γ-H2AX Foci Formation as a Pharmacodynamic Marker of DNA Damage Produced by DNA Cross-Linking Agents: Results from 2 Phase I Clinical Trials of SJG-136 (SG2000)

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Abstract

Purpose: To evaluate γ-H2AX foci as a pharmacodynamic marker for DNA damage induced by DNA interstrand cross-linking drugs.

Experimental Design: γ-H2AX foci formation was validated preclinically in comparison with the Comet assay, and evaluated pharmacodynamically in two phase I studies of different dosing schedules of the novel cross-linking agent SJG-136 (SG2000).

Results: The measurement of γ-H2AX foci in human fibroblasts and lymphocytes in vitro was more than 10-fold more sensitive than Comet assay measurement of cross-linking, with peak γ-H2AX response 24 hours after the peak of cross-linking. In lymphocytes from a phase I study (every three week schedule), γ-H2AX foci were detectable 1 hour following the end of administration, and in all patients, maximum response was observed at 24 hours. Significant levels of foci were still evident at days 8 and 15 consistent with the known persistence of the DNA damage produced by this agent. In two tumor biopsy samples, foci were detected 4 hours postinfusion with levels higher than in lymphocytes. Extensive foci formation was also observed before the third dose in cycle 1 in lymphocytes from a second phase I study (daily × 3 schedule). These foci also persisted with a significant level evident before the second cycle (day 21). An increased γ-H2AX response was observed during the second cycle consistent with a cumulative pharmacodynamic effect. No clear relationship between foci formation and administered drug dose was observed.

Conclusion: This is the first use of γ-H2AX as a pharmacodynamic response to a DNA cross-linking agent in a clinical trial setting. Clin Cancer Res; 19(3); 721–30. ©2012 AACR.

Introduction

The histone protein H2AX is phosphorylated in response to ionizing radiation resulting in γ-H2AX (1). Discrete nuclear foci form rapidly at the sites of DNA double-strand breaks, which can be visualized by immunohistochemistry (2). An essential role of γ-H2AX is in the recruitment and accumulation of DNA repair and cell-cycle checkpoint proteins to the sites of DNA double-strand break damage (1, 3), including sites of replication fork collapse (4). Because of the sensitivity and use for detection of DNA double-strand breaks, γ-H2AX has emerged as a potentially useful biomarker with clinical implications (5, 6). Persistence of these foci is considered to be an indicator of cell sensitivity after radiotherapy or treatment with radiomimetic drugs (7–9). We, and others, have also shown that the DNA damage produced by DNA interstrand cross-linking agents, including mechlorethamine, cisplatin, mitomycin C, and psoralen plus UV, can also induce γ-H2AX foci (9–13), raising the possibility that the measurement of γ-H2AX foci could be used as a sensitive pharmacodynamic marker of DNA damage by cross-linking agents in the clinic (6).

SJG-136 (SG2000, NSC 694501) is a rationally designed pyrrolobenzodiazepine dimer, which interacts sequence selectively in the minor groove of DNA (14). It spans 6 base pairs with a preference for 5'-purine-GATC-pyrimidine sequences, binding covalently to the N2 positions of guanine on opposite strands of DNA to form highly cytotoxic DNA interstrand cross-links spanning 4 base pairs (14–16). On the basis of the potent antitumor activity of SJG-136 in vitro and against several human tumors in vivo (16, 17) it has progressed to phase I clinical trials in the United
Translational Relevance

γ-H2AX foci are induced following DNA interstrand cross-linking drug treatment. This article documents the preclinical evaluation of this assay and pharmacodynamic results from two phase I studies in solid tumors evaluating different dosing schedules of the novel cross-linking agent SIG-136 (SG2000). This first use of the immunochemical measurement of γ-H2AX to detect DNA damage response to a DNA cross-linking agent in lymphocytes and solid tumor in a clinical trial setting suggests that it may have a role in cancer drug development and treatment optimization in the future.

Materials and Methods

Drug

SIG-136 was synthesized as described previously (14). For in vitro experiments, 1 mmol/L stock solutions were prepared in methanol and stored at −20°C. All subsequent drug dilutions were freshly prepared in serum-free medium before drug treatment. All other chemicals were from Sigma Chemical Co. unless otherwise stated.

Cell lines and peripheral blood lymphocytes

The normal human fibroblast AG01522B (AGO) cell line was kindly provided by Dr. Kevin Prise (Gray Cancer Institute, Oxford, UK) and maintained in α-minimum essential medium containing 2 mmol/L L-glutamine, 20% fetal calf serum (FCS), 1% nonessential amino acids, 100 U/ml penicillin, and 100 μg/ml streptomycin. Cells were grown in a humidified atmosphere at 37°C and 5% CO₂ and maintained in exponential growth. The cells were kept at low passage, returning to original frozen stocks every 3 to 6 months, and tested regularly for Mycoplasma.

Normal peripheral blood lymphocytes (PBL) were isolated using the Vacutainer CPT system (Becton Dickinson). Samples were centrifuged at 1,500 × g for 20 minutes at room temperature. The fluffy mononuclear layer at the interface of the 2 layers was removed using a Pasteur pipette and transferred to a 15 ml tube. Ten milliliters of cold RPMI-1640 tissue culture media was then added and the tube gently inverted and centrifuged immediately at 200 × g for 5 minutes at 4°C. The supernatant was then discarded and the cell pellet resuspended in RPMI-1640 containing 10% FCS and 2 mmol/L L-glutamine.

Patient samples

PBL samples were taken from 2 phase I clinical trials of SIG-136 in patients with advanced cancer and pharmacodynamic analysis was conducted in the United Kingdom and United States. In the CR-UK trial, whole blood samples (8 ml) were collected predose, 1, 4, 24 hours, day 8, and day 15 after the end of infusion for cycle 1 and pre-, 1, 4 hours, day 8, and day 15 after the end of infusion for cycle 2. PBLs were then isolated using the Vacutainer CPT system described above with final resuspension in 2 ml RPMI-1640 containing 20% FCS and 10% dimethyl-sulphoxide and stored at −80°C until analysis. Samples were analyzed for DNA interstrand cross-linking using the single-cell gel electrophoresis (Comet) assay (21) and the same samples (cycle 1 only) were then used for the quantification of γ-H2AX foci induction as the research end point.

Tumor biopsies were also obtained from 2 patients before treatment and between 2 and 4 hours postinfusion. A single-cell suspension was prepared from the tumor within 30 minutes of collection. The tumor was placed in a Petri dish with a small amount of cold RPMI-1640 medium, and using 2 scalpel blades, the tumor was chopped using a cross cutting action until a suspension of cells was formed. The cell suspension was then transferred to a 15 ml tube and centrifuged at 200 × g for 5 minutes at 4°C. The supernatant was then discarded and the cells resuspended in 2 ml RPMI-1640 containing 20% FCS and 10% dimethylsulphoxide and stored at −80°C until analysis.

In the NCI trial, PBLs were isolated using the Vacutainer CPT system described above and samples taken from the patients before the first and third doses of SIG-136 during cycles 1 and 2. As in the CR-UK trial, the formation of DNA interstrand cross-links were measured using a modification of the single-cell gel electrophoresis (Comet) assay was measured as a pharmacodynamic end point, and the same samples were then used for the quantification of γ-H2AX foci induction as a research end point.

All the patient samples were independently coded before analysis, processed, and the number of γ-H2AX foci scored blind.
In vitro drug treatment

For the single-cell gel electrophoresis (Comet) assay, AGO cells and normal PBLs were treated with SJG-136 for 1 hour at 37°C and 5% CO₂ in a humidified atmosphere. For AGO cells, drug treatments were carried out in a 6-well plate and following drug removal, cells were postincubated in medium supplemented with serum. For normal PBLs, the drug was removed by centrifugation at 200 × g for 5 minutes. The supernatant was removed and cells were resuspended in drug-free full media. Cells were then incubated at 37°C and 5% CO₂ in a humidified atmosphere for the required postincubation time.

For γ-H2AX foci induction, AGO cells and PBLs to be treated ex vivo were incubated with SJG-136 for 1 hour at 37°C and 5% CO₂ in a humidified atmosphere. For AGO cells, drug treatments were carried out in 8-well LAB-TEK II Chamber Slides (Nalge Nunc International), and the medium was replaced with drug-free medium following treatment with SJG-136. For PBLs, the drug was removed by centrifugation at 200 × g for 5 minutes, the supernatant removed, and cells resuspended in drug-free full media. Cells were then incubated at 37°C and 5% CO₂ in a humidified atmosphere as required.

Determination of DNA interstrand cross-link formation

The details of the single-cell gel electrophoresis (Comet) assay used to measure DNA interstrand cross-linking and repair are described in detail elsewhere (21). All procedures were carried out on ice and in subdued lighting. All chemicals were obtained from Sigma Chemical Co., unless otherwise stated. Immediately before analysis, cells were diluted to give a final concentration of 2.5 × 10⁶ cells/mL and irradiated (15 Gy) to deliver a fixed number of random DNA strand breaks. After embedding cells in 1% agarose on a precoated microscope slide, the cells were lysed for 1 hour in lysis buffer (100 mmol/L disodium EDTA, 2.5 mol/L NaCl, and 10 mmol/L Tris-HCl pH 10.5) containing 1% Triton X-100 added immediately before analysis, and then washed every 15 minutes in distilled water for 1 hour. Slides were then incubated in alkali buffer (50 mmol/L NaOH and 1 mmol/L disodium EDTA, pH 12.5) for 45 minutes followed by electrophoresis in the same buffer for 25 minutes at 18 V (0.6 V/cm), 250 mA. The slides were finally rinsed in neutralizing buffer (0.5 mol/L Tris-HCl, pH 7.5) and then saline.

After drying, the slides were stained with propidium iodide (2.5 μg/mL) for 30 minutes and then rinsed in distilled water. Images were visualized using a NIKON inverted microscope with high-pressure mercury light source, 510–560 nm excitation filter and 590 nm barrier filter at × 20 magnification. Images were captured using an on-line CCD camera and analyzed using Komet Analysis software 4.02 (Andor Technology). For each duplicate slide, 25 cells were analyzed. The tail moment for each image was calculated as the product of the percentage DNA in the comet tail and the distance between the means of the head and tail distributions (26). DNA interstrand cross-linking was expressed as percentage decrease in tail moment compared with irradiated controls calculated by the formula:

\[
\text{% decrease in tail moment} = \left[ 1 - \left( \frac{(T_{\text{coli}} - T_{\text{cu}})}{(T_{\text{co}} - T_{\text{cu}})} \right) \right] \times 100
\]

where \( T_{\text{coli}} \) = tail moment of drug-treated irradiated sample; \( T_{\text{cu}} \) = tail moment of untreated, unirradiated control; and \( T_{\text{co}} \) = tail moment of untreated, irradiated control.

γ-H2AX immunofluorescence

For AGO cells, 2 × 10⁶ cells per well were seeded in an 8-well LAB-TEK II Chamber Slides (Nalge Nunc International) and incubated overnight at 37°C. Cells were treated with SJG-136 for 1 hour after which the drug was removed and cells incubated at 37°C in drug-free medium. Cells were fixed with ice-cold methanol:acetone (50:50) for 8 minutes at 4°C. Cells were washed 3 times with cold PBS and then permeabilized with 0.5% Triton X-100 in PBS for 5 minutes at room temperature. Cells were then blocked overnight at 4°C with blocking buffer (0.1% Triton X-100, 0.2% skimmed dry milk in PBS). Blocked cells were incubated with anti-phospho-histone H2A.X (Ser139) monoclonal antibody (Millipore) for 1 hour at a 1:10,000 dilution in blocking buffer at room temperature. After washing 3 times with washing buffer (0.1% Triton X-100 in PBS), cells were then incubated for 1 hour at room temperature with Alexa Fluor 488 goat anti-mouse secondary antibody (Invitrogen) in blocking buffer. Cells were then washed with PBS.

For ex vivo treatment of PBLs, cells were treated with 10 nmol/L SJG-136 for 1 hour after which the drug was removed by centrifugation at 200 × g, cells resuspended, and incubated at 37°C in drug-free medium. For both ex vivo treated PBLs and patient samples (PBL and tumor), 5 × 10⁴ cells were adhered to Vision BioSystems Plus slides by cytopinning at 650 rpm for 5 minutes at room temperature. Slides were then dried at room temperature. Cells were fixed with ice-cold methanol:acetone (50:50) for 15 minutes at 4°C. Cells were washed 3 times with cold PBS and then permeabilized for 15 minutes at room temperature. Cells were then blocked in blocking buffer (0.1% Triton X-100 and 0.2% skimmed dry milk in PBS) overnight at 4°C. Blocked cells were incubated overnight at 4°C with anti-phospho-histone H2A.X (Ser139) monoclonal antibody (Millipore) at a 1:1,000 dilution in blocking buffer. After washing 3 times with washing buffer (0.1% Triton X-100 in PBS), cells were then incubated for 4 hours at room temperature with Alexa Fluor 488 goat anti-mouse secondary antibody (Invitrogen) in blocking buffer. Cells were then washed with PBS.

For all cell lines, normal lymphocytes, and patient samples, cells were counterstained with 2 μg/mL propidium iodide for 2 minutes. Slides were then rinsed in distilled water for 30 minutes, mounted with Vectashield (Vector Laboratories), and the edges sealed with clear nail polish. Images were visualized using Perkin Elmer Ultraview ERS Suite v 3.0.0 and confocal microscopy consisting of Zeiss Axiovert 200 inverted fluorescence microscope (× 40 oil
objective) equipped with 14 bit ECCD camera and argon and krypton gas excitation lasers at 488 and 568 nm. Z-stack acquisition using optimal slice distancing was conducted on each microscope image. Images were then compressed to produce a maximum intensity projection image to allow maximum foci detection. Foci were counted in 50 cells per time point and results are expressed as mean number of foci per cell from 3 independent experiments. All clinical samples were read blind to avoid any potential bias.

Statistical analysis

Statistical analysis was conducted using Prism 5.02 (GraphPad Software Inc.). For samples taken from the CR-UK phase I trial, all post-treatment samples were compared with pre-treatment samples by using repeated one-way ANOVA analysis. For the NCI phase I trial, the samples were compared by using one-tailed unpaired t test. The significance level was expressed as ns = non-significant; *, P < 0.05; **, P < 0.005; ***, P < 0.001.

Results

$\gamma$-H2AX foci formation following exposure to SJG-136 in vitro and in vivo

We have previously shown that exposure of cells to conventional clinical cross-linking agents and the novel minor groove sequence selective cross-linking agent SJG-136 can induce $\gamma$-H2AX foci (10, 27). Figure 1A shows a dose response of $\gamma$-H2AX foci formation in individual human fibroblast AGO cells 24 hours following a 1 hour exposure to SJG-136. Foci are observed at doses as low as 10 pmol/L reflecting the known efficiency of DNA interaction of this agent (14–16). Figure 1B shows the dose response in AGO cells of $\gamma$-H2AX foci formation above background 24 hours after 1 hour SJG-136 exposure (red) compared with the measurement of DNA interstrand cross-linking using the single cell gel electrophoresis (Comet) assay (blue) immediately after 1 hour drug exposure. The data clearly show that the $\gamma$-H2AX response is at least 10-fold more sensitive than direct measurement of DNA interstrand cross-linking using the Comet assay.

The reason for the difference in timing at which the assays are conducted is shown in Figure 1C. DNA interstrand cross-links form rapidly following exposure to SJG-136 and have reached a peak in AGO cells at the end of the 1-hour treatment. The nondistorting cross-links produced by this agent persist and are still detectable at high levels at 120 hours in these cells. In marked contrast, the $\gamma$-H2AX response is delayed and reaches a peak at 24 hours following the 1-hour treatment. The response then declines to around 30% of the peak level by 120 hours (Fig. 1C). Importantly, a similar $\gamma$-H2AX response is observed in human lymphocytes treated ex vivo with SJG-136, although in this case, the peak level at 24 hours is approximately 60% of that observed in AGO cells at the same dose of the drug (Fig. 1C).

The ability of the assay to detect $\gamma$-H2AX at pharmacologically relevant doses was tested in vivo. Data from a representative xenograft experiment are shown in Supplementary Fig. S1. Doses of SJG-136 of 0.15 and 0.3 mg/kg i.v. were chosen to give dose-dependent tumor growth
delay and measurable levels of cross-linking in tumor, peaking at 2 hours, as measured by the Comet assay. Levels of γ-H2AX foci increased with dose in both lymphocytes and tumor and were considerably higher at 24 hours than at the peak of cross-linking (2 hours), consistent with in vitro data. Both background and drug-induced levels of foci were higher in tumor than in lymphocytes.

Before use on clinical samples, validation experiments, to determine the variability of the assay, were carried out in human lymphocytes treated ex vivo with SJG-136 for 1 hour followed by post-incubation for 24 hours. Inter- and intra-assay data showing the high reproducibility of the assay are shown in Supplementary Fig. S2A and S2B. In addition, during analysis of all clinical samples, aliquots of internal standard samples of treated lymphocytes stored at −80°C were run. Data from the same internal standards from 10 runs of individual clinical sample analyses are shown in Supplementary Fig. S2C.

γ-H2AX foci formation in the CR-UK phase I clinical trial of SJG-136

The CR-UK study was designed as a 2 centre phase I dose escalation study of SJG-136, given as a 10-minute intravenous infusion every 21 days in patients with solid tumors (18). Seventeen patients were entered into the study and 16 patients were treated. Doses administered ranged from 15 to 240 mg/m². The schema for the dosing schedule and timing of sample for pharmacodynamic analysis are shown in Fig. 2 (top). The γ-H2AX foci data in lymphocytes from the individual patients at the different dose levels are shown in Fig. 3A with the pooled data in Fig. 3B. All samples were read blind to avoid any potential bias. The background level of γ-H2AX foci in the predose samples ranged from 0 to 10 foci per cell. Foci are detectable in all lymphocyte samples as early as 1 hour after the end of drug infusion (Fig. 3A) although the overall level did not reach significance over the predose level (Fig. 3B). A significant level of foci formation was, however, observed at 4 hours (P < 0.005), which then reached a peak at 24 hours. Interestingly, there is no clear dose response in γ-H2AX foci formation. Statistically significant levels of foci are still evident in the day 8 (P < 0.005) and day 15 (P < 0.05) samples.

In 2 patients with melanoma (both treated with 45 μg/m²), it was possible to obtain both predose and post-treatment (4 hour) tumor biopsy samples. The predose biopsy samples had a greater background level of γ-H2AX foci than in lymphocytes. This level, however, increased by more than 4-fold in patient 12 and more than 3-fold in patient 13 following treatment (Fig. 3C).

γ-H2AX foci formation in the NCI Vanderbilt phase I clinical trial of SJG-136

In the NCI trial, SJG-136 was administered via a 20-minute intravenous infusion using a daily x 3 dosing schedule every 3 weeks with steroid premedication (dexamethasone, 8 mg/day, day 1–3) and early diuretic treatment with spironolactone (19). The starting dose of SJG-136 was 20 mg/m²/d, which was escalated to 25, 30, and 35 mg/m²/d. The schema for the dosing schedule and timing of samples for pharmacodynamic assessment is shown in Fig. 2 (bottom). The γ-H2AX foci data in lymphocytes from the individual patients at the different dose levels are shown in Fig. 4A. The background level of γ-H2AX foci in the cycle 1 predose samples was less than 10 in all samples with the exception of one patient who had a level more than 20. In the cycle 1 day 3 samples (just before the administration of the third daily dose), γ-H2AX foci were observed in all samples ranging from 4 to 34 foci per cell. This level of foci was highly significant (P < 0.001) compared with the precycle 1 sample (Figure 4B), although no clear dose response was observed. Eighteen days later, just before the first administration of the second cycle (pre-C2, Fig. 4), the level of foci had decreased in all samples, but the mean level was still significantly (P < 0.005) above than that in the pre-cycle 1 samples (Fig. 4B). Cycle 2 day
3 (C2D3) gave the highest level of γ-H2AX foci, which was significantly higher than the pre-cycle 1 samples (P < 0.001), but also significantly higher than the cycle 1 day 3 (C1D3) samples (P < 0.05, Fig. 4B) indicating a cumulative DNA damage response with cycle.

Discussion

The current study was undertaken to evaluate the potential of γ-H2AX foci formation as a clinical pharmacodynamic marker of DNA damage produced by DNA cross-linking agents and its repair. We have previously shown in vitro that γ-H2AX can act as a highly sensitive and general marker of DNA damage induced by nitrogen mustard and platinum drugs and that it showed promise for predicting cellular chemosensitivity to interstrand cross-linking agents (10). γ-H2AX is likely marking sites of double-strand breaks generated after lesion processing by structure-specific endonucleases. A decline in γ-H2AX after the peak of formation suggests the resolution of the intermediate double-strand breaks by downstream pathways, for example, homologous recombination repair, translesion DNA synthesis, etc.

The novel DNA minor groove cross-linking agent was chosen for the current study as it was previously shown to be a highly efficient cross-linking agent (16) and the 2 phase I studies of this agent, using different dosing schedules where appropriately timed samples were already being taken for other pharmacodynamic analyses, made it ideal for the clinical evaluation of γ-H2AX response. In the
preclinical studies, the measurement of γ-H2AX foci was found to be at least 10-fold more sensitive than the Comet assay at detecting DNA damage induced by SJG-136. The modified Comet assay directly measures DNA interstrand cross-links, the critical cytotoxic lesion produced by bifunctional alkylating drugs and SJG-136. Although capable of producing other damage to DNA including intrastrand cross-links (28), SJG-136 rapidly and efficiently produces interstrand cross-links in cells, which persist (16, 29). This is in contrast to more conventional cross-linking drugs such as the nitrogen mustard and platinum drugs where the helix distorting DNA interstrand cross-links account for less than 5% of damage to the DNA and are repaired more readily (16, 30). In contrast to the Comet assay, the γ-H2AX assay does not directly measure the drug-induced lesion but is indicating a damage response and acts as a more general surrogate marker for the detection of the DNA damage produced by interstrand cross-linking agents. The γ-H2AX response following cross-linking agent exposure does not require cells to be actively dividing because it is observed in lymphocytes.

Interestingly, the γ-H2AX response following SJG-136 is markedly different to that produced by conventional cross-linking drugs. We have previously shown that the peak of γ-H2AX foci formation is approximately 1 hour following the peak of interstrand cross-linking (measured using the Comet assay) for nitrogen mustard and platinum drugs (10). In the case of SJG-136, however, the current study shows that the γ-H2AX response does not peak until 24 hours after the peak of the cross-linking. This may reflect the nondistorting nature of the cross-links produced by this agent (14, 16) and which may evade early detection. In addition to the increased sensitivity of the γ-H2AX assay, another potential advantage is that while the Comet assay is restricted to detecting the induction and initial incision/unhooking of DNA interstrand cross-links, it cannot detect defects in the downstream processing of unhooked cross-links, or the repair of cross-link–associated DNA double-strand breaks by homologous recombination (31). We have previously shown that γ-H2AX foci persist in cells defective in both the initial unhooking of interstrand cross-links (ERCC1 defective).
and homologous recombination repair (XRCC3 defective; ref. 10).

In the samples from the CR-UK study, γ-H2AX foci were detectable at 1 hour following the end of treatment and in all patients, the maximum response was observed at 24 hours, showing the same time course as was observed in the lymphocytes treated ex vivo. Significant levels of foci were still evident at day 8 and day 15 consistent with the known persistence of the DNA damage produced by this agent. In the 2 biopsy samples that were available, DNA damage was clearly detected 4 hours post-infusion with foci levels much higher than in the lymphocyte samples taken at the same time point. This clearly indicates that a significant level of drug had reached the tumor. It is interesting to note that in these 2 patients, the level of foci in the tumor at 4 hours was more than the level in lymphocytes from the same patients at 24 hours, the peak time of γ-H2AX response.

Extensive foci formation was also observed just before the third dose in cycles 1 in the lymphocytes from the NCI study. These foci were also shown to persist and a significant level was evident just before the second cycle (day 21). Consistent with this was the fact that low levels of cross-linking were observed just before cycle 2 in some patients measured using the Comet assay (19). An increased γ-H2AX response was observed during the second cycle consistent with a cumulative pharmacodynamic effect. It is interesting to note that in neither clinical study was there a clear relationship between lymphocyte foci formation and administered drug dose (Supplementary Fig. S3A and S3B) despite a clear dose response observed in vitro. In both clinical studies, linear drug pharmacokinetics was observed across the dose ranges tested. In the NCI study, the low levels of cross-linking observed in samples taken during cycle 1 correlated better with the systemic exposure to SJG-136 (as assessed by AUC or Cmax) than with the administered dose levels (19). The absence of measurable cross-linking in the CR-UK study and relatively low levels detected in the NCI study suggest that the levels produced were near the limits of detection of this assay for this drug. In the NCI study, there was no clear relationship between foci formation and cross-linking (Supplementary Fig. S3C). The loss of γ-H2AX observed in lymphocytes may not necessarily represent repair, but loss of damaged cells, which may partly explain the lack of dose response observed. It is interesting to note, however, that no significant myelosuppression was observed on the NCI study (19). The γ-H2AX assay, however, provided conclusive evidence of drug–DNA interaction by SJG-136 in lymphocytes from all patients, and in tumor in the 2 patients, where it was possible to evaluate.

One patient unexpectedly had a very high background of γ-H2AX foci in lymphocytes. In addition, the level of background in the tumor biopsy samples was found to be higher than in lymphocytes, as observed in vitro (Supplementary Fig. S1). Most circulating lymphocytes are quiescent and DNA synthesis is limited. In tumor, the fraction of cells in S-phase may be expected to have a higher γ-H2AX response than cells in other phases. Background levels of γ-H2AX have been shown to vary widely between cells in different tissues, culture, or different cell lines, and it has been found that elevated levels of γ-H2AX are present in a number of human cancer cell model systems (32, 33), suggesting that an increased level of DNA damage is a general characteristic of cancer development. In addition, the extent of γ-H2AX response to cross-links can also vary between different cells (as observed in this study for AGO cells and lymphocytes) and between different interstrand cross-linking agents (10, 12, 13).

The current study clearly shows that the measurement of γ-H2AX foci can act as a surrogate clinical marker of DNA damage induced by DNA interstrand cross-linking agents such as the novel sequence selective minor groove cross-linking agent SJG-136. The current clinical studies used primarily lymphocytes where the time course and persistence of γ-H2AX foci formation could be studied with good sensitivity. The data in biopsy material were limited in the current study due to the design of the clinical protocols, but importantly, showed that the assay was also applicable to target tumor tissue. Encouragingly, in the CR-UK study higher levels of foci were observed in tumor than in time-matched lymphocytes. Future studies should examine the relationship between cross-linking drug-induced γ-H2AX foci formation and persistence in relation to the clinical antitumor response. Indeed, γ-H2AX foci is being measured directly in tumor cells in 2 further studies of SJG-136: a phase II study in ovarian cancer and a phase I/II study in hematologic malignancies, and the results of these analyses will be presented in due course. A recent study has shown the potential of monitoring drug-induced γ-H2AX as a pharmacodynamic biomarker in individual circulating tumor cells (34). 2 studies have used flow cytometry measurement of H2AX phosphorylation following drug treatment in leukemic cells (35, 36), and an immunofluorescence assay for γ-H2AX has been validated as a pharmacodynamic marker of topoisomerase I inhibitor activity (37). The current study is the first to use the immunochromatographic measurement of γ-H2AX to detect DNA damage response to a DNA cross-linking agent in lymphocytes and solid tumor in a clinical trial setting. The central position of γ-H2AX in DNA damage detection and repair and its ease of detection suggest that it may have a significant role in cancer drug development and treatment optimization in the future (6).

Disclosure of Potential Conflicts of Interest

D. Hochhauser has a commercial research grant from Merck Serono and is a consultant/advisory board member of Roche. J.A. Hartley is employed (other than primary affiliation; e.g., consulting) in Spirogen Ltd. as a consultant/founder, has commercial research support and ownership interest (including patents) from Spirogen Ltd; and is a consultant/advisory board member of Spirogen Ltd. No potential conflicts of interest were disclosed by the other authors.

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