ABSTRACT

UDP-glucuronosyltransferase (UGT)-mediated glucuronidation of benzo(a)pyrene-trans-7,8-dihydrodiol (BPD), precursor to the potent mutagen benzo(a)pyrene-7,8-dihydrodiol-9,10-epoxide, may be an important pathway in the detoxification of benzo(a)pyrene. To better characterize this pathway in humans, high-pressure liquid chromatography (HPLC) was used to detect glucuronide conjugates of BPD formed in vitro. Three peaks were detected by HPLC after incubation of racemic BPD with human liver microsomes; these were identified as monoglucuronides by liquid chromatography-mass spectrometry analysis. Proton nuclear magnetic resonance spectroscopy of isolated fractions, combined with HPLC analysis of the glucuronide products from human liver microsomal incubations with purified benzo(a)pyrene-trans-7,8-dihydrodiol (+)-BPD and benzo(a)pyrene-trans-7R,8R-dihydrodiol (−)-BPD forms of BPD, indicated that peak 1 contained the 7-glucuronide of 7,8-S-BPD (BPD-7S-Gluc), peak 2 was a mixture of the 7-glucuronide of 7R,8R-BPD (BPD-7R-Gluc) and the 8-glucuronide of 7S,8S-BPD (BPD-8S-Gluc), and peak 3 contained the 8-glucuronide of 7R,8R-BPD (BPD-8R-Gluc). In liver microsomes, peak 1 (BPD-7S-Gluc) was the largest peak observed, whereas in microsomes from aerodigestive tract tissues, peak 2 (both BPD-7R-Gluc and BPD-8S-Gluc) was the largest HPLC peak observed. The liver enzymes UGT1A1 and UGT2B7 formed BPD-7S-Gluc as the major diastereomer, whereas UGT1A8 and UGT1A10, extrahepatic enzymes present in the aerodigestive tract, preferentially formed both BPD-7R-Gluc and BPD-8S-Gluc. In addition, both UGT1A9 and UGT1A7 preferentially formed BPD-7R-Gluc. No detectable glucuronidating activity against BPD was observed by UGT1A3, UGT1A4, UGT1A6, UGT2B4, UGT2B15, or UGT2B17. The affinity of individual UGT enzyme as determined by Km analysis was UGT1A10 > UGT1A9 > UGT1A1 > UGT1A7 for (−)-BPD and UGT1A10 > UGT1A9 > UGT2B7 > UGT1A1 > UGT1A7 for (+)-BPD. These results suggest that several UGTs may play an important role in the overall glucuronidation of BPD in humans, with UGT1A1, UGT1A7, UGT1A9, UGT1A10 and potentially UGT1A8 playing an important role in the glucuronidation of the precarcinogenic (+)-BPD enantiomer, and that the stereospecific activity exhibited by different UGTs against BPD is consistent with tissue-specific patterns of BPD glucuronidate diastereomer formation and UGT expression.

INTRODUCTION

BaP is an extensively studied polycyclic aromatic hydrocarbon that is highly carcinogenic in animals, and its presence is widespread in the environment including in emission exhausts, cigarette smoke, and charbroiled foods (1–3). This carcinogen is metabolized by phase I enzymes to a large number of metabolites including phenols, arene oxides, quinones, dihydrodiols, and diol epoxides and is also conjugated by phase II enzymes to glutathione, sulfate, and UDPGA-derived glucuronic acid to form more water-soluble, detoxified derivatives (1). Although several of these metabolites contribute to the high carcinogenicity of BaP, numerous studies have clearly identified the 7,8-diol-9,10-epoxide as the primary carcinogenic metabolite of BaP, with the anti- (+)-BaP-7R,8S-dihydrodiol-9,10R-epoxide diastereomer exhibiting enhanced mutagenic activity in vitro and in vivo (1, 2, 4–8). This penultimate carcinogen is formed from BaP by two rounds of cytochrome P450-mediated oxidation separated by a hydrolysis reaction involving epoxide hydrolase-mediated formation of the proximate carcinogen, BPD (see Fig. 1). In rats, 90–95% of BaP metabolism to the BaP-7,8-epoxide is to the (+)-7R,8S form (9, 10), and subsequent enzymatic hydrolysis of the (+)-7R,8S-epoxide results in formation of (−)-BPD. Upon oxidation, two isomeric diol-epoxides from each BPD enantiomer are formed, and although the relative amounts of each depend on the stereoselectivity of oxidation (8, 11, 12), conversion is primarily to the highly mutagenic anti- (+)-BaP-7R,8S-dihydrodiol-9,10R-epoxide (9). Although less well-characterized than that in rats, the metabolic profiles reported from work with human tissues are similar to those reported for other mammalian systems (2).

The UGT superfamily of enzymes catalyzes the glucuronidation of a variety of compounds including endogenous compounds like bilirubin and steroid hormones, as well as xenobiotics including drugs and environmental carcinogens (13–16). Based on differences in sequence homology and substrate specificity, two families of UGTs (UGT1 and UGT2) have been identified in several species, each containing several highly homologous UGT genes. The entire UGT1 family is derived from a single locus on chromosome 2 that codes for nine functional proteins differing only in their NH2 terminus because of alternate splicing of independent exon 1 regions to a shared COOH terminus encoded by exons 2–5 (17). In contrast to the UGT1A family, the UGT2B family is composed of several independent genes

Received 11/19/01; accepted 1/31/02.

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1 Supported by USPHS Grants R01-DE12206 and R01-DE13158 (National Institute for Dental and Craniofacial Research; to P. L.) and USPHS Grant PO1–68384 (National Cancer Institute; P. L., project leader; Steven Stellman, principal investigator) from the NIH, Department of Health and Human Services.

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coding for seven known functional human UGT enzymes clustered on chromosome 4 (18–22).

Several studies have demonstrated that UGTs exhibit a protective effect against the carcinogenicity mediated by BaP. The addition of UDPGA to the Ames test is associated with a reduction in BaP mutagenicity (23, 24). In studies of UGT-deficient homozygous (jj) and heterozygous (j/) RHA rats versus UGT-normal (+/+) RHA controls, reduced glucuronidation of BaP metabolites in vivo was correlated with increased covalent binding to hepatic DNA and microsomal protein (25). In addition, a similar correlation was observed after in vitro incubations of BaP with rat liver microsomes, lymphocytes, or skin fibroblasts from UGT-deficient RHA rats (25–27). Although previous studies have shown that several UGTs, including UGT2B7, UGT1A7, UGT1A8, UGT1A9, and UGT1A10, exhibit glucuronidating activity against several phenolic derivatives of BaP (28–32), there is little information regarding the identity of the UGTs involved in the glucuronidation of BPD. In rats, to date, only UGT1A7 has been shown to exhibit activity against BPD (29, 33), whereas of the human UGTs yet tested, only UGT2B7 has been shown to possess activity (28). One of the potential reasons for the general failure to identify BPD-glucuronidating UGT enzymes in previous studies may lie with the fact that TLC was used as the method of detection in most previous studies. To obtain increased assay sensitivity and better characterize this pathway in humans, we have developed a HPLC assay to detect glucuronide conjugates of BPD. In the present study, we used this HPLC detection assay to identify the different BPD glucuronides formed in human liver and compare with the BPD glucuronides observed in potential target tissues of BaP exposure such as tissues of the aerodigestive tract. We demonstrate that several human UGTs exhibit stereo- and regiospecific glucuronidating activity against BPD and that the pattern of diastereomer/regioisomer formation observed for different UGTs is consistent with the patterns of BPD glucuronide diastereomer/regioisomer formation and differential UGT expression observed in different tissues. Implications regarding UGT enzyme involvement in BaP detoxification in potential target tissues are discussed.

MATERIALS AND METHODS

Chemicals and Materials. 3-Hydroxy-BaP, (+)-BPD, (−)-BPD, and racemic BPD were obtained from the National Cancer Institute Chemical Carcinogen Repository (synthesized and characterized at Midwest Research Institute, Kansas City, MO), dissolved in DMSO, and stored protected from light at −70 °C. Imipramine, 1-naphthol, clofibric acid, androsterone, 4-nitrophenol, UDPGA, d,L-2-lysophosphatidyl choline palmital C16:0, and Escherichia coli β-glucuronidase were purchased from Sigma Chemical Co. (St. Louis, MO). [14C]UDPGA was obtained from NEN Life Scientific Products (Boston, MA; specific activity = 380 Ci/mol). DMEM was obtained from Mediatech (Hernndon, VA), and both fetal bovine serum and Geneticin (G418) were purchased from Life Technologies, Inc. (Grand Island, NY). Baculosome preparations overexpressing UGT1A1, UGT1A3, UGT1A7, UGT1A10, and UGT2B7 were purchased from PanVera Corp. (Madison, WI). HPLC-grade solvents were provided by various suppliers and used after filtration. All other chemicals were of analytical grade and used without further purification.

Tissue Samples and Microsome Preparation. Normal human liver tissues from patients undergoing hepatectomy were obtained from the Cooperative Human Tissue Network (Eastern Division, Philadelphia, PA). Normal human larynx and esophagus specimens were from individual patients undergoing cancer surgery at the H. Lee Moffitt Cancer Center and were obtained via the H. Lee Moffitt Cancer Center Tissue Procurement Facility. All protocols involving the analysis of tissue specimens were approved by the institutional review board at the University of South Florida and in accordance with assurances filed with and approved by the United States Department of Health and Human Services. Assurance was given by the Cooperative Human Tissue Network.
Network that samples were isolated and quick-frozen at 70 °C within 2 h after surgery.

Tissue microsomes were prepared through differential centrifugation as described previously (34) and stored (10–20 mg protein/ml) at −70 °C in 100–μl aliquots, with total protein concentrations measured using the BCA assay (Pierce, Rockford, IL). Microsome preparations of UGT2B17-overexpressing cells were prepared as described previously (32).

Cell Lines and Cell Homogenate Preparation. HK293 (human embryonic kidney fibroblast) cells and HK293 cell lines overexpressing UGT1A4, UGT1A8, UGT2B1, UGT2B7, or UGT2B15 were kindly provided by Dr. Thomas Tephly (University of Iowa, Iowa City, IA; Refs. 35–40), whereas V79 (Chinese hamster fibroblast) cells and V79 cells overexpressing UGT1A6 and UGT1A9 were kindly provided by Dr. Brian Burchell (University of Dundee, Dundee, United Kingdom; Ref. 41). The stable transfectant of the UGT2B4* overexpressing cell line has been described previously (16).

All V79 and HK293 cell lines were grown to 80% confluence in DMEM supplemented with 4.5 mM glucose, 10 mM HEPES, 10% fetal bovine serum, 0.1 g penicillin/mL, 100 units/mL streptomycin, and maintained in 700 μg/mL Geneticin for selection of UGT overexpression in a humidified incubator under an atmosphere of 5% CO2. Cells were suspended in Tris-buffered saline [25 mM Tris base, 138 mM NaCl, and 2.7 mM KCl (pH 7.4)] and subjected to three rounds of freeze-thaw before gentle homogenization. Cell homogenates (5–30 mg homogenate protein/ml) were stored at −70 °C in 100–μl aliquots. Total cell homogenate protein concentrations were determined using the BCA assay as described above.

Analysis of BPD Glucuronidating Activity. The rate of BPD glucuronidation was determined using the following conditions: tissue microsomes (1 mg of protein), cell homogenates (0.6–5 mg of protein), cell microsomes (50 μg of protein), or baculosomes (0.4–1.8 mg of protein) were incubated with 1–2 mM BPD, 4 mM UDPGA, and 1–2 μCi of [14C]UDPGA (where indicated) in 10 mM MgCl2 and 50 mM Tris-HCl (pH 7.4) in a total volume of 100–600 μl at 37 °C for 1–6 h (as indicated in the text). Where indicated, incubations were performed with D,L-2-lysophosphatidyl choline palmital.

Glucuronidation was determined using the following conditions: tissue microsomes supplemented with 4.5 mM glucose, 10 mM HEPES, 10% fetal bovine serum, 0.1 g penicillin/mL, 100 units/mL streptomycin, and 700 μg/mL Geneticin for selection of UGT overexpression in a humidified incubator under an atmosphere of 5% CO2. Cells were suspended in Tris-buffered saline [25 mM Tris base, 138 mM NaCl, and 2.7 mM KCl (pH 7.4)] and subjected to three rounds of freeze-thaw before gentle homogenization. Cell homogenates (5–30 mg homogenate protein/ml) were stored at −70 °C in 100–μl aliquots. Total cell homogenate protein concentrations were determined using the BCA assay as described above.

RESULTS

Identification of BPD Glucuronide Regioisomers and Diastereomers in Human Liver Microsomes. As shown in Fig. 1, four BPD monoglucuronides and two BPD diglucuronides could potentially be formed via glucuronidation of BPD. Previous studies have not examined the possible formation of any of these glucuronides. To identify possible diastereomeric BPD derivatives formed in human liver, separation of BPD glucuronides was performed by HPLC using racemic BPD as substrate. A typical HPLC trace demonstrating BPD glucuronide formation after incubation of human liver microsomes with racemic BPD is shown in Fig. 2. Three peaks corresponding to predicted BPD glucuronides (retention time = 22–28 min) were detected by both UV detection (254 nm; Fig. 2A) and UDPGA-derived 14C glucuronic acid incorporation (Fig. 2C). These HPLC peaks were sensitive to treatment with β-glucuronidase (Fig. 2, B and D), confirming that they correspond to glucuronidated BPD conjugates. It was originally hypothesized that the three HPLC peaks observed in our assays with human liver microsomes corresponded to the 7- and 8-monoglucuronides as well as the 7,8-diglucuronide of BPD. When the combined products of human liver microsomes were analyzed using LC with electrospray MS detection (Fig. 3), all three glucuronide peaks that had been observed by UV absorbance displayed molecular and fragment ions consistent with BPD monoglucuronide products. Each peak showed essentially the same negative ion mass.
spectra, with deprotonated molecules \([M - H]^+\) at \(m/z\) 461. A prominent fragment ion corresponding to the phenol derived from the UDPGA moiety \((m/z \text{ 267})\) was also observed, as were fragment ions from UDPGA \((m/z \text{ 193, 175, and 113})\). Positive ion mass spectra consisted primarily of the phenol fragment ion \((m/z \text{ 269})\), with smaller amounts of \((M + NH_4)^+\) at \(m/z\) 480 (data not shown).

The identity of the glucuronidates was established by \(^1\)H NMR analysis of the individual HPLC peaks, combined with information obtained from conducting incubations with the optically pure BDP isomers. To facilitate the interpretation, the spectrum of racemic BPD obtained from conducting incubations with the optically pure BDP was used. Analysis of the individual HPLC peaks, combined with information shown.

### Table 1

<table>
<thead>
<tr>
<th>Proton</th>
<th>BPD</th>
<th>BDP-7S-Gluc</th>
<th>BDP-7R-Gluc</th>
<th>BDP-8S-Gluc</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>8.20 d</td>
<td>8.19 m</td>
<td>8.19 m</td>
<td>8.19 m</td>
</tr>
<tr>
<td>2</td>
<td>8.00, t, J_{1,2} = J_{2,3} = 7.6</td>
<td>7.98, t, J_{1,2} = J_{2,3} = 7.6</td>
<td>7.99 m</td>
<td>7.99 m</td>
</tr>
<tr>
<td>3</td>
<td>8.18 d</td>
<td>8.18 m</td>
<td>8.19 m</td>
<td>8.19 m</td>
</tr>
<tr>
<td>4</td>
<td>8.42 d</td>
<td>8.06, d, J_{4,5} = 8.9</td>
<td>8.10 m</td>
<td>8.10 m</td>
</tr>
<tr>
<td>5</td>
<td>8.42 d</td>
<td>8.18, m</td>
<td>8.10 m</td>
<td>8.10 m</td>
</tr>
<tr>
<td>6</td>
<td>8.09, s</td>
<td>8.79, s</td>
<td>8.48, s</td>
<td>8.48, s</td>
</tr>
<tr>
<td>7</td>
<td>5.08, dd, J_{7,8} = 10.8</td>
<td>5.40, d, J_{7,8} = 10.1</td>
<td>5.35, d, J_{7,8} = 9.7</td>
<td>5.31, d, J_{7,8} = 9.7</td>
</tr>
<tr>
<td>8</td>
<td>4.58, ddd, J_{8,9} = 10.1; J_{9,10} = 2.5; J_{10,11} = 2.1</td>
<td>6.27, dd, J_{9,10} = 10.1; J_{9,10} = 2.3</td>
<td>6.27, dd, J_{9,10} = 10.1; J_{9,10} = 2.5</td>
<td>6.27, dd, J_{8,9} = 10.1; J_{8,10} = 2.5</td>
</tr>
<tr>
<td>9</td>
<td>6.29, dd, J_{9,10} = 10.1; J_{9,10} = 2.5</td>
<td>7.55, dd, J_{9,10} = 10.3; J_{9,10} = 2.3</td>
<td>7.56, m</td>
<td>7.56, m</td>
</tr>
<tr>
<td>10</td>
<td>7.56, dd, J_{9,10} = 10.1; J_{9,10} = 2.1</td>
<td>8.41, d, J_{10,11} = 9.4</td>
<td>8.42, d, J_{10,11} = 9.3</td>
<td>8.43, d, J_{10,11} = 9.4</td>
</tr>
<tr>
<td>11</td>
<td>8.42, d, J_{11,12} = 9.3</td>
<td>8.12, d, J_{11,12} = 9.3</td>
<td>8.10, m</td>
<td>8.10, m</td>
</tr>
<tr>
<td>12</td>
<td>8.13, d</td>
<td>4.94, d, J_{11,12} = 7.3</td>
<td>4.75, d, J_{12,13} = 7.3</td>
<td>4.70, d, J_{12,13} = 7.7</td>
</tr>
<tr>
<td>1'</td>
<td></td>
<td></td>
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<td></td>
</tr>
</tbody>
</table>

**a** Recorded in methanol-\(d_4\).

**b** The assignment may be reversed.

**c** Abbreviations for coupling patterns: s, singlet; d, doublet; t, triplet; m, multiplet.

**d** Obscured by the residual methanol resonance; identified by two-dimensional COSY.

In conclusion, the results presented here provide evidence for the regio- and stereoselectivity of BPD glucuronidation and the potential of glucuronides as biomarkers of BPD exposure. The study also highlights the importance of understanding the metabolic pathways involved in BPD glucuronidation for the development of strategies aimed at reducing the risk of BPD-related toxicity.
against racemic BPD (Fig. 4). In all cases, the optimal rate of BPD glucuronide formation was observed in incubations without detergent (d,l-2-lyso phosphatidyl choline palmital C16:0) and in Tris-HCl buffer (pH 7.4). No detectable glucuronidation of racemic BPD was observed for homogenates of cell lines overexpressing UGT1A4, UGT1A6, UGT2B4, or UGT2B15; for UGT1A3-overexpressing baculosomes; or for microsomes from UGT2B17-overexpressing cells in incubations, with or without detergent (d,l-2-lyso phosphatidyl choline palmital C16:0) or in different buffer systems at various pHs (see “Materials and Methods”; results not shown).

As shown by HPLC, there were significant differences in the relative amount of BPD glucuronide diastereomers formed by homogenates from cells or baculosomes overexpressing the different UGTs in incubations with racemic BPD. The HPLC peaks 1:2:3 ratio exhibited by UGT1A1-overexpressing baculosomes was 1:0.5:0.2 (Fig. 4A), a ratio similar to that observed for human liver microsomes (1:0.4:0.1; see Fig. 2). In addition to being the major peak observed for homogenates of UGT1A1-overexpressing cells, HPLC peak 1, corresponding to the formation of BPD-7S-Gluc, was the only peak observed for incubations with homogenates from UGT2B7-overexpressing cells (Fig. 4B) or UGT2B7-overexpressing baculosomes (results not shown). UGT1A7 (Fig. 4C), UGT1A8 (Fig. 4D), UGT1A9 (Fig. 4E), and UGT1A10 (Fig. 4F) all exhibited a glucuronide diastereomer/regioisomer pattern with HPLC peak 2 (corresponding to the formation of BPD-7R-Gluc and/or BPD-8S-Gluc) being the major peak. Little or no peak 3 formation (corresponding to BPD-8R-Gluc) was observed for UGT1A1 (Fig. 4A), or UGT1A7-overexpressing baculosomes (Fig. 4C) or for UGT1A9-overexpressing cell homogenates (Fig. 4E) in incubations with racemic BPD. Higher rates of HPLC peak 3 (BPD-8R-Gluc) versus peak 1 (BPD-7S-Gluc) formation were observed for homogenates from both UGT1A8 (Fig. 4D)- and UGT1A10 (Fig. 4F)-overexpressing cells.

To better characterize the stereo- and regiospecificity and the kinetics of each UGT against BPD enantiomers, reactions were performed using either (−)-BPD or (+)-BPD as the substrate. The BPD glucuronide isomer ratios observed by HPLC for the different UGTs and each BPD isomer [(+)-BPD and (−)-BPD; Table 2] were consistent with the HPLC peak ratios observed for racemic BPD (Fig. 4). For UGT1A1- and UGT1A7-overexpressing baculosomes and UGT1A9-overexpressing cell homogenates, HPLC peak 1 was preferentially formed in incubations with (+)-BPD, whereas HPLC peak 2 was preferentially formed in incubations with (−)-BPD, indicating that these UGTs preferentially glucuronidate the 7 position of BPD. HPLC peak 2 was the major peak for both UGT1A7- and UGT1A9-overexpressing cell homogenates, whereas peak 1 was the major peak for UGT1A1-overexpressing cell homogenates in incubations with racemic BPD. These data suggest that UGT1A1 preferentially forms BPD-7S-Gluc, whereas UGT1A7 and UGT1A9 preferentially form BPD-7R-Gluc. Consistent with observations in incubations with racemic BPD, homogenates from UGT2B7-overexpressing cells exhibited significant activity against (+)-BPD, with HPLC peak 1 (corresponding to BPD-7S-Gluc) being the only peak observed; no detectable activity was observed for UGT2B7-overexpressing cell homogenates against (−)-BPD. HPLC peaks 2 and 3 were both observed for incubations with UGT1A8- and UGT1A10-overexpressing baculosomes with (−)-BPD, whereas HPLC peak 2 was preferentially formed in incubations with (+)-BPD, indicating that both the 7 and 8 positions of (−)-BPD and the 8 position of (+)-BPD were glucuronidated by these UGTs.

The relative affinities for each BPD enantiomer as reflected by the apparent $K_m$ were UGT1A10 $>$ UGT1A9 $>$ UGT2B7 $>$ UGT1A1 $>$ UGT1A7 for (+)-BPD and UGT1A10 $>$ UGT1A9 $>$ UGT1A1 $>$ UGT1A7 for (−)-BPD (Table 2). UGT1A10 and UGT1A9 exhibited similar affinity for both the (−)-BPD and (+)-BPD, whereas UGT1A7 and UGT1A1 exhibited higher affinity for (−)-BPD. Consistent with the isomer patterns observed in incubations with either racemic BPD or each of the purified (+)-BPD or (−)-BPD enantiomers, UGT2B7 exhibited higher overall activity for (−)-BPD as compared with (−)-BPD (as determined by the $V_{max}/K_m$ ratio), whereas UGT1A7 and UGT1A9 exhibited higher overall activity for (−)-BPD. Similarly, the high levels of HPLC peak 2 formation observed for both UGT1A1 and UGT1A10 with racemic BPD (Fig. 4) are consistent with their similar overall activity for each of the purified BPD enantiomers (Table 2). Although UGT1A8 exhibited
detectable levels of activity against racemic BPD (see Fig. 4D), kinetic analysis could not be performed due to low overall rates of BPD glucuronidation for the UGT1A8-overexpressing cell line.

**BPD Glucuronidation in Aerodigestive Tract Tissues.** Previous studies have demonstrated differential expression of UGTs in different human tissues (31, 43–46). To better assess the role of differential UGT expression on BPD glucuronidation in aerodigestive tract tissues (target tissues for BaP exposure), separation of BPD glucuronides by HPLC was performed for both human laryngeal (Fig. 5A) and esophageal (Fig. 5C) microsomes after incubation with racemic BPD. As observed for human liver microsomes, three peaks corresponding to predicted BPD glucuronides (retention time = 22–28 min) were detected. These HPLC peaks were sensitive to treatment with -glucuronidase (Fig. 5, B and D). The levels of total BPD glucuronide formation in liver microsomes were approximately 250- and 500-fold that observed for laryngeal and esophageal microsomes, respectively, in incubations with racemic BPD. In contrast to human liver microsomes, in which HPLC peak 1 was the preferential peak formed (comprising 71% of the total BPD glucuronide peaks), peak 2 was the preferential peak formed with microsomes from both aerodigestive tract tissues, with peak 1 comprising only 36% and 10% of the total BPD glucuronide peaks for laryngeal and esophageal microsomes, respectively (see Fig. 1). The pattern of stereo- and regiospecificity in aerodigestive tract tissues is similar to that observed for the aerodigestive tract tissue expressing UGT1A7, UGT1A8, and UGT1A10.

**DISCUSSION**

This is the first study to characterize the glucuronidation of BPD by human UGTs. Several human UGTs were shown to exhibit significant levels of activity against BPD, with different UGT enzymes exhibiting specific patterns of stereo- and regioselective BPD-monoglucuronide diastereomer/regioisomer formation. Whereas the UGT with the lowest $K_m$ and therefore the highest affinity for both (+)-BPD and (-)-BPD was UGT1A10, other UGTs including UGT1A1, UGT1A7, UGT1A8, and UGT1A9 also exhibited detectable levels of activity against both BPD enantiomers, whereas UGT2B7 exhibited significant levels of activity against (+)-BPD. Of these, only UGT2B7 has been shown to exhibit activity against BPD in previous studies (28).

No activity against BPD was observed for UGT1A8 and UGT1A10 in transiently transfected COS-7 cells (30), whereas no detectable glucuronidation of BPD was observed for HK293 cells stably transfected with human UGT1A7 (32). It is likely that these discrepancies are due to decreased assay sensitivity in previous studies. In contrast to the transient transfection studies of Mojarrabi and Mackenzie (30), the UGTs analyzed in the present study were from either stably transfected cell lines or overexpressing baculosomes. Moreover, whereas a sensitive HPLC assay was used to detect BPD-glucuronide formation in the present study, TLC was used to detect BPD-glucuronidating activities in previous studies (28, 30, 32).

In addition to increased sensitivity, the HPLC methodology used in the present study allowed for the detection and identification of individual BPD glucuronide isomers. As shown by mass and $^1$H NMR spectral analyses, none of the BPD glucuronides detected by HPLC in this study were diglucuronides; all were monoglucuronides at either the 7S or 8R position of BPD. Of the four possible BPD monoglucuronide isomers formed by glucuronidation of BPD, both the 7S- and 8R-glucuronides (HPLC peaks 1 and 3, respectively) were separated from other potential BPD glucuronide isomers using the HPLC meth-
Fig. 4. HPLC analysis of BPD glucuronidation formation in homogenates from UGT-overexpressing V79 and HK293 cells and UGT-overexpressing baculosomes. Cell homogenates or baculosomes were incubated at 37°C with 1 mg racemic BPD and 4 mM UDPGA as described in “Materials and Methods.” Shown are metabolites from incubations using UGT1A1-overexpressing baculosomes (0.8 mg of protein) (A), homogenates (0.6 mg of protein) from UGT2B7-overexpressing HK293 cells (B), UGT1A7-overexpressing baculosomes (1.8 mg of protein; C), homogenates (5 mg of protein) from UGT1A8-overexpressing HK293 cells (D), homogenates (1 mg of protein) from UGT1A9-overexpressing V79 cells (E), and UGT1A10-overexpressing baculosomes (0.4 mg of protein; F). Assays were performed for 2 h for incubations with UGT1A1, UGT2B7, UGT1A7, UGT1A9, and UGT1A10 and for 16 h for incubations with UGT1A8.

Table 2  Kinetic analysis of the glucuronidation of BPD isomers by human UGT enzymes

<table>
<thead>
<tr>
<th>UGT Enzyme</th>
<th>(−)-BPD</th>
<th>(+)-BPD</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$K_m$ (μM)</td>
<td>$V_{max}$ (pmol min$^{-1}$ mg$^{-1}$)</td>
</tr>
<tr>
<td>UGT1A1$^{c}$</td>
<td>290 ± 17$^{d}$</td>
<td>5.0 ± 0.5</td>
</tr>
<tr>
<td>UGT1A7</td>
<td>695 ± 62</td>
<td>0.8 ± 0.2</td>
</tr>
<tr>
<td>UGT1A8</td>
<td>Not performed$^{e}$</td>
<td></td>
</tr>
<tr>
<td>UGT1A9</td>
<td>244 ± 22</td>
<td>166 ± 17</td>
</tr>
<tr>
<td>UGT1A10</td>
<td>183 ± 20</td>
<td>9.3 ± 0.4</td>
</tr>
<tr>
<td>UGT2B7</td>
<td>ND$^{f}$</td>
<td>ND</td>
</tr>
</tbody>
</table>

$^a$ BPD glucuronide regiosomer ratios were calculated based on HPLC peak areas, with peak 2 as the referent.

$^b$ BPD glucuronide regiosomer ratios were calculated based on HPLC peak areas, with peak 1 as the referent.

$^c$ Incubations were performed without detergent in Tris-Cl (pH 7.4) buffer at 37°C for 2 h (UGT1A1, UGT1A7, and UGT1A10), 4 (UGT1A17), 16 (UGT1A18), or 0.5 h (UGT2B7), as indicated in “Materials and Methods.”

$^d$ Data are presented as mean ± SD for three independent experiments.

$^e$ Kinetic analysis was not performed for UGT1A8 due to low overall glucuronidating activity of UGT1A8-overexpressing cell homogenates (see text).

$^f$ ND, not detectable.
The results of this study suggest that UGT1A1, UGT1A7, UGT1A8, which cells and tissues protect against BaP-induced carcinogenicity. The results of the present study strongly implicate several UGT isozymes in the glucuronidation of the important procarcinogen BPD and support recent evidence that glucuronidation is an important detoxification pathway for BaP in multiple tissues. Therefore, several UGT enzymes may serve as important targets for cancer chemoprevention in the future.

ACKNOWLEDGMENTS

We thank Richard D. Beger for obtaining the NMR spectra and Kim Journault for the preparation of membrane fractions of UGT2B17-overexpressing cells.

REFERENCES


Characterization of Benzo(a)pyrene-trans-7,8-dihydrodiol Glucuronidation by Human Tissue Microsomes and Overexpressed UDP-glucuronosyltransferase Enzymes

Jia-Long Fang, Frederick A. Beland, Daniel R. Doerge, et al.


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