Cytochrome P450 Profile of Colorectal Cancer: Identification of Markers of Prognosis

Meera Kumarakulasingham,1 Patrick H. Rooney,1,2 Sinclair R. Dundas,1 Colin Telfer,2 William T. Melvin,2 Stephanie Curran,1 and Graeme I. Murray1

Abstract

Purpose: The cytochromes P450 (P450) are a multigene family of enzymes with a central role in the oxidative metabolism of a wide range of xenobiotics, including anticancer drugs, carcinogens, and endogenous compounds. The purpose of this study was to define the P450 profile of colorectal cancer and establish the prognostic significance of expression of individual P450s in colorectal cancer.

Experimental Design: Immunohistochemistry for a panel of 23 P450s was done on a colorectal cancer tissue microarray consisting of 264 primary colorectal cancers, 91 lymph node metastasis, and 10 normal colorectal samples. The intensity of immunoreactivity in each sample was established by light microscopy.

Results: The most frequently expressed form of P450 in normal colon was CYP3A4. In primary colorectal cancer, several P450s (CYP1B1, CYP2S1, CYP2U1, CYP3A5, and CYP51) were present at a significantly higher level of intensity compared with normal colon. P450 expression was also detected in lymph node metastasis and the presence of several P450s (CYP1B1, CYP2A/2B, CYP2F1, CYP4V2, and CYP39) in the lymph node metastasis strongly correlated with their presence in corresponding primary tumors. The presence of strong CYP51 (log-rank = 12.11, P = 0.0005) or strong CYP2S1 (log-rank = 6.72, P = 0.0095) immunoreactivity were associated with poor prognosis. CYP51 was also an independent marker of prognosis (P = 0.009).

Conclusions: The expression of individual P450s has been established in colorectal cancer. Several P450s show increased expression in colorectal cancer. High expression of CYP51 or CYP2S1 were associated with poor prognosis and CYP51 is an independent marker of prognosis.

Colorectal cancer is one of the most common cancers in the Western world. The 5-year survival rate, although slowly improving, is still relatively poor at 40% (1). A significant proportion of patients present with locally advanced disease and current therapy for advanced colorectal cancer, which is based on a 5-fluorouracil regimen, results only in a modest improvement in survival (1, 2). Most large bowel cancers arise from adenomas and ~5% of these adenomatous polyps progress to malignant tumors within 5 to 10 years (3). Environmental factors and genetic susceptibility both make important contributions to the development of colorectal cancer (3, 4).

The P450s have a major role in tumor development via their metabolism of many carcinogens (9). Compounds implicated in the etiology of colon cancer include polycyclic aromatic hydrocarbons and more especially heterocyclic amines, many of which require metabolic activation by P450s before exerting their genotoxic effect (10). Specific P450s have also been shown to be expressed in tumors; in particular, CYP1B1 is overexpressed in a range of tumors (7, 11, 12). Because the P450s are involved in the oxidative metabolism (activation and deactivation) of many anticancer drugs, they are capable of influencing the response of tumors to anticancer therapy (12, 13). The outcome in terms of activation (i.e., cytotoxicity) or deactivation (i.e., resistance) is determinant upon the relative amount and activity of specific P450s in individual tumor cells (7). Several therapeutic strategies are now being developed to exploit the presence, overexpression, and activity of P450s in tumors (14, 15). These approaches include P450 vaccines (16), P450-mediated prodrug activation (12, 17–19), and P450 inhibitors (20). The presence of CYP1B1 in tumors is currently being exploited as a tumor antigen. A phase 1 trial of a CYP1B1...
DNA vaccine has been successfully completed (16) and a phase 2 trial of this vaccine will begin patient recruitment shortly. A number of prodrugs designed to be selectively activated by P450 enzymes are also currently being evaluated (12, 14, 17, 19). The bioreductive prodrug AQ4N, a topoisomerase inhibitor, is activated to the cytotoxic amine AQ4 by cytochrome P450–mediated bioreduction selectively under the hypoxic conditions found in tumor tissue. CYP3A4, CYP1A1, and CYP1B1 all contribute to bioreduction of AQ4N (17, 18). Several inhibitors of individual P450s are also

<table>
<thead>
<tr>
<th>P450 antibody</th>
<th>Source</th>
<th>Type</th>
<th>Immunogen</th>
<th>Antigen retrieval* and antibody dilution for immunohistochemistry</th>
</tr>
</thead>
<tbody>
<tr>
<td>CYP1A1</td>
<td>Chemicon</td>
<td>Polyclonal</td>
<td>Peptide, amino acid sequence not stated in datasheet</td>
<td>20 min, 1/1,000</td>
</tr>
<tr>
<td>CYP1B1</td>
<td>Own laboratory</td>
<td>Monoclonal</td>
<td>Peptide, PENFDHARFSLDKDGL (amino acids 437-451)</td>
<td>20 min, undiluted tissue culture supernatant</td>
</tr>
<tr>
<td>CYP2A6/2B6</td>
<td>Own laboratory</td>
<td>Monoclonal</td>
<td>C terminal peptide, RNYTMSFLPR (CYP2A6 sequence)</td>
<td>20 min, undiluted tissue culture supernatant</td>
</tr>
<tr>
<td>CYP2C8/9/19</td>
<td>Chemicon</td>
<td>Polyclonal</td>
<td>Peptide, amino acid sequence not stated in datasheet</td>
<td>No antigen retrieval, 1/500</td>
</tr>
<tr>
<td>CYP2D6</td>
<td>BD Bioscience</td>
<td>Monoclonal</td>
<td>Expressed human CYP2D6</td>
<td>No antigen retrieval, 1/20</td>
</tr>
<tr>
<td>CYP2E1</td>
<td>Oxford Biomedical Research</td>
<td>Polyclonal</td>
<td>Expressed human CYP2E1</td>
<td>20 min, 1/2,000</td>
</tr>
<tr>
<td>CYP2F1</td>
<td>Own laboratory</td>
<td>Polyclonal</td>
<td>COOH-terminal peptide, RPFQLCLRPR</td>
<td>20 min, 1/1,000</td>
</tr>
<tr>
<td>CYP2J2</td>
<td>Own laboratory</td>
<td>Polyclonal</td>
<td>COOH-terminal peptide, SHRLCAVPOV</td>
<td>20 min, 1/200</td>
</tr>
<tr>
<td>CYP2R1</td>
<td>Own laboratory</td>
<td>Polyclonal</td>
<td>COOH-terminal peptide, OPYLICAERR</td>
<td>20 min, 1/1,000</td>
</tr>
<tr>
<td>CYP2S1</td>
<td>Own laboratory</td>
<td>Polyclonal</td>
<td>COOH-terminal peptide, TDLHSTTTQTR</td>
<td>20 min, 1/1,000</td>
</tr>
<tr>
<td>CYP2U1</td>
<td>Own laboratory</td>
<td>Polyclonal</td>
<td>COOH-terminal peptide, HPFNITISRR</td>
<td>20 min, 1/1,000</td>
</tr>
<tr>
<td>CYP3A4</td>
<td>Own laboratory</td>
<td>Monoclonal</td>
<td>Purified human CYP3A4</td>
<td>20 min, undiluted tissue culture supernatant</td>
</tr>
<tr>
<td>CYP3A5</td>
<td>Own laboratory</td>
<td>Monoclonal</td>
<td>COOH-terminal peptide, DSRDGTLSGE</td>
<td>20 min, undiluted tissue culture supernatant</td>
</tr>
<tr>
<td>CYP3A7</td>
<td>Own laboratory</td>
<td>Monoclonal</td>
<td>COOH-terminal peptide, ESRDETVSQA</td>
<td>20 min, undiluted tissue culture supernatant</td>
</tr>
<tr>
<td>CYP3A43</td>
<td>Own laboratory</td>
<td>Polyclonal</td>
<td>COOH-terminal peptide, HLRDGITSGP</td>
<td>20 min, 1/1,000</td>
</tr>
<tr>
<td>CYP4F11</td>
<td>Own laboratory</td>
<td>Monoclonal</td>
<td>COOH-terminal peptide, RVEPLGANSQ</td>
<td>20 min, 1/10</td>
</tr>
<tr>
<td>CYP4V2</td>
<td>Own laboratory</td>
<td>Polyclonal</td>
<td>COOH-terminal peptide, KLKRRNADER</td>
<td>20 min, 1/1,000</td>
</tr>
<tr>
<td>CYP4X1</td>
<td>Own laboratory</td>
<td>Polyclonal</td>
<td>COOH-terminal peptide, NGMYHLKKL</td>
<td>20 min, 1/1,000</td>
</tr>
<tr>
<td>CYP4Z1</td>
<td>Own laboratory</td>
<td>Polyclonal</td>
<td>COOH-terminal peptide, NGIHVIHAKKL</td>
<td>20 min, 1/1,000</td>
</tr>
<tr>
<td>CYP24</td>
<td>Own laboratory</td>
<td>Polyclonal</td>
<td>COOH-terminal peptide, RELPACOFQR</td>
<td>20 min, 1/1,000</td>
</tr>
<tr>
<td>CYP26A1</td>
<td>Own laboratory</td>
<td>Monoclonal</td>
<td>COOH-terminal peptide, PARFTHFHE</td>
<td>20 min, 1/10</td>
</tr>
<tr>
<td>CYP39</td>
<td>Own laboratory</td>
<td>Polyclonal</td>
<td>COOH-terminal peptide, QCRWEYKORI</td>
<td>20 min, 1/1,000</td>
</tr>
<tr>
<td>CYP51</td>
<td>Own laboratory</td>
<td>Polyclonal</td>
<td>COOH-terminal peptide, CPVIRYKRRSK</td>
<td>20 min, 1/1,000</td>
</tr>
</tbody>
</table>

*The antigen retrieval step consisted of microwaving the sections in 0.01 mol/L citrate buffer (pH 6.0) for 20 minutes in an 800 W microwave oven operated at full power.
currently in development (20) and AVI-4557, an antisense construct specifically targeted against CYP3A4, has recently completed a phase 1 study (21). Gene-directed prodrug therapy is also being used to deliver exogenous P450s (21, 22). The presence of other P450s that may interact with prodrug activation would, therefore, have important clinical implications.

In this study, we have conducted a comprehensive analysis of the expression of P450s in colorectal cancer and defined the expression profile of P450s in primary colorectal cancer, metastatic colorectal cancer, and normal colon. We have identified P450s that are overexpressed in colorectal cancer and those associated with poor prognosis.

Materials and Methods

Antibodies. A panel (n = 23) of P450 antibodies was used in this study. The development of monoclonal antibodies to CYP1B1 (23) and CYP3A4 (24) has been described previously. Polyclonal antibodies to the following P450s—CYP2J2, CYP2R1, CYP2S1, CYP2U1, CYP3A4, CYP4V2, CYP4X1, CYP24, CYP39, and CYP51—were produced by immunizing rabbits with the relevant COOH-terminal peptide (Table 1) conjugated to ovalbumin. The use of COOH-terminal peptides as immunogens has been previously used to successfully develop antibodies to individual P450 forms (25). Animals received two booster immunizations at 4- to 6-week intervals after the initial immunization. Animals were bled 7 to 10 days after the last injection and serum obtained by centrifugation of the clotted blood. Monoclonal antibodies to CYP2A6, CYP3A5, CYP3A7, CYP4F11, and CYP26A1 were produced as previously described (23, 24). In each case, the appropriate COOH-terminal peptide conjugated to ovalbumin was the immunogen. Briefly, mice were immunized with the relevant peptide conjugate and received booster immunizations. Spleens from mice that showed the highest antibody titers as assessed by ELISA using the peptide immunogen were fused with myeloma cells. After cloning of the hybridomas, antibody titers were again assessed by ELISA.

The specificity of the antibodies was confirmed by immunoblotting (23) against microsomes prepared from appropriate human tissues (Fig. 1). Some antibodies were also immunoblotted against the relevant expressed P450. Expressed human P450s (CYP1A1, CYP1A2, CYP1B1, CYP2A6, CYP2B6, CYP2C8, CYP2D6, CYP2E1, CYP3A4, CYP3A5, CYP3A7, and CYP4A11) were purchased from BD Biosciences (Bedford, MA). The CYP2A antibody recognized both CYP2A6 and CYP2B6, reflecting the very close sequence similarity of these two P450s and in particular the almost identical COOH-terminal amino acid sequences of these P450s. Therefore, this antibody has been designated CYP2A/CYP2B. All the antibodies described above are available from Auvation, Ltd. (Aberdeen, United Kingdom).

Polyclonal antibodies to CYP1A1 and CYP2C were purchased from Chemicon Europe (Chandlers Ford, United Kingdom), whereas a monoclonal antibody to CYP2D6 was bought from BD Biosciences (Oxford, United Kingdom) and a polyclonal antibody to CYP2E1 was obtained from Oxford Biomedical Research (Oxford, MI).

Tumor samples. This project had the permission of the Grampian Research Ethics Committee. There were 264 patients in the study (26) and the cases were selected from the Aberdeen colorectal tumor bank. All the patients had a diagnosis of primary colorectal cancer.
and had undergone elective surgery for colorectal cancer in Aberdeen between 1994 and 2003. The tumor samples had been submitted to the Department of Pathology, University of Aberdeen, for diagnosis. The tumor excision specimens were fixed in formalin, representative blocks were embedded in wax, and sections were stained with H&E. The clinicopathologic characteristics [age, gender, site of primary tumor, degree of primary tumor differentiation, microsatellite instability (MSI) status, and Dukes stage] of the patients included in this study are detailed in Table 2. Complete follow-up was available for all patients and ranged from 1 to 105 months. There were 71 deaths (26.9%) in the patient group with a median survival of >105 months. Fifty-four (58%) of Dukes C patients had received adjuvant chemotherapy, all with a 5-fluorouracil – based regimen.

Tissue microarray. An eight-block tissue microarray was constructed as described (26). The tissue microarray contained 264 primary colorectal cancer (Dukes A = 67, Dukes B = 104, and Dukes C = 93), 91 lymph node metastasis, and 10 normal morphologically colonic mucosal samples. The lymph node metastasis were from the corresponding Dukes C cases (adequate nodal metastatic tissue to sample was not available in two cases). The arrayed tumors reflected the distribution of the anatomic locations and Dukes stage of colorectal cancer in this population. A single normal colon sample was obtained from each of 10 of the colorectal cancer resection specimens (proximal = 2, distal = 3, and rectum = 5) and each sample was acquired from at least 10 cm distant from the tumor as previously described (27). One representative 1.6 mm core of tissue was taken from each donor block using a steel Menghini needle and arrayed into the recipient wax block. One section from each microarray was stained with H&E to confirm the histopathologic diagnosis and the adequacy of sampling.

Immunohistochemistry. Immunohistochemistry for each antibody was carried out using a Dako autostainer (DakoCytomation, Ely, United Kingdom). Sections (5 μm) of the tissue microarray were dewaxed, rehydrated, and an antigen retrieval step was done when required. The antigen retrieval step consisted of microwaving the sections in 0.01 mol/L citrate buffer at pH 6.0 for 20 minutes in an 800 W microwave oven operated at full power. The sections were then allowed to cool to room temperature. Primary antibody appropriately diluted (Table 1) in antibody diluent (DakoCytomation) was applied for 60 minutes at room temperature, washed with buffer (DakoCytomation), followed by peroxidase blocking for 5 minutes (DakoCytomation), and followed by a single 2-minute buffer wash. Prediluted peroxidase-polymer–labeled goat anti-mouse/rabbit secondary antibody (Envision, DakoCytomation) was applied for 30 minutes at room temperature, followed by further washing with buffer to remove unbound antibody. Sites of peroxidase activity were then shown with diaminobenzidine as the chromogen applied.
for three successive 5-minute periods. Finally, sections were washed in water, lightly counterstained with hematoxylin, dehydrated, and mounted. Tissues known to express the relevant P450 were used as positive controls. Omitting the primary antibody from the immunohistochemical procedure and replacing it with antibody diluent or nonimmune rabbit serum acted as negative controls. For the newly developed P450 antibodies, preincubating each antibody with their corresponding unconjugated peptide immunogen before performing immunohistochemistry with positive control tissues acted as a further control and resulted in a loss of immunohistochemical staining.

The sections were evaluated by light microscopic examination and the intensity of immunostaining in each section was assessed independently by two observers (M.K and G.M) using the scoring system described. There were very few discrepancies (<5% of cases) and these were resolved by simultaneous reevaluation. The intensity of immunostaining in each core was scored as negative = 0, weak = 1, moderate = 2, or strong = 3 (26).

The MSI status of the tumors was determined by immunohistochemistry as previously described (28). Sections were immunostained with monoclonal antibodies to hMLH1 (clone G168-728, BD Biosciences, Oxford, United Kingdom) used at a dilution of 1 in 50 and hMSH2 (clone Fe11, Oncogene, Merck Biosciences, Nottingham, United Kingdom) also used at a dilution of 1 in 50. Immunohistochemistry, including an antigen retrieval step for each antibody, was done as described above. Loss of expression when none of the tumor nuclei stained with either hMLH1 or hMSH2 was regarded as MSI-high (MSI defective), whereas staining of tumor nuclei for either hMLH1 or hMSH2 was considered as microsatellite stable (MSI low; ref. 28).

**Results**

**P450s in normal colon.** All the P450s with the exception of CYP2F1, CYP3A7, and CYP4Z1 showed immunoreactivity in normal colon (Figs. 2 and 3). Most of the P450s displayed low frequency and weak immunoreactivity in normal colon. Several P450s, CYP2S1, CYP2U1, CYP3A4, and CYP51, showed immunoreactivity in >50% of cores. Only CYP3A4 immunoreactivity was detected in all cores and this P450 also showed the highest intensity of immunoreactivity in normal colon. All P450s that showed positive immunohistochemical staining displayed cytoplasmic immunoreactivity in colonic epithelium with stronger staining in surface epithelial cells compared with crypt epithelial cells. CYP2S1 also displayed cytoplasmic staining of chronic inflammatory cells (lymphocytes, plasma cells, and macrophages) present in the lamina propria. There was no relationship between the expression of individual P450s and the anatomic site within the colon.

**P450s in colorectal cancer.** All P450s showed some immunoreactivity in colorectal cancer (Figs. 2 and 3). There was significantly greater intensity of immunohistochemical staining for CYP1B1 \( (P = 0.05) \), CYP2S1 \( (P = 0.02) \), CYP2U1 \( (P = 0.003) \), CYP3A5 \( (P = 0.02) \), and CYP51 \( (P = 0.0001) \) in colorectal cancer compared with normal colon. The highest percentage of strong immunoreactivity was observed for CYP2S1 with 48.9% of the tumors showing strong immunohistochemical staining. Whereas for CYP1A1, CYP2F1, CYP2R1, CYP4F11, CYP4V2, and CYP4Z1, >80% of the cores were negative for the respective P450.

All P450s that showed immunohistochemical staining displayed diffuse cytoplasmic immunoreactivity in tumor cells (Fig. 3). CYP2S1 also displayed staining of chronic inflammatory cells present in the surrounding tumor stroma. Comparison of the presence of individual P450s and Dukes
stage showed that there were significant correlations for CYP2S1 ($\chi^2 = 19.2, P = 0.004$), CYP2U1 ($\chi^2 = 14.8, P = 0.02$), CYP3A4 ($\chi^2 = 24.7, P = 0.001$), CYP3A5 ($\chi^2 = 20.7, P = 0.002$), CYP3A43 ($\chi^2 = 17.8, P = 0.007$), CYP4X1 ($\chi^2 = 37.1, P = 0.001$), and CYP51 ($\chi^2 = 40.1, P = 0.001$). Other P450s did not show any correlation between their expression and tumor stage.

**P450s in lymph node metastasis.** All the P450s showed some degree of immunoreactivity in lymph node metastasis (Figs. 2 and 3). The highest frequency of strong immunoreactivity was observed for CYP2S1 and CYP3A4. All P450s that showed immunohistochemical staining in lymph nodes displayed diffuse cytoplasmic immunoreactivity in tumor cells (Fig. 1).

Comparison of the Dukes C carcinomas and their corresponding metastases showed that there were significant correlations for CYP1B1 ($\chi^2 = 27.3, P = 0.001$), CYP2A/2B ($\chi^2 = 29.0, P = 0.001$), CYP2C ($\chi^2 = 18.1, P = 0.006$), CYP2F1 ($\chi^2 = 11.1, P = 0.001$), CYP4V2 ($\chi^2 = 10.7, P = 0.005$), and CYP39 ($\chi^2 = 8.2, P = 0.042$) between the presence of each of these P450s in the primary tumor compared with their expression in the secondary tumors. Other P450s did not show any correlation between their expression in the primary tumor and the lymph node metastases.

**P450 expression and survival in colorectal cancer.** There was a significant survival difference for patients whose tumors showed strong CYP51 immunoreactivity compared with those patients whose tumors showed negative, weak, or moderate CYP51 immunoreactivity (log-rank = 12.11, $P = 0.0005$; Fig. 4A). The median survival in the poor survival group was 61 months, whereas the median survival in the good survival group was >105 months. Similarly, there was a significant survival difference for patients whose tumors showed strong CYP2S1 immunoreactivity compared with those patients whose tumors showed negative, weak, or moderate CYP2S1 immunoreactivity (log-rank = 6.72, $P = 0.0095$; Fig. 4B). The median survival in the poor survival group was 81 months, whereas in the good survival group it was >105 months. The other significant survival factors by univariate analysis were Dukes stage (log-rank = 15.9, $P = 0.003$), tumor site (log-rank = 7.9, $P = 0.02$), and age (log-rank = 5.4, $P = 0.02$).

CYP51 (hazard ratio, 0.46; 95% confidence interval, 0.26-0.82; $P = 0.009$) remained independently prognostically significant after multivariate analysis with the prognostic model including Dukes stage (hazard ratio, 0.52; 95% confidence interval, 0.27-0.99; $P = 0.05$), age (hazard ratio, 1.60; 95% confidence interval, 0.92-2.76; $P = 0.1$), and tumor site (hazard ratio, 1.63; 95% confidence interval, 0.85-3.12; $P = 0.14$). CYP2S1 was not independently significant (hazard ratio, 1.5; 95% confidence interval, 0.88-2.57; $P = 0.14$).

**Discussion**

In this study, we have analyzed, by immunohistochemistry, P450 expression in colorectal cancer, corresponding lymph node metastasis, and normal colon. We have also defined the expression profile for individual P450s and established the prognostic significance of individual P450 expression in colorectal cancer.

CYP3A4 was the main form (most frequently expressed and at the highest intensity) of P450 present in normal colon and this finding is consistent with previous studies (29, 30). CYP2S1 was one of the other P450s that also showed frequent high-intensity expression in normal colon. This P450 has only recently been cloned and although assigned to the CYP2 family on the basis of nucleic acid and amino acid sequence homology, it is dioxin inducible (31, 32). All other dioxin-inducible P450s are members of the CYP1 family and this suggests that CYP2S1 may have similar functional characteristics and metabolic substrates as CYP1 P450s (31, 32). The immunohistochemical localization of CYP2S1 protein in normal colon is a novel finding although a high level of CYP2S1 mRNA has previously been identified by real-time quantitative PCR in this tissue (33). CYP2S1 was localized to both epithelial cells and chronic inflammatory cells present in the lamina propria. This finding contrasts with other P450s that were only localized to epithelial cells of normal colon.

It is becoming increasingly recognized that individual forms of P450, most notably CYP1B1 (11), are overexpressed in specific types of cancer and that the P450s are emerging as important cancer therapeutic targets (12, 14), both as a
consequence of their overexpression and because of the distinct microenvironment in which tumors exists. Hypoxia is one of the main features of the tumor microenvironment that is currently being exploited by P450-targeted therapy. AQ4N is a CYP3A-activated prodrug that, in hypoxic conditions, is activated to a highly potent topoisomerase inhibitor and is currently being evaluated in clinical trials (17).

It is, therefore, important to define the expression profile of P450 in colorectal cancer and identify which P450s are overexpressed and also establish their prognostic significance. Previous studies of P450 expression and activity in colon cancer have studied only a limited number of P450s (30, 34–36). CYP3A immunoreactivity (30) and CYP3A-associated activity (34) have both been detected in colon cancer. In this study, we found that a range of P450s were present in colorectal cancer and several P450s showed more frequent and greater intensity of expression compared with normal colon. Importantly, we confirmed that CYP1B1 was overexpressed in colorectal cancer, consistent with both our previous study that used a polyclonal antibody to CYP1B1 (11) and the findings of others (37). We also found that CYP2S1, CYP2U1, CYP3A5, and CYP51 were significantly overexpressed. In particular, we identified several P450s that have not previously been identified in colon cancer, most notably CYP51 and CYP2S1. Not only are these distinct P450s overexpressed but the patients with strongly expressing tumors showed poorer prognosis compared with patients whose tumors showed less or no immunoreactivity and CYP51 expression is independently prognostically significant.

Biologically, CYP51 is involved in the synthesis of sterols (38, 39) that are incorporated into membranes. Greater activity of this P450 may allow tumor cells to retain a greater degree of membrane integrity and/or membrane fluidity, thus promoting tumor cell survival and motility and hence invasive capacity (40, 41). Clinically, this would be ultimately reflected in poorer patient survival.

We also found that CYP2S1 was overexpressed in tumors and that high expression of CYP2S1 was associated with poor prognosis. There have been no previous studies of this P450 in tumors. CYP2U1 was also overexpressed in primary colorectal cancer. This novel P450, which has only recently been identified, catalyses the ω and ω – 1 hydroxylation of fatty acids, suggesting a role for this P450 in intracellular signaling pathways (42, 43). There have been no previous studies of this P450 in tumors.

The expression pattern of P450s in lymph node metastasis have not previously been studied in colorectal cancer. This is important because it cannot necessarily be assumed that the pattern of expression in the primary tumors will be reflected in the lymph node metastasis. Because most chemotherapeutics is targeted at metastatic tumors, it is important to have knowledge of the expression profile of P450s in the lymph node metastasis and how this relates to the expression pattern in the corresponding primary tumors. In this study, we found a correlation between the expression of a subset of P450s including CYP1B1, CYP2A/2B, CYP2C, CYP2F1, CYP4V2, and CYP39 in the primary tumors and the corresponding lymph node metastases. We have previously shown that CYP1B1 expression in primary and secondary ovarian carcinoma correlate (44). However, for most P450s, there was no relationship between their presence in primary tumor compared with their immunoreactivity in the secondary tumors, suggesting that the tumor microenvironment is an important factor in influencing the expression of many individual P450s. Several P450s have recently been identified in hepatic metastases of colorectal cancer by one-dimensional gel electrophoresis and mass spectrometry (45). However, in that study, only six metastases were investigated and comparative data for the corresponding primary colorectal cancers was not available. We believe that to maximize therapeutic efficiency, it will be necessary to directly phenotype lymph node metastasis for many individual P450s because expression cannot be inferred from the corresponding primary tumor.

In conclusion, we have defined the P450 profile of colorectal cancer, lymph node metastasis, and normal colon. We have identified overexpression of several P450s in colorectal cancer, most notably CYP51 and CYP2S1. Both of these enzymes show prognostic significance and CYP51 is an independent marker of prognosis in colorectal cancer.

Acknowledgments

We thank Joan Aitken and Nicky Fyfe for technical assistance.

References

13. Kivisto KT, Kroemer HK, Eichelbaum M. The role of human cytochrome P450 enzymes in the metabolism of anticancer agents: implications for drug interac-


Clinical Cancer Research

Cytochrome P450 Profile of Colorectal Cancer: Identification of Markers of Prognosis


Updated version  Access the most recent version of this article at:
http://clincancerres.aacrjournals.org/content/11/10/3758

Cited articles  This article cites 44 articles, 9 of which you can access for free at:
http://clincancerres.aacrjournals.org/content/11/10/3758.full#ref-list-1

Citing articles  This article has been cited by 17 HighWire-hosted articles. Access the articles at:
http://clincancerres.aacrjournals.org/content/11/10/3758.full#related-urls

E-mail alerts  Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions  To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions  To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.