Pharmacogenomic Dissection of Resistance to Thymidylate Synthase Inhibitors

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ABSTRACT

Chemoresistance is a major obstacle for successful cancer treatment. Gene amplification and altered expression are the main genetic mechanisms of tumor chemoresistance. Previously, only a limited number of genes were analyzed in each individual study using traditional molecular methods such as Northern and Southern blotting. In this study, the global gene expression patterns of 1176 genes in a panel of five thymidylate synthase (TS) inhibitor [raltitrexed (TDX) and 5-fluorouracil (5-FU)] resistant and sensitive parent cell lines were investigated using cDNA array technology. Only 28 of 1176 genes were altered >1.5-fold among resistant cells, with 2 genes (TS and YES1) consistently higher in the panel. TS mRNA and protein were consistently overexpressed in all drug-resis-
tant tumor cell lines compared with the sensitive parent cell lines. Southern blot and FISH analysis demonstrated that the TS gene was amplified in 5-FU- and TDX-resistant cell lines. YES1 mRNA and protein were overexpressed in four drug-resistant tumor cell lines but were not over-
expressed in the lymphoblast cell line W1L2,TDX, although the YES1 gene was highly amplified in these cells. The fact that W1L2 has high level (>10-fold) resistance to TS inhibitor in the absence of high YES1 expres-
sion leads to a conclusion that YES1 has no direct role in this drug resistance process. By narrowing the search from 1176 to 2 genes, the analysis of in vitro TDX and 5-FU resistance becomes more straightfor-
ward for confirmatory studies. These data provide encouragement that comprehensive transcript analysis will aid the quest for more enlightened therapeutics.

INTRODUCTION

Chemotherapy has improved the outcome of cancer treatment. However, tumor resistance to chemotherapeutic agents is still a major obstacle in the clinical management of human cancers. Numerous molecular genetic events are involved in chemoresistance to agents with distinct molecular targets. Until recently, most studies have focused on the expression of a limited number of candidate genes using traditional methods, such as reverse transcription-PCR, Northern blotting, and Western blotting. The global molecular alterations in chemoresistant tumors and cell lines are largely unknown. In contrast to traditional methods, advances in molecular technology now allow for global assessment of the genome (CGH), transcrip
tome (cDNA microarray), or proteome (1–3). Therefore, the molecular basis for drug resistance can be evaluated without prior assumptions as to the putative mechanism(s) of resistance. Elucidation of these genetic aberrations in drug-resistant tumor cells may help to more fully explain resistance and provide strategies to restore chemosensitivity.

To dissect the pharmacogenomics of chemoresistance, thymidylate synthase inhibitor-resistant cell lines were used as a model in this study. A critical step in the de novo pathway of DNA synthesis is the production of the pyrimidine nucleotide dTMP from dUMP. Because this reaction is catalyzed by TS (EC 2.1.1.45), using CH_2THF (5,10-
methylene tetrahydrofolate, a folate substrate), and is the only de novo source of cellular thymidylate, TS is an attractive target for cytotoxic drugs (4, 5). TDX is a specific inhibitor of TS and has demonstrated activity in many solid tumors in experimental systems (6). This drug has also been used in the treatment of human tumors such as colorectal, breast, and lung cancers (7–9). Another commonly used anti-
cancer drug, 5-FU, also inhibits TS activity, as well as damaging tumor DNA and RNA by incorporation of fluoro-nucleotides (10). As with other anticancer drugs, acquired or inherent resistance to these drugs are still the main barriers for their clinical effectiveness. The resistant cells often express high levels of TS protein, which can antagonize the cytotoxic effect of TDX and 5-FU (11). CGH results have shown that TDX-resistant cell lines have a gain of genomic material on chromosome 18 at the location of the TS gene (18p11.32; Ref. 12). It is possible that abnormal expression of other genes on 18p11.32 and other regions of the genome may also influence the response of tumor cells to TS inhibitors.

The aim of this study was to set up a model for the global analysis of gene expression patterns in chemoresistant cells using five pairs of TS inhibitor-sensitive and -chemoresistant tumor cell lines and to identify the common molecular genetic events involved in resistance to TS inhibitors in different tumors. Overexpression of two genes located at chromosome 18p (TS and YES1) was detected by cDNA array analysis and confirmed by Northern blotting. Gene amplification and protein overexpression status of these two genes were investigated using FISH, Southern, and Western blotting analysis. The putative relationship between gene amplification and overexpression of mRNA or protein is discussed. In addition, the data highlight the discordance between the observation of gene amplification and a true role in resistance, providing the context in which current oncogenic studies must be interpreted.

MATERIALS AND METHODS

Cell Culture. For expression analysis, four TDX-resistant cell lines (colo-
rectal tumor, H630,TDX; and RKO,TDX; breast tumor, MCF-7,TDX; lympho-
blistoid, W1L2,TDX), one 5-FU-resistant cell line (H630,FU), and the sensitive parent cell lines were cultured in RPMI 1640 (Life Technologies, Inc., Glass-
gow, United Kingdom) supplemented with 10% FCS, 50 units/ml penicillin, 50 

\mu \text{gADM streptomycin, and relevant concentrations of TDX (H630,TDX: 1 } \mu \text{M; RKO,TDX, MCF-7,TDX; W1L2,TDX: 2 } \mu \text{M; and 5-FU (H630,FU, 10 } \mu \text{M) in 75-cm}^2 \text{ flasks at } 37^\circ \text{C and 5% CO}_2 \text{ until 80–90\% confluent (11, 13). The cells were then harvested by trypsinization and used for further analysis.}

cDNA Array Analysis. Total RNA was extracted using the method recom-
ended by the cDNA array manufacturer (Clontech Laboratories, Palo Alto, CA), poly(A)^+ mRNA was extracted using the Oligotex mRNA mini purification kit (Qiagen, Inc., Santa Clarita, CA) following the supplier’s instruction.

The Human Cancer 1.2 Array containing cDNAs from 1176 genes on a nylon membrane (Clontech Laboratories, Inc., Palo Alto, CA) was used to interrogate the gene expression patterns of the different cell lines. Nine housekeeping genes were also present on the membrane. Membranes were hybridized at 68°C overnight in 1.5 ml of ExpressHyb solution (Clontech) containing 32P-labeled cDNA probes (>1 \times 10^6 \text{ cpm/ml).}

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cDNA probes were produced by reverse transcription from 1 μg of mRNA using primers specific for the 1176 genes (Clontech). The membranes were stringently washed as recommended by the supplier. The array signals were detected by exposing the membranes to a Fuji Phosphor Plate overnight. The blotted RNA was immobilized to a Hybond-N+ nylon membrane (Amersham, Buckinghamshire, United Kingdom) by capillary transfer overnight. The blotted RNA was hybridized with [32P]dATP random labeled probes at 68°C overnight. The membranes were exposed to Kodak X-ray film overnight at −70°C. The intensities of the bands were analyzed using Bio-Rad Molecular Analyst software. Blots were stripped and rehybridized with different probes. T5 and YES1 genes were subjected to Northern blotting analysis, and the GAPDH gene was used as an internal control. The probes were reverse transcribed and amplified from 1 μg of mRNA.

Table 1 The genes with altered expression in chemoresistant cell lines compared with the sensitive parent cell lines (resistant/sensitive ratio).

<table>
<thead>
<tr>
<th>Gene W1L2-TDX</th>
<th>RKO-TDX</th>
<th>MCF-TDX</th>
<th>H630-TDX</th>
<th>H630-5FU</th>
</tr>
</thead>
<tbody>
<tr>
<td>Thymidylate synthase</td>
<td>3.61</td>
<td>3.54</td>
<td>5.80</td>
<td>1.45</td>
</tr>
<tr>
<td>YES1 proto-oncogene</td>
<td>0.41</td>
<td>0.27</td>
<td>3.23</td>
<td>1.82</td>
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<tr>
<td>T-cell protein-tyrosine phosphatase</td>
<td>0.53</td>
<td>0.19</td>
<td>3.84</td>
<td>1.21</td>
</tr>
<tr>
<td>Activator 1 40-kDa subunit</td>
<td>0.88</td>
<td>1.22</td>
<td>2.10</td>
<td>NE</td>
</tr>
<tr>
<td>CAK1 antigen</td>
<td>NE</td>
<td>0.79</td>
<td>1.53</td>
<td>0.78</td>
</tr>
<tr>
<td>RPD3 protein</td>
<td>0.56</td>
<td>0.86</td>
<td>1.38</td>
<td>NE</td>
</tr>
<tr>
<td>Checkpoint suppressor 1</td>
<td>1.10</td>
<td>0.89</td>
<td>1.24</td>
<td>1.07</td>
</tr>
<tr>
<td>α1 catenin</td>
<td>0.97</td>
<td>1.06</td>
<td>1.22</td>
<td>NE</td>
</tr>
<tr>
<td>TGF-β3</td>
<td>0.79</td>
<td>0.84</td>
<td>1.11</td>
<td>NE</td>
</tr>
<tr>
<td>Semaphorin III</td>
<td>0.88</td>
<td>0.79</td>
<td>1.09</td>
<td>NE</td>
</tr>
<tr>
<td>Ephrin type-B receptor 2 precursor</td>
<td>1.03</td>
<td>1.44</td>
<td>1.09</td>
<td>0.93</td>
</tr>
<tr>
<td>Lymphotixin β receptor precursor</td>
<td>0.61</td>
<td>0.66</td>
<td>1.08</td>
<td>NE</td>
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<tr>
<td>c-rel proto-oncogene protein</td>
<td>0.95</td>
<td>1.21</td>
<td>1.02</td>
<td>1.36</td>
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<tr>
<td>Stem cell factor precursor</td>
<td>NE</td>
<td>NE</td>
<td>0.99</td>
<td>1.08</td>
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<tr>
<td>Interleukin-4 precursor</td>
<td>NE</td>
<td>1.22</td>
<td>0.95</td>
<td>0.68</td>
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<td>Interferon-inducible protein 9–27</td>
<td>0.89</td>
<td>0.89</td>
<td>0.92</td>
<td>1.23</td>
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<tr>
<td>CD91 antigen</td>
<td>1.12</td>
<td>0.94</td>
<td>0.91</td>
<td>NE</td>
</tr>
<tr>
<td>Fibroblast growth factor receptor 1 precursor</td>
<td>1.09</td>
<td>1.21</td>
<td>0.67</td>
<td>0.88</td>
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<td>p58-rk T3 oncogene</td>
<td>NE</td>
<td>NE</td>
<td>0.63</td>
<td>1.32</td>
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<tr>
<td>Procollagen 3 α1 subunit precursor</td>
<td>1.61</td>
<td>0.73</td>
<td>0.62</td>
<td>0.97</td>
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<tr>
<td>Integrin α9</td>
<td>1.40</td>
<td>0.81</td>
<td>0.59</td>
<td>1.13</td>
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<td>β NGF</td>
<td>1.31</td>
<td>1.55</td>
<td>0.59</td>
<td>0.99</td>
</tr>
<tr>
<td>Retinoic acid receptor α1</td>
<td>NE</td>
<td>2.92</td>
<td>0.40</td>
<td>1.42</td>
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<tr>
<td>PRSM1 metallopeptidase</td>
<td>0.72</td>
<td>1.12</td>
<td>NE</td>
<td>1.18</td>
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<tr>
<td>Mitotic feedback control protein MADP2 homologue</td>
<td>0.97</td>
<td>1.14</td>
<td>0.40</td>
<td>NE</td>
</tr>
<tr>
<td>c-myc oncogene</td>
<td>1.26</td>
<td>1.20</td>
<td>0.29</td>
<td>1.32</td>
</tr>
<tr>
<td>Metalloproteinase inhibitor 3 precursor</td>
<td>1.26</td>
<td>1.28</td>
<td>NE</td>
<td>NE</td>
</tr>
<tr>
<td>DNA topoisomerase IIβ</td>
<td>0.88</td>
<td>NE</td>
<td>NE</td>
<td>0.97</td>
</tr>
</tbody>
</table>

* NE, not evaluable.
RESULTS

Array Analysis of Gene Expression in Chemoresistant Cell Lines. The expression patterns of cell lines resistant to TS inhibitors were compared with those of the wild-type cell lines (Fig. 1). A total of 28 of 1176 genes (2.4%) had altered expression in the different chemoresistant cell lines (Table 1). More genes were altered in H630F cells (22 genes) than the TDX-resistant cell lines (1–9 genes; Table 1). However, only TS and YES1 genes were consistently overexpressed, with a resistance:sensitive ratio ≥1.5 in 5 (TS) and 4 (YES1) of the chemoresistant cell lines. YES1 mRNA was not overexpressed in W12TDX cells in which TS mRNA was markedly overexpressed (Table 1). Because TS and YES1 are within 50 kb of...
each other at chromosome 18p11.32 (15), further genomic analysis was performed to dissect the involvement of the two genes in resistance.

Comparison of TS and YES1 DNA, mRNA, and Protein. To confirm the cDNA array results, the expression levels of the TS and YES1 genes were determined by Northern blot analysis (Fig. 2A). The relative expression levels of TS and YES1 were closely matched between cDNA array and Northern blotting (Fig. 3). The protein expression levels in each cell line reflected mRNA expression, with corresponding increase in TS and YES1 within four of five cell lines (Fig. 4, A and B). W1L2 did not demonstrate a significant change in YES1 protein between sensitive and resistant cells (Figs. 2B and 4B).

Gene amplification is one of the most common mechanisms of overexpression in cancer cells, and Southern analysis demonstrated that the TS and YES1 genes were amplified in all chemoresistant cell lines (Figs. 2C and 4, C and D). TS gene amplification ranged from 1.8- to 5.7-fold, whereas YES1 was amplified 3.0–5.3-fold in the resistant cells. In each chemoresistant cell line, the TS and YES1 genes were amplified at a comparable level (Fig. 5). FISH was performed using a P1 clone containing TS to confirm gene amplification at the cytogenetic level (Fig. 6). In concordance with the Southern analysis, MCF-7 TDX, RKO TDX, and W1L2 TDX show the largest degree of TS amplification by FISH (>20 copies), compared with H6305FU (>10 copies) and H630 TDX (6 copies).

The relative TS and YES1 mRNA expression levels in chemoresistant cell lines were evaluated to provide context to the findings in the resistant cells. W1L2 wild-type cells expressed much lower YES1 mRNA, compared with the other wild-type cell lines (1.9–2.8-fold lower). In contrast, TS mRNA was 1.3–2.0-fold higher in W1L2 wild-type compared with the other wild-type cell lines.

DISCUSSION

Chemoresistance is a major barrier for the successful treatment of malignant diseases with chemotherapy. The global analysis of gene expression patterns in drug-resistant cell lines may help to more fully elucidate the underlying mechanisms involved. In this study, the gene expression profiles of five TS inhibitor-resistant cell lines were compared with parent cell lines using a cDNA array. Surprisingly, only 2 of 1176 genes (0.17%) were consistently altered across the cell line panel, TS and YES1. Overexpression of TS is strongly associated with the resistance of cell lines to TS inhibitors (11, 16). cDNA array analysis showed high expression of TS mRNA in all TDX- and 5-FU-resistant cell lines (Fig. 1). Overexpression of YES1 mRNA was also observed in four of five drug-resistant cell lines. The cDNA array results were confirmed by Northern blot analysis. Western analysis
showed that TS and YES1 protein levels had the same pattern of expression as that observed for mRNA in the drug-resistant cell lines. DNA analysis found concordance between TS and YES1 gene amplification. These results are not unexpected, because the TS and YES1 genes lie 50 kb apart on chromosome 18p11.32 (15). Previous CGH studies showed an amplification of genomic material at 18p11.32 and beyond in the resistant cell lines (12), and FISH data demonstrated a large amplicon of the TS-containing region of 18p in drug-resistant cell lines (Fig. 6). Therefore, it is likely that the amplicon would contain both TS and YES1. However, the discordance between DNA-mRNA-protein for the resistant:sensitive cells is surprising. No alteration in YES1 mRNA was observed in the W1L2 TDX cell line in the context of YES1 gene amplification and TS overabundance at the DNA, mRNA, and protein level.

These findings have important implications for the interpretation of data in the postgenome era. There have been a large number of putative oncogenes and tumor suppressor genes that are the “victims” of guilt by association or, more precisely, localization. For example, over 10 different genes in chromosome 20q have been found to be amplified in a number of human solid tumors and purported to have defining roles in tumor biology (14, 17). However, CGH analysis has found the entire 20q arm to be amplified, suggesting that many amplified genes are being “taken along for the ride” rather than “driving” the malignant process (14). The data presented here support this theory. Although the TS and YES1 genes are both amplified in all of the resistant cells, only TS is strongly overexpressed at the mRNA and protein levels in all cell lines. YES1 is an oncogene with kinase activity in a number of solid tumors, including colon (18, 19). WIL2 is a lymphoblastoid cell line, whereas the others are derived from carcinomas of colon and breast, consistent with tissue-specific transcriptional control as the basis for the discordance between gene copy number and mRNA/protein in this cell line. The fact that WIL2 has high level (>10-fold) resistance to TS inhibitor in the absence of high YES1 expression leads to a conclusion that YES1 has no direct role in this drug resistance process.

The FISH analysis showed that TS amplification occurs as a highly replicated amplicon, rather than as a double minute chromosome or random integration into the genome. Therefore, strategies to reverse resistance from TS amplification will need to use direct approaches [e.g., TS ribozymes (20) rather than chemoelimination of extra chromosomal DNA (21)].

A major concern with the use of cDNA microarray analysis in cancer therapeutics is that the assessment of a large number of genes (i.e., 1176 in the Atlas array) may identify an overwhelming number of “associated” genes. This would lead to a great amount of fruitless effort to try and confirm involvement in resistance and bring confusion, rather than clarity, to the understanding of drug action. However, this study is an example of the promise of the microarray approach. Although multiple genes (n = 28) were altered in the various resistant clones, only TS and YES1 were changed consistently. By narrowing the search from 1176 to 2 genes, the analysis of in vitro TDX and 5-FU resistance becomes more straightforward for confirmatory studies. Similar approaches can now be conducted in clinical samples to establish the in vivo mechanisms of resistance to TDX, 5-FU, and other active agents. It is not known if a proportional degree of clarity would be reached with microarrays containing larger numbers of genes. These data provide encouragement that comprehensive transcript analysis will aid the quest for more enlightened therapeutics.

ACKNOWLEDGMENTS

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Fig. 6. FISH with a TS-containing P1 probe showing amplification of the TS region of 18p in resistant cells. a, MCF-7 sensitive; b, MCF-7_TDX; c, WIL2 sensitive; d, WIL2_TDX.
REFERENCES

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