IMPORTANCE OF UDP-GLUCURONOSYLTRANSFERASE 1A10 (UGT1A10) IN THE DETOXIFICATION OF POLYCYCLIC AROMATIC HYDROCARBONS: DECREASED GLUCURONIDATIVE ACTIVITY OF THE UGT1A10^{139LYS} ISOFORM

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ABSTRACT:

UDP-glucuronosyltransferase 1A10 (UGT1A10) is an extrahepatic enzyme expressed in aerodigestive tract tissues that exhibits significant glucuronidation activity against the important procarcinogenic benzo(a)pyrene (BaP) metabolite, BaP-trans-7,8-dihydrodiol (BPD), and the UGT1A10 codon 139 (Glu>Lys) polymorphism was previously implicated in risk for orolaryngeal cancer by Elahi et al. in their 2003 study. To better assess the potential role of UGT1A10 in risk for tobacco-related cancers, the glucuronidation activity of UGT1A10 was compared with that of other known UGT enzymes against selected polycyclic aromatic hydrocarbons, and the effects of the codon 139 polymorphism on UGT1A10 function were examined in vitro. UGT1A10 exhibited considerably more glucuronidation activity as determined by \( V_{\text{max}}/K_{\text{m}} \) against 3-hydroxy (OH)-BaP, 7-OH-BaP, 9-OH-BaP, and 1-OH-pyrene than any other UGT1A family member. Although a kinetic comparison using \( V_{\text{max}} \) could not be performed against family 2B UGTs, UGT1A10 exhibited a 1.7- to 254-fold lower \( K_{\text{m}} \) than active family 2B UGTs against 3-OH-BaP, 7-OH-BaP, and 1-OH-pyrene. A significantly (\( p < 0.01 \)) higher \( V_{\text{max}}/K_{\text{m}} \) was observed for homogenates from wild-type UGT1A10^{139Glu}-overexpressing cells against all four BaP metabolites tested (3-OH-BaP, 7-OH-BaP, 9-OH-BaP, and BPD). A similarly significant (\( p < 0.05 \)) increase in \( V_{\text{max}}/K_{\text{m}} \) was observed for homogenates from wild-type UGT1A10^{139Glu}-overexpressing cells against 1-OH-pyrene. Significant differences in \( K_{\text{m}} \) were observed for homogenates from wild-type UGT1A10^{139Glu}-overexpressing cells against 1-OH-pyrene (\( p < 0.05 \)) and 3-OH-BaP (\( p < 0.01 \)). Reverse transcription-polymerase chain reaction of total lung RNA showed low levels of UGT1A10 expression in human lung tissue. Together, these studies implicate UGT1A10 as an important detoxifier of polycyclic aromatic hydrocarbons in humans and that the UGT1A10 codon 139 polymorphism may be an important determinant in risk for tobacco-related cancers.

The UDP-glucuronosyltransferase (UGT) superfamily of enzymes catalyzes the glucuronidation of a variety of endogenous compounds such as bilirubin and steroid hormones, as well as xenobiotics such as drugs and environmental carcinogens (Tephly and Burchell, 1990; Owens and Ritter, 1995; Gueraud and Paris, 1998; Ren et al., 2000). Based on structural and sequence homology, UGTS are classified into several families and subfamilies (Jin et al., 1993). UGT family 2B members are derived from independent genes, whereas the entire several families and subfamilies (Jin et al., 1993). UGT family 2B UGTs are expressed in the liver (Ciotti et al., 1997; Levesque et al., 1997; Beaulieu et al., 1997). Several family 1A UGTs have been implicated in the detoxification of tobacco carcinogen metabolites including the tobacco-specific nitrosamine, NNK (Ren et al., 2000; Wiener et al., 2004b), and polycyclic aromatic hydrocarbons (PAHs) like benzo(a)pyrene (BaP) (Ciotti et al., 1997; Levesque et al., 1997; Beaulieu et al., 1998; Bélanger et al., 1998; Carrier et al., 2000). Although most family 1A UGTs are expressed in the lung (Ciotii et al., 1997; Burchell and Hume, 1999; Levesque et al., 1999; Guillemette et al., 2000), several UGTs are extrahepatic (Tukey and Strassburg, 2000) and are expressed in several target tissues for tobacco-induced cancers, including tissues in the aerodigestive tract (Zheng et al., 2002).

Polymorphisms have been previously identified for many of the UGT genes, and several recent studies have examined their potential role in tobacco carcinogenesis and in risk for tobacco-induced cancers. In studies examining UGT family 1A variants, the “TATA” box polymorphism in the promoter region of UGT1A1, commonly associated with Gilbert’s syndrome, is associated with reduced function in the UGT1A1 transcriptional promoter (Burchell and Hume, 1999) and is associated with decreased formation of the glucuronide conjugate of regions to a shared carboxy terminus encoded by exons 2 through 5 (Beaulieu et al., 1997). Several family 1A UGTs have been implicated in the detoxification of tobacco carcinogen metabolites including the tobacco-specific nitrosamine, NNK (Ren et al., 2000; Wiener et al., 2004b), and polycyclic aromatic hydrocarbons (PAHs) like benzo(a)pyrene (BaP) (Ciotti et al., 1997; Levesque et al., 1997; Beaulieu et al., 1998; Bélanger et al., 1998; Carrier et al., 2000). Although most family 1A UGTs are expressed in the lung (Ciotii et al., 1997; Burchell and Hume, 1999; Levesque et al., 1999; Guillemette et al., 2000), several UGTs are extrahepatic (Tukey and Strassburg, 2000) and are expressed in several target tissues for tobacco-induced cancers, including tissues in the aerodigestive tract (Zheng et al., 2002).

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the important procarcinogenic BaP metabolite, BaP-trans-7,8-dihydrodiol (BPD), in liver microsomes (Fang and Lazarus, 2004). UGT1A7-specific genetic variants are associated with reduced UGT1A7 metabolic function against BaP phenols (Guillemette et al., 2000) and are strongly linked to increased risk for orolaryngeal cancer (Zheng et al., 2001), pancreatic (Ockenga et al., 2003), and lung (Araki et al., 2005) cancer. Recent studies have shown an association between liver microsomal O-glucuronide conjugate formation activity against NNAL, the major metabolite of NNK, and a Pro>Thr polymorphism at codon 24 of the UGT1A4 gene (Wiener et al., 2004a). Among the family of 2B polymorphic variants, recent studies have shown an association between both the UGT2B7 codon 268 polymorphism and the UGT2B17 gene deletion polymorphism and the O-glucuronidation of NNAL in liver microsomes (Wiener et al., 2004a; Lazarus et al., 2005).

UGT1A10 is an extrahepatic enzyme expressed in aerodigestive tract tissues (Zheng et al., 2002) that exhibits significant glucuronidation activity against BPD (Fang et al., 2002). Previous studies have shown that polymorphism in codon 139 of the UGT1A10 gene, resulting in a nonconservative Glu>lys amino acid change, was linked to altered risk for orolaryngeal cancer (Elahi et al., 2003). No such association was observed for the UGT1A10 codon 244 polymorphism, which results in a conservative amino acid change of Leu>Ile. To better assess the potential role of UGT1A10 in risk for tobacco-related cancers, the glucuronidation activity of UGT1A10 was compared with that of other known UGT enzymes against selected PAHs, UGT1A10 expression was examined in lung tissue, and the effects of the codon 139 polymorphism on UGT1A10 function were examined in vitro. Results are presented showing that UGT1A10 appears to be the most highly active UGT against a number of tobacco carcinogen metabolites, that UGT1A10 is expressed in lung, and that the UGT1A10/139Glu-encoding variant exhibits reduced enzyme activity against all the substrates tested compared with the wild-type UGT1A10/139Glu-encoded isofrom in vitro.

Materials and Methods

Chemicals and Materials. 3-Hydroxy (OH)-BaP, 7-OH-BaP, 9-OH-BaP, and BPD were obtained from the National Cancer Institute Chemical Carcinogen Repository (Midwest Research Institute, Kansas City, MO). UDP-glucuronic acid (UDPGA), N2-N-sulfophosphatidyl choline palmital C16:0, 1-hydroxypyrene (1-OH-pyrene), 1-naphthol, 4-nitrophenol, and 4-methylumbelliferone were purchased from Sigma (St. Louis, MO). [14C]-UDPGA (specific activity: 300 μCi/mmol) was obtained from Amersham (Arlington Heights, IL). Dulbecco’s modified Eagle’s medium was obtained from Mediatech (Herndon, VA), and fetal bovine serum was purchased from BD Gentest (Woburn, MA), and the anti-β-actin monoclonal enhancer solution (Invitrogen), 100 to 500 μg of template DNA minipreps were screened for the codon 139 variant by digestion with the UGT1A10 sequence was confirmed by dideoxy sequencing. The pcDNA3.1/V5-His-TOPO mammalian expression vector was used as a control vector in experiments with the three different cell lines.

Reverse transcription (RT)-PCR from normal human lung tissue was performed as described above except that total RNA from histologically normal human lung tissue specimens, obtained from the Tissue Procurement Facility at the H. Lee Moffitt Cancer Center (Tampa, FL), was used as a template. The primers used to amplify exon 1 of UGT1A10 were described previously (Zheng et al., 2002). All the protocols involving the analysis of tissue specimens were approved by the Institutional Review Board at Penn State College of Medicine and in accordance with assurances filed with and approved by the U.S. Department of Health and Human Services.

Site-Directed Mutagenesis, Generation of Cell Lines, and Cell Homogenate Preparation. The UGT1A10/139Gluc variant was generated by PCR amplification of the pcDNA3.1/V5-His-TOPO vector containing the wild-type UGT1A10 sequence using site-directed mutagenesis primers specific for the polymorphic site. The primers used to generate this variant were UGT1A10-m139F (5’-CTTTCTTCTCTTAAGACCA-3’), corresponding to nucleotides +556 to +578 relative to the UGT1A10 translation start site in the UGT1A10 cDNA sequence, and UGT1A10-m139R (5’-CCGAGAACACTGCCAAACTA AA-GACCTTCTCTAAGTCTAC-3’), corresponding to nucleotides +25 to +43 with respect to the UGT1A10 translation stop codon) primers, and 2.5 units of Pfu DNA polymerase. Incubations were performed in a GeneAmp 9700 thermocycler (Applied Biosystems, Foster City, CA) as follows: 1 cycle of 94°C for 2 min, 41 cycles of 94°C for 30 s, 55°C for 30 s, and 72°C for 2 min, followed by a final cycle of 7 min at 72°C. The PCR product was purified after electrophoresis in 1.5% agarose using the QIAEX II gel extraction kit (QIAGEN, Valencia, CA) and subsequently subcloned into the pcDNA3.1/V5-His-TOPO mammalian expression vector using standard methodologies. Confirmation of insert orientation was performed by restriction enzyme digestion, and the UGT1A10 sequence was confirmed by dideoxy sequencing of the entire PCR-amplified UGT1A10 cDNA product (performed at the Molecular Biology Core Facility at Penn State University College of Medicine) using two vector primers (T7 and BGH; Integrated DNA Technologies, Coralville, IA) and one internal sense primer (UGT1A10S2, 5’-CCCTTCTTCTATGGCCTACGAA3’, corresponding to nucleotides +556 to +578 relative to the UGT1A10 translation start site in the UGT1A10 cDNA sequence) by comparison with the UGT1A10 cDNA sequence described in GenBank accession no. BC020971.

Reverse transcription (RT)-PCR was performed using total RNA from the Tissue Procurement Facility at the H. Lee Moffitt Cancer Center (Tampa, FL), was used as a template. The primers used to amplify exon 1 of UGT1A10 were described previously (Zheng et al., 2002). All the protocols involving the analysis of tissue specimen were approved by the Institutional Review Board at Penn State College of Medicine and in accordance with assurances filed with and approved by the U.S. Department of Health and Human Services.
cells were passaged and subsequently grown in genecin (700 μg/ml medium) for the selection of genecin-resistant cells, with selection medium changed every 3 to 4 days. Cell homogenates were prepared by resuspending pelleted cells in Tris-buffered saline (25 mM Tris base, 138 mM NaCl, 2.7 mM KCl, pH 7.4) and subjecting them to three rounds of freeze-thaw before gentle homogenation. Cell homogenates (5–30 mg/ml homogenate protein) were stored at 70°C in 100–μl aliquots. Total cell homogenate protein concentrations were determined using the BCA assay from Pierce Biotechnology (Rockford, IL) after protein extraction using standard protocols.

**Western Blot Analysis.** Levels of UGT1A protein in UGT-overexpressing cell lines were measured by Western blot analysis using the anti-UGT1A antibody (1:5000 dilution as per the manufacturer’s instructions), whereas β-actin protein levels were assayed using a 1:5000 dilution of the monoclonal anti-β-actin antibody. UGT1A protein was detected by chemiluminescence using the SuperSignal West Dura Extended Duration Substrate (Pierce Biotechnology). Secondary antibodies supplied with the Dura enhanced chemiluminescence kit (anti-rabbit and anti-mouse) were used at 1:3000. UGT1A protein levels were quantified against a known amount of human UGT1A4 protein and normalized based on UGT1A protein levels for individually overexpressed UGT enzymes, 1-OH-pyrene glucuronidation activity was detected for all the UGTs tested except that homogenates from UGT1A6-overexpressing cells exhibited no glucuronidation activity.

**Glucuronidation Assays.** The rate of glucuronidation by cell homogenates was determined essentially as described previously (Ren et al., 2000; Fang et al., 2002; Wiener et al., 2004b). For kinetic analysis, family 1A UGT activities were normalized based on UGT1A protein levels as determined by Western blot analysis (Fig. 1A). A similar anti-UGT1A antibody and a similar glucuronidation activity were detected for all the UGTs tested except that homogenates from UGT1A6-overexpressing cells exhibited no detectable activity against any of these substrates. Cell homogenates from cell lines overexpressing UGT1A4 or UGT2B4 were active against other known aglycones (results not shown).

**Results**

**Kinetic Analysis of Human UGT Isoform Activity against Mono-hydroxylated PAH.** Several UGT family members have been shown to glucuronidate PAHs, including metabolites of BaP, with UGT1A10 exhibiting higher glucuronidation activity against both the (−) and (+) isomers of BP compared with other UGT enzymes (Fang et al., 2002). To determine whether UGT1A10 exhibits a similarly high activity against other PAHs, the relative activities of individual UGT enzymes were screened against 1-OH-pyrene and three hydroxylated metabolites of BaP, 3-OH-BaP, 7-OH-BaP, and 9-OH-BaP. In screening assays using cell homogenate or baculosomal protein for individually overexpressed UGT enzymes, 1-OH-pyrene glucuronidation activity was detected for all the UGTs tested except UGT1A4 and UGT2B4 (Table 1). The same pattern of activity was observed against all the monohydroxylated BaP metabolites tested, except that homogenates from UGT1A6-overexpressing cells exhibited no detectable activity against any of these substrates. Cell homogenates from cell lines overexpressing UGT1A4 or UGT2B4 were active against other known aglycones (results not shown). For kinetic analysis, family 1A UGT activities were normalized based on UGT1A expression in the individual UGT-overexpressing cell homogenates or baculosomes based on Western blot analysis (Fig. 1A). A similar analysis for the UGT2B was not performed because an antibody that recognizes all the UGT2B family members was not available. As shown in Table 1, UGT1A10 was considerably more active against all the PAHs tested than any other UGT family member as determined by V_{max}/K_{m} values. UGT1A9 exhibited similar activity against all three BaP metabolites as determined by V_{max}/K_{m} and UGT1A8 exhibited similar activity to UGT1A9 against 3-OH-BaP. UGT1A enzymes exhibiting significant activity as determined by

### Table 1

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<tr>
<th>UGT</th>
<th>3-OH-BaP</th>
<th>7-OH-BaP</th>
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<th>1-OH-Pyrene</th>
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<td>V_{max}/K_{m} (μM)</td>
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<td>1588 ± 314</td>
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N.D., not detected; N.P., not performed.

a Kinetic data are reported as mean ± S.D. for three independent experiments. K_{m} apparent. b V_{max} values are adjusted per milligram of the corresponding UGT1A protein as determined by Western blot analysis.

c Incubation for 30 min.

The rate of glucuronidation by cell homogenates was measured using cell homogenate or baculosomal preparations for individually overexpressed UGT enzymes, and incubations were for 1 h or 30 min.

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a Kinetic data are reported as mean ± S.D. for three independent experiments. K_{m} apparent. b V_{max} values are adjusted per milligram of the corresponding UGT1A protein as determined by Western blot analysis.

**: Student's t-test (two-sided) was used for comparing rates and kinetic values of glucuronide formation for the UGT1A10**

ROC and UGT1A10**196-39** isoforms against the different substrates examined in this study.
V_{\text{max}}/K_{\text{m}} against 1-OH-pyrene in addition to UGT1A10 were UGT1A6 and UGT1A8. Although a comparison using $V_{\text{max}}$ could not be performed against family 2B UGT, UGT1A10 exhibited a 1.7- to 254-fold lower apparent $K_{\text{m}}$ than active family 2B UGTs against 3-OH-BaP, 7-OH-BaP, and 1-OH-pyrene. Overall, the affinity of individual UGT enzymes as determined by apparent $K_{\text{m}}$ analysis was $1A10 > 1A1 > 1A9 > 1A7 > 1A8 > 2B17 > 1A3 > 2B15 > 2B7$ for 3-OH-BaP, $1A10 > 1A3 > 1A9 > 1A7 > 2B7 > 1A8 > 1A1 > 2B15 > 2B7$ for 7-OH-BaP, and $1A7 > 1A10 > 2B7 > 2B15 > 1A9 > 1A3 > 1A1 > 2B17 > 1A8$ for 9-OH-BaP. UGT1A10 was not detected in human lung in RT-PCR assays for multiple human lung specimens (Zheng et al., 2002). UGT1A10 was not expressed in normal human lung tissue, but only when assayed as a single amplification with one primer set specific for UGT1A10 (Fig. 1B, lane 4); consistent with previously reported results (Zheng et al., 2002). UGT1A10 was not detected in human lung when multiplex RT-PCR was performed (Fig. 1B, lane 6). The amplified product was confirmed to be UGT1A10 by sequencing analysis (data not shown). Similar results were obtained in RT-PCR assays for multiple human lung specimens (data not shown). No UGT1A10 expression was detected using HEK293 cell total RNA as template when assays were performed using UGT1A10 primers alone or when multiplexed with primers for $\beta$-actin (results not shown). This is the first demonstration of UGT1A10 expression in the human lung.

Expression of UGT1A10 in Human Lung. Previous studies have shown that UGT1A10 and UGT1A7 are the only UGTs expressed in all the aerodigestive tract tissues examined, including floor of mouth, larynx, tonsil, esophagus, and tongue (Zheng et al., 2002). In the same studies, UGT1A10 was not detected in lung tissue by multiplex RT-PCR. Recent studies have suggested that UGT1A10 was expressed in an irinotecan-resistant lung adenocarcinoma cell line and capable of glucuronidating SN-38, the active metabolite of irinotecan (Oguri et al., 2004). To better assess whether UGT1A10 is in fact expressed in human lung, RT-PCR of UGT1A10 exon 1 alone or in a multiplex assay with $\beta$-actin was performed using total RNA extracted from normal human lung tissue. As shown for a representative lung RNA specimen (Fig. 1B), UGT1A10 was expressed in normal human lung tissue, but only when assayed as a single amplification with one primer set specific for UGT1A10 (Fig. 1B, lane 4); consistent with previously reported results (Zheng et al., 2002). UGT1A10 was not detected in human lung when multiplex RT-PCR was performed (Fig. 1B, lane 6). The amplified product was confirmed to be UGT1A10 by sequencing analysis (data not shown). Similar results were obtained in RT-PCR assays for multiple human lung specimens (data not shown). No UGT1A10 expression was detected using HEK293 cell total RNA as template when assays were performed using UGT1A10 primers alone or when multiplexed with primers for $\beta$-actin (results not shown). This is the first demonstration of UGT1A10 expression in the human lung.

Analysis of UGT1A10<sup>139Glu</sup> Function Using UGT1A10-Overexpressing Cell Lines. To determine whether the Glu>Ly s amino acid change at codon 139 of the UGT1A10 gene affects UGT1A10 enzyme activity, stable HEK293 cell lines overexpressing either the UGT1A10<sup>139Glu</sup> or UGT1A10<sup>139Lys</sup> isoforms were created. The overexpressed UGT1A10 wild-type and polymorphic cDNA were PCR-amplified and fully sequenced as described under Materials and Methods. The UGT1A10 cDNA sequence of both cell lines matched with 100% identity to the UGT1A10 cDNA sequence described in GenBank (accession no. BC030974) with the only difference between the cell lines being the polymorphic G>A transition at nucleotide
UGT1A10 polymorphisms have been identified, including a missense polymorphism at codon 139 that results in a Glu to Lys amino acid change. This polymorphism was recently implicated in the metabolism of polycyclic aromatic hydrocarbons (PAHs). The purpose of the present study was to further evaluate the role of UGT1A10 in the metabolism of PAHs and to examine the effects of the UGT1A10 codon 139 polymorphism.

Semiquantitative Western blot analysis showed high levels of UGT1A10 protein in homogenates of both the UGT1A10139Glu- and UGT1A10139Lys-overexpressing HEK293 cell lines (Fig. 1C). The levels of UGT1A10 relative to β-actin (as an internal reference for expression) measured by densitometry revealed that the level of expression of the UGT1A10139Lys polymorphic variant was 2.1-fold greater than the expression of the UGT1A10139Glu wild-type isoform. No UGT1A10 expression was detected by Western blot analysis in the HEK293 cell line.

As shown in a representative chromatogram (Fig. 2), glucuronidation activity was clearly discernable for both the UGT1A10139Glu- and UGT1A10139Lys-overexpressing cell lines against 4-nitrophenol (top and middle). A 4-nitrophenol-glucuronide peak (retention time = 12 min) was no longer observed after addition of β-glucuronidase to the reaction (Fig. 2, bottom). For a comparative activity assay, the glucuronidation activities of both cell lines were initially examined using a variety of commonly tested noncarcinogenic substrates, including 4-nitrophenol, 4-methylumbelliferone, and 1-naphthol, with the relative UGT1A10 enzymatic activity normalized according to UGT1A10-overexpressing cell homogenate.

<table>
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<th>Substrate</th>
<th>UGT1A10139Glu</th>
<th>UGT1A10139Lys</th>
</tr>
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<tr>
<td>4-Nitrophenol</td>
<td>348 ± 39</td>
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</tr>
<tr>
<td>4-Methylumbelliferone</td>
<td>669 ± 24</td>
<td>290 ± 59²</td>
</tr>
<tr>
<td>1-Naphthol</td>
<td>365 ± 19</td>
<td>172 ± 11²</td>
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</table>

* Significant (p < 0.005) differences in glucuronidation activity were observed for UGT1A10139Glu versus UGT1A10139Lys-overexpressing cell homogenates.

To assess whether these differences in activity were also manifested against PAH, kinetic analysis was performed against 1-OH-pyrene and four BaP metabolites, BPD, 3-OH-BaP, 7-OH-BaP, and 9-OH-BaP (Table 3). Differences in glucuronidation kinetics were observed between homogenates from the UGT1A10139Glu and UGT1A10139Lys cell lines against all the substrates tested. A significantly higher Vmax/Km was observed for homogenates from wild-type UGT1A10139Glu cells against all four BaP metabolites tested. A similarly significant (p < 0.05) increase in Vmax/Km was observed for homogenates from wild-type UGT1A10139Glu cells against 1-OH-pyrene. Significantly lower apparent Km values were observed for homogenates from wild-type UGT1A10139Glu cells against 1-OH-pyrene (p < 0.05) and 3-OH-BaP (p < 0.01). Interestingly, the apparent Km observed in the present study for homogenates from the wild-type UGT1A10139Glu cell line against racemic BPD (46.8 μM) was almost 4-fold lower than that observed for wild-type UGT1A10-overexpressing baculosomes in previous studies (Fang et al., 2002).

**Discussion**

UGT1A10 is an extrahepatic enzyme that is expressed in tissues of the digestive tract (Strassburg et al., 1999) and aerodigestive tract (Zheng et al., 2002). UGT1A10 has been implicated in the glucuronidation of several important carcinogens that probably play an important role in cancer initiation at these sites, including PAH-like BaP-7,8-dihydrodiol, precursor to the ultimate carcinogenic metabolite of BaP, BaP-7,8-dihydrodiol-9,10-epoxide (Fang et al., 2002), and 2-hydroxymethyl-1-methyl-6-phenylimidazo[4,5-b]pyridine (N-hydroxy-PhiP), the reactive intermediate of PhiP, a heterocyclic amine found in charbroiled meats (Malfatti and Felton, 2004). Previous reports identified two missense polymorphisms for UGT1A10, one at codon 139 that results in a nonconservative change in amino acids (Glu>Lys), and another at codon 244 that results in a conservative (Leu>Ile) amino acid change (Elahi et al., 2003). Both polymorphisms were somewhat prevalent (0.04–0.05) in African Americans but much less prevalent in other racial groups, including Caucasians and Asians (<0.01 for both groups). In a small hospital-based case/control study of 230 African American subjects, only the codon 139 polymorphism was associated with orolaryngeal cancer risk, with subjects with the UGT1A10139Lys variant exhibiting a significantly decreased risk for orolaryngeal cancer (Elahi et al., 2003).

The purpose of the present study was to further evaluate the role of UGT1A10 as a potentially important enzyme in the metabolism of PAH and to examine the effects of the UGT1A10 codon 139 polymorphism on UGT1A10 activity against the same PAH in vitro. Results presented here clearly show that of all the UGTs examined, UGT1A10 exhibits the highest glucuronidation activity against the various PAHs tested. These results are consistent with the high relative activity previously observed for UGT1A10 against both the (+)
and (−) isomers of BPD (Fang et al., 2002). This suggests that UGT1A10 could be playing a major role in the detoxification of PAH in important target sites, including tissues within the digestive and aerodigestive tracts, where exposure to PAH via charbroiled meats or tobacco smoke may be important in cancer induction.

Results from this study also showed detectable levels of expression of UGT1A10 in lung tissue, indicating that UGT1A10 may also be playing a role in the detoxification of tobacco smoke PAH within the lung. The fact that UGT1A10 was not observed to be expressed in lung tissue in previous studies is likely because of differences in assay sensitivity because previous studies were performed using multiplex RT-PCR using β-actin as an internal control for amplification (Zheng et al., 2002). Although excellent for quality control, the use of multiple primers for the amplification of multiple genes in single PCR reactions can affect overall amplification sensitivity and can interfere with the amplification of low-copy number mRNA (Markoulakos et al., 2002), a possibility for UGT1A10 in lung. Alternatively, it is possible that UGT1A10 may be localized to different regions within the lung, and that the lung specimens examined in the two studies were from different lung sites, or that UGT1A10 may have been differentially induced in the lungs from the different individuals from whom the specimens were obtained. Future studies will be necessary to evaluate these possibilities.

Results from the present study show that the UGT1A10*3Lys* variant exhibits significantly decreased glucuronidation activity against several PAHs, including metabolites of BaP and 1-OH-pyrene in vitro. The decreased activity observed for UGT1A10*3Lys* cell homogenates against these PAHs was reflected by significantly decreased \( V_{\text{max}} \) and, in some cases, significantly higher apparent \( K_m \), compared with UGT1A10*3Hua* cell homogenates. Similarly significant decreases in glucuronidation activity were observed for UGT1A10*3Lys* cell homogenates against all the noncarcinogenic aglycones examined in this study. The fact that there were differences in the apparent \( K_m \) for the wild-type UGT1A10 against BPD in the present study versus previous studies (Fang et al., 2002) is likely because UGT1A10-overexpressing baculosomes were used in previous studies, whereas a UGT1A10-overexpressing cell line was used in the present analysis. Recent studies have suggested that UGT1A10 activity is phosphorylation-dependent, potentially involving kinases that may not be present or as active in insect cells versus human cells (Basu et al., 2004).

Together, these results suggest that the nonconservative amino change of Glu to Lys at codon 139 renders UGT1A10 less active. Interestingly, this decrease in glucuronidation activity for the UGT1A10*3Lys* variant is not consistent with the protective effect observed for this allele in orolaryngeal cancer case/control studies (Elahi et al., 2003). One possibility that could explain this is that the two variants may have different optimal assay conditions in vitro. Another possibility is that the previous case/control study was small (115 individually matched African American case/control pairs) and that the association observed was an aberration. However, credence to the results of this study was provided by the fact that an association with orolaryngeal cancer risk was not observed with the more conservative codon 244 missense UGT1A10 polymorphism examined in the same population. The most likely possibility that could explain the differences observed between these molecular epidemiologic studies and the functional studies outlined in this report is that the UGT1A10*3Lys* allelic variant may be linked by haplotype to one or more other genetic variations within the UGT1A loci that not only compensate for the detrimental effect on UGT1A10 function by the presence of the codon 139 Lys residue but also serves to provide an overall protective effect against orolaryngeal cancer risk. A haplotype analysis of potential variants within the UGT1A10 coding region was performed in previous studies, where the UGT1A10-specific exon 1 was screened for polymorphisms in a total of 102 subjects (53 Caucasians and 49 African Americans) (Elahi et al., 2003). The allelic variant encoding the UGT1A10*3Lys* isoform (termed UGT1A10*2) was not observed to be linked to any other UGT1A10 exon 1 polymorphisms in these studies. Alternatively, linkage could be with variants within the UGT1A10 promoter region, sequences that were not examined in these previous studies, or in linkage with other genetic variations within the UGT family 1A loci that somehow affect UGT1A10 expression. Another possibility is that the UGT1A10 codon 139 polymorphism may be linked to functionally relevant polymorphism(s) in another family 1A UGT that is important in orolaryngeal cancer risk. Previous studies have shown that function-altering polymorphisms in the UGT1A7 gene are strongly associated with tobacco smoking-related orolaryngeal cancer risk in both Caucasians and African Americans (Zheng et al., 2001). Like UGT1A10, UGT1A7 was also shown to be the only other UGTs to be well expressed in all the aerodigestive tract tissues examined (Zheng et al., 2002) and, as described in this and previous reports (Fang et al., 2002; Guillemette et al., 2000), UGT1A7 exhibits glucuronidating activity against various PAHs including BPD. It is not yet known whether a genetic linkage exists between the UGT1A10 codon 139 polymorphism and polymorphisms in other regions within the UGT family 1A loci including UGT1A17. Studies attempting to identify UGT1A10 codon 139-inclusive haplotypes within the UGT family 1A locus by large-scale sequencing analysis of individuals with a UGT1A10*2 allele are currently in progress.

In summary, UGT1A10 is the most active UGT in the glucuronidation of various PAHs and is expressed in various target tissues where PAH exposure may be important in cancer induction, including tissues within the digestive and aerodigestive tracts and potentially within the...
lung. Further investigations will be required to fully elucidate the mechanism underlying the observed protective phenotype in orolaryngeal cancer risk associated with the functionally less-active UGT1A10139Lys polymorphic variant.

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References


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