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1 **Terbium Fluorescence as a Sensitive, Inexpensive Probe for**
2 **UV-induced Damage in Nucleic Acids**

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7 **Abstract**

8 Much effort has been focused on developing methods for detecting damaged nucleic acids.
9 However, almost all of the proposed methods consist of multi-step procedures, are limited,
10 require expensive instruments, or suffer from a high level of interferences. In this paper, we
11 present a novel simple, inexpensive, mix-and-read assay that is generally applicable to nucleic
12 acid damage and uses the enhanced luminescence due to energy transfer from nucleic acids to
13 terbium(III) (Tb^{3+}). Single-stranded oligonucleotides greatly enhance the Tb^{3+} emission, but
14 duplex DNA does not. With the use of a DNA hairpin probe complementary to the
15 oligonucleotide of interest, the Tb^{3+} /hairpin probe is applied to detect ultraviolet (UV)-induced
16 DNA damage. The hairpin probe hybridizes only with the undamaged DNA. However, the
17 damaged DNA remains single-stranded and enhances the intrinsic fluorescence of Tb^{3+} ,
18 producing a detectable signal directly proportional to the amount of DNA damage. This allows
19 the Tb^{3+} /hairpin probe to be used for sensitive quantification of UV-induced DNA damage. The
20 Tb^{3+} /hairpin probe showed superior selectivity to DNA damage compared to conventional
21 molecular beacons probes (MBs) and its sensitivity is more than 2.5 times higher than MBs with

22 a limit of detection of 4.36 ± 1.2 nM. In addition, this probe is easier to synthesize and more than
23 eight times cheaper than MBs which makes its use recommended for high-throughput,
24 quantitative analysis of DNA damage.

25 **Keywords**

26 Terbium, Fluorescence, Nucleic Acid damage, Hairpin probe, Fluorescence sensor.

27 **1. Introduction**

28 Exposure of nucleic acids to solar UV radiation gives rise to a wide range of photochemical
29 products such as cyclobutane pyrimidine dimers (CPDs), [6-4] pyrimidine-pyrimidinones, dewar
30 pyrimidinone photoproducts and uracil and thymine photohydrates [1,2]. On the other hand, free
31 radicals, such as reactive oxygen species, leads to oxidation products, such as 8-oxoguanosine
32 and photohydrates. Other damage agents, such as reactive chemicals and ionizing radiation, lead
33 to other DNA lesions, such as single- and double-strand breaks, adducts, and cross-links. All
34 these damage products lead to miscoding during DNA replication and may result in mutagenesis,
35 carcinogenesis and cell death [3-6].

36 Fluorescent methods have been shown to be superior for detecting DNA damage over previous
37 destructive, time-consuming techniques such as gel electrophoresis [7], capillary electrophoresis
38 [8,9], electrochemical [9,10], HPLC [11], mass spectrometric [12-14] and polymerase chain
39 reaction (PCR) amplification [15] methods. Fluorescent probes offer enhanced sensitivity and the
40 potential for use *in situ* or *in vivo*. Differences in the fluorescence lifetime of a dye intercalated in
41 undamaged and damaged DNA have also been used to detect DNA damage [16]. Fluorescently-
42 labeled antibodies provide a highly selective probe of particular damage photoproducts, such as
43 thymine cyclobutyl photodimers [17].

44 The use of fluorescent nucleic acid probes, such as molecular beacons (MBs) and smart
45 probes, have become powerful tools for application in detection of nucleic acid targets in general
46 [18,19,20], and broad-spectrum detection of different types of DNA and RNA damage such as
47 radiation, oxidative and chemical damage [2,21-24]. For the design of such a probe, the
48 recognition capabilities of DNA through hybridization reactions are well-established, but
49 adequate reporters are needed to generate a physically measurable signal from the hybridization
50 event. This is normally accomplished by labeling the same DNA probe with a fluorophore-
51 quencher pair so that the Förster resonance energy transfer (FRET) can take place. Despite the
52 wide applications and the exquisite sensitivity and selectivity of MBs, they have some readily-
53 apparent limitations [25-30], such as the synthetic and purification difficulties, and limitations
54 associated with site-specific labeling of each terminus of the hairpin [25,26,28,30], incomplete
55 attachment of the quencher [3,7], and its ability to probe only undamaged DNA [2,21-24]. For
56 this last limitation, the MB signal is inversely proportional to the damage, or negative detection,
57 lowering the sensitivity and selectivity of the assay.

58 The main focus of this work is to design an inexpensive probe for the positive detection of
59 DNA damage, in which the produced signal is directly proportional to the amount of DNA
60 damage. We have previously reported two methods for the positive detection of DNA damage.
61 The first is by using a 2-aminopurine (2AP) hairpin probe [31]. This probe offers high sensitivity
62 and selectivity for the detection of DNA damage, as well as overcoming most of the MB probe's
63 limitations. However, these are expensive probes, especially with an increasing number of 2AP
64 bases incorporated in the probe to increase sensitivity. A hypochromism probe [32] was also
65 designed. The hypochromic effect arises from the formation of the double-stranded hybrid of the
66 undamaged target and hairpin. With accumulated UV exposure, the target-hairpin hybrid

67 concentration decreases and the absorbance increases. This probe is more selective and is more
68 than ten times cheaper than MBs, but is less sensitive [32]. The goal of this paper is to design a
69 more sensitive, selective and cheaper probe for the positive detection of DNA damage.

70 Terbium(III) (Tb^{3+}) is a trivalent lanthanide cation that possesses low intrinsic fluorescence in
71 aqueous solutions owing to its low absorption cross-section and non-radiative deactivation
72 through the O-H vibrations of the coordinated water molecules [33-40]. Upon chelation of the
73 ion by ligands that, when excited with light, undergo intersystem crossing from the ligand's
74 excited singlet state to an excited triplet state. Following this crossing, radiationless energy
75 transfer occurs from the excited triplet state of the ligand to the lanthanide ion, resulting in
76 population of its excited state. This process leads to longer emission lifetimes with significant
77 fluorescence enhancement, due to the involvement of the long-lived triplet state [33-40]. This
78 property, which allows for efficient intra-molecular energy transfer from ligand to central atom,
79 along with the fact that there is an insignificant degree of radiationless deactivation in the
80 chelated ion [41], has made Tb^{3+} ions extremely valuable as fluorescent probes for detecting
81 DNA [42-45] as well as detecting alkaline metal binding sites in proteins [46,47], tRNA [48], and
82 rRNA [49,50]. Similarly, lanthanides, especially Tb^{3+} , have been employed to study the structure
83 of tRNA [48,51], rRNA [49] and DNA [52,54]. In addition, the enhancement of Tb^{3+} emission in
84 the presence of single-stranded oligonucleotides has been utilized in the detection of distorted
85 DNA regions [55], single base mismatches in DNA duplexes [56] and DNA- and RNA-drug
86 interactions [57,58].

87 In this paper, we explore the enhanced emission of Tb^{3+} as a potential tool to probe UV-
88 induced DNA damage. This is accomplished by the use of a DNA hairpin probe complementary
89 to the DNA target of interest. The Tb^{3+} /hairpin probe detects UV-induced DNA damage through

90 the hybridization of the hairpin probe to the undamaged target DNA. The damaged DNA-hairpin
91 hybrid is destabilized, and the probe preferentially acquires the hairpin structure while the
92 damaged target remains single-stranded. The Tb^{3+} then directly coordinates to the unpaired
93 nucleobases of the single-stranded damaged DNA. This enhances the intrinsic fluorescence of
94 Tb^{3+} , producing a detectable signal proportional to the amount of DNA damage. Thus, the
95 recognition of DNA damage is accomplished by the hairpin probes through hybridization
96 reactions and the Tb^{3+} is the reporter that generates a physically measurable signal reflecting the
97 amount of damage. The Tb^{3+} /hairpin probe has superior selectivity and sensitivity for DNA
98 damage compared to conventional DNA MBs, and is almost an order of magnitude less
99 expensive.

100 **2. Experimental**

101 *2.1. Materials*

102 Single-stranded oligonucleotide targets and hairpin probes (Scheme 1) were obtained from
103 Integrated DNA Technologies Inc. (Coralville, Iowa). The oligonucleotide samples were purified
104 by standard desalting. The terbium(III) chloride ($TbCl_3$) was obtained from Sigma-Aldrich
105 Canada Ltd. (Oakville, Ontario), magnesium chloride ($MgCl_2$) and sodium chloride ($NaCl$) were
106 obtained from EMD Chemicals Inc. (Gibbstown, New Jersey), and Tris was obtained from ICN
107 Biomedicals, (Aurora, Ohio). All chemicals were used as received. Nanopure water from a
108 Barnsted Nanopure (Boston, Massachusetts) system was used for all solutions. The
109 oligonucleotide samples were each dissolved in nanopure water and kept frozen at $-20\text{ }^{\circ}C$ until
110 needed.

111 *2.2. Instrumentation*

112 Absorption spectra were recorded at intervals throughout the irradiation period on a
113 Hewlett-Packard (Sunnyvale, California) 8452A diode array spectrophotometer. For the
114 fluorescence measurements were done using a Photon Technologies International
115 (Birmingham, New Jersey) fluorescence spectrophotometer. The change in temperature was
116 monitored by means of a Cole-Parmer DiGi-SENSE thermocouple (Niles, Illinois).
117 Oligonucleotide samples were irradiated in a Luzchem (Ottawa, Ontario) DEV photoreactor
118 chamber with UVC light from lamps emitting principally at 254 nm with an irradiation dose
119 of 75 W m⁻².

120 2.3. Procedures

121 2.3.1. UV Irradiation

122 Nitrogen-purged aqueous solutions of 10 μM oligonucleotide targets were irradiated in sealed,
123 UV-transparent 1 cm path length cuvettes. The cuvettes were placed in a water bath in a UV-
124 transparent water dish to keep the temperature constant throughout the irradiation.
125 Oligonucleotide samples were irradiated in the photoreactor chamber with UVC light. The
126 samples were constantly stirred during irradiation, and the photoreactor was purged with
127 nitrogen throughout the irradiation to flush out oxygen and any ozone subsequently generated
128 from the UVC lamps. Control samples were handled identically, but were not exposed to UV
129 radiation. The UVC lamps were turned on ~20 min before the start of irradiation to stabilize the
130 lamp output.

131 2.3.2. Absorption and fluorescence measurements

132 Absorption spectra were recorded by placing the irradiated cuvettes containing the target
133 oligonucleotide solutions directly into the spectrophotometer. For the fluorescence

134 measurements, a 10 μL aliquot of each irradiated solution was taken at various time intervals and
135 was later mixed with appropriate amounts of the hairpin probes and 2 mM Tris buffer solution
136 (pH 7.5) to give final concentrations of 2 μM oligonucleotide targets and 2 μM hairpin probes.
137 These solutions were then incubated in the dark at room temperature for about 24 h. A 40 μM
138 TbCl_3 solution was added to the hybridized solutions prior to the fluorescence measurements.
139 For the MB fluorescence measurements, a 10 μL aliquot of each irradiated solution was taken at
140 various time intervals and was later mixed with an appropriate amount of the MB probe and 10
141 mM Tris buffer solution (3 mM MgCl_2 , 1 mM EDTA, pH 7.5) to give final concentrations of
142 1 μM oligonucleotide target and 200 nM MB probe. These solutions were then incubated in the
143 dark at room temperature for about 24 h.

144 Fluorescence spectra of 100 μL aliquots of the incubated hybridization mixtures were
145 measured. The spectra were recorded between 450 and 600 nm with excitation at 290 nm for the
146 Tb^{3+} fluorescence measurements, and between 500 and 700 nm with excitation at 490 nm for the
147 MB fluorescence measurements. A 1 cm path length Suprasil quartz fluorescence cuvette was
148 used for these measurements.

149 The Tb^{3+} /hairpin probe was characterized by a thermal denaturation profile experiment, in
150 which temperature-dependent fluorescence measurements were carried out on a buffered 2 μM
151 solution of the hairpin probe incubated in the absence or presence of either the target
152 oligonucleotide sequence or the UV-damaged target sequence at 2 μM concentration. The
153 temperature was varied from 20 to 60 $^\circ\text{C}$ in 4 $^\circ\text{C}$ increments at a heating rate of 1 $^\circ\text{C min}^{-1}$ and
154 5 min settling time for each step of the heating cycle.

155 3. Results and discussion

156 The hairpin probes used in this study are carefully designed to maximize their performance
157 as a specific probe for UV-induced nucleic acid damage. This design ensures that the probes can
158 selectively discriminate single damage sites in oligonucleotides. Scheme 1 shows the structure of
159 the hairpin probes used in this study. Each probe is composed of a loop and a stem region
160 composed of six base pairs. The design of the hairpin maximizes discrimination of damaged
161 *versus* undamaged targets, due to the melting temperatures (T_m 's) of the stem and hybrid;
162 designing the hairpin to have a T_m for the stem 5 – 10 °C higher than the T_m of the hybrid
163 ensures maximum selectivity [21].

164 The fluorescence at 545 nm of Tb^{3+} alone, in the presence of single-stranded DNA (ssDNA)
165 and in the presence of double-stranded DNA (dsDNA) is shown in Figure 1. The intrinsic
166 fluorescence of Tb^{3+} is enhanced by ~15 times in the presence of ssDNA, while almost complete
167 fluorescence quenching occurs in the presence of dsDNA (Figure 1). After UV damage, the
168 hairpin probe will hybridize only with the undamaged DNA, while the damaged DNA remains
169 single-stranded, binding Tb^{3+} and enhancing its fluorescence. In this way, the Tb^{3+} produces a
170 detectable signal proportional to the amount of DNA damage. In order to optimize Tb^{3+} /hairpin
171 detection of DNA damage to obtain the maximum discrimination between damaged and
172 undamaged oligonucleotides, we studied the effect of ionic strength, oligonucleotide
173 concentrations, and Tb^{3+} concentration on the fluorescence of Tb^{3+} .

174 3.1. *Optimizing DNA damage detection*

175 The analysis of DNA damage is commonly carried out in the presence of high ionic strength
176 buffers with metal ions such as magnesium and sodium ions present. Such ions are essential for
177 stabilizing the hairpin structure of the probe and the hybrid between the probe and undamaged
178 target [2,21-24]. We studied the effect of magnesium and sodium ions on the enhancement of

179 Tb³⁺ fluorescence in the presence of ssDNA. Figure 2A shows the fluorescence of the Tb³⁺-
180 ssDNA complex at 545 nm as a function of different concentrations of magnesium and sodium
181 ions that have been previously used in buffers for the detection of DNA damage [2,21-24]. The
182 results show that the highest fluorescence is from solutions of buffers having no Mg²⁺ and Na⁺.
183 The Tb³⁺ fluorescence decreased with increasing sodium concentrations, with increasing
184 magnesium concentration, and with increasing concentration of both (Figure 2A). These results
185 can be attributed to blocking of Tb³⁺ binding sites on the negatively charged phosphate backbone
186 by the Na⁺ and Mg²⁺ ions, lowering the Tb³⁺ fluorescence. Figure 2A also shows that the
187 presence of Mg²⁺ in the buffer has a more drastic effect on the enhancement of Tb³⁺ fluorescence
188 than Na⁺, indicating that the higher valance ions lower the enhancement of the Tb³⁺ fluorescence
189 more. To maximize the fluorescence enhancement of Tb³⁺, 2 mM Tris buffer with no Na⁺ and
190 Mg²⁺ ions added was used for all subsequent measurements.

191 Figure 2B shows a plot of the fluorescence of 25 μM Tb³⁺ as a function of the nucleobase
192 concentration of the single-stranded and double-stranded DNA. In the absence of DNA, Tb³⁺
193 fluorescence is very low (Figure 2B). Upon addition of the ssDNA, the Tb³⁺ emission increases
194 linearly with increasing ssDNA nucleobase concentration. After the addition of ~29 μM ssDNA
195 bases, the fluorescence enhancement starts to gradually level. This result is expected, as the Tb³⁺
196 concentration is 25 μM, and indicates that one Tb³⁺ binds, on average, to one base. The annealed
197 duplex solutions did not enhance the Tb³⁺ fluorescence (Figure 2B), as expected, because all the
198 electron donating groups of the nucleoside bases are base-paired and are not free to coordinate to
199 Tb³⁺. This result confirms that binding to the phosphate backbone, without direct coordination to
200 the base, doesn't result in efficient energy transfer [59,60]. It is worth mentioning that the
201 fluorescence of solutions of both Tb³⁺- ssDNA and Tb³⁺-dsDNA complexes did not change over

202 6 h. This result indicates that the presence of Tb^{3+} with dsDNA does not force the equilibrium to
203 shift to the ssDNA formation over the 6 h period of time and acts only as a multivalent cation
204 stabilizing the hybrid secondary structure.

205 The fluorescence spectra and intensities of Tb^{3+} -ssDNA complexes strongly depend on the
206 amount of complexed Tb^{3+} (Figure 2C). In the absence of Tb^{3+} , the solution is non-fluorescent as
207 expected. When Tb^{3+} is added to the annealed duplex solutions, no fluorescence enhancement is
208 observed and the fluorescence is constant at the background level. After the addition of Tb^{3+} to
209 the ssDNA solutions, the emission of Tb^{3+} is greatly enhanced, and the fluorescence intensity
210 increases linearly with increasing Tb^{3+} concentration. As shown in Figure 2C, when the
211 Tb^{3+} :nucleobase ratio reaches 1:1, the fluorescence intensity saturates. To ensure complete
212 complexation with ssDNA, a 1.3-fold excess of Tb^{3+} was used in the following experiments to
213 form the Tb^{3+} -ssDNA complexes.

214 3.2. *Selectivity of Tb^{3+} /hairpin detection of DNA damage*

215 To examine the selectivity of this method for the detection of UV-induced DNA damage, we
216 measured the fluorescence at 545 nm of 40 μM Tb^{3+} in the presence of the hairpin probe alone,
217 the annealed duplexes of the hairpin probe with the undamaged target, and with the 5 minute-
218 and 60 minute-UV damaged ssDNA targets for 5 and 60 min as a function of temperature. Figure
219 3 shows their thermal denaturation profiles. At low temperatures, the fluorescence of Tb^{3+} in the
220 presence of the hairpin probe remains constant at a slightly enhanced fluorescence signal level
221 due to the interaction of Tb^{3+} with the nucleobases in the single-stranded loop of the hairpin
222 probe. At temperatures close to the melting temperature of the stem of hairpin probe (~ 42 °C),
223 the Tb^{3+} fluorescence gradually increases with temperature, because the proportion of single-
224 stranded DNA increases as the stem melts. For the hybrid between the probe and undamaged

225 target, there is no fluorescence enhancement at low temperatures, because the undamaged target
226 is completely hybridized with the probe and all the nucleobases are involved in hydrogen
227 bonding. At temperatures close to the hybrid melting temperature ($\sim 39^\circ\text{C}$), the fluorescence
228 intensity gradually increases due to the interaction of Tb^{3+} with the unpaired nucleobases of the
229 undamaged target.

230 It is clear that the thermal denaturation profile of the undamaged target-hairpin probe hybrid in
231 the presence of Tb^{3+} shows an opposite trend to that of the MB probe [2,21-24] and this is what
232 causes the Tb^{3+} fluorescence signal to increase with increasing damage to the target. This result
233 is demonstrated in Figure 3, where the hybrid between the hairpin probe and the oligonucleotide
234 target subjected to UVC light for 5 min in the presence of Tb^{3+} shows higher fluorescence
235 intensity than that of the hairpin-undamaged target hybrid and is essentially flat with increasing
236 temperature. The slight decrease in fluorescence with increasing temperature has been observed
237 before [21,22,31] and is attributed to a higher rate of non-radiative relaxation in the fluorophore
238 at higher temperature. The thermal denaturation profile of the hybrid between the hairpin probe
239 and the oligonucleotide target subjected to UV-C light for 60 min in the presence of Tb^{3+} shows
240 a very similar trend to that of the 5 min-irradiated target-hairpin hybrid. This result indicates that
241 most of the oligonucleotide targets are damaged within 5 minutes of UVC irradiation and are in
242 the single-stranded structure causing maximum enhancement of the Tb^{3+} fluorescence. As
243 shown in Figure 3, there is good discrimination in the fluorescence between the undamaged and
244 damaged targets hybridized with the hairpin probe in the presence of Tb^{3+} at 20°C . Therefore,
245 we have chosen this hybridization temperature for detecting the formation of the UV-induced
246 photoproducts.

247 In order to confirm that these are the secondary structures of the probe-target hybrids for the
248 undamaged and 5 minute UV-damaged targets, we also measured the 260 nm absorbance of
249 these solutions as a function of temperature (Figure 3 inset). As shown in the inset, the hybrid
250 between the hairpin probe and the UV-damaged target shows a higher absorbance than that of
251 the hybrid between the hairpin and the undamaged target at low temperatures. The increase in
252 absorbance of the damaged solution is due to less hypochromism from the single-stranded
253 damaged target. This confirms that the UV-damaged target-probe hybrid after 5 min is unstable
254 due to damage and the probe preferentially acquires the hairpin structure with the damaged target
255 in the single-stranded form.

256 To confirm the selectivity of Tb^{3+} to detect single-stranded DNA in the presence of
257 complementary duplexes, we measured the fluorescence intensity as a function of the
258 dsDNA:ssDNA concentration ratio at a total target concentration equal to the Tb^{3+} concentration.
259 Figure 4 shows the resulting calibration curve obtained. At zero ssDNA concentration, i.e. only
260 dsDNA is present in the mixture, Tb^{3+} shows no fluorescence. Upon increasing ssDNA
261 concentration, the Tb^{3+} fluorescence increases linearly. The sensitivity, calculated as the slope of
262 the calibration curve, is $8.21 \times 10^{11} \text{ cps M}^{-1}$ and the limit of detection (LOD), calculated as 3
263 times the standard deviation of the blank divided by the sensitivity, is found to be 28.5 nM. By
264 dividing the concentration of the ssDNA bases by the LOD, we are able to calculate that Tb^{3+}
265 can detect one unpaired nucleobase in the presence of ~ 10600 paired ones in double-stranded
266 form.

267 3.3. *Detection of UV-induced photoproducts*

268 In order to investigate the selectivity of the Tb^{3+} /hairpin probe to detect nucleic acid damage,
269 T_{random} and T_{dT17} oligonucleotide targets were irradiated separately at constant temperature. The
270 Tb^{3+} fluorescence was measured (Figure 5) after aliquots of both the irradiated and unirradiated
271 samples of these solutions were incubated with the complementary hairpin probes and Tb^{3+} . It
272 should be noted that the hairpin probes were not irradiated, they were only incubated with
273 aliquots of either the irradiated oligonucleotides or unirradiated controls. As shown in Figure 5A
274 and 5B, the Tb^{3+} fluorescence increases with target UV irradiation dose and continues to increase
275 with increasing dose until it reaches a plateau. This plateau is reached within the first 3 min of
276 target irradiation under the conditions used here. No fluorescence is observed from the
277 unirradiated controls. This result indicates that after 3 min irradiation, the entire probe is in the
278 hairpin form and Tb^{3+} exhibits its maximum fluorescence enhancement.

279 The fluorescence signal as a function of irradiation time for the T_{random} and T_{dT17}
280 oligonucleotide targets (Figure 5A, 5B) were fit to a single exponential growth function. This
281 increase in the fluorescence intensity represents the decreased stability of the damaged target-
282 hairpin hybrid. Therefore, the faster the increase in the fluorescence intensity, the faster the rate
283 of UV-induced damage in the oligonucleotide targets. The damage constants obtained by fitting
284 these fluorescence damage curves are shown in Table 1 for both the T_{random} and T_{dT17}
285 oligonucleotide targets. It is clear from Table 1 that the damage constant of the T_{dT17} target is
286 ~ 2.8 times faster than that of the T_{random} target. This indicates that the T_{dT17} target is more
287 damaged under UV irradiation than the T_{random} target. Comparing the number of photoreactive
288 damage sites in each target reveals that the T_{dT17} target has 8 TT sites that are most prone to UV
289 damage. However, the T_{random} target has only one TT site, one TC site, three CT sites, one AA
290 site and two AT sites. CPDs are produced preferentially at TT and TC sites, whereas CC and CT

291 dipyrimidine sites are poorly photoreactive [13], and dipurine sites are photostable compared to
292 dipyrimidine sites [1]. So the T_{random} target contains a total of five dipyrimidine sites, in which
293 four of them are less photoreactive than the TT site. Thus, it should exhibit slower photodamage
294 kinetics, consistent with Figure 5. This result confirms that we can get information on the
295 amount of UV damage accumulated in different targets by comparing the damage constant
296 values obtained by the same probe.

297 The selectivity of the Tb^{3+} /hairpin probe was compared to the MB for detecting nucleic acid
298 damage. The MB probe (Scheme 1) used in this study was designed to have the same sequence
299 as the hairpin probe, i.e. complementary to the $T_{\text{dT}_{17}}$ target. In this target, the 260 nm absorption
300 band bleaches with increasing irradiation time, quantifying photoproduct formation via the loss
301 of the $\text{C}_5=\text{C}_6$ and yielding an independent spectroscopic marker for DNA damage.

302 As explained above, the MB fluorescence is quenched in the hairpin position when the FAM
303 fluorophore and DABCYL quencher are in close proximity, and the fluorescence intensity is
304 high in the presence of complementary target when the MB forms a hybrid with the target. As
305 damage accumulates on the target strand, the MB-target hybrid becomes less stable, effectively
306 decreasing the fluorescence intensity until the closed, hairpin form is the more stable form of the
307 MB. This trend is shown in Figure 5C, in which the MB fluorescence intensity decreases with
308 longer target irradiation time until reaching a constant minimum corresponding to the quenched
309 fluorescence of the MB in the hairpin structure. The damage curve for MB-detected UV damage
310 was fit to a single exponential decay function. The damage constant obtained is shown in Table
311 1. The selectivity of the probe is directly related to the damage constant; the faster the
312 fluorescence intensity increases in case of Tb^{3+} /hairpin probe (Figure 5B) or decreases in case of

313 the MB probe (Figure 5B), the more selective the probe is at detecting UV-induced DNA
314 damage under identical irradiation conditions for the same target. Table 1 shows that the damage
315 constant of the Tb³⁺/hairpin probe is 6 times faster than that of the DNA MB. This proves that
316 the Tb³⁺/hairpin probe has superior selectivity for detection of UV damage in nucleic acids
317 compared to the DNA MB method.

318 UV absorbance measurements as a function of T_{dT17} target irradiation time (Figure 5D) were
319 used to quantify the amount of UV damage and to develop calibration curves for the Tb³⁺/hairpin
320 probe. This curve was fit to a double-exponential function and the damage constants are listed in
321 Table 1. The results show that the damage constant of the Tb³⁺/hairpin probe is 15 times faster
322 than the fastest absorption damage constant. This confirms that the fluorescent Tb³⁺/hairpin
323 probe has superior selectivity for detection of UV damage in nucleic acids over the absorption
324 method [2,22,31].

325 3.4. *Sensitivity of the Tb³⁺/hairpin probe*

326 In order to check the sensitivity of the Tb³⁺/hairpin probe for damage detection, we used the
327 UV absorbance measurements as a function of target irradiation time to quantify the amount of
328 UV damage and to develop calibration curves of the UV-induced photoproducts detected by the
329 Tb³⁺/hairpin probe. The procedure and calculation of the photoproducts concentration from the
330 absorbance measurements of the irradiated solutions have been explained previously [31]. Figure
331 6 shows the calibration curve obtained upon plotting the Tb³⁺ fluorescence intensity as a function
332 of the concentration of the photoproducts calculated for both the Tb³⁺/hairpin probe (Figure6A)
333 and the fluorescence signal for the MB probes (Figure 6B). In Figure 6A, the fluorescence at
334 zero concentration of the photoproducts represents the background level corresponding to the

335 quenched Tb^{3+} fluorescence as the hairpin probe is completely hybridized with the undamaged
336 target. The Tb^{3+} fluorescence increases linearly with increasing damage. At high damage
337 concentrations, the hybrids formed between the hairpin probe and the damaged strands are
338 completely unstable, and the probe acquires the hairpin structure with the damaged target in the
339 single-stranded form leading to maximum enhancement of Tb^{3+} fluorescence. Additional
340 formation of photoproducts cannot lead to any more dehybridization, so the fluorescence signal
341 shows saturation-like behaviour.

342 For the DNA MB (Figure 6B), any decrease in fluorescence signal requires a minimum 2.59
343 μM concentration of the photoproducts. The constant fluorescence signal of the DNA MB over
344 the range of 0 – 2.59 μM of the photoproducts concentration can be attributed to the lower
345 selectivity of the DNA MB to UV-induced DNA damage as discussed above. At high
346 photoproduct concentrations, the hybrid formed between the DNA MB and the damaged strand
347 is completely unstable, and the DNA MB preferentially acquires the hairpin structure where the
348 fluorophore and the quencher are in close proximity and the fluorescence is the lowest. Further
349 damage doesn't lead to any additional decrease in fluorescence and the signal remains constant,
350 showing a saturation-like behaviour.

351 Although the MB probe used in this study was designed to have the same sequence as the
352 hairpin probe (Scheme 1), the Tb^{3+} /hairpin probe proved to be more selective and sensitive to
353 UV-induced DNA damage than the MB probe. This can be attributed to the difference in the
354 reporting mechanism between the two probes. In the MB probe, the reporting mechanism is
355 through FRET between a fluorophore-quencher pair on the hairpin probe, while in the
356 Tb^{3+} /hairpin probe, it is through direct emission from the coordinated Tb^{3+} via energy transfer
357 from the unpaired nucleobases. This is reflected in Figure 6A where the low fluorescence

358 background allowed the Tb^{3+} to show an immediate fluorescence increase upon photoproduct
359 formation, leading to better sensitivity. Also, it has been previously shown that single
360 mismatches in the sequence of a duplex DNA lead to selective Tb^{3+} fluorescence enhancement
361 [56]. Our result showing that Tb^{3+} is sensitive to very low photoproduct concentrations is
362 consistent with this past work. For the MB probe (Figure 6B), the high fluorescence background
363 of the quenched fluorophore decreases the sensitivity of this probe.

364 Table 2 shows the parameters for the quantification of UV-induced DNA damage from Figure 6.
365 The calibration curve for the Tb^{3+} /hairpin probe shows a similar linear dynamic range to the MB
366 probe (Table 2), taking into account the MB threshold response of $2.59 \mu M$ photoproduct. The
367 sensitivity of detection is larger by a factor of ~ 2.5 for the Tb^{3+} /hairpin probe, leading to a lower
368 limit of detection (LOD) and limit of quantification (LOQ) by approximately an order of
369 magnitude. It is worth mentioning that the values recorded in Table 2 for the LOD and LOQ for
370 the MB method for the detection of DNA damage is obtained by using the standard deviation of
371 the blank measurements and the sensitivity of the method, while the LOD and LOQ will be
372 practically limited to the threshold $2.59 \mu M$ (Figure 6B) photoproduct concentration. From this
373 data, we calculate that the Tb^{3+} /hairpin probe can detect one damage site in the presence of
374 ~ 8000 undamaged sites, compared to one damage site in the presence of ~ 820 undamaged sites
375 with the MB probe. This again confirms the superior sensitivity of the Tb^{3+} /hairpin probe over
376 the MB probe. Considering the volume of the DNA target solution used in one analysis (100
377 μL), our technique allows the detection of 0.4 picomoles of UV-damaged sites. The detection
378 limit of this technique compares favorably with those reported for other DNA damage
379 techniques, such as mass spectrometry [12], alkaline gel electrophoresis [61], immunoassay
380 coupled with laser-induced fluorescence [17], ELISA [62], electrochemical detection [10] and

381 HPLC-MS/MS [63]. This detection limit allows the Tb^{3+} /hairpin probe to be used in high-
382 throughput, quantitative analysis of DNA damage.

383

384 **Conclusions**

385 These results conclusively show that the Tb^{3+} /hairpin probe is a sensitive tool for detecting
386 UVC-induced oligonucleotide damage. Changing the fluorescence reporting mechanism of the
387 probe from a fluorophore-quencher pair attached to the hairpin probe to Tb^{3+} coordinated to
388 ssDNA allows positive detection of DNA damage with a fluorescence signal that increases with
389 increasing damage. The Tb^{3+} /hairpin probe proves to have superior selectivity and sensitivity to
390 DNA damage than the MB probe, while also being much cheaper and easier to synthesize. The
391 Tb^{3+} /hairpin probe represents a promising tool in the design of biosensors for the *in vivo*
392 detection of the nucleic acid damage. The only limitation of this technique is that a specific
393 probe sequence must be designed for each DNA target. Upon comparing this requirement to the
394 complexity of other available and widely used techniques for the detection of DNA damage,
395 such as HPLC-MS/MS and fluorescently labelled antibodies, the Tb^{3+} /hairpin probe method is
396 still cheaper and simpler.

397 **4. Acknowledgements**

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402 **5. References**

- 403 [1] B. P. Ruzsicska, D. G. E. Lemaire, in: W. M. Horspool, P.-S. Song, (Eds.), DNA
404 Photochemistry, CRC Handbook of Organic Photochemistry and Photobiology; CRC
405 Press, New York. 1995, pp. 1289-1317.
- 406 [2] S. Yarasi, C. McConachie, G. R. Loppnow, Photochem. Photobiol. 81 (2005) 467-473.
- 407 [3] B. Ames, L. Gold, W. Willett, Proc. Natl. Acad. Sci. U.S.A. 92 (1995) 5258-5265.
- 408 [4] T. Lindahl, Nature. 362 (1993) 709-715.
- 409 [5] L. Marnett, P. Burcham, Chem. Res. Toxicol. 6 (1993) 771-785.
- 410 [6] L. Marrot, J. Meunier, J. Am. Acad. Dermatol. 58 (2008) S139-S148.
- 411 [7] M. Weinfeld, K. Soderlind, Biochemistry (N.Y.) 30 (1991) 1091-1097.
- 412 [8] X. Le, J. Xing, J. Lee, S. Leadon, M. Weinfeld, Science. 280 (1998) 1066-1069.
- 413 [9] B. Haab, R. Mathies, Anal. Chem. 67 (1995) 3253-3260.
- 414 [10] K.C. Kucharikova, M. Fojta, T. Mozga, E. Palecek, Anal. Chem. 77 (2005) 2920-2927.
- 415 [11] H. Kaur, B. Halliwell, Biochem. J. 318 (1996) 21-23.
- 416 [12] I. D. Podmore, M.S. Cooke, K.E. Herbert, J. Lunec, Photochem. Photobiol. 64 (1996)
417 310-315.
- 418 [13] T. Douki, J. Cadet, Biochemistry (N.Y.) 40 (2001) 2495-2501.
- 419 [14] J. Ravanat, T. Douki, J. Cadet, Photochem. Photobiol. B Biol. 63 (2001) 88-102.
- 420 [15] A. Kumar, M. Tyagi, P. Jha, Biochem. Biophys. Res. Commun. 318 (2004) 1025-1030.
- 421 [16] C.C. Trevithick-Sutton, L. Mikelsons, V. Filippenko, J. C. Scaiano, Photochem.
422 Photobiol. 83 (2007) 556-562.
- 423 [17] J. Xing, J. Lee, S. Leadon, M. Weinfeld, X. Le, Methods 22 (2000) 157-163.
- 424 [18] S. Tyagi, D. Bratu, F. Kramer, Nat. Biotechnol. 16 (1998) 49-53.

- 425 [19] S. Tyagi, F. Kramer, *Nat. Biotechnol.* 14 (1996) 303-308.
- 426 [20] K. Wang, Z. Tang, C. J. Yang, Y. Kim, X. Fang, W. Li, Y. Wu, C. D. Medley, Z. Cao, J.
427 Li, P. Colon, H. Lin, W. Tan, *Angew. Chem. Int. Ed. Engl.* 48 (2009) 856-870.
- 428 [21] A. F. El-Yazbi, G. R. Loppnow, *Can. J. Chem.* 89 (2011) 402-408.
- 429 [22] S. A. Oladepo, G. R. Loppnow, *Anal. Bioanal. Chem.* 397 (2010) 2949-2957.
- 430 [23] Z.J. Shire, G. R. Loppnow, *Photochem. Photobiol.* 88 (2012) 645-650.
- 431 [24] Z.J. Shire, G. R. Loppnow, *Anal. Bioanal. Chem.* 403 (2012) 179-184.
- 432 [25] K. Stohr, B. Hafner, O. Nolte, J. Wolfrum, M. Sauer, D. Herten, *Anal. Chem.* 77 (2005)
433 7195-7203.
- 434 [26] J. Knemeyer, N. Marme, M. Sauer, *Anal. Chem.* 72 (2000) 3717-3724.
- 435 [27] A. Misra, P. Kumar, K.C. Gupta, *Anal. Biochem.* 364 (2007) 86-88.
- 436 [28] T. Heinlein, J. Knemeyer, O. Piestert, M. Sauer, *J. Phys. Chem. B* 107 (2003) 7957-7964.
- 437 [29] Y. Kim, C. J. Yang, W. Tan, *Nucl. Acids Res.* 35 (2007) 7279-7287.
- 438 [30] A. Misra, M. Shahid, *Bioorg. Med. Chem.* 17 (2009) 5826-5833.
- 439 [31] A. F. El-Yazbi, G. R. Loppnow, *Anal. Chim. Acta.* 726 (2012) 44-49.
- 440 [32] A. F. El-Yazbi, G. R. Loppnow, *Can. J. Chem.* (2013) In press
- 441 [33] N. Sabbatini, M. Guardigli, J. Lehn, *Coord. Chem. Rev.* 123 (1993) 201-228.
- 442 [34] S. Rigault, C. Piguet, G. Bernardinelli, G. Hopfgartner, *Angew. Chem. Int. Ed.* 37 (1998)
443 169-172.
- 444 [35] N. Martin, J. Bunzli, V. McKee, C. Piguet, G. Hopfgartner, *Inorg. Chem.* 37 (1998) 577-
445 589.
- 446 [36] C. Piguet, J. Bunzli, G. Bernardinelli, G. Hopfgartner, S. Petoud, O. Schaad, *J. Am.*
447 *Chem. Soc.* 118 (1996) 6681-6697.

- 448 [37] V. Alexander, *Chem. Rev.* 95 (1995) 273-342.
- 449 [38] G. Choppin, Z. Wang, *Inorg. Chem.* 36 (1997) 249-252.
- 450 [39] P. Valente, S. Lincoln, K. Wainwright, *Inorg. Chem.* 37 (1998) 2846-2847.
- 451 [40] M. Wolbers, F. van Veggel, B. SnellinkRuel, J. Hofstraat, F. Geurts, D. Reinhoudt, J.
452 *Am. Chem. Soc.* 119 (1997) 138-144.
- 453 [41] R. C. Leif, L. M. Vallarino, M.C. Becker, S. Yang, *Cytometry A* 69A (2006) 767-778.
- 454 [42] M. Li, P. R. Selvin, *Bioconjug. Chem.* 8 (1997) 127-132.
- 455 [43] A. Saha, K. Kross, E. Kloszewski, D. Upson, J. Toner, R. Snow, C. Black, V. Desai, J.
456 *Am. Chem. Soc.* 115 (1993) 11032-11033.
- 457 [44] P. Ioannou, T. Christopoulos, *Anal. Chem.* 70 (1998) 698-702.
- 458 [45] P. Hurskainen, P. Dahlen, J. Ylikoski, M. Kwiatkowski, H. Siitari, T. Lovgren, *Nucl.*
459 *Acids Res.* 19 (1991) 1057-1061.
- 460 [46] S. Ghosh, A. Misra, A. Ozarowski, A. Maki, *J. Phys. Chem. B.* 107 (2003) 11520-11526.
- 461 [47] A. Leonov, B. Voigt, F. Rodriguez-Castaneda, P. Sakhaii, C. Griesinger, *Chem. Eur. J.*
462 11 (2005) 3342-3348.
- 463 [48] M. J. Belousoff, P. Ung, C. M. Forsyth, Y. Tor, L. Spiccia, B. Graham, *J. Am. Chem.*
464 *Soc.* 131 (2009) 1106-1114.
- 465 [49] M. Lambert, J. Hoerter, M. Pereira, N. Walter, *RNA* 11 (2005) 1688-1700.
- 466 [50] A. Trentani, P. Testillano, M. Risueno, M. Biggiogera, *Eur. J. Histochem.* 47 (2003) 195-
467 200.
- 468 [51] M. Roy, L. Wittenhagen, S. Kelley, *RNA* 11 (2005) 254-260.
- 469 [52] B. Jolles, A. Laigle, J. Liquier, L. Chinsky, *Biophys. Chem.* 46 (1993) 179-185.
- 470 [53] S. Klakamp, W. Horrocks, *J. Inorg. Biochem.* 46 (1992) 175-192.

- 471 [54] D. Gersanovski, P. Colson, C. Houssier, E. Fredericq, *Biochim. Biophys. Acta.* 824
472 (1985) 313-323.
- 473 [55] Z. Balcarova, V. Brabec, *Biophys. Chem.* 33 (1989) 55-61.
- 474 [56] P. Fu, C. Turro, *J. Am. Chem. Soc.* 121 (1999) 1-7.
- 475 [57] L. Pearlman, H. Simpkins, *Biochem. Biophys. Res. Commun.* 131 (1985) 1033-1040.
- 476 [58] Y. Ci, Y. Li, X. Liu, *Anal. Chem.* 67 (1995) 1785-1788.
- 477 [59] A. Canfi, M. Bailey, B. Rocks, *Analyst.* 114 (1989) 1405-1406.
- 478 [60] A. Abusaleh, C. Meares, *Photochem. Photobiol.* 39 (1984) 763-769.
- 479 [61] S.E. Freeman, A.D. Blackett, D.C. Monteleone, R.B. Setlow, B.M. Sutherland, J.C.
480 Sutherland, *Anal. Biochem.* 158 (1986) 119-129.
- 481 [62] M.S. Cooke, I.D. Podmore, N. Mistry, M.D. Evans, K.E. Herbert, H.R. Griffiths, J.
482 Lunec, *J. Immunol. Methods* 280 (2003) 125-133.
- 483 [63] F. Zhang, W.T. Scott, A.J. Clark, M.R. Schisler, J.J. Grundy, B.B. Gollapudi, M.J.
484 Bartels, *Rapid Commun. Mass Spectrom.* 21 (2007) 3949-3955.

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493 6. Figure captions

494 **Scheme 1.** Sequences of the probes used in this work. The Tb^{3+} /hairpin probes are
495 complementary to T_{random} (A) and to T_{dT17} (B). The MB probe is complementary to T_{dT17} (C).
496 “FAM” denotes the 6-carboxyfluorescein fluorophore and “DABCYL” denotes the dabcyyl
497 quencher. T_{random} and T_{dT17} are the oligonucleotide targets used in this study.

498 **Figure 1.** The fluorescence spectra of Tb^{3+} alone (—), in the presence of single-stranded DNA
499 (-----) and in the presence of double-stranded DNA(·-·-·-·-). The fluorescence excitation
500 wavelength was 290 nm and the spectra were recorded at room temperature. “c.p.s.” denotes
501 counts per second.

502 **Figure 2.** Tb^{3+} fluorescence intensity as a function of (A) sodium and magnesium ion
503 concentrations in 2 mM Tris (pH 7.5) buffer and 25 μM Tb^{3+} , (B) nucleobase concentration of
504 single-stranded DNA (open squares) and double-stranded DNA (filled squares) in 2 mM Tris
505 buffer (pH 7.5) and 25 μM Tb^{3+} , and (C) Tb^{3+} concentration of single-stranded DNA (open
506 squares) and double-stranded DNA (filled squares) in 2 mM Tris buffer (pH 7.5) and 34 μM
507 nucleobases. Fluorescence excitation and emission wavelengths were 290 and 454 nm,
508 respectively. Each data point is an average of three replicate measurements and the error bars
509 correspond to the standard deviation of each measurement. “c.p.s.” denotes counts per second.

510 **Figure 3.** Fluorescence thermal denaturation profiles for 40 μM Tb^{3+} /hairpin probe alone (open
511 circles), 40 μM Tb^{3+} /hairpin probe in the presence of an equimolar amount of the complementary
512 oligonucleotide target sequence (filled circles), and 40 μM Tb^{3+} /hairpin probe in the presence of

513 an equimolar amount of the UV-irradiated oligonucleotide target sequence for 5 min (filled
514 squares) and 60 min (filled triangles). The inset shows the absorption thermal denaturation
515 curves for the same solutions of 40 μM Tb^{3+} /hairpin probe in the presence the complementary
516 oligonucleotide target (filled circles), and the 5 min UV-irradiated oligonucleotide target (filled
517 squares) in 1 cm cuvettes. The lines are guides for the eye.

518 **Figure 4.** Calibration curve of the detection of ssDNA in a mixture of single-stranded and
519 double-stranded DNA with 40 μM Tb^{3+} . $[\text{dsDNA}]$ and $[\text{ssDNA}]$ are in μM . Each data point is an
520 average of three replicate measurements and the error bars correspond to the standard deviation
521 of the measurements. The linear regression coefficient squared, R^2 , calculated from the
522 calibration curve is 0.993, the sensitivity, calculated as the slope of the calibration curve, is 8.21
523 $\times 10^{11}$ cps M^{-1} , the limit of detection (LOD), calculated as 3 times the standard deviation of the
524 blank divided by the sensitivity, is found to be 28.5 nM, and the limit of quantification (LOQ),
525 calculated as 3.3 times the LOD, is equal to 95.1 nM. For the determination of the blank standard
526 deviation, 20 solutions of 40 μM Tb^{3+} were measured and the standard deviations of these
527 measurements were 0.7×10^4 .

528 **Figure 5.** UV damage plots of Tb^{3+} /hairpin probe fluorescence intensity ($\lambda_{\text{ex}} = 290$ nm, $\lambda_{\text{em}} =$
529 545 nm) as a function of target irradiation time for T_{random} (A) and $T_{\text{dT}_{17}}$ (B). (C) MB hairpin
530 probe fluorescence ($\lambda_{\text{ex}} = 490$ nm, $\lambda_{\text{em}} = 520$ nm) as a function of target irradiation time for $T_{\text{dT}_{17}}$.
531 (D) 260 nm absorbance as a function of target irradiation time for $T_{\text{dT}_{17}}$. For all experiments, the
532 2 μM irradiated oligonucleotide targets (open squares) and the 2 μM unirradiated control (filled
533 squares) were hybridized with the probe at 20 $^{\circ}\text{C}$. The solid line through the irradiated sample
534 fluorescence points in (A) and (B) is a single exponential growth fit to $I_{\text{F}} = I_{\text{F},0} + a(1 - e^{-t/\tau})$,

535 where (A) $I_{F,0} = (0.10 \pm 0.01) \cdot 10^5$ cps, $a = 4.6 \pm 0.01$, and $\tau = 1.1 \pm 0.02$ min, and (B) $I_{F,0} =$
536 $(0.17 \pm 0.01) \cdot 10^5$ cps, $a = 3.7 \pm 0.01$, and $\tau = 0.40 \pm 0.01$ min. The MB damage curve in (C) is a
537 single exponential decay fit to $I_F = I_{F,0} + a e^{-t/\tau}$ where $I_{F,0} = (1.2 \pm 0.04) \cdot 10^5$ cps, $a = 2.5 \pm 0.10$,
538 and $\tau = 2.36 \pm 0.10$ min. The solid line through the absorbance points (open squares) is the least-
539 squares fit to an offset, double exponential function, $A = A_0 + A_1 e^{-t/\tau_1} + A_2 e^{-t/\tau_2}$, where the
540 absorbance damage constants are 6.1 ± 0.07 min (τ_1) and 91.8 ± 2.0 min (τ_2), and the amplitudes
541 are $A_1 = 0.52 \pm 0.01$ and $A_2 = 0.66 \pm 0.02$. The offset (A_0) is 0.21 ± 0.02 . The control points
542 (filled squares) are fit to a straight line with zero slope by eye.

543 **Figure 6.** Calibration curve of DNA photodamage formed upon UV irradiation of the T_{dT17} target
544 for the (A) Tb^{3+} /hairpin probe and (B) DNA MB. The inset shows the fit to the linear portions of
545 the calibration curves. Each data point is an average of three replicate measurements and the
546 error bars correspond to the standard deviation of the measurements.

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556 **Table 1. Damage constants of the different DNA damage assay methods.**

Method	Damage constant (min)^a
Tb ³⁺ /hairpin probe fluorescence	$\tau_{dT_{17}} = 0.40 \pm 0.01$ $\tau_{\text{random}} = 1.10 \pm 0.02$
DNA MB fluorescence	$\tau_{dT_{17}} = 2.36 \pm 0.20$
Absorbance	$\tau_1 = 6.1 \pm 0.07$ $\tau_2 = 92 \pm 2.00$

557 ^aThe damage constants (τ) were obtained from the exponential fits in Figure 5.

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568 **Table 2. Analytical parameters for the quantification of UV-induced DNA damage with**
 569 **Tb³⁺/hairpin probe and DNA MB**

Parameter ^a	Detection of UV-damaged DNA	
	Tb ³⁺ /hairpin probe	DNA MB
Linear Dynamic Range (μM)	0.00 – 1.72	2.59 – 4.53
R²	0.975	0.995
Sensitivity (cps M⁻¹)	2.38 × 10 ¹²	9.84 × 10 ¹¹
LOD (nM)	4.36	41.4
LOQ (nM)	14.5	138

570 For the determination of the blank standard deviation, 20 solutions of 40 μM Tb³⁺ and 200 nM
 571 DNA MB were used, respectively. The standard deviations of these measurements were 0.7 ×
 572 10⁴ and 1.3 × 10⁴ c.p.s., respectively. ^aIn this table, linear dynamic range is the concentration
 573 range corresponding to the linear region in the calibration curve, R² is the linear regression
 574 coefficient squared, sensitivity is the slope of the calibration curve, LOD is the limit of detection
 575 and is 3 times the standard deviation of the blank divided by the sensitivity, and LOQ is the limit
 576 of quantification and is 3.3 times the LOD.

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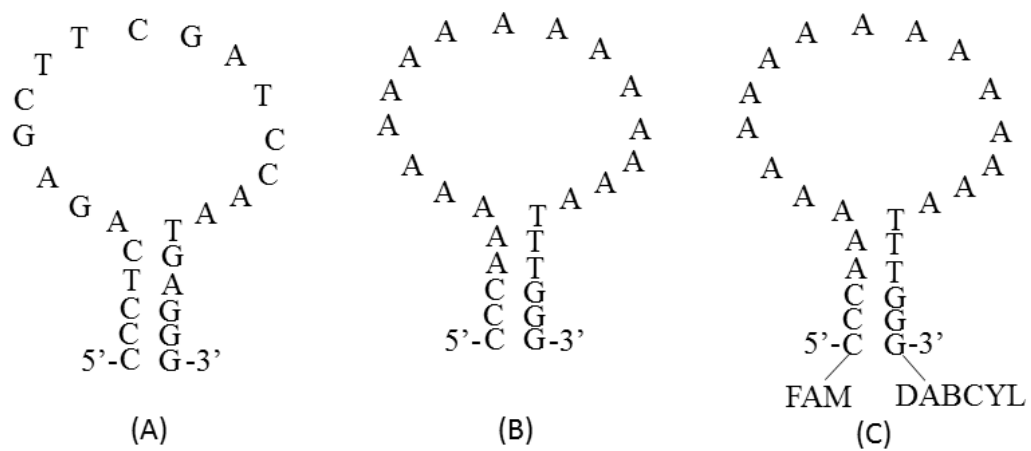
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586 Scheme 1



T_{dT17} : 3'-TTT TTT TTT TTT TTT TT-5'

T_{random} : 3'-CTC GAA GCT AGG TTA CT-5'

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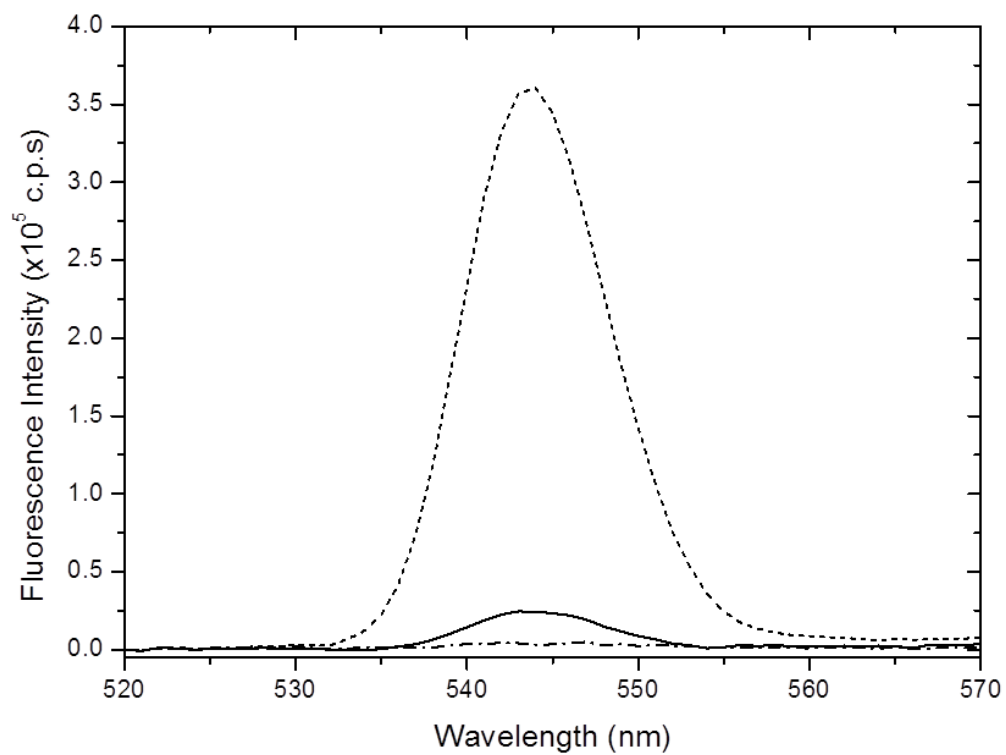
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Figure 1

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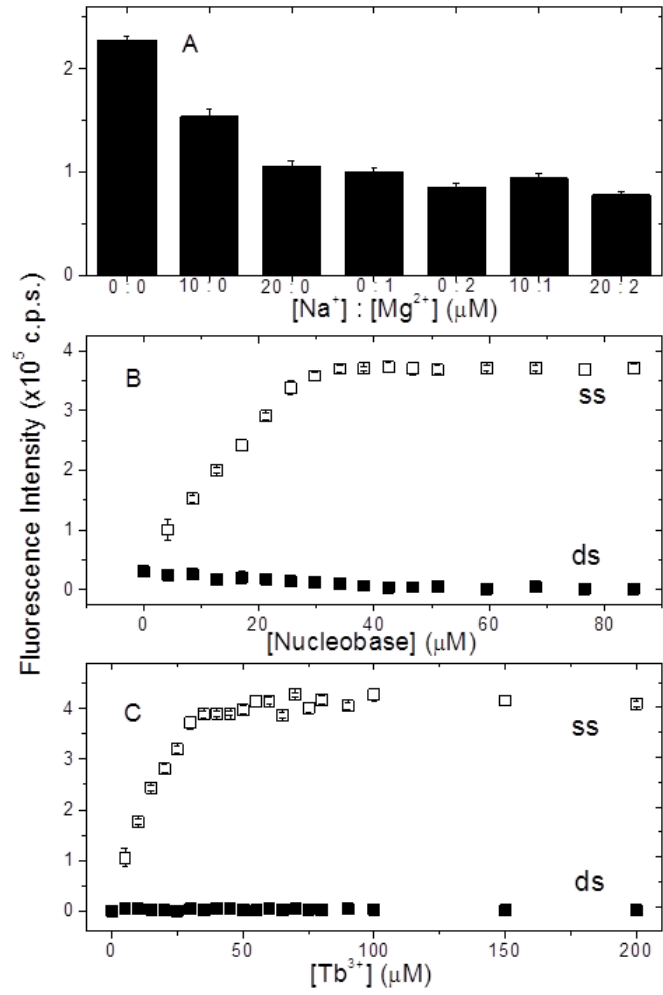


Figure 2

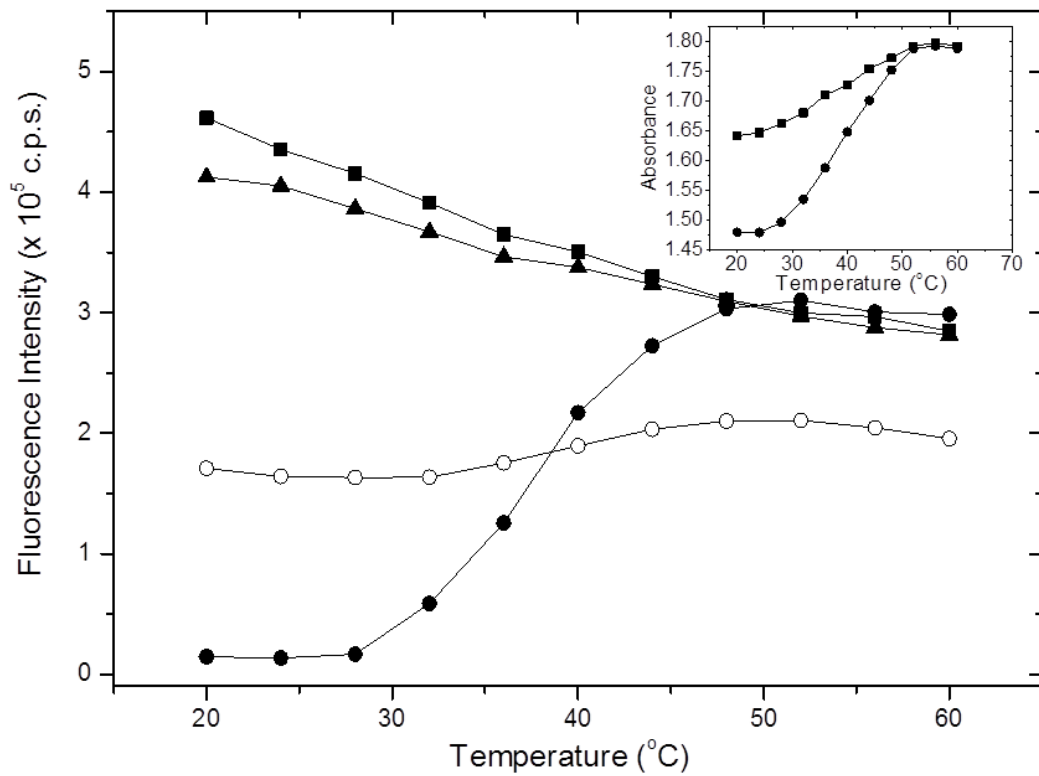
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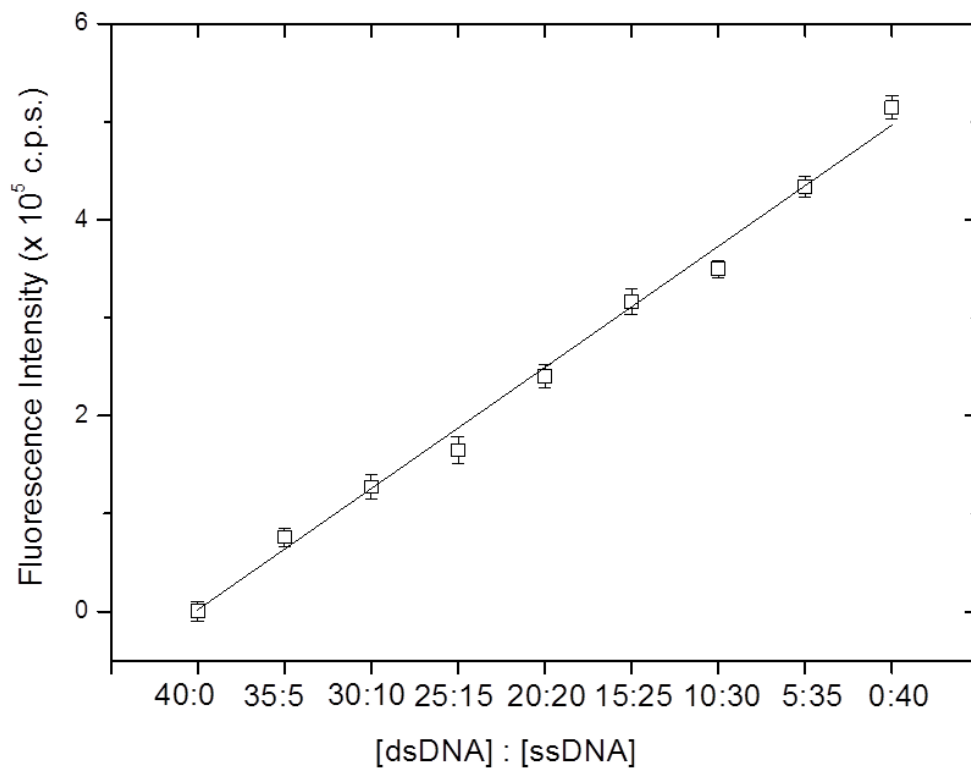
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Figure 3

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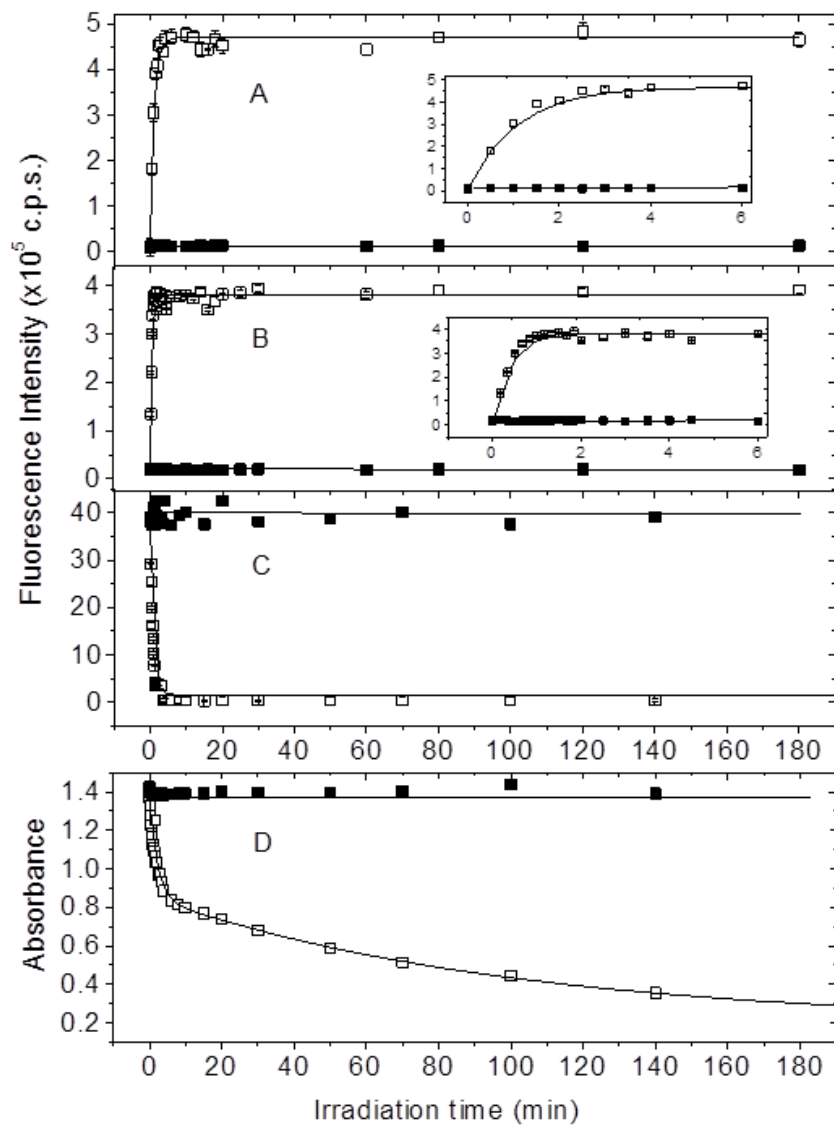
Figure 4

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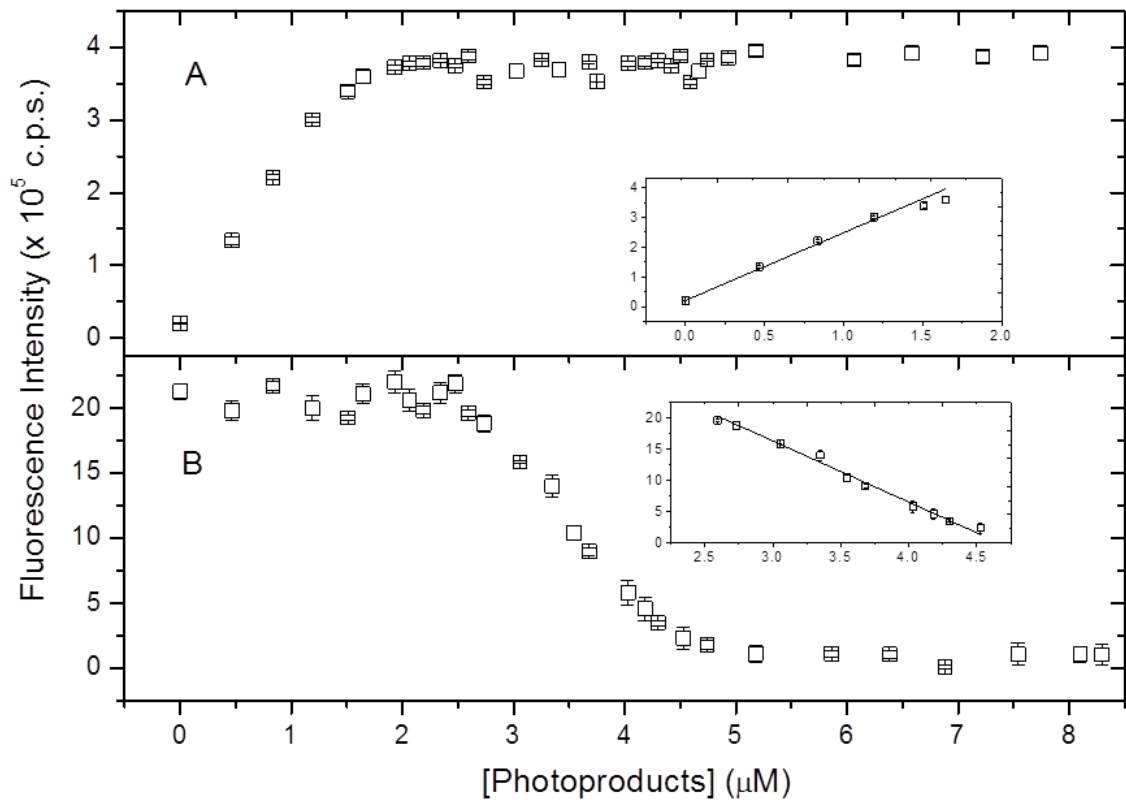
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Figure 5

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Figure 6

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