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Molecular Cancer Therapeutics



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BRCA2 and RAD51 Promote Double-Strand Break Formation and Cell Death in Response to Gemcitabine

Rebecca M. Jones¹, Panagiotis Kotsantis¹, Grant S. Stewart¹, Petra Groth², and Eva Petermann¹

Abstract

Replication inhibitors cause replication fork stalling and double-strand breaks (DSB) that result from processing of stalled forks. During recovery from replication blocks, the homologous recombination (HR) factor RAD51 mediates fork restart and DSB repair. HR defects therefore sensitize cells to replication inhibitors, with clear implications for cancer therapy. Gemcitabine is a potent replication inhibitor used to treat cancers with mutations in HR genes such as *BRCA2*. Here, we investigate why, paradoxically, mutations in HR genes protect cells from killing by gemcitabine. Using DNA replication and DNA damage assays in mammalian cells, we show that even short gemcitabine treatments cause persistent replication inhibition. *BRCA2* and *RAD51* are recruited to chromatin early after removal of the drug, actively inhibit replication fork progression, and promote the formation of MUS81- and XPF-dependent DSBs that remain unrepaired. Our data suggest that HR intermediates formed at gemcitabine-stalled forks are converted into DSBs and thus contribute to gemcitabine-induced cell death, which could have implications for the treatment response of HR-deficient tumors. *Mol Cancer Ther*; 13(10); 2412–21. ©2014 AACR.

Introduction

Many cytotoxic anticancer treatments target proliferating cells by interfering with DNA replication, thus generating lethal DNA damage. Such treatments exploit the high proliferation rates of cancer cells, and can be further potentiated by cancer-specific defects in DNA repair (1). The mechanisms of action of two replication inhibitors, the ribonucleotide reductase (RNR) inhibitor hydroxyurea (HU) and the DNA polymerase inhibitor aphidicolin, have been studied in detail. Both cause slowing or stalling of replication forks, generating excessive amounts of ssDNA as DNA polymerases stall but the replicative helicase continues to unwind DNA. Replication inhibition activates the ATR-dependent S-phase checkpoint, which stabilizes stalled forks and downregulates new replication initiation (origin firing) to prevent further damage (2). After removal of the inhibitor, replication restarts and the checkpoint is inactivated. Depending on the length of treatment, restart occurs either by resumption of replication fork progression or through new origin firing (2, 3). After a few hours of

replication block, structure-specific nucleases such as MUS81-EME1 begin to process the stalled forks into double-strand breaks (DSB; refs. 3, 4). Accumulation of these DSBs creates a requirement for the DSB repair pathways homologous recombination (HR) and nonhomologous end joining (NHEJ) for cellular resistance to replication inhibitors (5). HR depends on the recombinase *RAD51* and mediator proteins such as *XRCC3* and *BRCA2*, which promote the loading of *RAD51* onto ssDNA. In addition to their roles in DSB repair, *BRCA2* and *RAD51* also prevent excessive MRE11-dependent resection of the daughter strands at stalled forks (6, 7) and *RAD51* promotes restart of stalled forks after release from HU (3). All of these findings are of potential clinical importance as several types of cancer can have genetic defects in HR. This includes breast and pancreatic cancer, where familial and sporadic forms can display inactivating mutations or promoter methylations in *BRCA1*, *BRCA2*, *PALB2*, *BRIP1*, and other genes of the Fanconi Anemia pathway (8–11). Breast and pancreatic cancer are treated with the replication inhibitor gemcitabine (2',2'-difluorodeoxycytidine). In the cells, gemcitabine is converted into its di- and triphosphates, which inactivate RNR and inhibit DNA polymerase after incorporation into nascent DNA (12). This strongly inhibits DNA synthesis and causes p53-independent apoptosis. The cytotoxic DNA lesions induced by gemcitabine and the DNA repair pathways that respond to them are poorly understood. Intriguingly, previous studies found that Chinese hamster cells mutated in *BRCA2* or another HR mediator, *XRCC3*, and the *FANCC*-mutated pancreatic cancer cell line PL11 were less sensitive to gemcitabine treatments than their HR-proficient counterparts (13–15).

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Here, we investigate the molecular mechanism by which the HR factors BRCA2 and RAD51 promote gemcitabine-induced cell death. Our data suggest that even after short gemcitabine treatments, replication forks remain stalled and are converted into DSBs that persist in the cells. BRCA2 and RAD51 are recruited to chromatin, inhibit fork progression, and promote the formation of DSBs that are dependent on the structure-specific endonucleases MUS81 and XPF. Our data suggest that HR intermediates formed at stalled forks promote gemcitabine cytotoxicity, which could have implications for the treatment response of HR-deficient tumors.

Materials and Methods

Cell lines and reagents

Human cell lines were all obtained from ATCC more than 2 years ago and were therefore authenticated using 8-locus short tandem repeat profiling (LGC standards). Human U2OS osteosarcoma cells were last authenticated in April 2013. H1299 lung carcinoma cells were last authenticated in March 2011 and have not been cultured since. BxPC3 pancreatic adenocarcinoma cells, MCF7 breast cancer cells, and OVCAR3 human ovarian cancer cells were last authenticated in April 2014.

VC8 and VC8-B2 cells were obtained from Małgorzata Z. Zdzenicka (16, authentication not available). Cells were confirmed mycoplasma-free and grown in DMEM with 10% FCS in a humidified atmosphere containing 5% CO₂. OVCAR3 cells were grown in DMEM with 10% FBS, 0.01 mg/mL insulin, and 1% nonessential amino acids (Sigma). Gemcitabine (Tocris Bioscience) was used at 2 or 5 μ mol/L for 2 hours. DNA-PK inhibitor NU7441 (Tocris Bioscience) was used at 1 μ mol/L. BLM inhibitor ML216 (Sigma-Aldrich) was used at 1.8 μ mol/L as previously described (17).

DNA fiber analysis

Cells were labeled with 25 μ mol/L CldU and 250 μ mol/L IdU as indicated. For release from gemcitabine, cells were washed three times with warm PBS. Controls were labeled with CldU and IdU for 20 minutes each. DNA fiber spreads were prepared as described (3). Acid-treated fiber spreads were incubated with rat anti-BrdU (detects CldU, BU1/75; AbD Serotec) and mouse anti-BrdU (detects IdU, B44; Becton Dickinson) for 1 hour. Slides were fixed with 4% formaldehyde and incubated with anti-rat IgG AlexaFluor 555 and anti-mouse IgG AlexaFluor 488 (Molecular Probes) for 1.5 hour. Images were acquired on an E600 Nikon microscope using a Plan Apo 60 \times (1.3NA) oil lens (Nikon), a digital camera (C4742-95; Hamamatsu) and the Velocity acquisition software (PerkinElmer). Images were analyzed using ImageJ (<http://rsbweb.nih.gov/ij/>). For quantification of replication structures, 60 to 250 structures were counted per independent experiment.

Immunofluorescence

For phospho-Histone H2AX, 53BP1, Lamin B, and phospho-Histone H3, cells were fixed with 4% formalde-

hyde and permeabilized with 0.2% Triton X-100 for 5 minutes. For RAD51 foci, cells were pre-extracted with 0.2% Triton X-100 for 1 minute. For colocalization with replication foci, antibodies were fixed with 4% formaldehyde before DNA denaturation with HCl and immunostaining for thymidine analogues. Primary antibodies were rat monoclonal anti-BrdU (BU1/75, AbD Serotec, 1:400) to detect CldU, mouse monoclonal anti-BrdU (B44, Becton Dickinson, 1:50) to detect IdU, mouse monoclonal anti-phospho-Histone H2AX (Ser139; JWB301, Merck Millipore, 1:1000), rabbit polyclonal anti-RAD51 (H-92, Santa Cruz Biotechnology, 1:500), rabbit polyclonal anti-53BP1 (Bethyl, 1:3000), goat polyclonal anti-Lamin B (Santa Cruz Biotechnology, 1:400), and rabbit polyclonal anti-phospho-Histone H3 (Ser10; Merck Millipore, 1:500). Secondary antibodies were anti-Rat IgG AlexaFluor 555, anti-mouse IgG AlexaFluor 488, anti-rabbit IgG AlexaFluor 555, or AlexaFluor 647 and anti-goat IgG AlexaFluor 594 (Molecular Probes). DNA was counterstained with 4',6-diamidino-2-phenylindole dihydrochloride (DAPI) and images acquired as above.

Cell survival assays

For clonogenic survival, defined numbers of cells were plated before treatment with gemcitabine (0.1–5 μ mol/L) for 2 hours. Colonies of >50 cells were allowed to form in fresh medium, fixed and stained with 50% ethanol, 2% methylene blue for 10 minutes. Apoptosis was quantified by counting fragmented nuclei after DAPI staining and mitotic catastrophe was quantified by counting fragmented nuclei displaying Lamin B staining.

Flow cytometry

A total of 5×10^5 cells per sample were treated as indicated, harvested and fixed with cold 70% ethanol before staining with propidium iodide (10 μ g/mL). Cell-cycle profiles were gathered using the C6 Flow Cytometer system (Accuri) and analyzed with CFlow Plus.

Pulsed-field gel electrophoresis

A total of 2×10^6 cells per sample were treated as indicated, harvested, and melted into 1.0% InCert-Agarose (Lonza) inserts. Inserts were digested in 0.5 mol/L EDTA-1% N-laurylsarcosyl-proteinase K (1 mg/mL) at room temperature for 48 hours and washed three times in Tris-EDTA (TE) buffer. Inserts were loaded onto a separation gel (1.0% chromosomal-grade agarose; Bio-Rad). Separation was performed using a CHEF DR III (Bio-Rad; 120-field angle, 240-second switch time, 4 V/cm⁻¹, 14°C) for 20 hours. Images of ethidium bromide-stained gels were acquired using a Syngene G:BOX gel imaging system. DSBs (chromosome fragments >2 Mbp) were quantified by densitometry using ImageJ. Intensity of DNA entering the gel was normalized to total DNA and untreated control was subtracted to obtain final values.

siRNA treatment

siRNA against human RAD51 (14), MUS81 (siGENOME SMARTpool D-016143), and XPF (ERCC4; OnTARGETplus

SMARTpool L-019946-00) were from Thermo Fisher. "All-stars negative control siRNA" (nonT) was from Qiagen. Cells were transfected with 50 nmol/L of each siRNA using Dharmafect 1 (Thermo Fisher) for 24, 48 (RAD51), or 72 hours (XPF and MUS81) before treatment with gemcitabine.

Western blotting

Primary antibodies were rabbit polyclonal anti-RAD51 (H-92, Santa Cruz Biotechnology, 1:500), mouse monoclonal anti-MUS81 (MTA30 2G10/3, Santa Cruz Biotechnology, 1:500), mouse monoclonal anti-XPF (219, Fisher Scientific, 1:200), mouse anti- α Tubulin (B512, Sigma, 1:5,000), rabbit polyclonal anti- β -actin (Cell Signaling Technology, 1:1,000), and mouse monoclonal anti-PARP1 (F-2, Santa Cruz Biotechnology, 1:500). For further antibody information, see Supplementary Materials and Methods.

Statistical analysis

The mean and $1 \times$ SEM of independent repeats are shown. Statistical significance was determined using the Student *t* test (*, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$).

Results

We used *BRCA2*-mutated VC8 and *BRCA2*-complemented VC8-B2 Chinese hamster fibroblasts (*p53* mutated), an isogenic model for *BRCA2* function that has successfully been used to study the role of *BRCA2* in chemotherapy response (18). We tested short gemcitabine treatments in the micromolar range, similar to clinically relevant concentrations (19, 20). Although VC8 cells were hypersensitive to cisplatin as expected (Supplementary Fig. S1A), they were less sensitive than VC8-B2 cells to higher concentrations of gemcitabine (Fig. 1A). Similar results were obtained after siRNA-depleting RAD51 in human U2OS osteosarcoma and BxPC3 pancreatic cancer cell lines (both *p53* wild-type), suggesting that this was not due to secondary mutations acquired in VC8 cells, but to loss of RAD51 function (Fig. 1B and C and Supplementary Fig. S1B).

We initially used 2 μ mol/L gemcitabine, which has been shown to inhibit fork progression and allowed about 50% survival in our cell lines, and measured replication restart using DNA fiber analyses (Fig. 1D). Even at this low concentration, most forks remained stalled and did not resume progression for at least 24 hours after release from 2 hour gemcitabine (Fig. 1D). Levels of fork stalling were comparable between *BRCA2*-proficient and -deficient cells and similar results were obtained using RAD51-depleted U2OS cells (Fig. 1E and F). Levels of phospho-S139-H2AX (γ H2AX), a marker of stalled forks (3), increased after gemcitabine release and remained high for at least 72 hours, suggesting that stalled forks persisted for several days (Fig. 1G and H). The induction of γ H2AX was comparable in *BRCA2*-proficient and -deficient as well

as control- and RAD51-depleted cells (Fig. 1G and H). However, *BRCA2*-deficient cells displayed lower γ H2AX staining after 72 hours release, suggesting a quicker recovery from gemcitabine-induced DNA damage (Fig. 1G). Overall these data did not suggest that promotion of fork restart by *BRCA2* or RAD51 plays a role in response to cytotoxic gemcitabine treatments.

Despite persistent fork stalling, cells resumed replication between 6-hour and 24-hour release, firing new origins and resuming slow progression through S phase (Fig. 2A and B). Nevertheless, markers of S-phase checkpoint signaling remained active during replication restart (Supplementary Fig. S2). Cell-cycle progression was accompanied by apoptosis and mitotic catastrophe (MC), which peaked after 2 to 3 days release (Fig. 2B and C). The appearance of MC suggests that some cell death did result from aberrant mitotic entry in presence of unrepaired DNA damage (21). VC8 cells displayed lower induction of MC and apoptosis after 5 μ mol/L gemcitabine (Fig. 2D), which was not due to VC8 cells being prevented from cycling and mitotic entry. Instead, VC8 cells displayed higher percentages of cells positive for phospho-histone H3 (Fig. 2E) and faster progression into the next G_1 phase 1 day after release compared with VC8-B2 cells (Fig. 2F). Initial accumulation in S phase was also not lower in *BRCA2*-deficient cells (Fig. 2F), confirming that reduced gemcitabine sensitivity was not due to fewer cells entering S phase. Interestingly, VC8 cells displayed fewer γ H2AX-positive cells and a lower percentage of S-phase cells at 3 days after release, suggesting a quicker recovery from gemcitabine in absence of *BRCA2* (Fig. 1G and 2F).

We decided to further investigate the role of *BRCA2* and RAD51 at gemcitabine-stalled replication forks. In addition to promoting fork restart, RAD51 and *BRCA2* also prevent shortening of daughter strands at stalled forks (6, 7), and RAD51 inhibits fork progression during cisplatin and camptothecin treatments (22, 23). To investigate if either of these processes occurs after release from gemcitabine, we compared the length of DNA replicated during 2-hour gemcitabine treatment and after 4-hour release from 5 μ mol/L gemcitabine in VC8 and VC8-B2 cells (Fig. 3A). Tracks replicated during the 2-hour gemcitabine treatment were longer in presence of *BRCA2*, as has been described before (6). However, after release from gemcitabine, replicated tracks in *BRCA2*-proficient cells remained the same length, whereas tracks in *BRCA2*-deficient cells further increased in length, suggesting that some forks were still progressing (Fig. 3B, C, and F). Similar results were obtained using RAD51-depleted U2OS cells (Fig. 3D, E, and G). Our data suggest that after release from gemcitabine, *BRCA2* and RAD51 are recruited to forks where RAD51 promotes transactions that inhibit further fork progression. In HR-proficient cells, RAD51 foci indeed accumulated and persisted for 72 hours after release (Fig. 3H and I), suggesting that HR was initiated but not completed during that time.

Next, we tested whether gemcitabine-stalled forks were processed into DSBs. We first measured accumulation of

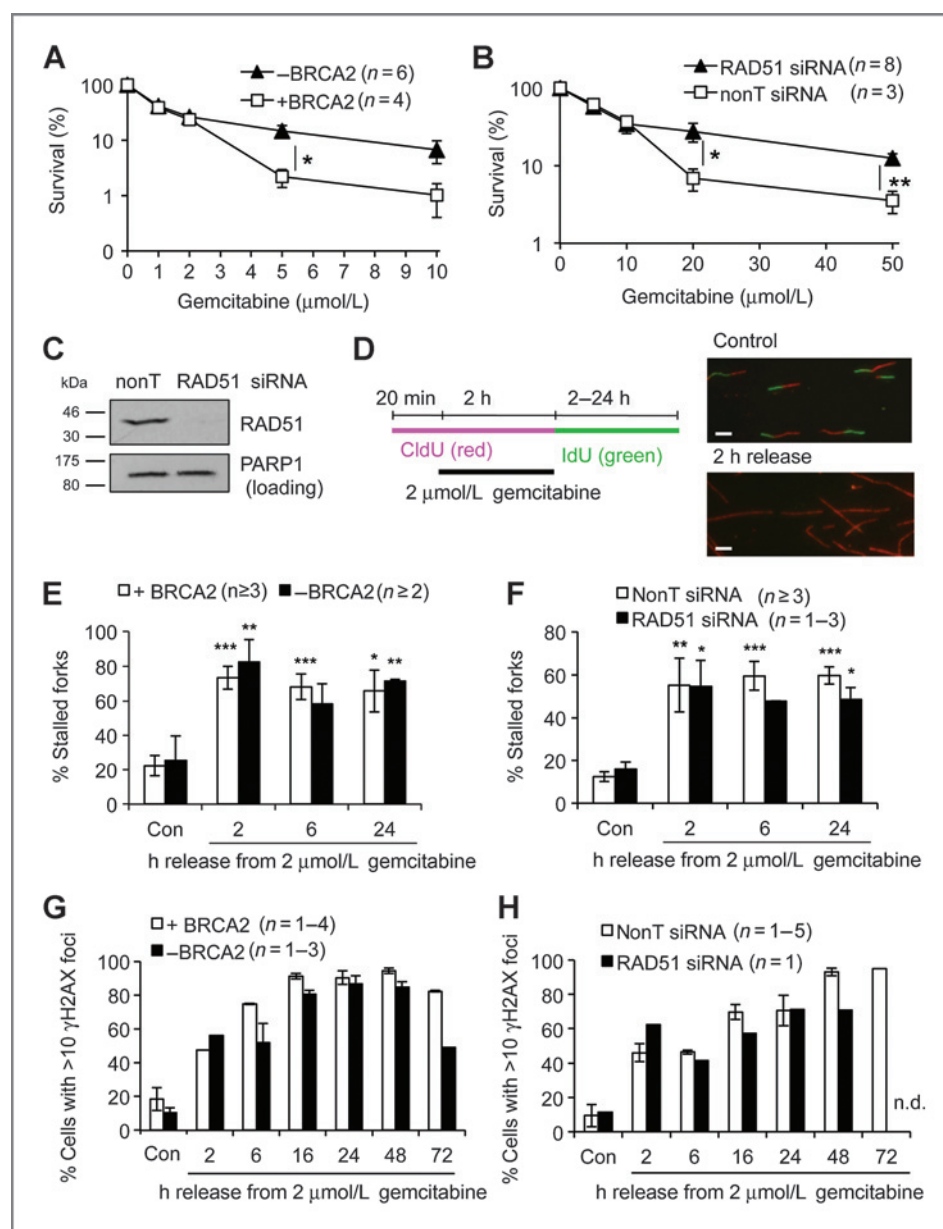


Figure 1. HR defects protect from cell death, but have no effect on irreversible replication fork stalling after release from gemcitabine. **A**, clonogenic survival of VC8 (–BRCA2) and VC8-B2 (+BRCA2) cells treated with gemcitabine for 2 hours and released into fresh medium. **B**, clonogenic survival of U2OS cells ± RAD51 treated as in **A**. **C**, protein levels of RAD51 and PARP1 (loading control) in U2OS cells 24 hours after transfection with RAD51 or nonT siRNA. **D**, schematic and representative images for DNA fiber labeling. CldU-only labeled tracks (stalled forks) were normalized to all CldU-containing tracks. Bars, 10 μm. **E**, quantification of stalled forks in VC8 and VC8-B2 cells (asterisks compared with Con). **F**, quantification of stalled forks in U2OS cells ± RAD51 siRNA (asterisks compared with Con). **G**, percentages of cells displaying more than 10 γH2AX foci after release from gemcitabine. **H**, percentages of U2OS cells ± RAD51 siRNA displaying more than 10 γH2AX foci after release from gemcitabine. Error bars, SEM; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$, Student t test.

nuclear 53BP1 foci, which mark sites of DSBs (24). High numbers of 53BP1 foci that colocalized with replication foci accumulated after 2- and 16-hour release in U2OS and VC8-B2 cells, respectively (Fig. 4A and B). Compared with γH2AX foci (Fig. 1G and H), 53BP1 foci formation was delayed and only around half of γH2AX-positive cells also contained 53BP1 foci. This supports the idea that γH2AX marks all stalled replication forks as well as DSBs, whereas 53BP1 only accu-

mulates at the subset of forks that have been processed into DSBs. Pulsed-field gel electrophoresis (PFGE) of genomic DNA confirmed that the increase in 53BP1 foci correlated with an increase in DSB levels (Fig. 4C and Supplementary Fig. S3A). As with RAD51 foci, DSB levels remained high for 2 to 3 days after release, suggesting that little DSB repair was occurring.

As DSBs are highly toxic DNA lesions and likely to contribute to gemcitabine toxicity, we next analyzed

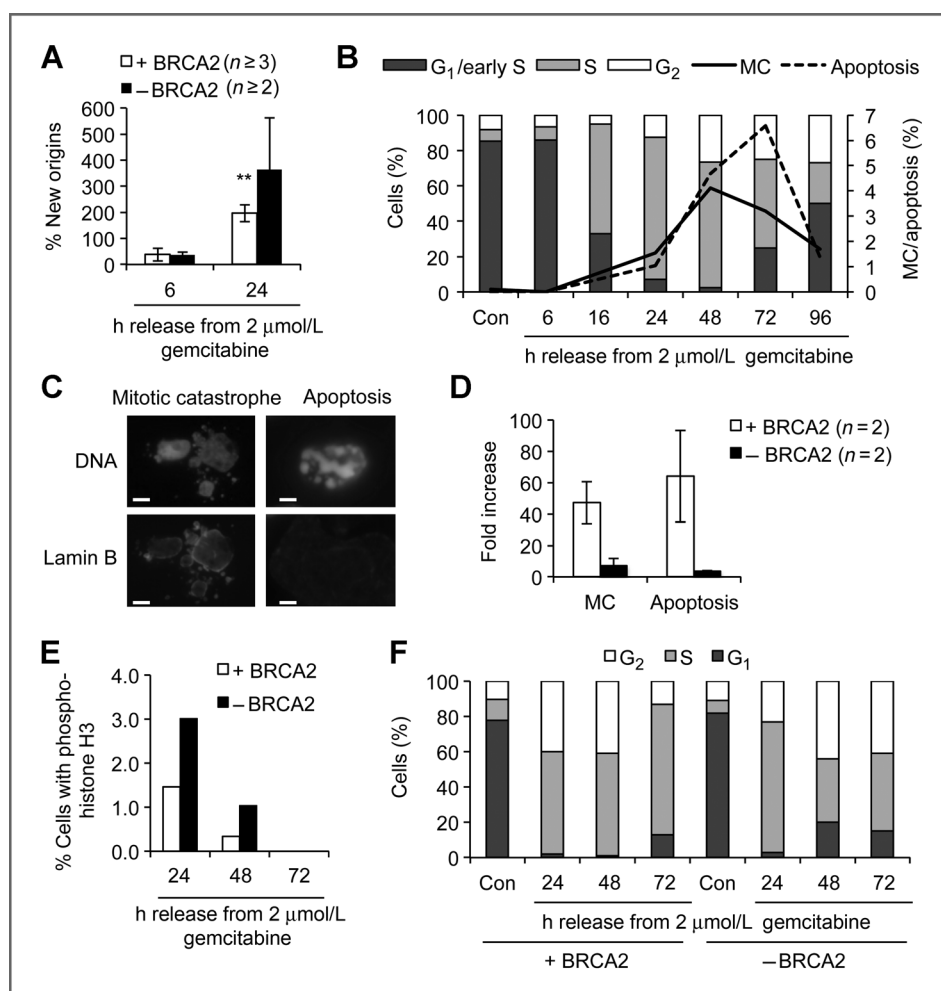


Figure 2. BRCA2-deficient and -proficient cells display aberrant cell-cycle progression after release from gemcitabine. **A**, new origin firing in VC8 and VC8-B2 cells after release from gemcitabine. DNA fiber labeling was performed as in Fig. 1D and IdU-only labeled tracks (new origins) were normalized to all CldU-containing tracks. **B**, FACS analysis of cell-cycle progression and time course of mitotic catastrophe (MC) and apoptosis in VC8-B2 cells after release from gemcitabine. **C**, representative images of DAPI- and Lamin B1-stained VC8-B2 cells with mitotic catastrophe or apoptotic phenotypes after 48-hour release from gemcitabine. Bars, 10 μm . **D**, increase in MC and apoptosis in VC8 and VC8-B2 cells after release from 5 $\mu\text{mol/L}$ gemcitabine. **E**, percentages of VC8-B2 and VC8 cells positive for phospho-histone H3 staining following release from gemcitabine in the presence of 1.5 $\mu\text{mol/L}$ nocodazole. **F**, cell-cycle progression in VC8 and VC8-B2 cells after release from 5 $\mu\text{mol/L}$ gemcitabine for 24 to 72 hours. Error bars, SEM; **, $P < 0.01$, Student t test.

whether gemcitabine-induced DSB formation depended on BRCA2 and RAD51. Indeed, PFGE showed that although VC8 cells displayed higher background levels of unrepaired DSBs, the additional increase in DSBs after gemcitabine was higher in the presence of BRCA2 (Fig. 4D and E and Supplementary Fig. S3B). Similarly, RAD51-depleted U2OS cells accumulated fewer 53BP1 foci than control cells after release from gemcitabine (Fig. 4F–H). Comparable results were obtained in RAD51-depleted human cancer cell lines derived from pancreatic (BxPC3, *p53* wild-type), breast (MCF7, *p53* wild-type), and ovarian cancer (OVCAR3, *p53* mutated; Supplementary Figs. S4–S6). HR-deficient cells thus accumulate fewer DSBs after gemcitabine treatment.

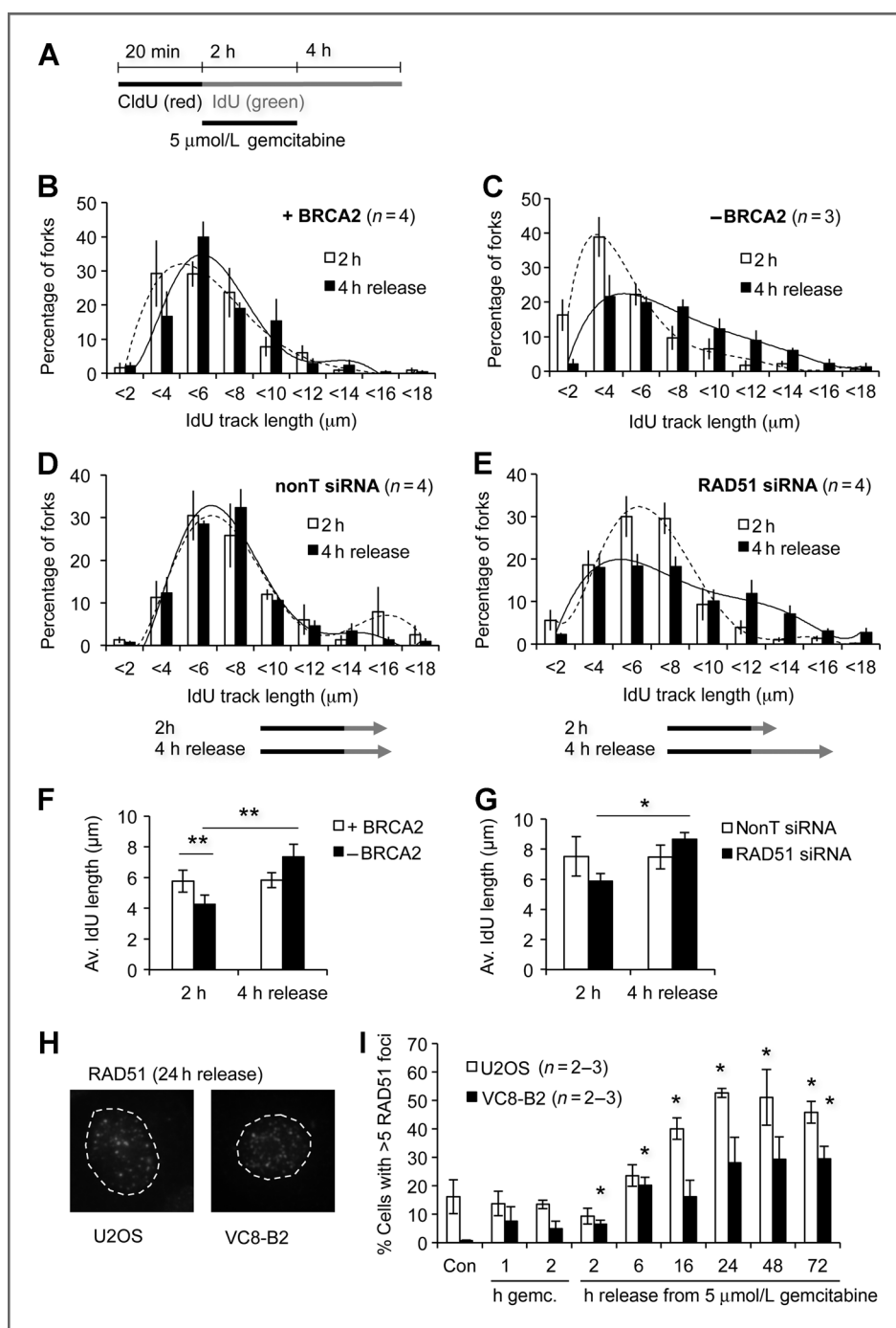
In addition to HR, NHEJ acts as an alternative and competing repair pathway for DSBs. Although NHEJ may not be able to faithfully repair one-ended DSBs at collapsed replication forks, it can promote resistance to replication inhibitors such as HU, suggesting that some replication-dependent breaks are substrates for NHEJ (5). We considered that reduced gemcitabine sensitivity in HR-deficient cells might result from DSBs being more efficiently repaired by NHEJ in absence of HR. We inhibited NHEJ

using DNA-PK inhibitor NU7441 to test whether this could sensitize HR-deficient cells to gemcitabine. NU7441 alone increased the background levels of unrepaired DSBs (Supplementary Fig. S3B). However, cotreatment with NU7441 did not increase gemcitabine toxicity (Fig. 5A) or gemcitabine-induced DSB levels in BRCA2-deficient cells (Fig. 5B and Supplementary Fig. S3B). In contrast, BRCA2-proficient cells treated with NU7441 were more sensitive to gemcitabine and accumulated more DSBs early after release from gemcitabine (Fig. 5A and B), suggesting that some BRCA2-dependent DSBs are repaired by NHEJ.

To further support a role for HR in gemcitabine-induced DSB formation and cell death, we used a small-molecule inhibitor of the BLM helicase, ML216 (17). BLM counteracts RAD51 function in the initiation of HR by resolving D-loop structures (25). If RAD51-mediated HR is responsible for gemcitabine-induced DSBs and cell death, then BLM inhibition should exacerbate both DSB formation and cell death. Indeed, we observed a small but reproducible increase in DSBs and cell death in cells treated with BLM inhibitor (Fig. 5C and D).

Finally, we used siRNA depletion in U2OS cells to test which enzymes were responsible for converting stalled

Figure 3. BRCA2 and RAD51 inhibit replication fork progression after release from gemcitabine. **A**, labeling protocol for DNA fiber analyses. Cells were labeled with CldU, treated with IdU and 5 μ mol/L gemcitabine for 2 hours and released into IdU for 4 hours. **B**, length distributions of IdU-labeled tracks from VC8-B2 cells (+BRCA2). **C**, length distributions of IdU-labeled tracks from VC8 cells (–BRCA2). **D**, length distributions of IdU-labeled tracks from U2OS cells treated with nonT siRNA. **E**, length distributions of IdU-labeled tracks from U2OS cells treated with RAD51 siRNA. **F**, average lengths of IdU tracks in VC8 and VC8-B2 cells treated as in **A**. **G**, average lengths of IdU tracks in U2OS cells \pm RAD51. **H**, representative images of RAD51 foci in cells released from 5 μ mol/L gemcitabine for 24 hours. **I**, percentages of cells displaying more than 5 RAD51 foci during 1 and 2 hours gemcitabine treatment and after release from gemcitabine (asterisks compared with Con). Error bars, SEM; *, $P < 0.05$; **, $P < 0.01$, Student t test.



forks into DSBs, focusing on the MUS81-EME1 and XPF-ERCC1 structure-specific endonucleases. *In vitro*, only MUS81-EME1 cleaves stalled replication fork structures, but *in vivo* XPF-ERCC1 and MUS81-EME1 can act in parallel pathways to process joint molecule recombination intermediates such as Holliday junctions (26, 27). Cells were transfected with XPF or MUS81 siRNA for 72 hours, treated with 5 μ mol/L gemcitabine for 2 hours, and released for up to 72 hours. Proteins remained deplet-

ed for at least 2 days after treatment (Fig. 6A–C). Depletion of MUS81 or XPF could prevent gemcitabine-induced DSB formation, with codepletion of both proteins being more effective (Fig. 6D and E). DSBs in gemcitabine-treated cells thus depend on BRCA2 and RAD51, and therefore likely on RAD51 loading and filament formation for the initiation of HR, and on endonucleases that cleave HR intermediates. These data suggest that these DSBs arise not only simply through endonucleolytic cleavage of stalled

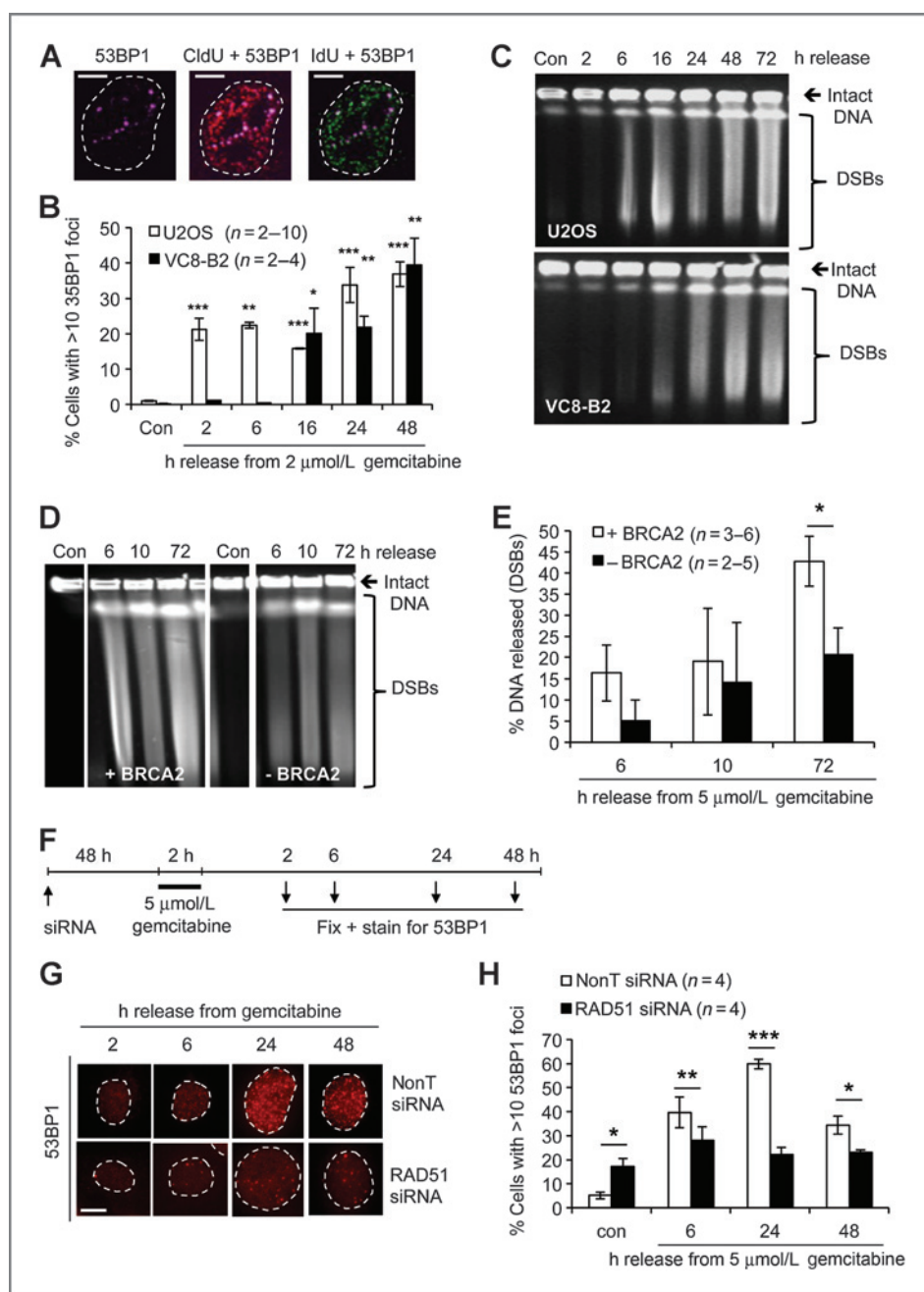


Figure 4. Gemcitabine causes DSBs that depend on BRCA2 and RAD51. **A**, 53BP1 foci (far-red) and colocalization with replication foci (CldU, red and IdU, green) in VC8-B2 cells 6 hours after release from 2 μ mol/L gemcitabine. Bars, 10 μ m. **B**, percentages of cells displaying more than 10 53BP1 foci after release from gemcitabine (asterisks compared with Con). **C**, PFGE showing DSB induction after release from 2 μ mol/L gemcitabine in U2OS and VC8-B2 cells (see Supplementary Fig. S3A for quantification). **D**, PFGE of DSB induction in VC8-B2 and VC8 cells after release from 5 μ mol/L gemcitabine (cropped lanes are from one gel, see Supplementary Fig. S3B). **E**, percentages of DNA released from plugs in DSB in VC8-B2 and VC8 cells. **F**, outline of experimental design for 53BP1 foci quantification. Twenty-four hours after transfection with RAD51 or nonT siRNA, U2OS cells were treated with 5 μ mol/L gemcitabine for 2 hours, released for the times indicated, fixed and stained for 53BP1. **G**, representative images of 53BP1 foci in U2OS cells \pm RAD51 siRNA released from 5 μ mol/L gemcitabine. Bar, 10 μ m. **H**, percentages of U2OS cells \pm RAD51 siRNA displaying more than 10 53BP1 foci after release from 5 μ mol/L gemcitabine. Error bars, SEM; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$, Student t test.

replication forks, but also through processing of recombination intermediates.

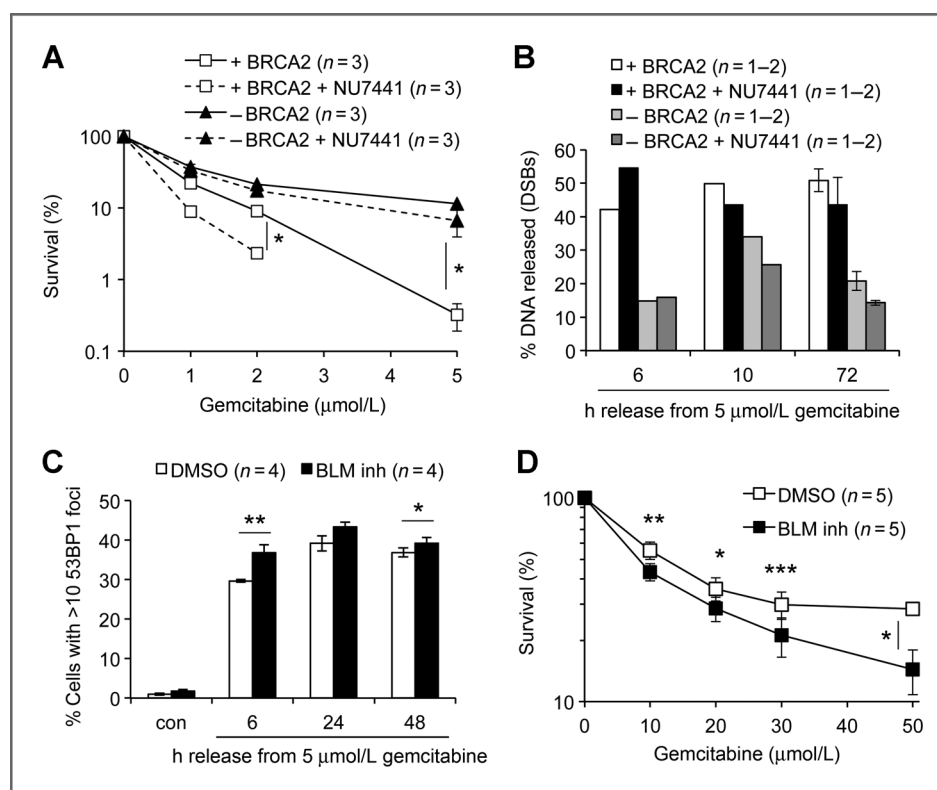
Discussion

We report that after release from gemcitabine treatment, BRCA2 and RAD51 inhibit replication fork progression, promote MUS81/XPF-dependent DSB formation, and exacerbate cell death. This supports the idea that initiation of HR is required for DNA damage formation at gemcitabine-stalled replication forks. HR, normally a pathway that prevents accumulation of DNA damage, can

thus promote the formation of DNA damage after gemcitabine treatment.

We speculate that in response to gemcitabine, BRCA2-assisted loading of RAD51 onto replication forks promotes the generation of HR intermediates, which inhibit further fork progression. This is likely the same mechanism as the RAD51-mediated fork slowing previously observed in cisplatin- or camptothecin-treated cells (22, 23), although the cellular consequences of this phenomenon have not been described. We speculate that these HR intermediates, likely D-loops and Holliday junctions, present substrates for endonucleolytic processing

Figure 5. Roles of NHEJ and BLM helicase in the response to gemcitabine. **A**, clonogenic survival of VC8-B2 and VC8 cells treated with gemcitabine and 1 $\mu\text{mol/L}$ NU7441 for 2 hours and released into fresh medium containing 1 $\mu\text{mol/L}$ NU7441, compared with survival without NU7441 (Fig. 1A). **B**, percentages of DNA released from plugs in DSB in VC8-B2 and VC8 cells released from treatment with 5 $\mu\text{mol/L}$ gemcitabine in presence or absence of 1 $\mu\text{mol/L}$ NU7441 (see Supplementary Fig. S3B for gel). Error bars, SD. **C**, percentages of U2OS cells \pm BLM inhibitor displaying more than 10 53BP1 foci after release from 5 $\mu\text{mol/L}$ gemcitabine. Cells were preincubated with 1.8 $\mu\text{mol/L}$ BLM inhibitor for 1 hour before gemcitabine treatment and released in fresh medium containing BLM inhibitor. **D**, clonogenic survival of U2OS cells \pm BLM inhibitor treated with gemcitabine for 2 hours as in C. Error bars, SEM; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$, Student t test.



by MUS81 and XPF to generate DSBs (Fig. 6F). Gemcitabine-induced DSBs are not efficiently repaired, which could explain why HR does not protect from cell death. We speculate that the processes described here also occur at forks that have been stalled by other types of replication inhibitors, but this may not be obvious if the inhibitor also induces DSBs by other mechanisms and does not prevent HR-mediated DSB repair. Our data suggest that for transient treatments, DNA damage response factors that promote rearrangements and nuclease processing of stalled forks can be expected to cause sensitivity to gemcitabine (Fanconi Anemia proteins, BRCA2, XRCC3, RAD51), whereas factors involved in later steps of DSB repair should promote survival or have little effect (DNA Ligase IV, RAD54).

Our data also suggest that the very persistent effects of even short exposures to gemcitabine are important for its cytotoxic action. Gemcitabine inactivates RNR irreversibly and gemcitabine nucleotides accumulate in cells after treatment (12), which likely underlies the prolonged replication inhibition observed. After release from gemcitabine, stalled replication forks and DNA damage signaling therefore persist, but cannot prevent the eventual resumption of cell-cycle progression. A similar phenomenon has been observed during prolonged HU treatments and could be common to all situations of prolonged replication fork stalling (4, 28). This cell-cycle progression in presence of unresolved DNA lesions contributes to cell death by mitotic catastrophe and likely also to DSB formation and apoptosis, as mitotic CDK1 activity has been suggested to

promote MUS81-dependent DSB formation at perturbed forks (29).

These peculiarities of transient gemcitabine treatments could explain why reports on the impact of HR status on gemcitabine sensitivity are still conflicting. Previous studies have variously used continuous or transient treatments. For example, RAD51 depletion sensitizes cells to continuous treatment with low doses of gemcitabine (30, 31), but both RAD51 depletion and mutations in BRCA2 decrease sensitivity when combined with transient treatments at higher doses, which seem more relevant for clinical applications (15 and this study). Indeed, a recent study showed that ATR and CHK1 inhibitors could sensitize ovarian cancer cells to transient but not to continuous gemcitabine treatments (32). As ATR and CHK1 protect stalled forks from DSB formation, this suggests that the danger of DSB is higher after release from gemcitabine than during continuous treatment, possibly due to increased cell-cycle progression. In agreement with this, our preliminary data suggest that more DSBs can be detected after release from transient gemcitabine treatment compared with continuous treatment for the same time (Supplementary Fig. S7). On the other hand, mutations in the HR genes XRCC3 and FANCC can promote resistance even to continuous gemcitabine treatments (13, 14). This suggests that more research into the time course of gemcitabine action is needed, especially as this information could be crucial for optimal scheduling in combination treatments such as gemcitabine/carboplatin.

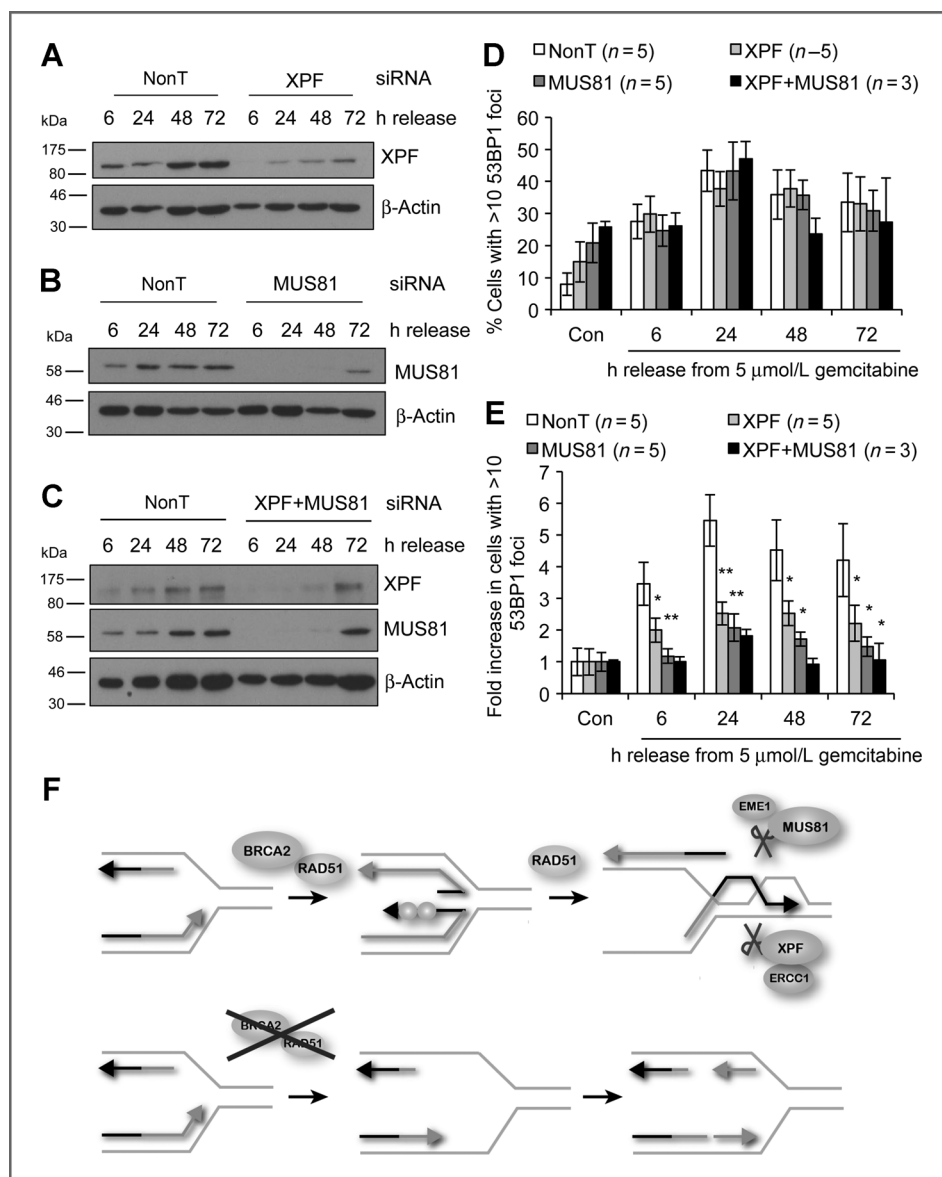


Figure 6. Gemcitabine-induced DSBs depend on MUS81 and XPF. A, protein levels of XPF and β -actin (loading control) after transfection with nonT or XPF siRNAs for 72 hours, treated with 5 μ mol/L gemcitabine for 2 hours and release for the times indicated. B, protein levels of MUS81 after transfection with nonT or MUS81 siRNAs as in A. C, protein levels of XPF, MUS81, and β -actin (loading control) after transfection with nonT or MUS81 and XPF siRNAs as in A. D, percentage of U2OS cells \pm XPF and MUS81 displaying more than 10 53BP1 foci after release from gemcitabine. E, quantification of increase in cells displaying more than 10 53BP1 foci as in D (asterisks compared with nonT siRNA). F, suggested model for HR-dependent replication fork slowing and DSB formation. Forks affected by gemcitabine treatment are recognized by BRCA2 and RAD51 and remodeled into joint molecule HR intermediates such as D-loops. These intermediates are preferentially cleaved by MUS81 and XPF. Error bars, SEM; *, $P < 0.05$; **, $P < 0.01$, Student t test.

There are three published case studies of patients with pancreatic cancer carrying *BRCA2* or *PALB2* mutations that did not respond or responded poorly to gemcitabine, but responded well to a subsequent treatment with the crosslinking agents cisplatin or mitomycin C (33–35). Although we do not consider these data evidence that HR-deficient pancreatic cancers are more resistant to gemcitabine than other pancreatic cancers, they do show that cancers that have proven resistant to one DNA-damaging agent (gemcitabine) can be hypersensitive to a different DNA-damaging agent (e.g., carboplatin). This also suggests that in the case of gemcitabine/platinum combination therapies, the hypersensitivity of HR-deficient tumors to platinum compounds could compensate for any gemcitabine resistance in these tumors.

Taken together, our data have potential implications for the scheduling of gemcitabine combination treatments in general and pose the question as to whether HR-deficient tumors would respond well to single-agent gemcitabine treatments.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors' Contributions

Conception and design: R.M. Jones, P. Kotsantis, E. Petermann
Development of methodology: R.M. Jones, P. Kotsantis, E. Petermann
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): R.M. Jones, P. Kotsantis, G.S. Stewart, P. Groth
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): R.M. Jones, P. Kotsantis, P. Groth, E. Petermann
Writing, review, and/or revision of the manuscript: R.M. Jones, P. Kotsantis, G.S. Stewart, E. Petermann
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