6} change in corresponding MF of hemizygous LOH events and (iii) 5.1×10^{-6} to 3.1×10^{-6} reduction in corresponding MF of homozygous LOH events. Thus, the MF of a non-LOH event in primed cells was reduced to 27% of the non-primed MF. The induction of hemizygous events, on the other hand, was barely influenced by priming. As far as homozygous events go, their corresponding MF was reduced to 61% of the original level, which was similar to level of reduction in total MF (62%).

3.4. Analysis of LOH tracts on chromosome 17

Fig. 2 shows the deleted or replaced regions of chromosome 17 in each LOH mutant. Mutants reflected both type 1 and type 2 LOH events. Type 1 defines a terminal event; that is, the deleted or exchanged chromosome segment extends to the telomere marker (D17S928). Type 2 defines an interstitial deletion; the altered segment does not reach the telomere marker.

In the present study, most hemizygous LOH mutations, which are considered to be the result of DSB non-homologous end-joining (NHEJ) repair, reflected

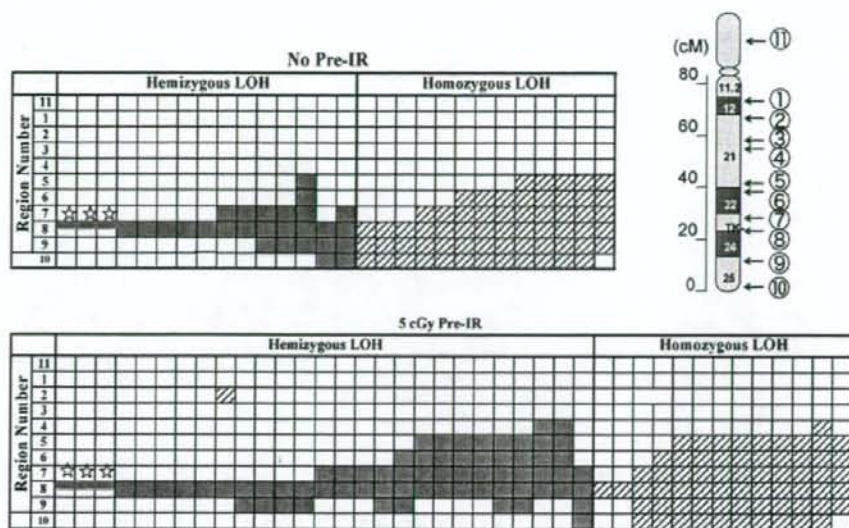


Fig. 2. Chromosome mapping of the LOH mutants. We analyzed the LOH mutants selected after a 2 Gy of challenging X-ray irradiation to determine the extent of the deleted or exchanged portions of the chromosome. The upper panel shows the profiles of 28 LOH mutants selected from non-primed cells, and the lower panel shows the profiles of 40 LOH mutants selected from cells primed with 5 cGy of X-rays. Each column represents a single LOH mutant. The rows represent regions of chromosome 17 diagrammed in the upper right insert. Shaded squares represent deleted regions and hatched squares represent exchanged regions (see text). The region numbers refer to the 11 microsatellite regions: (1) D17S588; (2) D17S1784; (3) D17S785; (4) D17S789; (5) D17S802; (6) D17S807; (7) D17S928; (8) D17S932; (9) D17S1299; (10) D17S1566; (11) THRA (see ref. [29]). The star symbol represents a "small" type 2 hemizygous event in which the deletion is restricted to *TK* locus.

type 2 events in both the non-primed (13 of 15 mutants) and primed (26 of 27 mutants) groups. Small type 2 deletions – those restricted to the *TK* locus (Fig. 2) – were infrequent in both groups (3 of 15 mutants in non-primed cells and 3 of 27 in primed cells). Similarly, the proportion of large deletion mutants (expanding to the region beyond region 8, Fig. 2) was also similar in the primed (18 of 27 mutants) and non-primed (7 of 15 mutants) groups. Homozygous LOH events, on the other hand, which are considered to be the result of homologous recombination (HR) repair of DSBs, were primarily identified as type 1 events in both primed (10 of 13) and non-primed (12 of 13) groups. Interestingly, small homozygous LOH events (where only a single region was replaced, Fig. 2) were recovered from the primed cells (2 of 13 (3 of 14)), but not from the non-primed cells (0 of 13).

3.5. Analysis of non-LOH-mutants

We detected many types of alterations in the non-LOH mutant cDNAs (Table 5). The proportion of single base-substitutions among all the mutations identified as this class was 1/8 (13%) in the primed cells, and this value

was clearly lower than 7/18 (87%) in the unprimed cells. G and C bases were targeted in base substitution mutations, except for a single case of an A to T transversion (Table 5). Most (4/5) of the double-base changes consisted of a single base deletion (causing a frameshift) and a base substitution, except for a single case of a GC to TA double transversion in a radioadapted mutant. It is difficult to estimate the effect of priming on the induction of the double-base change events from the limited number of cells involved. Similar difficulties were also found in the other mutational events in this class such as triple-base changes, multiple-base changes and exon skipping. In addition, the proportion of abnormal transcription events (both functional and non-functional *TK* alleles are equally transcribed) was also similar in the radioadapted (1/8, 13%) and the non-adapted (3/18, 17%) group, although its origin was not identified.

4. Discussion

The radioadaptation conditions used in this study (5 cGy of priming X-rays followed in 6 h by 2 Gy of challenging X-rays) were similar to those used in other studies [4,6,11,12,14,16]. The *TK* mutation frequency

Table 5
Nature of the isolated non-LOH mutants

| Type of mutation | Specific changes | [Position: exon] | Number of identified mutants | |
|--|--------------------------------------|------------------|------------------------------|--------------------------|
| | | | Non-primed exposure | Primed (5 cGy pre-X-ray) |
| Single base substitutions | | | 7 | 1 |
| G → A (Gly → Glu) | [56:1] | | 3 | 0 |
| C → T (Gln → Stop) | [64:1] | | 1 | 0 |
| C → A (Ser → Stop) | [89:2] | | 1 | 0 |
| A → T (Ser → Cys) | [97:2] | | 1 | 0 |
| G → C (Leu → Phe) | [108:2] | | 0 | 1 |
| G → A (Glu → Lys) | [430:6] | | 1 | 0 |
| Double base changes | | | 3 | 2 |
| G → A (Gly → Glu)/Del. C | [56:1/676:7] | | 1 | 0 |
| G → C (Leu → Phe)/Del. A | [108:2/686:7] | | 0 | 1 |
| Add. C/Del. G | [232:4/641:7] | | 1 | 0 |
| GC → TA (Leu Asp → Leu Asn) | [372 and 373:5] | | 0 | 1 |
| G → A (Glu → Lys)/Del. G | [430:6/447:6] | | 1 | 0 |
| Triple base changes | | | 0 | 1 |
| Del. G/C → T (Ile → Ile)/C → T (Leu → Leu) | [92:1/288:4/561:7] | | 0 | 1 |
| Multiple base changes | | | 1 | 1 |
| CC → AT (Thr Gln → Thr Stop)/G → A (Gln → Gln)/G → A (Gln → Gln)/Add. C/Del. G | [51 and 52:1/66:1/667:7/232:4/641:7] | | 0 | 1 |
| Base changes at 20 sites | | | 1 | 0 |
| Exon skipping, abnormal splicing and deletion | | | 3 | 2 |
| Del. of a part of exon 1 (48 bases) | [161–209: 1] | | 1 | 1 |
| Abnormal splicing of intron (between exons 1 and 2) | | | 1 | 0 |
| Skipping of exon 3 (Del. 111 bases) | [99–203: 3] | | 1 | 0 |
| Skipping of exon 5 (Del. 90 bases) | [304–393: 5] | | 0 | 1 |
| Abnormal transcription | | | 3 | 1 |
| Both functional and non-functional alleles are equally transcribed | | | | |
| Unidentified | | | 1 | 0 |
| Total | | | 18 | 8 |

we observed after the challenge X-rays (18.3×10^{-6}) was reduced by the 5-cGy priming exposure to about 62% of the non-primed level (11.4×10^{-6}). Taking into consideration the *TK* spontaneous mutation frequency observed in our recent study (3.0×10^{-6}) [32], the increase in MF induced by 2 Gy of X-rays was reduced from 6.1-fold to 3.8-fold.

We originally planned this study to determine whether radioadaptation would alter the characteristics of X-ray-induced LOH events. X-ray-induced interstitial deletions are likely to be the result of NHEJ repair of DSBs, and this type of mutation was the one we recovered most frequently after 2 Gy X-ray irradiation in our previous study [24]. We also found that carbon-ion beam irradiation induced interstitial deletions more efficiently than the same dose of X-rays [26,27], which we interpreted as the result of a higher occurrence of inaccurately

repaired DSBs. In the present study, however, we found that the frequency of hemizygous LOH mutations, as well as their size and the distribution of deleted regions on chromosome 17, was similar for radioadapted and non-adapted cells. Those results are not consistent with reports suggesting that enhanced repair of DSBs reduces chromosomal alterations [21,22]. An entire genome assay might lead to results similar to the ones in those reports, but our observations were restricted to the *TK* locus on chromosome 17.

On the other hand, we observed a decrease in the induction of homozygous LOH events in the primed cells, which suggests that priming enhanced the HR repair of DSBs. We recently constructed a model system to follow the fate of a single DSB introduced by the restriction enzyme *I-sceI* at a specific site in the *TK* gene in TK6 cells [31]. In preliminary exper-

iments, low dose/low-dose rate γ -irradiation (30 mGy at 1.2 mGy/h) did not significantly affect end joining (EJ) repair of this specific DSB, but it enhanced the efficiency of HR repair by about 50% (unpublished data). The small homozygous LOH events we observed in the primed cells in the present study (3/14) might reflect this enhanced HR, but we must examine whether the adaptive response was really involved because we also recovered small homozygous LOH mutants after the low-dose/low-dose rate γ -ray exposures [32]. The decrease in the frequency of single-base substitutions that we observed in primed cells (1/48) versus non-primed cells (7/46) (Tables 4 and 5) is rarely influenced by counting base substitutions accompanied by single base deletions (which would result in 2/48 for primed cells and 9/46 for non-primed cells), so the most likely mechanism for the reduced induction of non-LOH mutants was suppression of base substitutions.

One of the possible targets for radioadaptation is oxidative base damage. In fact, down-regulation of the human *CDC16* gene that occurs after oxidative stress causes more rapid and efficient repair in adapted (2 cGy pre-irradiated) human lymphoblastoid cells challenged with 4 Gy irradiation [6]. On the other hand, oxidative base excision repair enzymes, including DNA glycosylases, hOGG1 and hNth1, are reportedly not up-regulated at the post-transcriptional level in γ -ray-primed TK6 cells [33]. Since DNA glycosylase can suppress base substitution, we need to examine whether radioadaptation enhances the enzyme's activity under the present condition. Alternatively, base substitution activity might not accurately reflect DNA glycosylase activity because attempted base excision repair of IR damage by the enzyme can lead to lethal and mutagenic DSBs [34].

A variety of untargeted effects may contribute to the short- and long-term fate of a cell exposed to IR [35]. An example is the possible involvement of a "radioadaptive bystander" effect in human lung fibroblasts [36]. The reduction of radiosensitivity in cells with a wild type *p53* gene by a radiation-induced, nitric oxide (NO)-mediated bystander effects may be a manifestation of the radioadaptive response [37,38]. This possibility is supported by the finding that the NO-induced apoptosis observed in lymphoblastoid and fibroblast cells depends on the phosphorylation and activation of *p53* [39]. However, it is still unclear whether the NO-mediated pathway also contributes to the mutagenic adaptation. The de novo protein synthesis is required for expression of adaptive responses [22,40], and gene expression studies are improving our understanding of the molecular mechanisms underlying the radioadaptive response [9,10,40,41]. Our laboratory is also focusing on the molecular mechanisms involved

in radioadaptation, especially the expression of genes involved in DNA base and nucleotide excision repair.

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Miscoding Properties of 2'-Deoxyinosine, a Nitric Oxide-Derived DNA Adduct, during Translesion Synthesis Catalyzed by Human DNA Polymerases

Manabu Yasui^{1*}, Emi Suenaga², Naoki Koyama¹, Chikahide Masutani³, Fumio Hanaoka³, Petr Gruz¹, Shinya Shibutani⁴, Takehiko Nohmi¹, Makoto Hayashi¹ and Masamitsu Honma¹

¹Division of Genetics and Mutagenesis, National Institute of Health Sciences, 1-18-1 Kamiyoga, Setagaya, Tokyo 158-8501, Japan

²Division of Pharmacognosy, Phytochemistry and Narcotics, National Institute of Health Sciences, 1-18-1 Kamiyoga, Setagaya, Tokyo 158-8501, Japan

³Cellular Biology Laboratory, Graduate School of Frontier Biosciences, Osaka University, 1-3 Yamada-oka, Suita, Osaka 565-0871, Japan

⁴Department of Pharmacological Sciences, State University of New York at Stony Brook, Stony Brook, NY 11794-8651, USA

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Chronic inflammation involving constant generation of nitric oxide (¹NO) by macrophages has been recognized as a factor related to carcinogenesis. At the site of inflammation, nitrosatively deaminated DNA adducts such as 2'-deoxyinosine (dI) and 2'-deoxyxanthosine are primarily formed by ¹NO and may be associated with the development of cancer. In this study, we explored the miscoding properties of the dI lesion generated by Y-family DNA polymerases (pols) using a new fluorescent method for analyzing translesion synthesis. An oligodeoxynucleotide containing a single dI lesion was used as a template in primer extension reaction catalyzed by human DNA pils to explore the miscoding potential of the dI adduct. Primer extension reaction catalyzed by pol α was slightly retarded prior to the dI adduct site; most of the primers were extended past the lesion. Pol η and pol κ Δ C (a truncated form of pol κ) readily bypassed the dI lesion. The fully extended products were analyzed by using two-phased PAGE to quantify the miscoding frequency and specificity occurring at the lesion site. All pils, that is, pol α , pol η , and pol κ Δ C, promoted preferential incorporation of 2'-deoxycytidine monophosphate (dCMP), the wrong base, opposite the dI lesion. Surprisingly, no incorporation of 2'-deoxythymidine monophosphate, the correct base, was observed opposite the lesion. Steady-state kinetic studies with pol α , pol η , and pol κ Δ C indicated that dCMP was preferentially incorporated opposite the dI lesion. These pils bypassed the lesion by incorporating dCMP opposite the lesion and extended past the lesion. These relative bypass frequencies past the dC:dI pair were at least 3 orders of magnitude higher than those for the dT:dI pair. Thus, the dI adduct is a highly miscoding lesion capable of generating A \rightarrow G transition. This ¹NO-induced adduct may play an important role in initiating inflammation-driven carcinogenesis.

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Keywords: inflammation; nitric oxide; DNA adduct; translesion synthesis; nonradioactive analysis

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*Corresponding author. E-mail address: m-yasui@nih.go.jp

Abbreviations used: ¹NO, nitric oxide; dI, 2'-deoxyinosine; dX, 2'-deoxyxanthosine; dA, 2'-deoxyadenosine; 8-Oxo-dG, 8-oxo-2'-deoxyguanosine; dNTP, 2'-deoxynucleoside triphosphate; Alexa546, Alexa Fluor 546 dye; pol α , human DNA polymerase α ; pol η , human DNA polymerase η ; pol κ , human DNA polymerase κ ; pol κ Δ C, a truncated form of pol κ ; F_{ins} , frequency of insertion; F_{ext} , frequency of extension; 8-NO₂-dG, 8-nitro-2'-deoxyguanosine; dCMP, 2'-deoxycytidine monophosphate; dTMP, 2'-deoxythymidine monophosphate; dTTP, 2'-deoxythymidine triphosphate; dC₁TP, 2'-deoxycytidine triphosphate; dGTP, 2'-deoxyguanosine triphosphate; Cy3, Cyanin 3; endo V, endonuclease V.

Introduction

Chronic inflammation involving constant generation of nitric oxide (^1NO) by macrophages has been recognized as a factor related to carcinogenesis.¹⁻³ ^1NO can attack neighboring epithelial and stromal cells by damaging the DNA, altering their genome stability. There are two possible major pathways for the ^1NO reaction (Fig. 1). One pathway involves the combination of ^1NO and superoxide with the formation of highly toxic peroxynitrite (ONOO^-). Spontaneous hydrolysis of peroxynitrite under physiological conditions generates secondary radical species ($^1\text{NO}_2$, ^1OH , and $\text{CO}_3^{\cdot-}$) that induce oxidation and nitration of diverse DNA adducts^{4,5} such as 8-oxo-2'-deoxyguanosine (8-OxodG) and 8-nitro-2'-deoxyguanosine (8- NO_2 -dG).^{6,7} A second involves nitrosative deamination of DNA base by ^1NO via formation of several nitrosating agents, which predominantly exist as nitrous anhydride (N_2O_3) at physiological pH.⁸ The DNA base products by nitrosative deamination mainly involve conversion of adenine to hypoxanthine [2'-deoxyinosine (dI)] (Fig. 2), guanine to xanthine [2'-deoxyxanthosine (dX)], and cytosine to uracil.⁹⁻¹²

The spectrum of nitrosative DNA adducts in N_2O_3 -treated plasmid DNA was composed of approximately 2% dG-dG cross-links, 4-6% abasic sites, and 25-35% each of dI, dX, and 2'-deoxyuracil.^{12,13} Moreover, dI and dX, as well as lipid peroxidated adducts, were increased in the cellular DNA of tissues from the ^1NO -overproducing SJL mouse model of inflammation.¹⁴ The increased production of ^1NO was associated with an increased mutation frequency.¹⁵ When human TK6 cells were exposed to ^1NO , the increase in mutation rates observed at hypoxanthineguanine

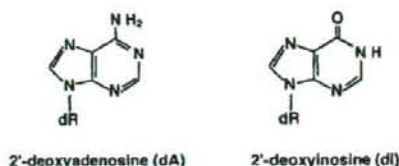


Fig. 2. Structures of dA and dI adducts.

phosphoribosyltransferase and thymidine kinase gene loci correlated with the 40-fold increase of dI and dX more than did that of the controls in the cellular DNA.¹⁰ Thus, the dI adduct is one of the major ^1NO -derived DNA lesions and may contribute to the burden of carcinogenesis in inflammation tissue.

Site-specifically dI-modified oligodeoxynucleotides have been used as DNA templates for investigating the miscoding events using only mouse pol α and rat pol β .¹⁶ The previous report showed that rat pol β inserted only 2'-deoxycytidine monophosphate (dCMP) opposite the dI lesion and that mouse pol α tended to incorporate dCMP and 2'-deoxythymidine monophosphate (dTMP) opposite the lesion. However, the miscoding events were investigated with the detection of mismatched base pairs by loss of a restriction enzyme recognition site. No quantitative analysis, therefore, has been performed for determination of miscoding events generated by dI.

Human DNA pol η ¹⁷ and pol κ ^{18,19} that are associated with translesion synthesis past a variety of DNA lesions^{20,21} were examined. We have here explored the miscoding properties of the dI lesion that occurred during DNA replication catalyzed by

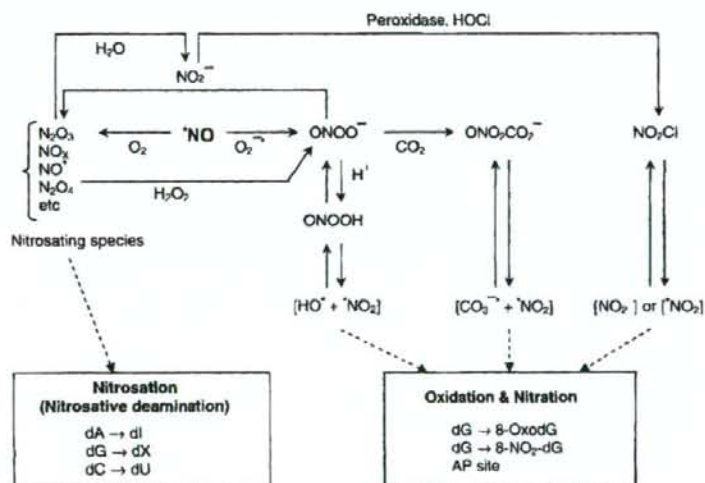


Fig. 1. Possible pathways for the formation of ^1NO -induced DNA adducts.