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Use of β -galactosidase (*lacZ*) gene α -complementation as a novel approach for assessment of titanium oxide nanoparticles induced mutagenesis

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ARTICLE INFO

Article history: Received 6 January 2012 Received in revised form 3 June 2012 Accepted 7 June 2012 Available online 15 June 2012

Keywords: Titanium dioxide Nanoparticles Mutagenicity E. coli β-galactosidase gene Transformation

ABSTRACT

The mutagenic potential of titanium dioxide nanoparticles (TiO₂-NPs) of an average size 30.6 nm was investigated using β -galactosidase (*lacZ*) gene complementation in plasmid pUC19/*lacZ⁻* Escherichia coli DH5 α system. Plasmid pUC19 was treated with varying concentrations of TiO₂-NPs and allowed to transfect the CaCl₂-induced competent DH5 α cells. The data revealed loss in transformation efficiency of TiO₂-NPs treated plasmids as compared to untreated plasmid DNA in DH5lpha host cells. Induction of multiple mutations in α -fragment of *lacZ* gene caused synthesis of non-functional β -galactosidase enzyme, which resulted in a significant number of white (mutant) colonies of transformed E. coli cells. Screening of mutant transformants based on blue: white colony assay and DNA sequence analysis of lacZ gene fragment clearly demonstrated TiO₂-NPs induced mutagenesis. Multiple alignment of selectable marker lacZ gene sequences from randomly selected mutants and control cells provided a gene specific map of TiO2-NPs induced mutations. Mutational analysis suggested that all nucleotide changes were point mutations, predominantly transversions (TVs) and transitions (TSs). A total of 32 TVs and 6 TSs mutations were mapped within 296 nucleotides (nt) long partial sequence of lacZ gene. The region between 102 and 147 nt within lacZ gene sequence was found to be most susceptible to mutations with nine detectable point mutations (8 TVs and 1 TSs). Guanine base was determined to be more prone to TiO₂-NPs induced mutations. This study suggested the pUC19/E. coli DH5 α lacZ gene α -complementation system, as a novel genetic approach for determining the mutagenic potential, and specificity of manufactured NPs and nanomaterials.

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1. Introduction

Extensive applications and an upsurge in synthesis of nanoparticles (NPs) in recent years pose a serious concern due to potential human and environmental risks [1–3]. Rapid commercialization of engineered NPs for use in a variety of industrial, chemical, medical and diagnostic applications presents a challenge to NPs manufacturers and regulators related to the safety of nanomaterial products. Indeed, the biological responses to NPs may exceed those elicited by micron-sized particles [4,5] due to their small size, high number per given mass, large specific surface area, and generation of free radicals [6]. It has been shown that NPs of titanium dioxide (TiO₂) and silica can enter the nucleus [7,8] where they produce intranuclear protein aggregates that can lead to inhibition of replication, transcription, and cell proliferation [9]. The titanium dioxide nanoparticles (TiO₂-NPs) have been reported to induce oxidative stress, and DNA damage in Chinese hamster ovary (CHO) cells,

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Syrian hamster embryo fibroblasts, human lymphoblastoids and human bronchial epithelial (BEAS-2B), and human amniotic epithelial (WISH) cell lines [10–15]. These NPs have also shown to induce apoptosis in human lymphocytes, U937 human monoblastoid cells, A549 alveolar epithelial cells, NRK-52E, LLC-PK1 renal proximal cells, and A431 human epidermal cells [16–19].

TiO₂-NPs are reported to be toxic to both Gram-negative and Gram-positive bacteria, and the antibacterial properties of these NPs have been exploited in water treatment reactors [20,21]. However, limited studies have been performed on the assessment of the mutagenic potential of TiO₂-NPs [22-24] in bacteria. Warheit et al. [25] have used the Ames bioassay to test the potential mutagenicity of TiO₂ using various bacterial strains. Pan et al. [26] compared the mutagenicity of several metal oxide NPs (TiO₂, Al_2O_3 , Co_3O_4 , CuO, and ZnO) to define the toxic potential of this group of nanomaterials. Recently, Kumar et al. [27] demonstrated the weak mutagenic potential of ZnO and TiO₂-NPs in Salmonella typhimurium strains TA98, TA1537 and Escherichia coli (WP2uvrA) of Ames test, underscoring the possible carcinogenic potential similar to certain mutagenic chemicals. Many chemical mutagens and carcinogens produce characteristic DNA adducts and base changes, allowing a correlation between the mutational spectrum of the

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^{1383-5718/\$ -} see front matter © 2012 Elsevier B.V. All rights reserved. http://dx.doi.org/10.1016/j.mrgentox.2012.06.002

mutated genes in tumors and the carcinogenic agents [28]. Therefore, it is important to identify the mutational specificity in DNA, damaged by a vast range of available metal oxide NPs and nanomaterials. In this study, we have chosen nano-sized TiO_2 (30.6 nm), a naturally occurring mineral, extensively being used in domestic and cosmetic products including food colorants, ceramics, antifouling paints, coatings, and additives in pharmaceuticals [29,30] to investigate its genotoxicity and mutagenicity.

To the best of our understanding, no significant information on mutational analysis encompassing the extent and nature of TiO₂-NPs induced mutations is available in literature. Further, the Ames tester strains designed for assessing the chemical mutagenesis have some limitations with NPs. Particularly the strains do not account for the physical interactions of the particles with DNA that could lead to mutation, which is contrary to the mechanism of chemical induced mutations, and are also known to generate false positive results [31,32]. This has prompted us to utilize the pUC19/lacZ⁻ E. *coli* DH5 α complementation as a simple and effective assay system for assessment of NPs induced mutagenesis. The mutational analysis was performed within the partial sequence of a 296 nt long α -fragment of *lacZ* gene insert in a commercially available 2.686 kb vector plasmid pUC19. The TiO₂-NPs induced DNA lesions in plasmid were processed (repaired and replicated) with in the E. coli cells, and validated the functionality of plasmid pUC19/E. coli DH5 α complementation assay, as a useful tool for studying the NPs induced mutagenesis.

2. Materials and methods

2.1. Materials

Powdered polyhedral rutile TiO₂-NPs, average size 30.6 nm, was a kind gift from the Centre of Excellence in Nanomaterials, Department of Applied Physics, AMU, Aligarh, India. TiO₂-NPs in Milli-Q water were sonicated using Pro Scientific Inc., USA for 15 min at 40 W to obtain a homogeneous suspension before the treatments. Plasmid pUC19 was prepared using QIAGEN plasmid Mini Kit, QIAGEN, USA. Ampicillin, MgCl₂, CaCl₂, 5-bromo-4-chloro-3-indolyl- β -p-galactoside (X-gal) and isopropyl β -D-1-thiogalactopyranoside (IPTG) were purchased from Sigma Chemical Company, St. Louis, MO, USA. All other chemicals were of analytical grade.

2.2. Effect of TiO₂-NPs on viability of E. coli DH5 α

Freshly grown cells (2 × 10⁸ CFU/ml) of *E. coli* DH5 α (F⁻, *endA1*, *glnV44*, *thi-1*, *recA1*, *relA1*, *gyrA96*, *deoR*, *nupG*, Φ 80d*lacZ* Δ M15, Δ (*lacZYA-argF*), U169, *hsdR17*(rK⁻ mK⁺), λ^-) stock were treated with increasing concentrations of 5, 10, 25, and 50 µg/ml of TiO₂-NPs in a total volume of 1 ml for 6 h at 37 °C. The aliquots of 0.1 ml of the treated and untreated control cells were serially diluted and plated on LB agar plates. The plates were then incubated at 37 °C for overnight. The colonies appeared on the plates were recorded as colony forming units (CFU) per ml. The percent survival was plotted as a function of increasing concentrations of TiO₂-NPs.

2.3. Preparation of competent E. coli cells

Cells from the freshly grown 100 ml culture (OD₆₀₀ ~0.5) of *E. coli* DH5 α were harvested by centrifugation at 2000 rpm for 8 min at 4 °C. The cells were gently suspended (1/10 volume) in 10 ml of ice-cold 10 mM CaCl₂ and subjected to centrifugation at 2000 rpm at 4 °C for 8 min. The cells were resuspended in 10 ml of cold 10 mM CaCl₂ and then kept on ice for 30 min. Cold suspension was again centrifuged at 2000 rpm for 8 min at 4 °C, and the cells were resuspended in 1 ml of cold 10 mM CaCl₂. The competent cells were used immediately for transformation.

2.4. Treatment of plasmid DNA with TiO_2-NPs and transformation in competent DH5 α cells

Plasmid pUC19 DNA (~100 ng) in Tris–HCl buffer (0.1 M, pH 7.5) was treated with increasing concentrations of 5, 10, 25, and 50 µg/ml of TiO₂–NPs, in a final volume of 50 µl at 37 °C for 2 h. The untreated and treated plasmid DNA were then incubated separately with 100 µl of competent (*lacZ*⁻) *E. coli* DH5 α host cells each at 4 °C for 30 min, followed by 90 s heat shock at 42 °C. To this nutrient broth (500 µl) was added and the cells were further incubated at 37 °C for 1 h for expression of antibiotic resistance. Cells were then plated on Luria broth (LB) agar plates containing ampicillin (60 µg/ml), X-gal (40 µg/ml) and IPTG (0.1 mM). The plates were incubated overnight at 37 °C. After incubation, the plates were transferred to 4 °C to allow the blue collared colonies to develop. Colonies were the nounted to score the number of mutants (white colonies) versus the number of normal (blue) colonies of Lac⁺ bacteria. This genetic event, in which the α fragment of *lacZ* gene derived from plasmid and ω fragment derived from the host cells constructs a functional gene producing β -galactosidase, is called α -complementation [33]. The *E. coli* DH5 α host cells, which undergo α -complementation, are easily recognized due to formation of blue colonies in the presence of a chromogenic substrate, X-gal. However, any mutation in the *lacZ* gene sequence of the plasmid, invariably produces an amino terminal fragment incapable of α -complementation, and therefore, results in formation of white (mutant) colonies.

2.5. Isolation of plasmid DNA from the mutants and its sequencing

Plasmid pUC19 DNA was isolated using QIAGEN plasmid Mini Kit, QIAGEN, USA, accordingly as suggested in the manufacturer's protocol. The purity and amount of DNA was determined by measuring the absorbance at 260 nm and ratio at 260/280 nm using Nanodrop 800 spectrophotometer (Thermo Scientific, USA). The quality of the isolated DNA was further validated on 1% agarose gel. The plasmid DNA was then subjected to sequencing of a fragment of the *lacZ* gene insert in vector plasmid using M13 reverse primer (5'CAGGAAACAGCTATGAC3') on an automated ABI Prism[®] 377 DNA sequencer (Applied Biosystems Inc., CA, USA) at DNA sequencing facility of the King Faisal Specialist Hospital and Research Centre, Riyadh, Saudi Arabia.

2.6. Multiple sequence alignments and mutation analysis

Partial sequences of a 296 nt *lacZ* gene in mutated plasmids isolated from ten randomly selected bacterial mutants (white colonies) were compared with the sequence of the untreated control. Multiple sequence analysis was performed by using CLUSTALW with default parameters [34]. The point mutations and their distribution across the specific region of *lacZ* sequence were manually identified.

3. Results

3.1. E. coli (DH5 α) host cell viability and transformation with TiO₂-NPs treated pUC19 plasmid

E. coli DH5 α cells treated with TiO₂-NPs at concentrations of 5, 10, 25, and 50 µg/ml for 6 h exhibited a decrease in the colony forming ability. The percent survival of TiO₂-NPs treated cells declined in a concentration dependent manner from 83.1 ± 3.9 to 38.1 ± 3.1 at 5 and 50 µg/ml, respectively (Fig. 1). Whereas, the pUC19 plasmid DNA treated *in vitro* with identical concentrations of TiO₂-NPs have not exhibited any alterations in its molecular size. Virtually no excision of DNA leading to size reduction or speciation was detected on an agarose gel, as compared with the untreated control (results not shown). The effect of TiO₂-NPs treated plasmid pUC19 DNA on transformation efficiency, using CaCl₂ induced competent *E. coli* cells has also been determined. The pUC19 DNA after treatment with TiO₂-NPs at a similar concentration range of 5, 10, 25, and 50 µg/ml were transfected into competent (*lacZ⁻*)



Fig. 1. Effect of TiO₂-NPs on viability of *E. coli* DH5 α cells. Values are expressed as mean ± S.D. of three independent experiments done in duplicate. (*) Significant difference from control (p < 0.01).



Fig. 2. Transformation capacity of TiO₂-NPs treated plasmid and induced mutagenesis. Panel (A) shows the TiO₂-NPs concentration dependent reduction in number of normal (blue) colonies with concomitant increase in the number of white (mutant) colonies on X-gal/IPTG medium. Panel (B) shows a linear decline in transformation frequency and an increase in mutation frequency as a function of TiO₂-NPs concentration.

E. coli DH5 α host cells. The results show a concentration dependent reduction in transformation frequency. The data obtained through blue:white colony assay, relies on the compromised functional activity of β -galactosidase enzyme due to unrepaired or misrepaired base alterations (point mutations) in a partial segment of *lacZ* gene sequence, and thus help demonstrate the TiO₂-NPs induced mutagenesis. A greater number of white (mutant) colonies of transformants were observed with significantly lesser transformation frequency at increasing concentrations of TiO₂-NPs (Fig. 2A and B). The loss of transformation capacity was found to be linearly correlated (*r*=0.99) with TiO₂-NPs concentration. The extent of reduction in bacterial transformation was recorded as 3.6 ± 2.5 , 11.4 ± 5.2 , 26.6 ± 1.15 and $42.4 \pm 1.2\%$ after 2 h treatment with 5, 10, 25 and 50 µg/ml of TiO₂-NPs, respectively.

3.2. Assessment of mutation profile of TiO₂-NPs in damaged pUC19 plasmid DNA

For determination of the types of mutations and their distribution upon processing of TiO_2 -NPs damaged plasmid DNA in *E. coli* cells, the mutant (white) and control (blue) colonies of Lac⁺ bacteria were randomly picked and the plasmid DNA isolated. Sequences of the partial α segment of the *lacZ* gene insert in plasmid were obtained using M13 reverse primer (5'CAGGAAACAGCTATGAC3') from both the blue and white colonies. Sequences of 296 nt long α fragment of a *lacZ* gene consisting of 46 base pairs multiple cloning sites (MCS) derived from plasmids were tagged as TiO₂-W1 to

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Profile of TiO₂-NPs induced mutations within *lacZ* gene in plasmid pUC19 DNA upon α -complementation in *E. coli* DH5 α cells.

<i>E. coli</i> DH5 α mutants	Number of point mutations	Nucleotide changes	Mutation map (nucleotides position on <i>lac</i> Z gene)
TiO ₂ -W1	3	C—G	33
		T—A	135
		T—A	218
TiO ₂ -W2	3	T—A	23
		*T-C	127
		C-A	263
TiO ₂ -W3	1	G—T	150
TiO ₂ -W4	3	T—A	127
-		*A–G	176
		*G-A	215
TiO ₂ -W5	4	A-T	19
		G–C	147
		T—A	180
		G-C	271
TiO ₂ -W6	2	C—G	107
		T—A	227
TiO ₂ -W7	3	A—T	102
		G–C	139
		*C-T	267
TiO ₂ -W8	5	A-T	06
		G-T	18
		A-T	64
		*CT	66
		G-T	214
TiO ₂ -W9	4	G-C	106
		A-T	163
		G-T	198
		*A—G	232
TiO ₂ -W10	4	G—C	73
		C—G	99
		T–A	223
		A-T	256

* Indicates transition mutations.

 TiO_2 -W10 and compared with that of untreated control. The results show that all the DNA sequences from randomly picked mutant colonies exhibited multiple point mutations ranging from 2 to 5, except the colony (TiO_2 -W3), which showed only 1 transition mutation at position 150 nt on treated plasmid. The randomly picked blue (control) colonies did not show any mutations.

The lacZ DNA sequences from mutants and control plasmids were aligned together and a consolidated map of TiO₂-NPs induced mutations was obtained through multiple sequence alignment analysis, as shown in Fig. 3. The mutational analysis revealed that all nucleotide changes were point mutations, mainly transversions (TVs) and transitions (TSs). Comparative nucleotide sequence analysis revealed a total of 32 transversions and 6 transitions mutations mapped along 296 nucleotides (nt) lacZ DNA sequence of the TiO₂-NPs treated pUC19 plasmids (Table 1). The region between 102 and 147 nt within lacZ DNA sequence was found to be most susceptible to mutations with nine detectable point mutations (8 TVs and 1 TSs) followed by the sequence regions between 214 and 250 nt and 6-33 nt with 6 point mutations (5 TVs and 1 TSs) and 5 TVs mutations, respectively. Amongst all the four nitrogenous bases, the guanine base was found to be the most susceptible to mutations (31% of detectable mutations) with 9 TVs and 1 TSs, followed by thymine (25% of detectable mutation) with 7 TVs and 1 TSs, adenine (25% of detectable mutation) with 6 TVs and 2 TSs, and cytosine (21% of detectable mutation) with 4 TVs and 2 TSs. Overall, the mutation spectra represented G:C – C:G transversions (12.5%), G:C - T:A transversions (12.5%), G:C - C:A transversions (3.1%) and G:C – A:T transition (3.1%).



Fig. 3. Multiple sequence analysis of β -galactosidase (*lacZ*) gene indicating the map of TiO₂-NPs induced mutations. Panel A shows the genetic organization of *lacZ* gene in a segment of pUC19 plasmid DNA. The dotted lines represent the *lacZ* gene amplicons of 296 nt including a 46 nt fragment of multiple cloning site (MCS) sequence. The gene sequences from untreated control and ten randomly selected mutant colonies, designated as TiO₂-W1 to W10, were aligned using CLUSTALW with default parameters for detecting the point mutations.

4. Discussion

The mutagenic potential of TiO2-NPs has been assessed through blue:white colony screening, and mutation mapping in a specific fragment of lacZ gene insert in pUC19 DNA processed in transformed *E. coli* DH5 α host cells. The data revealed that the *in vitro* TiO₂-NPs treatment to plasmid pUC19 DNA resulted in a significant loss in transformation efficiency and increased mutagenesis. The survival data also explicitly suggested the toxic effects of TiO₂-NPs on *E. coli* DH5 α cells, which supports the earlier toxicity studies on the Gram-negative and Gram-positive bacteria [35]. Indeed, the nano-sized TiO₂ at a higher concentration range of 100-1000 µg/ml has been reported as detrimental, and can disinfect the water containing 10⁵-10⁶ E. coli cells per ml within 30 min under illuminated conditions [20,21]. In our studies, the reduction in colony forming ability of DH5 α at a selected dose range of 5–50 μ g/ml TiO₂-NPs is attributed to decrease in viability due to cellular and genetic damage. Therefore, a similar dose range of TiO₂-NPs was chosen for treatment of plasmid pUC19, to determine the nature and extent of induced mutations. The results of transformation studies corroborates well with our earlier studies on reduction in transformation frequency of pBR322 DNA in E. coli AB1157 cells at pH 10.0, due to structural distortions and development of strand breaks (S1 nuclease sensitive sites) in super-coiled closed circular DNA [36]. The results also support the studies of Chakrabarty et al. [37] and Ahmad et al. [38], who have demonstrated significant reduction in transformation frequency of RP 1 DNA treated with DNase or by denaturation and sonication, and in plasmid Bluescript SK(+) treated with 200 µM resveratrol, respectively. Thus, the reduction in transformation of *E. coli* DH5α host cells with the treated plasmid DNA can be considered as an end-point for determining NPs toxicity, possibly due to induced DNA damage/structural alterations in plasmid DNA.

To elucidate the extent and nature of TiO2-NPs induced DNA damage and/or mutagenesis, the molecular size of the untreated and TiO₂-NPs treated plasmids, isolated from control and mutant E. coli cells was analyzed on an agarose gel. Comparative analysis revealed no excision of DNA, which suggests that toxic effects of TiO₂-NPs on plasmid DNA per se encompass the structural alterations and/or point mutations. Wang et al. [22] through the hprt forward mutation assay and comet assay have demonstrated that the TiO₂-NPs are capable of inducing point mutations and DNA strand breakages. TiO2-NPs are also known to induce oxidative damage, micronuclei formation, and increased hydrogen peroxide and nitric oxide production in human bronchial epithelial cells [14]. This may lead to mutagenesis, if the lesions in DNA due to chemicals or oxidative insults are not repaired or replicated with sufficiently high fidelity. In order to understand the TiO₂-NPs induced mutagenesis, we have employed plasmid pUC19-E. coli lacZ gene complementation system, as an effective one-step approach for delineating the mutational specificity of NPs. Similar approach using a pSP189 shuttle vector plasmid has been extensively used for determining the mutation profiles of a variety of chemicals such as nitric oxides, peroxinitrites, and sodium nitrite [39-41]. The procedure referred as supF assay generally involves two cycles of transformations involving the human cell line Ad293 and indicator bacterial strains E. coli MBM7070 or MBL 50 [41]. Many studies have employed this assay system for the advantage of picking up the mutations in supF gene by initially processing the damaged plasmid through a replication and repair machinery in cultured human cells followed by processing and screening in bacterial cells based on blue:white colony assay.

In this study, we have exploited a simple, one-step process for assessment of NPs-induced mutagenesis, where the TiO₂-NP damaged plasmid pUC19 DNA carrying an α -fragment of *lacZ* gene with the regulatory sequences and coding information for the first 146 amino acids of β -galactosidase, was allowed to be processed in *E. coli* cells. The carboxy terminal portion of the β -galactosidase is encoded by the bacterium *E. coli* DH5 α , which is used as a host for such vectors. In isolation, neither the plasmid-coded nor the host-coded fragments are themselves active, but in combination they can associate to form an enzymatically active protein. It is feasible to replicate the damaged plasmid DNA directly in *E. coli*, which results in mutations being generated during DNA lesions processing (repair and replication) in bacterial cells [41]. Ahmad et al. [38] have demonstrated the development of point mutations (deletions/substitutions) in resveratrol treated Bluescript SK(+) plasmid, consequent upon the damage processing in the DH5 α cells.

The types and distribution of TiO₂-NPs induced mutations in a partial (296 nt) fragment of *lacZ* gene insert were analyzed through sequencing and multiple sequence alignment analysis. The data revealed multiple point mutations, predominantly TVs and TSs in plasmid lacZ gene sequences. It is well known that point mutations and deletions are the possible factors for inactivation of tumor suppressor genes and activation of oncogenes [42]. The potential of TiO₂-NPs to elicit mutagenicity in metabolically more competent eukaryotes, as well as to induce frame shift mutations in TA98, TA1537 and oxidative mutagenic response in E. coli (WP2 uvrA) strains, both in presence and absence of S9 fraction, have been suggested earlier [25]. Pan et al. [26] have also reported an increase in mutagenic potential of TiO₂, when the particle size is reduced to lower than 100 nm. This corresponds well with our results, where TiO₂-NPs of primary particle size 30.6 nm exhibited significant mutagenesis.

Mutagenicity of TiO₂-NPs is a matter of health concern particularly for the reason that these NPs readily cross the cellular barrier and distribute in body organs [22,25]. Our recent study explicitly demonstrated the TiO₂-NPs induced changes in the levels of oxidative marker enzymes (GSH and catalase), intracellular ROS generation and consequent DNA damage in human amniotic epithelial (WISH) cells [15]. Earlier, Xu et al. [43] have suggested that TiO₂-NPs uptake by cells can induce kilo-base pair deletion mutations in a transgenic mouse mutation system. Peroxynitrite anions (ONOO-) have been identified as an essential mediator involved in mutations induced by TiO₂-NPs in gpt delta transgenic mouse primary embryo fibroblasts [44]. The nano-sized TiO₂ exposure has also been reported to increase the production of nitric oxide (NO) and oxidative DNA damage in human bronchial epithelial cells [14]. Most likely, NO reacts with superoxide anions $(O_2^{\bullet-})$ and can be rapidly converted into more reactive nitrogen compounds such as peroxynitrite (ONOO-) that can cause nitration of proteins, hydroxylation or nitration of DNA, and mutations [40]. The mutation spectra induced by ONOO- suggested the clustering of mutations within 5'region of the supF gene with 21-fold increased mutation frequency in treated pSP189 plasmid replicated in bacteria [40]. The pattern of mutations reported in supF gene in ONOO- treated plasmid pSP189, predominantly involves G:C -T:A transversions (65%), G:C - C:G transversions (28%) and G:C -A:T transitions (11%) in E. coli MBL 50 cells. Whereas, the mutation spectra induced by TiO₂-NPs revealed G:C - T:A and G:C -C:G transversions (12.5% each) in TiO₂-NPs treated pUC19 plasmid replicated in *E. coli* DH5α. Additionally, the NPs treatment induces T:A – A:T (21.8%) and A:T – T:A (18.7%) transversions, which were not recorded with ONOO- treatment [40] but were induced to the extent of 10% of total mutations with 1 M nitrite, pH 6.4 [39]. Since, guanine base in genomic DNA is highly susceptible to oxidative stress due to its lowest oxidation potential, therefore, G:C - T:A and G:C - C:G transversion mutations might occur more frequently under oxidative conditions. Also, the mutagenic lesion 8-oxo-7,8dihydro-guanine (8-oxoG), which can pair with adenine (A) may cause G:C – T:A transversion mutations [44]. However, the molecular basis of G:C - C:G transversions is not clear. Furthermore, the plausible reason for T:A – A:T and A:T – T:A transversions could be the SOS dependent mutator activity of recA[–] *E. coli* DH5 α . The increased SOS dependent mutator activity due to defect in the \in (3' \rightarrow 5' proofreading) subunit of DNA polymerase III, has been attributed to a specific increase in A:T – T:A, A:T – C:G and G:C – T:A transversions [45]. The differences in mutation spectra induced with the oxidants like ONOO–, nitric oxide, sodium nitrite following replication of a damaged shuttle vector in dual hosts system (human Ad293 cells and *E. coli* MBL 50/MBM7070) *vis-a-vis* TiO₂-NPs damaged pUC19 vector, processed in *E. coli* DH5 α alone, could be due to differences in the nature and extent of induced DNA damage, as well as the fidelity of DNA repair and replication machinery of the host cells.

5. Conclusions

The study provided a direct evidence of the TiO_2 -NPs induced mutagenicity through DNA sequence analysis, and suggested that the metal oxide NPs induced mutations can be easily detected through the normal processing of DNA lesions by the repair and replication machinery of indicator *E. coli* strain. Thus, the plasmid pUC19-*lacZ* gene complementation in *E. coli* DH5 α cells proved to be an important genetic approach for assessment of the mutation spectra of NPs.

Conflict of interest

The authors declare that there is no conflict of interest.

Acknowledgements

The authors are thankful to King Abdulaziz City for Science and Technology (KACST), Riyadh, Saudi Arabia, for research funding under the National Plan for Science and Technology (NPST) grant no. 10-NAN1115-02.

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