Predicting cisplatin and trabectedin drug sensitivity in ovarian and colon cancers

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Abstract
Molecular profiling of markers involved in the activity of chemotherapeutic agents can shed light on the successes and failures of treatment in patients and can also provide a basis for individualization of therapy. Toward those ends, we have used reverse-phase protein lysate microarrays to evaluate expression of protein components of the nucleotide excision repair (NER) pathways. Those pathways strongly influence the anticancer activities of numerous drugs, including those that are the focus here, cisplatin and ecteinascidin 743 (Et-743; Yondelis, Trabectedin). Cisplatin is generally more active in cell types deficient in NER, whereas Et-743 tends to be less active in those cells. We measured protein expression and sensitivity to those drugs in 17 human ovarian and colon cancer cell lines (13 of them from the NCI-60 panel) and five xeroderma pigmentosum (XP) patient cell types, each containing a different NER defect. Of the NER proteins giving reliable signals, XPF and XPG showed the highest correlations of protein expression with drug activity across all three tissue-of-origin groups. When we compared protein expression data with mRNA expression data from Affymetrix U133A chips, we found no consistent correlation between the two across the cell lines studied, which reinforces the conclusion that protein measurements can give more interpretable mechanistic information than can transcript measurements. The work reported here provides motivation for larger proteomic studies with more cell types focused on potential biomarkers in additional pharmacologically pertinent pathways. [Mol Cancer Ther 2008;7(1):10–8]

Introduction
Platinum derivatives are the mainstay of chemotherapy for many epithelial malignancies, including ovarian and colon cancers (1). For many advanced cancers, the rate of response to initial chemotherapy is quite high, but the patients tend to relapse (and then to be more refractory to second or third line treatment; ref. 2). For instance, 70% to 80% of advanced stage ovarian cancers respond to cisplatin-based primary therapy, with around 50% of the responders eventually relapsing due to clinical resistance (2). Nucleotide excision repair (NER) is the primary mechanism known to remove platinum-DNA adducts (including cisplatin-induced and oxaliplatin-induced intrastrand crosslinks) from DNA (1, 3–5), thereby increasing resistance to the drug. NER is composed of two subpathways for damage detection: (a) global genome NER, which maintains the integrity of the entire genome, and (b) transcription-coupled NER (TC-NER), which accounts for removal of damage in the transcribed strands of active genes. Impaired NER activity is associated with several rare autosomal recessive photosensitivity diseases, including xeroderma pigmentosum (XP), Cockayne syndrome, and trichothiodystrophy (6). NER factors are also mutated in some human cancers, including ovarian and testicular tumors (3, 7, 8), and can therefore contribute to clinical resistance to platinum derivatives (1).

Global genome NER and TC-NER are comparable in terms of mechanism, except for the initial damage recognition step (6). In global genome NER, helix-distorting base lesions are identified by XPC-hHR23B. In TC-NER, elongating RNA polymerase II encounters the lesion and recruits the Cockayne syndrome factors CSA and CSB. Subsequent stages of the two subpathways are the same. TFIIH is composed of XPD and XPD, helicase components that catalyze ATP-dependent unwinding of the DNA strands. XPA and replication protein A stabilize the open complex and position the other factors. Dual incision is done by ERCC1-XPF and XPG endonucleases, which cleave the damaged strand 5’ to 3’ of the lesion, respectively.
Finally, NER is completed by gap-filling DNA synthesis, followed by strand ligation.

Ecteinascidin 743 (Et-743; Yondelis, Trabectedin), a natural product isolated from a marine tunicate, is currently under registration for the treatment of soft tissue sarcomas and is being studied in a pivotal Phase III trial for ovarian cancer\(^4\) (9, 10). The mechanism by which Et-743 interacts with DNA and exerts its antitumor activity is different from those of other alkylating agents, such as cisplatin. Whereas cisplatin binds to the N7 position of guanine in the major groove of DNA (1), Et-743 forms monoaucts at the N2 position of guanine in the minor groove of DNA, forcing the minor groove toward the major groove and allowing possible interaction of the C-ring portion of the drug with the NER factors (11, 12).

Although the precise mechanism of action of Et-743 has not been fully elucidated, Et-743 has been found to be more active in cells with an enhanced TC-NER system, for example, in cisplatin-resistant cells (4, 13, 14). An understanding of the opposite relationships of cisplatin and Et-743 with the NER pathways could be useful, potentially yielding more effective molecularly targeted treatment strategies and suggesting that Et-743 could be used in a second-line regimen after cisplatin-based treatment or in combination with cisplatin.

To further our understanding of the relationship between NER and resistance to cisplatin and Et-743, we studied the expression of NER factors and the sensitivity to those two drugs in a set of cell types that express different levels of the NER components. Generally, that approach would involve assessment of transcript levels, for example, using oligonucleotide microarrays. However, it is well understood that transcript levels may or may not accurately reflect protein levels, depending on the particular molecular species and the biological specimens to be compared; see, for example, refs. (15, 16). Because proteins are the directly acting molecules in the NER pathway and the species most often useful as clinical biomarkers, we preferred to profile the proteins rather than the transcripts. In the present study, therefore, we used a high-throughput proteomic technology, the reverse-phase protein lysate microarray, to quantitate NER components and other proteins in ovarian cancer, colon cancer, and XP patient cells. One advantage of the reverse-phase microarray technology (15, 17) is that it permits direct comparison for a given protein species across samples on a single glass slide. That type of comparison is more useful than a direct comparison of different proteins in a given sample, as is obtained from two-dimensional gels, antibody arrays, and most mass spectrometry–based technologies.

After obtaining the NER protein profiles across cell lines, we compared them with patterns of sensitivity to Et-743 and cisplatin, which we determined using the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay. XPF and XPG showed the highest correlation with drug activity in the set of cell lines studied. Thirteen of the 17 colon and ovarian cancer cell types are included in the panel of 60 human cancer cell lines (NCI-60) used by the National Cancer Institute (NCI) to screen for anticancer agents (18). It will, therefore, be possible in future analyses to relate the NER protein expression levels presented here to the overall database of compounds screened and also to the large array of additional molecular characterizations of the NCI-60 at the DNA, RNA, protein, and small molecule levels. Those characterizations are represented in the “Spotlight on Molecular Profiling” series, inaugurated by Molecular Cancer Therapeutics in November of 2006 (19).

Materials and Methods

Cells, Drugs, and Antibodies

OVCAR3, OVCAR4, OVCAR5, OVCAR8, Igrov1, and Skov3 ovarian cancer cells were provided by Dr. R. Camalier, Division of Cancer Treatment and Diagnosis Tumor Repository, NCI. A2780 ovarian cancer cells and the cisplatin-resistant variant CP70 were provided by Dr. T. Fojo (Cancer Therapeutics Branch, NCI). The HeyA8 ovarian cancer cell line was provided by Dr. G. Mills of M.D. Anderson Cancer Center. HCC2998, SW620, HT29, COLO205, HCT116, KM12, and HCT116 colon cancer cells were purchased from the American Type Culture Collection. The Et-743–resistant HCT116 variant HCT116/ER5 has been reported previously (13). GM637 normal nonfetal transformed fibroblasts, GM4312 (XPA) transformed fibroblasts, GM2345 (XBP) transformed lymphoblasts, GM8207 (XPD) transformed fibroblasts, and GM8437 (XPF) transformed fibroblasts cells were purchased from Human Genetic Mutant Cell Repository, Coriell Institute for Medical Research. The XP20B (XPG) primary fibroblast cell line was provided by Dr. K. Kraemer (Laboratory of Molecular Carcinogenesis, NCI). Cells lines were maintained in RPMI or DMEM supplemented with 10% fetal bovine serum. All cell lines were regularly tested for Mycoplasma contamination by PCR analysis.

Et-743 was provided by the NCI Developmental Therapeutics Program, NCI. Cisplatin was purchased from Sigma. Anti-XPA, anti–ERCC1, anti–DNA polymerase β, anti–Rad51, anti–X-ray complementing defective 1 gene, anti–mismatch repair protein 2 (MSH2), anti-p300, anti–keratin 8, anti–keratin 7, anti–proliferating cell nuclear antigen, anti–MSH6, and anti–Ref 1 monoclonal antibodies were purchased from Neomarkers. Anti–XPB rabbit polyclonal antibody was obtained from Santa Cruz Biotechnology. Anti–breast cancer 1 gene monoclonal antibody (21A8) was donated by Dr. T. Ouchi from New York University. Anti–XPD was donated by Dr. J. Bradsher from NCI. Anti–XPC, anti–XPF, and anti–XPG rabbit polyclonal antibodies were donated by Dr. R. Wood of University of Pittsburgh. Secondary alkaline phosphatase–conjugated goat anti–rabbit and goat anti–mouse antibodies were purchased from Tropix.

\(^4\) http://www.pharmamar.com/en/pipeline/yondelis.cfm
Protein Lysate Preparation and Micro–Western Blot Analysis

Cell lines were grown to 50% to 80% confluence, then scraped from the flask and washed thrice with cold PBS. Cell pellets were lysed in buffer as described previously (15). Lysates were aliquoted and stored at −80°C to avoid repeated freeze/thaw cycles, and antibody specificity was determined by micro–Western blotting. Samples containing 10 μg of protein in an SDS standard loading buffer were electrophoresed in a 4% to 20% Tris-glycine Novex precise gels. After electrophoresis, the separated proteins were transferred to a nitrocellulose membrane, which was then incubated with I-Block blocking buffer (Tropix) with 0.1% Tween 20. The blot was incubated with specific primary antibodies and then incubated with secondary alkaline phosphatase–conjugated antibody. Protein bands were visualized by chemiluminescence using CDP-Star ready-to-use substrate solution (Tropix).

Reverse-Phase Protein Lysate Arrays

Arrays were designed and produced as previously described (15). Briefly, lysate samples were manually loaded into 384-well microtiter plates (Genetix) to produce ten 2-fold serial dilutions at a constant buffer composition for each sample. Arrays were made in batches of 20 by spotting samples from the microtiter plates onto 20 nitrocellulose-coated glass slides (FAST Slides, Schleicher & Schuell) using a pin-in-ring format Affymetrix GMS 417 arrayer. Lysate samples in microtiter plates were freeze/thawed no more than thrice. Arrays were stored at −20°C until use. The 1st and 20th array of each batch were stained with anti-p300 antibody to provide interbatch and intrabatch controls, and the remaining slides were stained with antibodies of interest. Slides 2 to 19 were processed through an automated Autostainer using the catalyzed signal amplification stain system (DAKO). Slides were then scanned using an ordinary optical flatbed scanner, the Perfection 1200S (Epson America), and the array spot images were converted to raw pixel values using the Peak Quantification with Statistical Comparative Analysis program.3

The dose interpolation algorithm (DI25), developed in a previous study (15), was used to analyze the array data. Briefly, the 25th percentile of each dose-response curve for each cell line was calculated for both target and total protein levels. Each experimental DI25 value was adjusted by total protein level for each cell line. Throughout this article, the term “protein level” from the microarrays refers to the DI25 value, which is expressed in terms of the 2-fold dilution number, hence in terms of a relative log base 2 of the protein expression level. Clustered image maps (20), also known as clustered “heat maps,” were generated using the CIMMiner program.6

Results

Protein Expression Profile of the NER Pathway in Ovarian Cancer Cell Lines

NER protein levels in ovarian cell lines and cell lines derived from XP patients (XPA, XPB, XPD, XPF, and XPG) are shown in Fig. 1. Included were six ovarian lines from the NCI-60 screen. Strong expression of XPD was observed in all of the cells, whereas other NER proteins were expressed to various extents in the different cell lines. For instance, many of the NER proteins were more strongly expressed in OVCAR3 and OVCAR5 than in OVCAR4, which expressed lower levels of XPA and XPF. The large differences in NER protein levels within the ovarian cancer cell line panel suggest possible functional differences in the pathway.

Figure 1. XP protein expression levels. Micro–Western blots of extracts from ovarian cancer and XP patient (XPA, XPB, XPD, XPF, and XPG) cell lines (top) probed with antibodies against NER proteins. For ERCC1, the XPF patient cell line was used because there is no ERCC1 patient cell line. GM637 are normal nontransformed human fetal fibroblasts. Tubulin was used as a loading control.

3 Available at http://abs.cit.nih.gov/pscan.
4 Available at http://discover.nci.nih.gov.
Differences in the NER pathway among ovarian and colon tumor cell lines were quantitated by using reverse-phase protein lysate microarrays. On Western blot, each antibody selected for the reverse microarray studies gave a specific and prominent band whose electrophoretic migration corresponded to the expected molecular mass of the target protein. Each array included ten 2-fold serial dilutions of each cell line and eight control lysate pools (prepared by mixing equal volumes of all of the cell lines together). Similar amounts of total protein were loaded on the array for all of the cell lines. Mouse and rabbit anti-Aspergillus niger glucose oxidase IgG1, used as a negative control antibody, showed only low, nonspecific signals (Fig. 2A). The median Pearson's correlation coefficient was +0.95 for the six pairwise comparisons of four replicate p300 arrays across all of the cell lines on the arrays. The dilution curves for XPA protein expression (Fig. 2B) are shown in Fig. 2C. OVCAR3 expressed the highest levels of XPA. The Spearman's (nonparametric) correlation coefficient between the micro–Western blot probing for XPA and the lysate microarray DI25 value was +0.84. Collectively, the results indicate that data from the arrays developed for this study of NER proteins are reproducible and quite reasonably concordant with the data from micro–Western blots.

Next, we tested the relationship between protein expression and mRNA levels. The mRNA levels were derived from our prior profiling of the NCI-60 using Affymetrix HG-U133 chips (16). None of the NER factors tested (XPA, XPC, XPF, and XPG) gave a significant correlation between mRNA and protein expression (all of the Pearson correlation coefficients were below 0.21). Rad51 gave a correlation

**Figure 2.** Reverse-phase protein lysate microarray. **A,** control slides include total protein staining with Sypro Ruby, CSA staining with p300, and negative controls (NC) with irrelevant mouse and rabbit IgGs (anti-Aspergillus niger) in place of the p300-specific antibody. **B,** CSA staining with XPA. **C,** dilution-intensity curves for each cell line on the array. Y axes, Peak Quantification with Statistical Comparative Analysis intensity read-outs; X axes, 2-fold dilution series.

**Validation of Reverse-Phase Protein Lysate Microarrays in Application to NER**

Differences in the NER pathway among ovarian and colon tumor cell lines were quantitated by using reverse-phase protein lysate microarrays. On Western blot, each antibody selected for the reverse microarray studies gave a specific and prominent band whose electrophoretic migration corresponded to the expected molecular mass of the target protein. Each array included ten 2-fold serial dilutions of each cell line and eight control lysate pools (prepared by mixing equal volumes of all of the cell lines together). Similar amounts of total protein were loaded on the array for all of the cell lines. Mouse and rabbit anti-Aspergillus niger glucose oxidase IgG1, used as a negative control antibody, showed only low, nonspecific signals (Fig. 2A). The median Pearson’s correlation coefficient was +0.95 for the six pairwise comparisons of four replicate p300 arrays across all of the cell lines on the arrays. The dilution curves for XPA protein expression (Fig. 2B) are shown in Fig. 2C. OVCAR3 expressed the highest levels of XPA. The Spearman’s (nonparametric) correlation coefficient between the micro–Western blot probing for XPA and the lysate microarray DI25 value was +0.84. Collectively, the results indicate that data from the arrays developed for this study of NER proteins are reproducible and quite reasonably concordant with the data from micro–Western blots.

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coefficient of 0.27. Only p300 showed a significant correlation between mRNA and protein (Pearson correlation coefficient, 0.63; \( P < 0.02 \)). Together those results suggest that proteins of the NER pathways should be measured directly rather than depending on the mRNA as a surrogate.

In addition, we compared the NER protein profiles with compound sensitivity \([-\log_{10}(\text{GI}_{50})]\) in the ovarian and colon cancer cell lines from the NCI-60 cell database (16, 21) and found a negative correlation between sensitivity to nitrosoureas and XPA protein levels (Table 1). The Pearson correlation coefficients were \(-0.77\) for lamustine \([1-(2\text{-chloroethyl})-3\text{-cyclohexyl}-1\text{-nitrosourea}]\) and \(-0.60\) for carmustine \([1,3\text{-bis}(2\text{-chloroethyl})-1\text{-nitrosourea}]\), whereas nonalkylating agents showed no correlation (correlation of \(-0.26\) for doxorubicin, \(-0.03\) for \(\text{t}\)-asparaginase, 0.02 for hydroxyurea, and 0.25 for paclitaxel).

**Clustered Image Map Representation of the Expression Profiles of NER and Other Proteins**

Many other factors, including repair pathways, may be involved in the cisplatin resistance of cancer cells. We therefore assessed the protein expression of a number of molecules that might show related changes: p53 (tumor suppressor protein p53), MSH2, p300 (E1A-binding protein), Rad51 (RecA homologue), keratin 8, keratin 7, proliferating cell nuclear antigen, poly[ADP-ribose] polymerase, DNA polymerase \(\beta\), X-linked inhibitor of apoptosis, nuclear factor-\(\kappa\)B, MSH6, X-ray complementing defective 1 gene, breast cancer 1 gene, and Ref1 (multifunctional DNA repair enzyme). Clustered image map—relating cells and proteins were generated using the calculated DI25 values (Fig. 3). All replicate samples clustered side by side with high positive Pearson’s correlation coefficients. For example, the GM637 cell line replicates clustered together with a correlation coefficient of +0.89, and the mean correlation coefficient for XPA, XPC, XPF, and XPG duplicate arrays was +0.92. Overall, the ovarian cancer and colon cancer cell lines did not cluster well by tissue-of-origin groups. A2780 and the A2780 cisplatin-resistant derivative CP70 clustered tightly with a Pearson correlation of +0.98. HCT116 and its Et-743 resistant derivative, ER5 (13), did not cluster tightly. HCT116 expressed higher levels of keratin 8, Rad51, and Ref1, whereas ER5 expressed higher levels of MSH2, p53, X-linked inhibitor of apoptosis, and nuclear factor-\(\kappa\)B. ER5, with a mutation in the XPG gene, expressed lower protein levels of XPG, XPF, and XPC (13). HCT116 is deficient in MSH2, and the array indeed showed low expression of that protein (22). Similarly, HCT15, known to be deficient in MSH6, expressed low amounts of that protein (23). Keratin 8, expressed in epithelial cancers, was expressed strongly in the colon and ovarian cancers with the exception of ER5, A2780, CP70, Igrov1, HeyA8, OVCAR5, and Skov3 (24). In contrast, keratin 7, an ovarian cancer marker, was expressed most prominently in the ovarian cell lines except for Igrov1, A2780, and CP70 (25). Igrov1 was the only ovarian line that did not express MSH2. The XBP and XPD cell lines clustered tightly, an interesting observation because both XBP and XPD function as helicases in the TFIIH NER complex to unwind DNA at the damage site. Cell lines from XP patients are known to express higher levels of p53 (26). The XPA, XBP, XPD, and XPF cell lines did, in fact, express high levels of p53. However, XPG, the only XP patient line we studied that is a nontransformed primary cell line, did not. Overall, the clustered image map showed the protein expression measurements to be technically reliable and biologically reasonable.

**Cisplatin and Et-743 Have Different Activity Profiles**

In the MTT assay, Et-743 and cisplatin showed different profiles of activity across the ovarian cancer, colon cancer, and XP patient cell lines (Fig. 4). The NER-deficient patient cell lines (XPA, XPB, XPD, XPF, and XPG) were, as a group, more sensitive to cisplatin than to Et-743. In comparison with GM637, the XP-deficient lines were more Et-743 resistant and cisplatin sensitive. Among the colon lines tested, HCC2998 and HT29 were highly resistant to cisplatin and sensitive to Et-743. In contrast, HCT15 and ER5 were highly resistant to Et-743 and sensitive to cisplatin. The ovarian lines OVCAR4 and Skov3 were sensitive to cisplatin and somewhat resistant to Et-743. The opposite was true for CP70, HeyA8, and OVCAR8, which were more sensitive to Et-743 and resistant to cisplatin. In the other ovarian and colon lines, the two drugs were similar in their potency.

**Best NER Predictors of Et-743 and Cisplatin Drug Sensitivity**

Developing more effective molecularly targeted therapies requires identification of biomarkers that predict sensitivity and resistance. In the present study, we attempted to identify potential biomarker proteins by assessing correlations between their expression levels and relative sensitivities to cisplatin and Et-743. To obtain a “drug preference score,” we subtracted the sensitivity (expressed as minus the logarithm base 10 of the 50% growth inhibitory concentration) to Et-743 from that to cisplatin. We then computed the correlation coefficient between that preference score and the expression level of each of the proteins profiled, focusing on the XP family (Table 2). Many of the

<table>
<thead>
<tr>
<th>NSC number</th>
<th>Drug name</th>
<th>XPA versus log10(GI50)</th>
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</thead>
<tbody>
<tr>
<td>79037</td>
<td>Lamustine (CCNU)</td>
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<tr>
<td>409962</td>
<td>Carmustine (BCNU)</td>
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<td>752</td>
<td>Thiouanilene</td>
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</tr>
<tr>
<td>125973</td>
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</table>

NOTE: Pearson correlation was calculated between the negative log10(GI50) and XPA protein expression (21).

Abbreviations: CCNU, 1-(2-chloroethyl)-3-cyclohexyl-1-nitrosourea; BCNU, 1,3-bis(2-chloroethyl)-1-nitrosourea.
proteins showed moderate correlations with the drug preference score, but the correlations were not highly significant. For instance, within the XP cell lines group, the $P$ value equaled 0.09, as computed by randomly permuting the cell lines labels for proteins and recomputing the correlations.

We also investigated correlations within tissue-of-origin groups and found several cases in which protein levels seemed to predict relative activities of cisplatin and Et-743. For example, levels of Rad51 showed a correlation of 0.55 with “cisplatin preference” among the ovarian lines, but an opposite correlation of $-0.78$ with cisplatin among the colon lines. Several other proteins showed similar patterns. Such large positive and negative correlations would quite possibly achieve statistical significance in a study based on a larger sample set, but they were only marginally significant ($P = 0.07$ by randomization test) for the small samples studied here. That is, they generated hypotheses to be investigated further.

Of the NER proteins, XPF and XPG showed the highest correlations with drug activity across all three tissue-of-origin groups (ovarian cancer, colon cancer, and XP cell lines). The increased protein expression was directly correlated with Et-743 sensitivity and cisplatin resistance. Those proteins were especially effective in predicting cisplatin and Et-743 activity in the NER-deficient lines but were only moderately well correlated with drug activity for the ovarian and colon tissue-of-origin groups (multiple comparisons–corrected $P$ values were $P = 0.11$ for XPG and $P = 0.16$ for XPF in randomization tests for ovarian and colon lines taken together). The differences observed in the panel of cell lines in the present study are consistent with the differential sensitivity to Et-743 and cisplatin of isogenic cell lines differentially expressing NER factors (4, 13).

**Discussion**

Promising evidence of antitumor activity and clinical benefit have been reported for Et-743 in clinical trials for many cancer types, including soft tissue sarcomas, breast cancers, and ovarian cancers (10, 27–30). A phase II clinical trial of Et-743 showed promising activity in relapsed ovarian cancer patients (31). As with other therapeutic...
agents, one is prompted to ask whether the success rate could be increased if therapy was selected on the basis of molecular profiles of the tumors. In the case of Et-743, logical molecules to consider as candidate biomarkers are the NER components. Et-743, in contrast, for example, to cisplatin (which is also used clinically against ovarian cancer), has been reported to be more active against NER intact cells than against NER-deficient ones. Although the role of NER in relation to the clinical activity of Et-743 and cisplatin remains to be understood comprehensively, the TC-NER pathway has been implicated in sensitivity and resistance of tumor cell lines to those drugs. Cells deficient in TC-NER have been reported as hypersensitive to UV radiation, cisplatin, and other alkylating agents, but resistant to Et-743 (4, 13, 14, 32). However, contradictory results have been published from various investigators attempting to correlate resistance to cisplatin therapy with elevated levels of genes and proteins of the NER pathway (1, 3, 33–37).

Here, we report expression profiles of the NER molecules in cells from five XP patients with various known NER defects and in a set of ovarian and colon cancer cell lines (all but four of them from the NCI-60 panel). Because of the opposite influences of NER defects on the activity of Et-743 and cisplatin (4, 13), we then asked how the expression levels relate to differences in activity between the two drugs. The simplest approach to profiling would have been at the transcript level, for example, by oligonucleotide microarray or reverse transcription–PCR. However, the relationship between transcript and protein expression is unknown for NER molecules, and the proteins are the directly active molecules. Hence, we used the reverse-phase lysate microarray platform for quantitation at the protein level (15, 17). That technology served our present purpose well, because it permitted direct comparison for each protein across all of the cell types on a single glass slide. To validate the microarray platform, we compared its results with those from micro–Western blots; the concordance was strong (e.g., +0.84 Spearman correlation for XPA). We also found the arrays to be highly reproducible (+0.95 correlation for replicate arrays assessing the control protein p300). We previously reported that some gene families show good correlation across the NCI-60 between transcript and protein expression profiles and some do not. In this study, the transcript and protein levels of NER molecules were poorly correlated. In general, proteomic profiling may yield more direct answers than transcript profiling because the majority of known biological effector molecules, diagnostic markers, and pharmaceutical targets are proteins (38, 39). It may be possible to hit pharmacologic targets more selectively if the pertinent pathways and their regulation are better understood at the protein level.

Individually, XPF and XPG showed the highest negative correlations with drug activity (cisplatin/Et-743 IC50

![Figure 4](mct.aacrjournals.org). Mean graph drug activity patterns (42) for Et-743 and cisplatin. The sensitivity of Et-743 and cisplatin against tumor cell lines measured using the MTT assay. Indicated values represent the averages of three independent experiments. Values are expressed relative to the mean across all cell lines tested using the equation \(-\log_{10}(IC_{50\text{individual cell line}} - IC_{50\text{mean}})\). Mean IC50 values for all cell lines tested were $5.4 \times 10^{-10}$ mol/L for Et-743 and $7.4 \times 10^{-9}$ mol/L for cisplatin.
protein expression of Rad51 correlated with Et-743 resistance. A microarray gene expression study identified many gene alterations in Igrov1 and the Et-743–resistant HCT116 colon cancer cell line (13) showed lower Rad51 protein level than did the Et-743–sensitive HCT116 cell line. That finding suggests a possible implication for Rad51 in acquisition of resistance to Et-743 in different cancer types. Other proteins that were increased in the ER5 cell line, p53, MSH2, X-linked inhibitor of apoptosis, and nuclear factor-a-B play diverse roles in processes, such as DNA repair, apoptosis, and transcription regulation. Collectively, the data developed here show the difficulty of identifying a single NER biomarker to predict drug sensitivity. The heterogeneity of cancers and the influence of NER-independent pathways probably contribute to this complexity.

Although many factors can influence the cisplatin and Et-743 sensitivity of cell lines, proteomic profiling with the reverse-phase protein microarrays provides a unique opportunity to relate drug sensitivity to key signal transduction proteins. The NER protein profiles presented here will be useful for analyses involving the large library of compounds screened against the NCI-60 and the array of molecular profiles at the DNA, RNA, protein, and small molecule levels available for those cells. We compared the NER protein levels (XPA, XPC, XPF, and XPG) with mRNA levels2 and found no significant correlation (Pearson correlation coefficient, <0.21). That result is not surprising given that transcript levels may not accurately reflect protein levels. In addition, we compared the NER protein profiles with NCI-60 cell line compound sensitivities and found a negative correlation between sensitivity to alkylating agents (nitrosoureas) and XPG protein levels in the ovarian and colon cancer cell lines. Those findings are consistent with the value of XPA as a protein biomarker for NER. The NER protein profiles presented here will be useful for future analyses involving the large library of compounds screened against the NCI-60 and the array of molecular profiles at the DNA, RNA, protein, and small molecule levels available for those cells.

It is clear that cell lines are not fully representative of tumors from patients, but they do have the advantages of reproducibility, availability, and homogeneity in cell lineage. We previously used colon and ovarian lines as the starting point for identification of molecular markers for differential diagnosis between advanced colon and ovarian cancers (41). That study suggested that useful information from patients’ tumors is retained in cultured cells. Further studies in tumors to correlate the NER protein levels with clinical data will clarify the biochemical roles of the NER proteins and their potential as therapeutic markers. Such a study might entail laser capture microdissection of tumor cells from biopsy materials and application of the resulting samples to reverse-phase protein arrays for mapping of protein pathways implicated in

## Table 2. NER biomarkers that predict cisplatin and Et-743 drug activity measured as correlations between mean “drug preference scores” and mean NER protein levels for subsets of cell lines

<table>
<thead>
<tr>
<th>Protein*</th>
<th>All</th>
<th>Ovarian cancer</th>
<th>Colon cancer</th>
<th>XP cell lines</th>
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<td>0.28</td>
<td>-0.52</td>
<td>0.88</td>
</tr>
<tr>
<td>XPF_2</td>
<td>-0.14</td>
<td>0.39</td>
<td>-0.60</td>
<td>0.91</td>
</tr>
<tr>
<td>XPG_1</td>
<td>-0.21</td>
<td>0.15</td>
<td>-0.52</td>
<td>0.88</td>
</tr>
<tr>
<td>XPG_2</td>
<td>-0.26</td>
<td>0.62</td>
<td>-0.28</td>
<td>0.90</td>
</tr>
</tbody>
</table>

NOTE: Drug preference score was calculated by subtracting the sensitivity \(-\log_{10}(IC_{50})\) to Et-743 from that to cisplatin. Correlation coefficient, shown in the table, is the correlation between the drug preference score and the XP protein expression levels.

* Nucleotide excision repair proteins (XPA, XPC, XPF, and XPG) profiled in duplicates (_1, _2).


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drug response. In summary, the work reported here on quantitation of the NER proteins in cancer cell lines may provide the basis for such future studies, with the goal of developing more effective molecularly targeted, patient-tailored therapies.

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