

Different Mechanisms of DNA Radiosensitization by 8-Bromoadenosine and 2'-Deoxy-2'-fluorocytidine Observed on DNA Origami Nanoframe Supports

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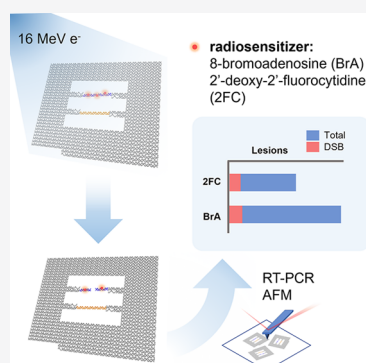


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ABSTRACT: DNA origami nanoframes with two parallel DNA sequences are used to evaluate the effect of nucleoside substituents on radiation-induced DNA damage. Double strand breaks (DSB) of DNA are counted using atomic force microscopy (AFM), and total number of lesions is evaluated using real-time polymerase chain reaction (RT-PCR). Enhanced AT or GC content does not increase the number of DNA strand breaks. Incorporation of 8-bromoadenosine results in the highest enhancement in total number of lesions; however, the highest enhancement in DSB is observed for 2'-deoxy-2'-fluorocytidine, indicating different mechanisms of radiosensitization by nucleoside analogues with the halogen substituent on base or sugar moieties, respectively. “Bystander” effects are observed, when the number of DSB in a sequence is enhanced by a substituent in the parallel DNA sequence. The present approach eliminates limitations of previously developed methods and motivates detailed studies of poorly understood conformation or bystander effects in radiation induced damage to DNA.



Understanding radiation damage to DNA is crucial for cancer radiotherapy. Irreparable damage to DNA suppresses cell proliferation, thereby exploring its mechanisms is important to the improvement of radio-therapeutic techniques.^{1,2} Several tools have been utilized to study radiation damage to DNA in solution, most of them relying on plasmid DNA and gel electrophoresis.^{3,4} These can provide quantitative data on DNA damage by ionizing radiation, although they are often influenced by the chosen analysis approach.^{5,6} Plasmid DNA-based systems have been useful in fundamental studies, for example, in disentangling direct and indirect effects of radiation on DNA damage^{3,7,8} or in studies identifying sources of synergism in chemo-radiation therapy.^{9–11} In certain cases, however, plasmid DNA and the necessity for stabilizing buffer solutions create a complex system that could be difficult to link to fundamental studies performed on isolated DNA building blocks.^{12,13} Therefore, there is also rising interest in studies of short DNA segments, incorporated into DNA strands¹⁴ or placed in a well-defined environment.^{15–17}

DNA origami nanostructures are promising tools to study radiation damage to DNA sequences and radiosensitivity modification by sensitizers such as nucleotides functionalized with electron affinic moieties. The hundreds of synthetic oligomers that compose the origami nanostructure allow for hundreds of unique binding sites that can be extended to support a wide array of probes and active agents at fixed nanometric spaces.¹⁸ A common DNA origami-based technique used to study DNA single strand breaks utilizes DNA origami nanotriangles deposited on Si/SiO₂ substrates

with atomic force microscopy (AFM) as the primary characterization technique to quantify strand breaks *in singulo*.¹⁹ Biotinylated DNA oligomers containing sequences of interest are attached to several locations on the origami nanostructure, free-standing above the surface, which can be irradiated in vacuum either by vacuum ultraviolet (VUV) or low energy electrons (LEE). The intact strands remaining after irradiation are amplified by the addition of streptavidin for subsequent visualization by AFM.¹⁹ The technique has been tested on various oligomer sequences with and without added radiosensitizers as well as biologically relevant secondary structures like G-quadruplexes generating values for strand break cross sections to represent the effects of secondary electrons.^{20–22} These studies are so far limited to irradiation in vacuum. Extending these studies to systems in aqueous solution as demonstrated in the present study would be beneficial in order to determine the respective contributions of direct effects deduced from said studies and those of indirect effects caused by reactive radiolysis products like OH radicals in environments close to that experienced by DNA in cellular environments. Some exploratory studies on bare origami nanostructures were also performed, indicating another

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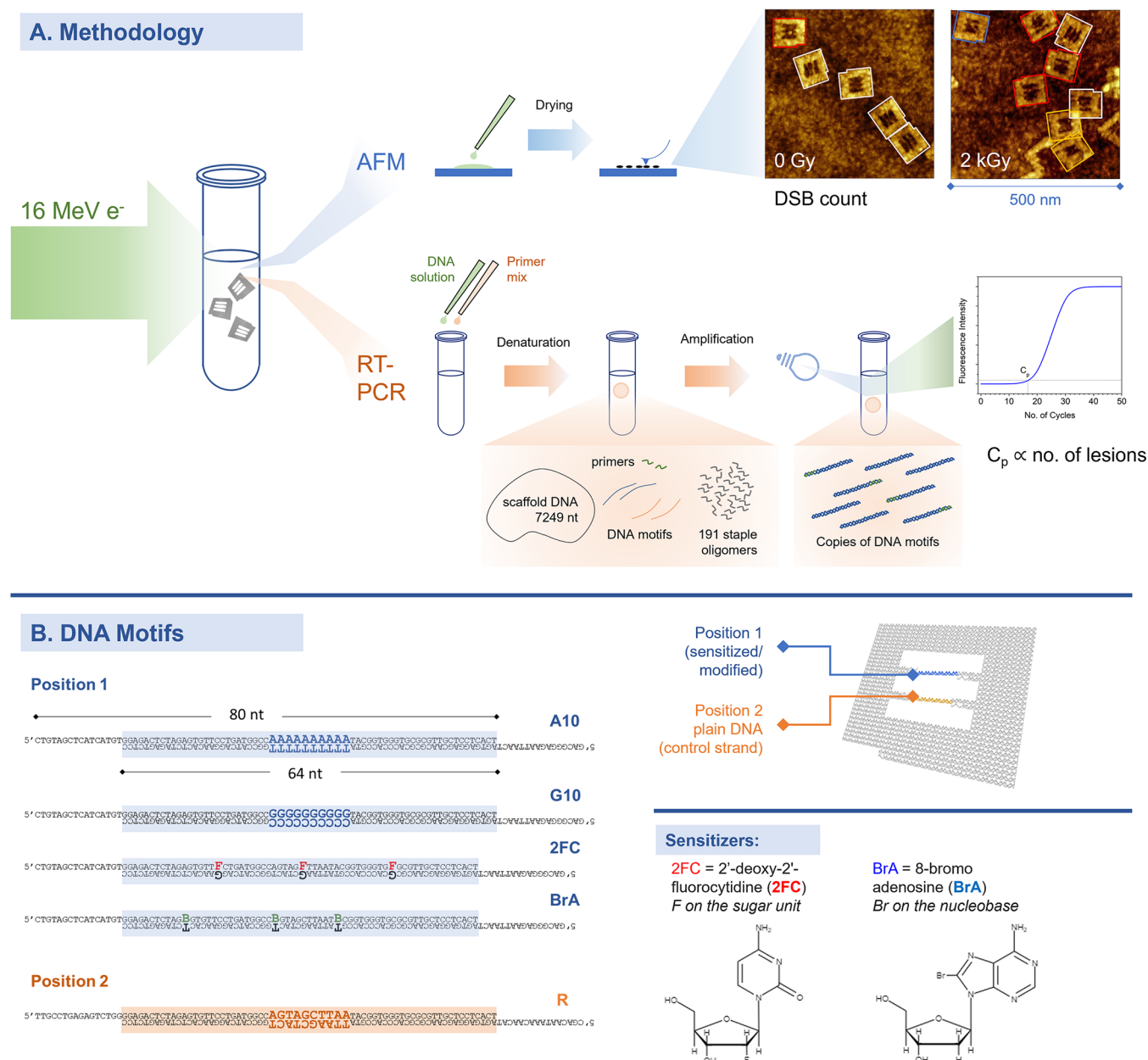


Figure 1. Scheme of the methods employed (A) and the various sequences studied, their positions in the origami nanostructure (image rendered in oxView),²⁵ and the chemical structures of the radiosensitizers used (B).

possible approach to study DNA damage in the aqueous environment using DNA origami templates. One of these made use of C_{60} in solution to generate 1O_2 reactive species upon photoexcitation, which then react with DNA origami²³ as observed through AFM. In another study, solutions containing DNA origami were irradiated by high doses of γ -rays and proton beams, demonstrating enhanced DNA origami stability compared to similarly sized plasmids, making it a suitable substrate for radiation damage studies.²⁴

The common use of DNA origami as a substrate with free-standing sequences of interest is limited to sequences of only several nucleotides due to the tendencies of longer sequences (~ 20 nucleotides) to fold.²⁶ Here we exploit an alternative method using DNA origami nanoframes, which enables studies of longer double stranded sequences (Figure 1A). The nanoframes are based on the design of the Sugiyama group,²⁷ where it was mostly used for state of the art

mechanistic studies on various DNA sequences.^{28,29} The frames are $\sim 80 \times 90$ nm in dimension and are constructed from an M13mp18 single-stranded DNA scaffold and 222 strategically designed staple oligomer sequences that tie the structure together. We had to trim the blunt ends by the removal of 31 staples on the sides to prevent agglomeration during deposition on the surface as a consequence of π - π stacking in between the end bases. The frames can support a couple of DNA motifs in their inner aperture, with at least 64 base-pairs in addition to 16 nucleotides that anchor to both sides of the origami frame (Figure 1B). In this design, two duplexes/motifs can be studied at the same time, allowing for direct comparison of damage to the strands, for example, in between two different DNA sequences or in between plain DNA and its sensitized form. We irradiated the samples in solution using 16 MeV electrons, deposited the treated solutions on Si substrates, and then visualized directly the

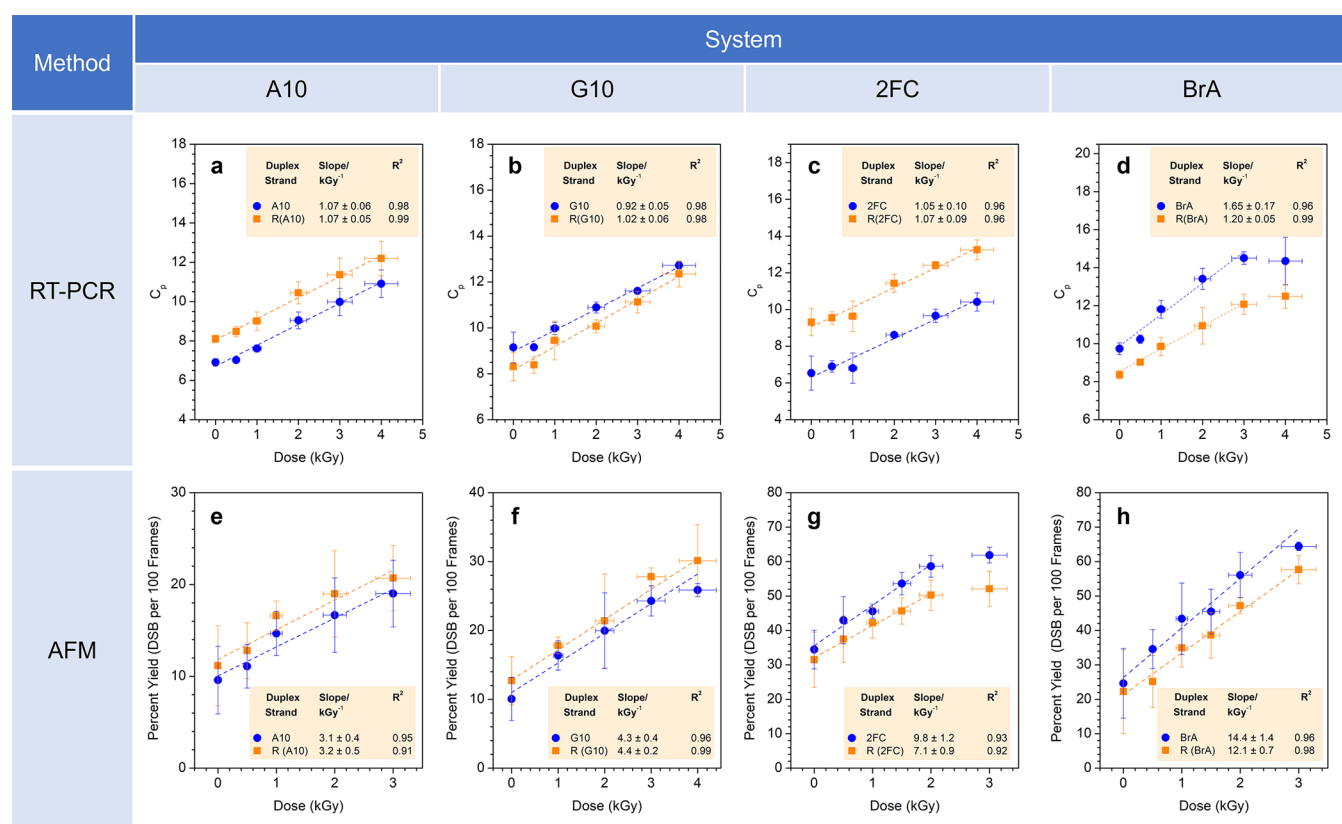


Figure 2. Dose response of C_p values (Mean \pm SD, $n = 3$) from RT-PCR analysis (a–d) and AFM counts of % DSB (Mean \pm SD, $n = 4$ –7) vs absorbed dose curves (e–h) of the various DNA motifs studied: A10, G10, 2FC, and BrA (blue circles) and their accompanying control (R) strand (orange squares). Linear fits were performed on each curve based on eqs 3 and 2 for data obtained from RT-PCR and AFM, respectively. Uncertainties in absorbed doses are within 10% as estimated from the measurements of dose rates on the irradiation platform.

strand breaks by AFM. The AFM count is limited to double strand breaks caused both by direct hits as well as double strand breaks from multiple SSBs on both strands of the DNA motif (clustered damages). The rest of the sample was then analyzed using a real-time polymerase chain reaction (RT-PCR), which was used as a complementary analytical technique to confirm dose-dependent damage to the DNA motifs. The latter can detect the relative amount of remaining, intact DNA motifs after irradiation; however, it cannot differentiate between the different types of lesions.

In this work, we investigated four systems, two of which deal with the effects of the AT and GC contents of the strands (referred to here as A10 and G10 systems); the other two concern the effects of the inclusion of model radiosensitizing nucleosides (referred to here as 2FC and BrA systems) (Figure 1B). The A10 system contains a higher AT content with A_{10} and complementary T_{10} fixed within the center of the DNA duplex in the top position (Position 1). The bottom position (Position 2) supports a control strand comprised of a scrambled DNA sequence (R(A10)). In the G10 system, the $A_{10} \cdot T_{10}$ section of the top strand is replaced by a $G_{10} \cdot C_{10}$ sequence. For the radiosensitized systems, the 64 bp free central sequence of the 2FC strand is similar to that of the R strand but with three cytosine nucleosides replaced by 2'-deoxy-2'-fluorocytidine, while in the BrA system, three adenosine nucleosides are replaced by 8-bromoadenosine (Figure 1B). Both are representative models for two types of electrophilic radiosensitizers, with halogen atoms incorporated in the sugar unit^{30,31} and the base unit^{32,33} of the nucleosides,

respectively. In both systems, the R sequence is retained in Position 2 serving as a control.

The breaks in the parallel duplex strands in the frame aperture can be distinguished and counted by AFM. The counts for each system at increasing absorbed dose are shown in Figure 2e–h. The dose response of DSB counted per DNA origami frame (N_{DSB} , with initial DSB count (N_{DSB_0}) in the unirradiated sample) can be described by an exponential with a saturation point (eq 1) and a decay rate corresponding to the double strand break yield (μ_{DSB}) due to the observed stochastic nature of the process.³⁴ The working range 0–4 kGy (see Supporting Information) before the frames become heavily damaged is still within the quasi-linear regime estimated by fitting a linear function whose slope is equal to μ_{DSB} (eq 2).

$$N_{DSB} = N_{DSB_0} + (1 - e^{-\mu_{DSB}D}) \quad (1)$$

$$N_{DSB} \approx \mu_{DSB}D + N_{DSB_0} \quad (2)$$

In the case of RT-PCR, the fraction of remaining intact strands ($\frac{N}{N_0}$) after irradiation is related to the measured C_p (crossing point or threshold value of fluorescence detection) as described in eq 3, taking into account the primer efficiency (E) obtained from standard curves (see Supporting Information), with C_{p,N_0} taken as the threshold value of the control containing N_0 strands.^{35,36} The measured curves are shown in Figure 2a–d. During irradiation, the strands can be nicked, and the remaining fraction of intact strands can be related to the absorbed dose (D) by an exponential decay function (eq

Table 1. Estimated Strand Break Yields of the Various DNA Motifs Studied after Irradiation with 16 MeV Electrons^a

DNA Motif	$\mu_{TL} \pm SD$ (total lesions·kGy ⁻¹)	EF (total lesions)	$\mu_{DSB} \pm SD$ (DSB·kGy ⁻¹)	EF (DSB)
A10	0.73 ± 0.04	1.02 ± 0.07	0.030 ± 0.005	0.98 ± 0.19
R(A10)	0.71 ± 0.03		0.031 ± 0.006	
G10	0.64 ± 0.04	0.95 ± 0.09	0.043 ± 0.004	0.98 ± 0.11
R(G10)	0.67 ± 0.04		0.044 ± 0.002	
2FC	0.70 ± 0.06	0.98 ± 0.12	0.118 ± 0.010	1.27 ± 0.13
R(2FC)	0.71 ± 0.06		0.093 ± 0.005	
BrA	1.19 ± 0.12	1.49 ± 0.16	0.144 ± 0.014	1.19 ± 0.13
R(BrA)	0.79 ± 0.04		0.121 ± 0.007	

^aThe enhancement factors are taken from the ratio of μ_{TL} or μ_{DSB} between the modified strand and the control strand (R) in each system.

Table 2. Strand Break Yields Obtained from This Work and Those Obtained from Gel Electrophoresis Results of High Energy Electron Irradiated Plasmid DNA in the Literature.^a

plasmid/system	electron energy (MeV)	scavenging capacity (s ⁻¹)	dose rate (Gy s ⁻¹)	$\mu_{SSB} \pm SD$ (SSB·Mbp ⁻¹ ·Gy ⁻¹)	$\mu_{DSB} \pm SD$ (DSB·Mbp ⁻¹ ·Gy ⁻¹)	ref			
64 bp duplex on DNA origami frames	16	10 ⁷	6.7	10.58 ± 0.53	0.51 ± 0.10	this work			
				9.85 ± 0.7	0.69 ± 0.03				
				9.64 ± 0.95	1.45 ± 0.08				
				10.51 ± 0.57	1.89 ± 0.11				
pBR322	16	7 × 10 ⁵	0.2	33.25 ± 3.21	0.19 ± 0.07	Perstin et al. 2022 ⁴⁰			
				47	12.22 ± 0.37		0.12 ± 0.04		
				93	13.57 ± 0.57		0.12 ± 0.05		
pBR322	6	10 ⁶	N.S.	7.94 ± 0.14	0.97 ± 0.10	Small et al. 2019 ⁴¹			
				10	11.00 ± 0.66		1.13 ± 0.08		
				15	7.71 ± 0.03		1.22 ± 0.01		
pBR322	100	10 ⁶	0.5	15.42 ± 0.86	0.35 ± 0.02	Small et al. 2021 ⁴²			
				150	17.63 ± 0.57		0.35 ± 0.03		
				200	20.19 ± 0.56		0.38 ± 0.02		
				100	10 ⁶		~10 ⁸ (flash)	20.31 ± 1.20	0.37 ± 0.03
				150			18.74 ± 0.52	0.37 ± 0.04	
200		21.22 ± 0.38	0.38 ± 0.02						

^aThe μ_{SSB} values from this work represent the minimum SSB and are estimated from $\mu_{TL} - \mu_{DSB}$ of the R strands in Table 1.

4). The decay rate (μ_{TL}) estimates the number of lesions per absorbed dose assuming a Poisson distribution of nicking events. The lesions include all double strand breaks and all damages to the modified strands that prevent PCR amplification such as single-strand breaks and base damages. Combining both equations relates the RT-PCR raw measurements in terms of C_p and the absorbed dose to directly obtain the number of lesions from the slope of the linear fit of the C_p vs D curves (eq 5).

$$\frac{N}{N_0} = (1 + E)^{(C_p, N_0 - C_p)} \quad (3)$$

$$\frac{N}{N_0} = e^{-\mu_{TL} D} \quad (4)$$

$$C_p = \frac{\mu_{TL} D}{\ln(1 + E)} - C_{p, N_0} \quad (5)$$

To discuss the effects of GC content, we can first look into the A10 and G10 systems. The values for PCR-evaluated lesions, AFM-evaluated DSB, and the corresponding enhancement factors when comparing the damages to the control strand in Position 2 are summarized in Table 1. Within the sensitivity of the present methods, increasing and decreasing the GC content by incorporation of contiguous G₁₀:C₁₀ and A₁₀:T₁₀ sequences do not show particular enhancement in the strand break yields. It has been observed that, with low energy

electron irradiated sequences in the dry state, oligomers with contiguous guanine and cytosine strands have lesser strand break cross section compared to adenine and thymine;¹⁹ however, certain studies on sequence dependence of γ radiation damage on plasmids in solution, where indirect effects play a significant role, identify cytosine as the preferred damage site for SSB and DSB and guanine for base damage.³⁷ It appears that both effects play a role in the damage observed for said systems within the radical scavenging conditions of the solution used in this experiment.

For the sensitized strands, in the 2FC system in which the halogen is attached to the sugar unit of the DNA, the total lesions are the same as the control strand as revealed by RT-PCR measurements; however, the double strand break yield is enhanced. So far radiosensitization of 2'-deoxy-2'-fluorocytidine has not yet been explored in the literature, but it appears that it does have a significant effect in increasing DSB damage in irradiated DNA. As the numbers of lesions in the modified and control DNA strands are the same, the mechanism can be explained by the different evolution of clustered damages in the two systems. While clustered DNA damages will remain non-DSB in the random sequence, they will result in DSB in the 2FC enhanced sequence. This can be caused by the formation of sugar radicals known to induce irreversible DNA damages,³⁸ possibly cutting the neighboring strands or just by the higher susceptibility of the 2FC strand to decay.

In the 8-bromoadenosine containing strand, both total lesions and DSB yields are amplified compared to the nonsensitized strand. The enhancement on DSB is lower than that on total lesions, which means that the strand breaks on the brominated base do not mostly result in DSB. The DNA sensitization by 8-bromoadenosine was explored in experiments with low-energy electrons irradiating single-stranded DNA sequences immobilized on DNA origami nanotriangles³⁹ and explained by experiments with isolated molecules.³³ An average enhancement factor of 1.9 ± 0.6 for irradiations by electrons in the 0.5–9 eV range was observed when comparing 8-bromoadenosine incorporated strands with the same sequence without the sensitizer, not far from the enhancement observed here for total lesions.

The damage profiles for 2FC and BrA indicate that the mechanisms of sensitization by these compounds are different. While BrA enhances number of single strand breaks, 2FC amplifies the number of DSB damages at the same SSB level.

It can be noted that the number of DSBs on the R strand in Position 2 is also increased by the presence of sensitized strands (R(2FC) and R(BrA) in Table 1) when compared to the R strand in the presence of A/G enhanced strands (R(A10) and R(G10) in Table 1). This can be explained as “bystander” effects, when release and diffusion of reactive species from the fragmentation of the sensitized strand can cause damages in the neighboring random sequence. In the present nanoframe design, the distance between the parallel strands is ~12 nm. However, the DNA origami technique allows for change of the distance by redesigning the nanoframe and can thus elicit more detailed exploration of this effect not only with respect to different sequences of DNA strands but also the incorporation of various types of radiosensitizers such as gold nanoparticles, which we plan to explore in the future.

Lastly, we can also compare the results of the strand break yields obtained from RT-PCR and AFM to that observed in plasmid irradiated studies at similar conditions. While DSBs can be directly compared, the number of lesions do not exactly correspond to the number of single-strand breaks. As described earlier, these encompass strand breaks and base damages on the PCR amplified strand of the double stranded DNA sequence, and therefore, the given numbers are only the lowest estimates of the SSBs. The estimates for the control strands are shown in Table 2 and are within the range of strand break yields observed in the literature. It is difficult to directly compare the values due to the differences in parameters such as the radical scavenging capacities and dose rates utilized, but both absolute values and SSB to DSB ratios are within the same range. We therefore believe that the present method can be a viable substitute or complementary technique to assess radiation induced damage to DNA sequences in solution. The nanoframe approach also allows new questions to be addressed in radiation damage such as evaluating “bystander” effects with nanometer precision as well as consequences of such damage to DNA conformation.

To conclude, we demonstrated the use of DNA origami frames to study radiation damage to doubly stranded DNA sequences in aqueous solution, particularly in assessing double strand breaks and radiosensitization/enhancement factors of halogenated nucleosides by AFM. RT-PCR was used to confirm dose-dependent damage by detecting the relative amount of remaining intact DNA motifs. The introduction of contiguous sequences of A-T and G-C base pairs did not result in changes in strand break yields detectable by the present

approach. Introducing fluorine on the sugar unit of the DNA does not significantly induce more lesions compared to the unsensitized DNA strand but has enhanced double strand break yields. Bromoadenosine consistently shows strand break enhancement both for total lesion and for double strand breaks. The strand break yields obtained using the method are close to those obtained in plasmid irradiated with MeV electrons; hence, it can be a promising tool to study radiation damage to DNA sequences of interest.

■ ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge at <https://pubs.acs.org/doi/10.1021/acs.jpcllett.2c00584>.

Methods, radiation damage to DNA origami nanoframes, and DNA origami staple sequences (PDF)

Transparent Peer Review report available (PDF)

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Notes

The authors declare no competing financial interest.

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