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X-ray structure and mechanism of RNA polymerase II stalled at an antineoplastic monofunctional platinum-DNA adduct

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DNA is a major target of anticancer drugs. The resulting adducts interfere with key cellular processes, such as transcription, to trigger downstream events responsible for drug activity. cis-Diamminedichloroplatinum(II), cDPCP or pyriplatin, is a monofunctional platinum(II) analogue of the widely used anticancer drug cisplatin having significant anticancer properties with a different spectrum of activity. Its novel structure-activity properties hold promise for overcoming drug resistance and improving the spectrum of treatable cancers over those responsive to cisplatin. However, the detailed molecular mechanism by which cells process DNA modified by pyriplatin and related monofunctional complexes is not at all understood. Here we report the structure of a transcribing RNA polymerase II (pol II) complex stalled at a site-specific monofunctional pyriplatin-DNA adduct in the active site. The results reveal a molecular mechanism of pol II transcription inhibition and drug action that is dramatically different from transcription inhibition by cisplatin and UV-induced 1,2-intrastrand cross-links. Our findings provide insight into structure-activity relationships that may apply to the entire family of monofunctional DNA-damaging agents and pave the way for rational improvement of monofunctional platinum anticancer drugs.

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The authors declare no conflict of interest.

Data deposition: The atomic coordinates have been deposited in the Protein Data Bank, www.pdb.org (PDB ID codes 3M4Q and 3M3Y).

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positioning of the pyriplatin-damaged guanosine residue is located above the bridge helix. This structure requires rotation of the cis-(Pt(NH$_3$)$_2$(py))$^{2+}$ moiety and its bound guanosine residue into a different configuration compared to that adopted in the pyriplatin-duplex DNA structure, in order to avoid a steric clash with bridge helix (7). Fig. 2B depicts this comparison. The rotation is energetically facilitated by the formation of hydrogen bonds between the ammine ligands on platinum with the phosphodiester moiety of the backbone between positions +1 and +2, with concomitant loss of a hydrogen bond between $\Omega^0$ of the platinate guanosine residue and an ammine ligand. An additional feature is that the pyridine group of the cis-(Pt(NH$_3$)$_2$(py))$^{2+}$ fragment, which points downstream toward the 5'-direction of the template DNA, forms van der Waals interactions with bridge helix residues Val 829 and Ala 832. The purine base of the guanosine residue at position +1 is displaced toward the major groove of the RNA–DNA duplex by comparison with structures having an undamaged base at this site in the post-translocation state (9–11).

Transcription Elongation Inhibited by a Pyriplatin–DNA Adduct. Because transcription inhibition is an important component in the mechanism of action of platinum anticancer drugs (12–20), we investigated the effect of a site-specific pyriplatin–DNA adduct on the kinetics of pol II transcription elongation. We performed an extension assay using platinate (Complex A, Table 1) and unplatted (Complex A', control, Table 1) pol II transcribing complexes having a 9mer RNA as primer. These complexes were then incubated with a mixture of ATP, CTP, and GTP. The RNA transcripts in A could be elongated from the 9mer to the 11mer, stopping at a position corresponding to the Pt-DNA lesion site observed in the pol II complex of the damaged template DNA, whereas RNA transcripts in A' were extended much farther downstream on the undamaged template control DNA (Fig. 3A). In order to avoid the possibility of misincorporation-induced transcription inhibition in this assay, we carried out a similar extension assay using an RNA containing a 3'-end CMP matched against the damaged base (pol II complex C, 11mer) (Table 1). A single matching GTP was incubated with this pol II complex to test whether the enzyme could bypass the Pt-DNA lesion. Consistent with the results of the previous assay, RNA transcripts could not be extended beyond an 11mer in the pol II complex with the damaged DNA template, whereas RNA transcripts were efficiently extended farther downstream along the undamaged DNA template (Fig. 3B). Similar extension assay results were obtained using a chain-terminated GTP analogue 3'-dGTP or an RNA primer of different length (complex B, 10mer) (Table 1) (Fig. 3C and D). Finally, to investigate whether the presence of the damaged base affects the rate of NTP incorporation in a single round, we used complex B (10mer) and complex C (11mer), incubating with CTP and 3'-dGTP, respectively. For CTP incorporation, RNA transcripts could be efficiently extended from the 10mer to the 11mer using both damaged and undamaged templates at a comparable rate (Fig. 3E), whereas no obvious extension of RNA transcripts from the 11mer to a 12mer was observed on the damaged DNA template (Fig. 3C). UTP failed to incorporate at the damaged template under the same conditions (Fig. S3A). No obvious intrinsic cleavage was observed for a pol II complex containing the 11mer RNA and Pt-damaged DNA template in the presence of 20 mM Mg$^{2+}$, suggesting that most of complex C (11mer) is not in the backtracked state (Fig. S3B) (21–23).

X-ray Structure of Pol II stalled at a Pyriplatin–DNA Adduct. To understand the nature of the pol II complex stalled at the pyriplatin-induced Pt–DNA adduct, we solved the x-ray crystal structure...
of the enzyme in complex with a platinated DNA using an RNA-containing CTP matched against the damaged guanosine residue. In this structure, pol II is in pre-translocation state, with the newly added CMP still occupying the addition site without translocation. The platinated guanosine residue forms Watson–Crick base pairs with the newly added CTP (Fig. 4A and B and Fig. S4). The cis-[Pt(NH$_3$)$_2$(py)$_2$]$^{2+}$ moiety is surrounded by the bridge helix at the bottom, part of the RpH2 fork region (528–534) on the left side, and the sugar-phosphate backbone connecting template DNA positions +1 and +2 on the right side (Fig. 4B). Interestingly, upon CMP incorporation, the cis-[Pt(NH$_3$)$_2$(py)$_2$]$^{2+}$ moiety adopts a different conformation. The pyridine group of this unit now faces toward 3′-direction of template DNA (Fig. 4A and B). The ammine group trans to pyridine is directed toward the bridge helix and forms hydrogen bonds with main chain atoms of Ala 828 and the side chain of Thr 831 (Fig. 4B). The residues in the bridge helix are highly conserved from yeast to humans. Because Thr 831 and Ala 828 are absolutely conserved between _S. cerevisiae_ and humans, the interactions we observe in the _S. cerevisiae_ pol II structure will also occur in human pol II.

These structural results provide important insights into the transcription stalling process at a monofunctional pyriplatin-DNA adduct. The adduct adopts a significantly different conformation within the pol II active site compared to that in duplex DNA (7). The present structural and biochemical evidence reveals that pol II stalls after efficient incorporation of CTP against the damaged guanosine residue. The conformation of the pyriplatin–DNA adduct changes significantly upon incorporation of CTP. The modified guanosine rotates into the pol II active site and serves as a template for base pairing with the matched substrate, and the cis-[Pt(NH$_3$)$_2$(py)$_2$]$^{2+}$ moiety is now directed toward 3′-end of the platinated DNA.
The result is that the RNA transcript fails to extend beyond the site of damage, subsequent translocation and nucleotide addition being strongly inhibited. Several factors contribute to such translocation inhibition, including (i) stabilization of the initial pre-translocation state by interaction between the platinated guanosine and pol II residues (Fig. 4B); (ii) a high translocation energy barrier; and (iii) an unfavorable subsequent post-translocation state induced by the DNA lesion. Hydrogen bonding interactions between an ammine group of the cis-[Pt(NH₃)₂Cl₂](py)²⁺ moiety and bridge helix residues are shown as black dashed lines. The loop of Rpb2 828–834 is shown in green.

**Fig. 4.** Structure of pol II transcribing complex stalled at a site-specific pyriplatin-DNA adduct after CMP incorporation. (A) The newly incorporated matched CMP is highlighted in yellow. Other colors are as in Fig. 2. Interactions of the damaged nucleotide and pol II residues are highlighted in (B). The view is taken roughly from an −90 degree clockwise rotation along the RNA/DNA helix axis from A. Nitrogen and oxygen atoms are depicted in blue and red, respectively. Hydrogen bonds between ammine group of the cis-[Pt(NH₃)₂Cl₂](py)²⁺ moiety and bridge helix residues are shown as black dashed lines. The loop of Rpb2 828–834 is shown in green.

**Discussion**

**Insights into Structure-Activity Relationships (SARs) for the Monofunctional Platinum Drug Family.** The original SARs pertaining to bifunctional platinum compounds such as cisplatin (8) were formulated to explain why anticancer activity appeared to require neutral, cis-[Pt(A₂X₂)] compositions, in which A is an amine ligand and X is a monoanionic leaving group. These rules are clearly violated by cationic, monofunctional platinum compounds such as pyriplatin (4, 5). Other monofunctional platinum complexes, including [Pt(dien)Cl]⁺, [Pt(NH₃)₂Cl]⁺, and trans-[Pt(NH₃)₂(py)Cl]⁺, are inactive and do not arrest pol II transcription, whereas the cis-[Pt(NH₃)₂(py)Cl]⁻ unit bound to guanosine blocks pol II transcription and has significant anticancer properties in mice when administered as pyriplatin (4, 5, 8, 24–32).

The present structure of pol II in complex with DNA site-specifically modified by pyriplatin provides unique insight into SARs to be expected for monofunctional platinum drug candidates. We constructed models of potential stalled transcription complexes containing DNA modified by the following three representative units, {Pt(NH₃)₂}, trans-[Pt(NH₃)₂(py)]²⁺, and cis-[Pt(NH₃)₂(py)]²⁺ bound to guanosine in DNA and positioned in either the −1 or +1 site of pol II, in order to mimic the...
post- and pre-translocation states, respectively (Fig. S1). For each modeled structure, we rotated the platinum unit about the Pt–N bond by 360° and computed van der Waals energies arising from contacts between platinum ligands and the rest of the pol II complex (Figs. S5–S9). The cis-\[Pt(NH}_3\]_2(py) \]^{2+} and trans-\[Pt(NH}_3\]_2(py) \]^{2+} monomers could readily be accommodated within the pol II active site over wide energy minima. The lack of a significant steric clash for these two groups, in either the −1 or +1 position of the pol II transcribing complex, indicates the absence of a barrier to transcriptional bypass (Figs. S6–S9). This finding agrees with experiment. In contrast, the energy barrier is prohibitively high for cis-\[Pt(NH}_3\]_2(py) \]^{2+} platinated DNA modeled at −1 position, which is consistent with its ability to block pol II bypass and the failure of pol II to reach the subsequent post-translocation state (Figs. S5 and S8). The presence of a pyridine or other bulky group in the cis configuration is important for restricting the rotation range of the cis-\[Pt(NH}_3\]_2(py) \]^{2+} moiety and thus rendering it a strong steric block to translocation. For a (Pt(NH}_3\]_2) \]^{2+} or trans-\[Pt(NH}_3\]_2(py) \]^{2+} adduct at the −1 position, such a steric clash can be avoided by rotation about the Pt–N bond, facilitating subsequent pol II translocation. These results are fully consistent with previous biochemical studies revealing that the latter two DNA adducts are inactive and fail to block transcription (5, 7, 12, 26–33).

**A Unique Molecular Mechanism of Pol II Transcription Inhibition.** The stalling mechanism of monofunctional platinum drugs of the pyriplatin family is dramatically different from transcription inhibition by cisplatin and UV-induced 1,2-intrastrand cross-links. For the latter two DNA-modifications, a translocation barrier prevents delivery of damaged bases to the active site and/or leads to misincorporation of NTPs against the damage site, respectively (19, 34). Monofunctional platinum-damaged residues, on the other hand, can cross over the bridge helix and be accommodated in the pol II active site. For Pt–dG adducts, the correct CMP nucleotide can be efficiently incorporated against the damaged guanosine. It is blockage of the subsequent translocation from this position after incorporation of the cytosine nucleotide that leads to inhibition of the RNA polymerase, but only when a bulky pyridine ligand is present in the cis coordination site.

In conclusion, we report here the structure of a pol II transcribing complex stalled at a site-specific monofunctional DNA adduct, revealing a unique mechanism of transcription inhibition by this kind of genome damage. The results establish a basis for SARs that govern the anticancer drug potential of monofunctional platinum-based DNA-damaging agents. Specific interactions between pol II active site residues and the platinum ligands are revealed, providing a structural framework for rational design of more potent monofunctional pyriplatin analogues. Because the spectrum of activity of pyriplatin is dramatically different from that of cisplatin against an extensive panel of cancer cell lines but with reduced potency (7), this information will be valuable for increasing the anticancer drug potential of this family of compounds based on pol II stalling with concomitant induction of apoptosis.

**Methods**

**Preparation of Pol II Transcribing Complexes.** Ten-subunit S. cerevisiae pol II was purified as described (35). RNA oligonucleotides were purchased from Dharmacon and DNA oligonucleotides were obtained from IDT. cis-\[Pt(NH}_3\]_2(py)/C/Cl] \] could be prepared by Ryan Todd at MIT. The site-specifically platinated template DNA was obtained as described (7).

Pol II transcribing complexes were assembled with the use of synthetic oligonucleotides (10). Briefly, DNA and RNA oligonucleotides were annealed and mixed with pol II in 20 mM Tris (pH 7.5), 40 mM KCl, and 5 mM DTT. The final mixture contained 2 µM pol II, 10 µM site-specific pyriplatin-damaged template DNA strand, and 20 µM nontemplate DNA and RNA oligonucleotides. The mixture was kept for 1 h at room temperature, and excess oligonucleotides were removed by ultraffltration. Crystals were obtained from solutions containing 390 mM (NH}_4\]_2HPO\]_4/NaH_2PO\]_4, pH 5.9–6.3, 50 mM dioxane, 10 mM DTT, and 9–11% PEG6000. Crystals of transcribing complexes were transferred in a stepwise manner to cryostreamer as described (10, 11). For the structure of the pol II complex with CTP incorporation, 10 mM CTP was added to the cryostreamer (10, 11).

**Crystal Structure Determination and Analysis.** Diffraction data were collected on beam line 11-1 at the Stanford Synchrotron Radiation Laboratory. Data were processed in DENZO and SCALEPACK (HKL2000) (36). Model building was performed with the program Coot (37), and refinement was done with REFMAC with TLS (CCP4) (Table S1). In the structure of pol II complex with a CTP incorporation against damaged guanosine residue, we also observed additional weaker density within the second channel in comparison to the nucleoside residue at the +1 position, which may correspond to nonspecific binding of a second CTP molecule through the soaking process. All structure models in the figures were superimposed with nucleoside residues near the active site using PYMOL (38).

**Transcription Assay.** Transcription assays were performed essentially as described (11). In a typical reaction, 3H-labeled RNA oligonucleotide (10 pmol) was annealed with template DNA 29 mer (20 pmol, damaged or nondamaged template) and nontemplate DNA 14 mer (30 pmol) in elongation buffer (20 mM Tris–HCl, pH 7.5, 40 mM KCl, 0.5 mM MgCl\]_2 in a final volume of 20 µL. An aliquot of the annealed RNA/DNA hybrid was incubated with a five-fold excess of pol II (final concentration of pol II 1.1 µM), of RNA oligonucleotide 0.22 µM, and of DNA oligonucleotides 0.44 µM) for 10 min at room temperature. Equal volumes of the NTP mixture solution were added (final concentrations 25 µM) and the mixture was then incubated for 0, 0.5, 1, 2, 3, 4, 8, 15, 30, 45, 60, 90, 120, 180, 300, and 600 min at 37 °C before addition of stop solution (final concentrations 5 M urea, 44.5 mM Tris–HCl, 44.5 mM boric acid, 26 mM EDTA, pH 8.0, Xylene Cyanol and Bromophenol Blue dyes). RNA products were analyzed by PAGE in the presence of urea. Visualization and quantification of products were performed with the use of a PhosphoImager (Molecular Dynamics).

**Computer Modeling Analysis.** Three representative platinum units, \[\text{cis-}[\text{Pt(NH}_3\]_2(py)]^{2+}, \text{trans-}[\text{Pt(NH}_3\]_2(py)]^{2+}, \text{cis-}[\text{Pt(NH}_3\]_2(py)]^{2+} bound to guanosine in DNA and positioned in either the −1 or +1 site of pol II were modeled to mimic the post- and pre-translocation states, respectively. The vdV interaction energies between the three ligands at different orientations and the rest of the pol II complex were systematically computed and taken as direct indicators of steric effects.

The structure of the \[\text{cis-}[\text{Pt(NH}_3\]_2(py)]^{2+} fragment on DNA in pol II is available from the current structure. Partial configurations for the other two units, \[\text{cis-}[\text{Pt(NH}_3\]_2(py)]^{2+} \] and \[\text{trans-}[\text{Pt(NH}_3\]_2(py)]^{2+} \] were obtained by modeling. Briefly, the same configuration of pol II, DNA, and RNA as found in the structure containing \[\text{cis-}[\text{Pt(NH}_3\]_2(py)]^{2+} \] was used for these two complexes. The geometry of \[\text{cis-}[\text{Pt(NH}_3\]_2(py)]^{2+} \] moiety was taken from a previous structure where it binds to a B-DNA dodemacer (PDB ID: SNBA) (39). Docking was achieved by aligning the damaged guanosine base of the two structures. Finally, trans-amine group in \[\text{Pt(NH}_3\]_2(py)]^{2+} was replaced with pyridine ligand, and the Pt–N bond length was appropriately adjusted to obtain the structure for \[\text{trans-}[\text{Pt(NH}_3\]_2(py)]^{2+} \]. The same procedure was used to generate structures at both +1 and −1 positions.

The vdV energies were computed for different configurations generated by rotating about the Pt–N bond from −180° to 180° for each platinum modification (see Figs. S5–S7). The rotation angle (φ) was defined to be positive when rotating in the antitclockwise direction. In the configuration with φ = 0°, the plane component of two Pt–N bonds of the ligand which are perpendicular to the Pt–N bond was set to be parallel to the damaged guanosine base. We noticed that, for \[\text{cis-}[\text{Pt(NH}_3\]_2(py)]^{2+} \] and \[\text{trans-}[\text{Pt(NH}_3\]_2(py)]^{2+} \], two trans amine groups were accommodated at slightly different configurations, with φ = 0° due to the different local environment, which leads to slightly different energies between conformations with φ and φ ± 180°. Because the purpose of our modeling study is to identify major steric clashes instead of accurately computing free energy changes associated with rotation of the ligand, which requires extensive conformational sampling, we performed a simple average of the two energies (\(E_1(\phi) \) and \(E_2(\phi = 180°) \)) based on their Boltzmann weights (T = 298 K), eq 1,

\[ E = (e^{-\beta E_1}E_1 + e^{-\beta E_2}E_2)/(e^{-\beta E_1} + e^{-\beta E_2}) \]  

to get a better estimate of dV energy profiles.
The GROMACS simulation package was used to compute vDW energies between the ligands and the pol II complex (40). A 20-Å cutoff was adopted for computing the vDW interactions. The AMBER03 force field was used for the pol II complex including protein, RNA, and DNA (41). The vDW force field (Leonard–Jones potential) parameters for ligands were generated from the AM1-BCC parameters of the AMBER9 package (42) using the general AMBER force field (GAFF) (43) developed for rational drug design. Since the Pt atom is not in direct contact with the pol II complex and does not contribute significantly to any steric effects, we excluded it from our vDW energy calculations.

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