DNA damage signaling induced by the G-quadruplex ligand 12459 is modulated by PPM1D/WIP1 phosphatase

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ABSTRACT
The triazine derivative 12459 is a potent G-quadruplex ligand that triggers apoptosis or delayed growth arrest, telomere shortening and G-overhang degradation, as a function of its concentration and time exposure to the cells. We have investigated here the DNA damage response induced by 12459 in A549 cells. Submicromolar concentrations of 12459 triggers a delayed Chk1-ATR–mediated DNA damage response associated with a telomeric dysfunction and a G2/M arrest. Surprisingly, increasing concentrations of 12459 leading to cell apoptosis induced a mechanism that bypasses the DNA damage signaling and leads to the dephosphorylation of Chk1 and γ-H2AX. We identified the phosphatase Protein Phosphatase Magnesium dependent 1D/Wild-type P53-Induced Phosphatase (PPM1D/WIP1) as a factor responsible for this dephosphorylation. SiRNA-mediated depletion of PPM1D/WIP1 reactivates the DNA damage signaling by 12459. In addition, PPM1D/WIP1 is activated by reactive oxygen species (ROS) induced by 12459. ROS generated by 12459 are sufficient to trigger an early DNA damage in A549 cells when PPM1D/WIP1 is depleted. However, ROS inactivation by N-acetyl cysteine (NAC) treatment does not change the apoptotic response induced by 12459. Because PPM1D expression was recently reported to modulate the recruitment of DNA repair molecules, our data would suggest a cycle of futile protection against 12459, thus leading to a delayed mechanism of cell death.

INTRODUCTION
Telomeres that cap chromosome ends are composed of tandem repeats of the sequence TTAGGGn with a 3’-single-stranded extension associated with proteins from the shelterin complex (1). This nucleoprotein structure is essential to avoid end of chromosomes to be recognized as a double-strand break by the DNA repair machinery and to trigger the DNA damage response (1). Two mechanisms have been reported in the maintenance of telomere length. The first requires telomerase to add TTAGGG repeats at the 3’-end (2). The second involves recombination between telomeres and is known as Alternative Lengthening of Telomeres (ALT) (3). Telomeres can fold into t-loop, a structure that may correspond to the invasion of the 3’-single-stranded extension into duplex DNA or into G-quadruplex DNA, a non-canonical four-stranded DNA structure based on the formation of guanine quartets.

G-quadruplexes are well-characterized conformations of sequences containing several repeats of guanines that arrange in guanine tetrads, stabilized by Hoogsteen hydrogen bonding and coordinated by central cations (4). Human telomeric sequence can form intramolecular G-quadruplexes showing an antiparallel conformation in sodium containing solutions or a parallel ‘propeller’ structure in potassium containing dehydrated solutions or in crystal (5).

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Evidence is accumulating that G-quadruplexes can form among telomere repeats during lagging strand DNA replication and at the 3'-telomeric G-overhang (6). Although their existence in mammalian cells is based on indirect evidences (7), it has been demonstrated using specific antibodies that G-quadruplexes are formed in the macronuclei from ciliates (8). Further bioinformatic analysis of the human genome indicated the presence of thousand potential G-quadruplex-forming sequences (PQS) with a specific enrichment in regulatory regions such as gene promoters, UnTranslated Regions (UTRs) and splice sequences (9), suggesting a role for G-quadruplexes in the regulation of gene expression.

A strategy based on the interaction of small molecule ligands with telomeric G-quadruplex has emerged during the past decade (10). These compounds, also called telomere targeting agents, were initially derived from DNA intercalators and now present remarkable selective binding properties to G-quadruplex relative to duplex DNA (11). Several pieces of evidence suggest that these ligands are deleterious for the stability of telomeres in both telomerase positive and ALT tumor cell lines. These ligands are able to interfere directly with the binding of essential shelterin components, such as Protection Of Telomere 1 (POT1) and Telomeric Repeat Factor 2 (TRF2) in telomerase positive cell lines (6,10) or TRF2 and TopoIIIz in ALT cell lines (12). This action induces a DNA damage response and the evidence of telomere-dysfunction induced foci (TIFs) has been demonstrated for several G-quadruplex ligands (13–15). It must be noticed that these ligands also induced telomere-independent DNA damage foci that might be related to the presence of G-quadruplexes in other regions of the genome enriched in PQS (14,16,17) as evidenced recently for pyridostatin (18).

During telomere replication, the transient recruitment of DNA damage proteins is observed and controlled by the coordinating action of POT1 and TRF2 that, respectively, repress the ATR and ATM DNA damage signaling (19,20). A recent study suggests that the pentacyclic acridinium salt RHPS4 can interfere with telomere replication, triggering an ATR-dependent damage response pathway (15). In addition, ATR deficiency strongly sensitizes cells to the pyridine dicarboxamide derivative 360A and provokes telomere aberrations generated during telomere replication (21). In contrast, telomestatin does not affect telomere replication, as revealed by Co-FISH experiments in mouse embryonic fibroblast (22), but rather induces an ATM-dependent DNA damage response in human leukemia cell lines (23). Furthermore, 360A also triggers telomere aberrations in ATM-deficient cell lines (24).

These data suggested that the DNA damage response induced by G-quadruplex ligands may differ as a function of the chemical structure of the ligand or the nature of the cell line used. In addition, the cell proliferation defect also varies as a function of the ligand concentration used. Indeed, triazine derivatives trigger short-term (short-term corresponded to a treatment with 12459 for <72 h and long-term to a treatment with 12459 ≥8 days,) apoptosis (within 48–72 h) at high micromolar range concentrations (>5 μM) and a delayed growth arrest associated with a cell senescence phenotype in the low micromolar range concentrations after long-term treatment (25). The establishment of cell lines resistant to the triazine derivative 12459 by either progressive adaptation or by ethyl methyl sulfonate (EMS) mutagenesis also pointed out significant differences between short-term and long-term effects of the ligand (26,27). Cross resistance to other G-quadruplex ligands (telomestatin, Braco-19) is observed for the long-term senescence induction but is absent for short-term treatment (26,27). Some of the clones selected for resistance to 12459 also present an overexpression of the Bcl-2 protein, and A549 cells transfected by Bcl-2 display a resistance to the apoptotic action of 12459 (28). However, the Bcl-2 overexpression is not sufficient to confer resistance to the long-term effect of 12459, thus suggesting that 12459-directed senescence is uncoupled from apoptosis, a result that fits well with the differences of resistance mechanism obtained after short-term or long-term exposure with the ligand (28).

Here, we report that 12459 at submicromolar concentrations triggers a Chk1/ATR-mediated DNA damage response associated with G2/M arrest and telomeric dysfunction. However, using higher concentrations that induced apoptosis, 12459 triggers a mechanism that bypasses the DNA damage signaling and leads to the dephosphorylation of Checkpoint kinase 1 (Chk1). We identified the phosphatase Protein Phosphatase Magnesium dependent 1D/Wild-type P53-Induced Phosphatase (PMP1D/WIP1) as a factor responsible for this dephosphorylation. PMP1D/WIP1 is activated at early stage by reactive oxygen species (ROS) induced by 12459. ROS induced by 12459 correlated with the early activation of PMP1D/WIP1 but their scavenging by N-acetyl cysteine (NAC) do not modify the apoptotic response induced by 12459.

**MATERIALS AND METHODS**

**Cell culture and drug treatment**

Human A549 lung carcinoma cell line was obtained from the American Type Culture Collection (Rockville, MD, USA). Cells were cultured in Dulbecco’s modified Eagle’s medium (DMEM) with glutamax, supplemented with 10% fetal calf serum and 1% penicillin-streptomycin (Invitrogen) at 37°C in an atmosphere containing 5% CO2.

For drug treatment, the triazine derivative 12459 (synthesized according to the patent WO-0140218) was dissolved in dimethylsulfoxide (DMSO) at 10 mM, and aliquots of this stock solution were kept at −20°C. Dilution to 1 mM was made in DMSO, and further dilutions were made in water. NAC (Sigma Aldrich) was dissolved in phosphate buffered saline (PBS) at 1 M and adjusted to pH 7.3 with sodium hydroxide.

For cell senescence experiments, A549 cells were seeded at 15 000/ml in 25 cm² culture dish. After 4 days of treatment, cells were trypsinized, counted and replated at 15 000/ml. At each passage, population doubling (PD) from untreated or 12459-treated cultures were calculated.
According to the following formula: PD = Log Cell density Day 4 – Log 15 000/Log 2.

For siRNA experiments, A549 cells were plated in six-well culture plates at 1.5 × 10^5 cells/well in 2 ml DMEM without antibiotics. After 12 h, 100 nM siRNA were transfected for 4 h, using Lipofectamin 2000 (Invitrogen). Two days after transfection, cells were splitted at 1.5 × 10^5 cells/well in new culture dishes for two additional days. Four days after transfection, 12459, NAC or H2O2 were added for 4 h, and then treated cells were processed for western blotting or immunofluorescence experiments. The siRNA used here are: SiRNA PPM1D/WP1: 5'-GGUUUCCUG UUGUACC-3', SiRNA control: 5'-UGCGCUACGAA GGACGAUG-3'.

**Antibodies and western blot analysis**

All experiments were performed with cells in a logarithmic phase by controlling the plating density. Cells were washed with ice-cold PBS and lysed in RIPA buffer [Tris–HCl 50 mM, pH 7.4, sodium deoxycholate 0.25%, NaCl 150 mM, ethylenediaminetetraacetic acid (EDTA) 1 mM, phenylmethylsulfonyl fluoride (PMSF) 1 mM] including a protease inhibitor cocktail at 1 μg/ml (Mini complete protease, Roche Diagnostics). After 30 min on ice, lysates were cleared by centrifugation. Protein concentration was quantified with the Bio-Rad protein assay. Cell lysates containing equal amounts of total protein (25–40 μg) were resolved on a 12% or 10% sodium dodecyl sulphate–polyacrylamide gel by electrophoresis, transferred to polyvinylidene fluoride (PVDF)-membrane (Macherey-Nagel) by electro-blotting in 25 mM Tris, pH 7.5, containing 0.15 M NaCl, 0.1% Tween 20 and 5% nonfat dry milk. Primary and secondary immunodetection, as well as washes, were performed in the same buffer using 5% dry milk. Western blot analysis was accomplished according to standard procedure using SuperSignal West Pico chemiluminescent substrate (Pierce). The following primary antibodies were used (1:1000 unless otherwise indicated): anti-phospho-histone (ser 139) γ-H2AX (Upstate), monoclonal anti-β-actin clone AC-15 (Sigma) (1:5000), anti-cleaved PARP asp 214 (Cell signaling), anti-P53 (Upstate), anti-phospho P53 Sampler Kit (Cell Signaling), anti P21 (BD Pharmingen), anti-Chk1, anti-phospho-Chk1(Ser317), anti-Chk2 and anti-phospho-Chk2 (Thr 68) (Cell Signaling), rabbit anti-PPM1D (BL 3066 Bethyl Laboratories).

**Immunofluorescence**

A549 cells were plated in six-well culture plates on glass coverslips. After drug treatment, cells were washed with PBS (pH 7.2), fixed with 4% paraformaldehyde and permeabilized with 20 mM Tris–HCl (pH 8.0), 50 mM NaCl, 3 mM MgCl2, 300 mM sucrose and 0.5% v/v Triton X-100 for 15 min at room temperature. Cells were then washed twice with PBS (pH 7.2). Cells were blocked with 1% bovine serum albumin in PBS for 1 h and incubated with primary antibodies for 1–2 h at room temperature [1 ng/μl for TRF1 rabbit polyclonal ab1423 (Abcam) and/or 2 ng/μl for antiphospho γ-H2AX (Ser139) (Upstate)]. The nuclear DNA was stained with 1 μM of Hoechst 33342. After washing with PBS, proteins of interest were detected by incubation for 30 min with fluorescently labeled secondary antibodies (anti-mouse antibody labeled with Alexa 568 and anti-rabbit antibody labeled with Alexa 488 (Molecular Probes), then washed with PBS. The nuclear DNA was stained with 1 μg/ml Hoechst 33342 in PBS (pH 7.2) for 4 min.

Cells were mounted in Shandon Immumount medium (Thermo Scientific). Samples were observed with a DMR Leica microscope, and images were captured with a Cool Snap HQ camera (Roper Scientific) controlled by Metamorph software (Roper Scientific). Final images are composed of arithmetic stacks of 15–25 deconvoluted images, each 0.2 μm in z-step. Stacks of 15–30 images (16-bit grayscale) were acquired with a z-step of 0.2 μm with low illumination intensity.

**ROS experiments**

ROS production was determined using carboxy fluorescein-AM (CF) (Molecular Probes). After cell treatment, 5 μM CF was added for 30 min to the cell culture. Cells were then washed by PBS trypsinized and analyzed by spectrofluorimetry using 488 nm for excitation and 515 nm for fluorescent emission measurements. Results were normalized relative to untreated A549 cells, defined as 100%.

**Flow cytometry**

Cells were cultured in presence or absence of 1 μM of 12459. Cells were always seeded at the same density (7.5 × 10^5 cells/75 cm^2 flask) in the same medium volume (15 ml). At indicated time points, cells were harvested with trypsin and either seeded for the next time point or collected for subsequent cell cycle analysis. They were then washed in PBS containing 20 mM EDTA and fixed with 70% ethanol at –20°C.

When the experiment was completed, cells were collected by centrifugation, washed in PBS containing 20 mM EDTA and incubated in PBS containing 20 mM EDTA, 100 mg/ml RNase A (Sigma) and 20 mg/ml propidium iodide (Sigma) for 30 min at 37°C. Cell cycle analysis was assessed on a C6 Accuri flow cytometer (Becton Dickinson) and data treated with the FCS Express 4 software.

**RESULTS**

12459 induces a DNA damage response at telomeres associated with senescence

To evaluate whether 12459 triggers a DNA damage response in A549 cells, we have investigated the formation of DNA damage foci due to the presence of phosphorylated H2AX (γ-H2AX), a phosphorylated variant of histone 2A that associates with DNA double-strand breaks (29). Cells treated with increasing concentrations of 12459 (0.5, 1, 2 and 5 μM) for 4 days were analyzed by immunofluorescence for γ-H2AX-containing foci (Figure 1). Interestingly, a marked DNA damage
response was observed for low concentrations of 12459 (0.5 and 1 μM), while this DNA damage response is decreased using higher concentrations of 12459 (2 and 5 μM) (see later in the text). At low concentration conditions (0.5 and 1 μM for 4 days), 12459 induces a cell growth inhibition that precedes cell senescence, as no evidence of P21 expression was detected by western blotting (Figure 2A and B). Prolongation of 12459 treatment to 8 days provokes a cell growth arrest where P21 expression became readily detectable, suggesting the onset of cell senescence (Figure 2A and B).

To determine whether this 12459-induced DNA damage corresponds to damaged telomeres, A549 cells treated with 12459 (0.5 μM) for 8 days were analyzed for γ-H2AX-containing foci that co-localized with TRF1 (Figure 2C and Supplementary Figure S1). Results showed that DNA damage foci induced by 12459 co-localized with TRF1 and corresponded to TIFs (Telomere-dysfunction Induced Foci). TIFs were strongly increased [9.92 ± 8.34 (n = 38) TIFs/nuclei in treated cells, as compared with 3.17 ± 1.43 (n = 23) in control cells, \( P < 0.001 \)], thus suggesting that 12459 induced a massive telomeric dysfunction associated with the onset of cellular senescence.

12459 triggers an ATR-mediated DNA damage response associated with G2/M arrest

To get further insight in the DNA damage checkpoint signaling associated with the cellular response to 12459-induced senescence, several effectors of ATM- or ATR-kinases have been evaluated. Results presented in Figure 2B indicate that 12459 treatment of A549 cells (0.5–2 μM) induces a transient overexpression of p53 after 4 days, with a slight activation of p53 at Ser 15 but without significant activation at Ser20. This activation of p53 disappears after 8 days during senescence. No obvious activation of Chk2(Thr68) was evidenced during 12459 treatment. In contrast, a significant activation of Chk1(Ser317) was found at the onset of senescence after 8 days that coincides with the expression of p21.

Cell cycle experiments were performed by fluorescence-activated cell sorting (FACS) in the presence or in the absence of the ligand (1 μM) and evaluated at days 3, 6, 9 and 13 (Figure 3). Results clearly indicated an effect of 12459 starting at day 6 corresponding to a G2/M accumulation together with a S phase decrease, in contrast to the G1/S arrest expected with replicative senescence (see discussion). No evidence of sub-G1 accumulation was found, in agreement with the absence of apoptosis detectable in these conditions for 12459 (28).

Therefore, the DNA damage signaling induced by 12459 corresponds to a late involvement of the ATR-Chk1 pathway occurring at the onset of the growth arrest, which is consistent with a mechanism of telomere deprotection through POT1 targeting (7,30). Although a marked DNA damage was evidenced by γ-H2AX foci after 4 days, this damage does not lead to a significant signalization through Chk1 or Chk2, thus suggesting an unusual processing, as compared with classical DNA
damaging agents, such as doxorubicin that was used as a control in experiments presented in Figures 1 and 2 (0.5 μM, 24 h).

Pro-apoptotic concentration of 12459 induced a delayed DNA damage signalization

We previously reported that 12459 induces apoptosis after a 48 h delay for high drug concentrations (>5 μM) (25,28). In these conditions, the apoptotic pathway predominates over the appearance of senescent cells or growth-arrested cells. Surprisingly, we observed a marked dose-dependent decrease in the appearance of γ-H2AX foci in A549 cells under 12459 treatment (Figure 1). Only few A549 cells remain γ-H2AX positive in the presence of 12459 at 5μM for 4 days and no positive γ-H2AX cells were detected using 10μM 12459 for 4 days. Because these

Figure 3. 12459 induced a G2/M accumulation associated with senescence. Delayed DNA damage signalization induced by 12459 in A549 cells. (A) A549 cells untreated or treated with 12459 (1 μM) for 3, 6 and 13 days were analyzed by FACS for cell cycle progression. (B) Quantifications of the percentage of cells in G2/M, S and G1 for the different conditions. Analysis was performed using the FSC Express 4 software.
concentrations induced a dramatic decrease in cell viability [see Figure 4 in (28)], it is possible that the apoptotic processes had eliminated cells presenting DNA damage. Therefore, we have examined the DNA damage induced by 12459 at early time treatment on A549 cells. The experiment presented in Figure 4A showed that A549 treatments with 12459 (10 and 20 μM) for 4 h and with 12459 (10 μM) for 24 h do not provoke any γ-H2AX foci, in contrast to 12459 (0.5 μM) for 8 days used as a positive control. In addition, a time-course western blot experiment (2–48 h) using 10 μM 12459 indicates that the ligand does not induce phosphorylation of γ-H2AX (data not shown). Interestingly, these data may suggest that 12459 treatment induces a dephosphorylation process.

When cellular extracts from the same experiment were blotted with Chk1(Ser317) antibodies, we also observed a dephosphorylation process, as compared with untreated control, that takes place between 2 and 4 h of drug treatment. Interestingly, a partial recovery of Chk1(Ser317) phosphorylation is observed at 8–16 h, that precedes a peak of p53 accumulation between 14 and 48 h corresponding to the onset of apoptosis (Figure 4B and data not shown, see also Supplementary Figure S2A). In these conditions, we do not observe any activation of the ATM-Chk2 signaling pathway because no phosphorylation of Chk2 was detected between 2 and 48 h (Figure 4B). These results are, however, consistent with the delayed apoptosis reported for this compound and suggest a mechanism that bypasses the DNA damaging signaling through the ATR-Chk1 pathway.

12459 triggers p53 phosphorylation at Ser392 and induces p53 accumulation in nucleoli

Because p53 accumulation is detected at the onset of apoptosis, between 14 and 48 h after 12459 treatment, we wished to determine to which signaling pathway it corresponds. A549 cells treated for 24 h with 10 μM 12459 were blotted with different specific antibodies recognizing phosphorylated serines at different positions (Ser 6, 9, 15, 20, 37, 46 and 392) and corresponding to different specific phosphorylation sites by kinases activated during the DNA damage signalization (Figure 5) (31). Interestingly, the only serine residue phosphorylated in response to 12459 treatment corresponded to Ser392 (Figure 5 and Supplementary Figure S2), known to be activated by ultraviolet (UV) light exposure or DNA-damaging anticancer agents, but not by gamma radiation (32). Some slight variations of reproducibility for p53 activation (between 14 and 48 h) were observed in the different experiments performed at these apoptotic concentrations that we attribute to the poor solubility of the compound at stock concentrations used for cell treatment (2 mM) to limit DMSO.

Data from literature indicated that p53 phosphorylation at Ser392 is also increased after p14ARF overexpression and is associated with p53 sequestration in nucleoli (33). Thus, we have investigated the nucleolar accumulation of p53 in 12459-treated A549 cells. As shown in Figure 6, 12459 treatment (10 μM for 24 h) induced a p53 accumulation in nuclei together with a nucleolar localization, in contrast to doxorubicin where p53 nuclear accumulation exclude nucleoli.

Altogether, our results indicate that 12459 triggers a specific phosphorylation of p53 at Ser392 together with

**Figure 4.** Delayed DNA damage signalization induced by 12459 in A549 cells. (A) Cells untreated or treated with 12459 for 4 h (10 and 20 μM) and for 24 h (10 μM) were examined for γ-H2AX foci (red). Hoechst staining of DNA is shown in blue. As a positive control for DNA damage, A549 cells were treated with 12459 (0.5 μM) for 8 days.

**Figure 5.** 12459 induces P53 phosphorylation at Ser 392. Western blot analysis of P53 and phosphorylation sites at Ser 6, 9, 15, 20, 37, 46 and 392 in A549 cells untreated or treated with 12459 (10 μM) for 24 h. β-Actin was used as a control for protein loading, and doxorubicin 0.5 μM for 24 h (Dox) was used as a positive control for the DNA damage response.
were examined for P53 nuclear localization (red). Hoechst staining of UV irradiation (0.005 J/cm²) or treatment with H2O2 to activate PPM1D/WIP1, i.e. we also found the activation of PPM1D/WIP1, using conditions previously described to activate PPM1D/WIP1, i.e. 12459 (10 μM) for 4 h (Figure 7B, see also Supplementary Figure S4). Results showed that siRNA PPM1D treatment restore the phosphorylation of Chk1(Ser317), suggesting that PPM1D/WIP1 is responsible for the dephosphorylation. Indeed, we also observe a reactivation of γ-H2AX DNA damage foci induced by the siRNA directed against PPM1D in cells treated with 12459 (15 μM, 4 h) (Figure 7C). These results suggest that PPM1D/WIP1 is responsible for the inhibition of the ATR-Chk1 signaling pathway in the presence of apoptotic concentrations of 12459.

Reactive oxygen species are responsible for PPM1D/WIP1 activation but do not influence apoptosis induced by 12459

We have previously published that 12459 triggers a delayed apoptosis involving the mitochondrial pathway through alteration of Bcl2/Bax (28). However, we also observed that 12459 is able to trigger other rapid cellular events such as a decrease of the mitochondrial membrane potential and an increase of ROS within 2–4 h [see figure 3 in (28)]. We thus seek to determine the influence of ROS in PPM1D/WIP1 activation and 12459-mediated apoptosis. Treatment of A549 cells with H2O2 (0.5 mM) for 4 h reveals the presence of γ-H2AX foci (Figure 8). Interestingly, the DNA damage foci induced by H2O2 were found more pronounced when A549 cells were treated with siRNA against PPM1D than with siRNA controls, thus confirming that PPM1D is able to negatively regulate DNA damage induced by ROS. Interestingly, pretreatment of A549 cells with the ROS scavenger NAC (10 mM) is able to both protect A549 cells from DNA damage foci induced by H2O2 (Figure 8) and to decrease the activation of PPM1D by apoptotic concentration of 12459 (10 μM, 4 h) (Figure 9A). In these conditions, no γ-H2AX foci were observed (see Figure 8). Interestingly, NAC treatment partially protects A549 cells from DNA damage foci induced by 12459 when PPM1D/WIP1 is depleted by siRNA treatment, as only few figures of γ-H2AX positive cells remained (see NAC+12459 in siRNA PPM1D-treated cells in Figure 8). These data suggested that ROS induced by 12459 are sufficient to induce an early DNA damage response when PPM1D/WIP1 is depleted by siRNA. Interestingly, we have also found that apoptosis induced by 12459 (10 μM, 48 h) in A549 cells was not affected by pretreatment of A549 cells by NAC (7.5 mM), as no modification of Poly-ADP-Ribose Polymerase (PARP) cleavage occurred during these conditions (Figure 9B). As a control, ROS production
induced by 12459 was found decreased by NAC pretreatment (Figure 9C and Supplementary Table S1). In addition, 12459 or pretreatment with NAC does not alter telomere length by TRF analysis after 48 h treatment (Supplementary Figure S5). We conclude from these experiments that ROS induced at early stage (4 h) of 12459 treatment are able to activate the expression of PPM1D/WIP1 but do not participate to the apoptotic processes induced by 12459.

DISCUSSION

Our results suggest that submicromolar concentrations of 12459 induced the onset of ‘senescence’, as evidenced by a delayed growth inhibition and induction of SA-beta-galactosidase (25) together with the activation of p21 (this study), which is a figure already reported for different G-quadruplex ligands [i.e. BRACO-19 (37), see Supplementary Figure S7 for the chemical structures cited here] and a G2/M arrest. The onset of ‘senescence’ is also associated with the presence of DNA damage that mostly co-localized with telomere, suggesting that telomeric DNA is one of the cellular targets for 12459, in agreement with previous studies with G4 ligands (13–16). In addition, our study suggests that the DNA damage signaling response associated with 12459-induced senescence corresponds to the Chk1/ATR signaling pathway, thus suggesting that most of the damage are generated during DNA replication (38,39) and significantly differs from the replicative senescence induced in normal fibroblast cultures where the ATM signaling pathway was initially found predominant at shortened telomeres (40). Recent works challenged the current paradigm that the checkpoint response to eroded telomeres occurs primarily in G1/S (41,42). These reports also linked the post-replicative damage response at eroded telomeres to G2 arrest signaling in normal senescent cells. In addition, senescence in tumor cells may be driven at G2/M by DNA damage and is controlled by Chk1/P21...
when P53 is functional (42,43). In that case, arrested G2/M cells may enter a downstream senescence or undergo a mitotic catastrophe. Interestingly, our results indicated that 12459 triggers a G2/M arrest, in agreement with these recent findings.

The activation of Chk1/ATR by 12459 is in agreement with one of the proposed mechanisms of action of this class of compounds in which G-quadruplex stabilization blocks the binding of POT1 at G-overhang and/or at lagging strand during replication, leading to a replication stress with the accumulation of single-stranded DNA regions (7). Consistently, other G4 ligands, such as RHPS4 and pyridostatin, also induced a replication-dependent DNA damage response (17,18). An ATR-dependent ATM activation is also observed with RHPS4 (15), similar to that triggered by replication stress-inducing agents (44), and the DNA damage response induced by pyridostatin was found dependent on ATM, suggesting that the induction of DSB was mediated by mechanisms related to transcription-coupled repair (18). This contrasts with our results using 12459, where no evidence of Chk2 induction was found. This suggests subtle differences in the molecular pathways activated by these different G-quadruplex ligands that may be related to the nature of the cell line used for these studies. Alternatively, the nature of telomere deprotection (i.e. removal of POT1 and/or TRF2 from telomeres) may orient the nature of the DNA damage response to ATM and ATM pathways (30). It is noteworthy that telomestatin, which is able to trigger POT1 and/or TRF2 removal from telomeres, also triggers an ATM DNA damage response (14,23,45), while RHPS4 mostly removes POT1 from telomeres (15,17). However, all these G-quadruplex ligands, including 12459, do not present selectivity toward other potential DNA or RNA G-quadruplexes (46). Thus, we could not exclude that 12459 induced its DNA damage response through an alternation of TERRA transcription. Indeed, TERRA was found to facilitate ORC recruitment at telomeres, and its siRNA depletion induced telomeric aberrations, TIFs and loss of cell viability (47).

Another important finding of this study is the delayed DNA damage signaling associated with the induction of PPM1D/WIP1 phosphatase using pro-apoptotic concentrations of 12459. Our data indicate that 12459 induces an early activation of PPM1D/WIP1 and promotes the dephosphorylation of Chk1(Ser317) and γ-H2AX. WIP1 is a nuclear serine/threonine phosphatase of the PP2C family encoded by PPM1D gene (48) characterized by inhibitory functions on several tumor suppressor pathways, including p53 (49). PPM1D/WIP1 was initially reported to dephosphorylate proteins phosphorylated by the DNA damage-activated sensor kinases ATM, ATR and DNA-PK, such as Chk1, Chk2 and p53, thus reducing the cell cycle checkpoint activities and p53 stability (49). More recently, PPM1D/WIP1 was shown to interact with γ-H2AX and to mediate a delayed γ-H2AX dephosphorylation after DNA damage to promote the resolution of the DNA damage foci (50,51). The premature dephosphorylation of γ-H2AX after DNA damage by WIP1 expression also results in failure to recruit DNA repair molecules to DNA damage foci and attenuates the DNA damage response (52). PPM1D/WIP1 also maintains cellular competence to divide during an ongoing DNA damage response in G2 (53). This would explain the delayed apoptosis associated with the absence of DNA damage signaling triggered by 12459. At these
concentrations, 12459 induced a marked reduction of telomeric G-overhang (28) leading to enhanced telomeric dysfunction, the presence of sub-G2 cell population accumulating after 48 h of treatment (Supplementary Figure S6) that finally lead to cell death. In agreement, siRNA depletion of PPM1D/WIP1 restore the 12459-induced DNA damage signaling pathway, as evidenced by the early activation of Chk1(Ser 317) and γ-H2AX (Ser 139).

A late activation of p53 at Ser 392 together with p53 nucleolar accumulation was also observed under 12459 treatment. Such figure was already reported to occur preferentially in response to UV radiations or to treatment with cisplatin (32,54). Interestingly, a model in which p53(Ser392) accumulates was proposed when uncoupling between p53 accumulation and degradation occurs in response to various stimuli (55,56). Because PPM1D/WIP1 directly or indirectly dephosphorylates p53 at various residues, except at Ser392 (35,49), the late accumulation of p53 (Ser 392) and the lack of activation of p53 (Ser 6, 9, 15, 20, 37 and 46) may rather result from the accumulation of non-degraded forms of p53 than from an active signaling process.

Finally, our results indicated that ROS induced by 12459 treatment were responsible for the early activation of PPM1D/WIP1. Treatment of A549 cells with NAC decreased the activation of PPM1D/WIP1 by 12459 due to the early activation of ROS that was previously reported in the same cellular model (28). The production of ROS by 12459 was found to be dose-dependent (C. Douarre, unpublished data) and correlated with the dose-dependent decrease of γ-H2AX foci reported in this study (Figure 1). Because ROS have been shown to induce a DNA damage response at telomere (57), one may ask whether ROS induced by 12459 participates in the telomere deprotection effect. Our study indicates that at short-term (4 h) ROS triggered by 12459 are sufficient to induce a significant early DNA damage when PPM1D/WIP1 is partially depleted. In addition, NAC treatment strongly decreases the DNA damage response of 12459 when PPM1D/WIP1 is depleted. Because apoptosis at 48 h is not greatly affected by NAC treatment, it is tempting to conclude that PPM1D/WIP1 activation by 12459 provides enough protection to avoid a massive effect of ROS on telomeres but does not eliminate the damages induced by G-quadruplex formation at telomeres or in other G-rich parts of the genome. However, we cannot exclude that a combination between the direct effects of the compound at telomeres and indirect effects triggered by ROS is responsible for this cell death response, and future studies will aim to solve this issue. Another piece of evidence against the sole involvement of ROS in the telomeric effects of the ligand is provided by the study of the JFD9 resistant cell line to 12459 (26,28). The production of ROS by 12459 was found to be dose-dependent (C. Douarre, unpublished data).

In conclusion, our data suggest that ROS activation of PPM1D/WIP1 by 12459 in A549 cells may represent a mechanism of futile protection, leading to an inhibition of DNA repair signaling that further accumulates G-quadruplex-induced telomeric dysfunction or other genomic DNA damages but that finally lead to a delayed cell death.

SUPPLEMENTARY DATA
Supplementary Data are available at NAR Online: Supplementary Table 1 and Supplementary Figures 1–7.

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