



Role of Nitroreductases but Not Cytochromes P450 in the Metabolic Activation of 1-Nitropyrene in the HepG2 Human Hepatoblastoma Cell Line

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ABSTRACT. 1-Nitropyrene is an environmental contaminant that is mutagenic in many prokaryotic and eukaryotic systems, including the hypoxanthine-guanosine phosphoribosyl transferase (HGPRT) locus in the human hepatoma cell line HepG2. Metabolism and DNA adduct formation of [³H]1-nitropyrene in the HepG2 were quantified to understand the role of nitroreduction and/or cytochrome P450-mediated C-oxidation of 1-nitropyrene in DNA adduct formation and mutagenicity. In uninduced HepG2 cells, 10 μM [³H]1-nitropyrene was metabolized principally by nitroreduction to 1-aminopyrene (516 pmol/24 hr/10⁶ cells), and by cytochrome P450-mediated C-oxidation to K-region *trans*-dihydrodiols (37 pmol/24 hr/10⁶ cells), 1-nitropyren-3-ol (51 pmol/24 hr/10⁶ cells), and 1-nitropyren-6-ol and 1-nitropyren-8-ol (77 pmol/24 hr/10⁶ cells). Pretreatment of the HepG2 cells for 24 hr with 5 nM 2,3,7,8-tetrachlorodibenzo-*p*-dioxin (TCDD) resulted in a complete change in the metabolism of [³H]1-nitropyrene, with 1-nitropyren-6-ol and 1-nitropyren-8-ol formation (449 pmol/24 hr/10⁶ cells) being 80-fold greater than 1-aminopyrene formation (6 pmol/24 hr/10⁶ cells). This increase in C-oxidation of 1-nitropyrene was consistent with increased levels of cytochrome P450 1A. The only DNA adduct detected using the ³²P-postlabeling assay in the HepG2 cells administered 1-nitropyrene was *N*-(2'-deoxyguanosin-8-yl)-1-aminopyrene (dG-C8-AP). Induction of C-oxidative metabolism through TCDD treatment resulted in a concomitant decrease in dG-C8-AP formation. DNA adducts for oxidized 1-nitropyrene metabolites were not detected in the TCDD-treated HepG2 cells administered 1-nitropyrene, which indicates that cytochrome P450-mediated C-oxidative pathways are detoxification pathways in HepG2 cells. *BIOCHEM PHARMACOL* 54:8:927–936, 1997. © 1997 Elsevier Science Inc.

KEY WORDS. 1-nitropyrene; HepG2; nitroreductase; DNA adducts; metabolism; cytochromes P450; metabolic activation

Nitro-PAHs§ are important environmental pollutants that have been detected from a wide variety of sources. Nitro-PAHs are generated as a result of fuel combustion [1, 2], and their emission from factories and automobiles results in the contamination of urban atmospheres and sediments [3–5]. In addition, these compounds are generated from sources in the home environment, such as kerosene heaters, wood smoke, and grilled foods [2, 6]. The *in situ* formation

of nitro-PAH in rodent lungs following administration of pyrene and exposure to nitrogen dioxide gas has also been reported [7, 8]. Therefore, the risk of long-term exposure to nitro-PAHs needs to be addressed in humans.

1-Nitropyrene, a prototypical nitro-PAH, is mutagenic in several prokaryotic and eukaryotic systems [5, 9, 10]. One pathway for the bioactivation of 1-nitropyrene is through nitroreduction to the nitroso and hydroxylamino species, with the subsequent formation of a C8 deoxyguanosine adduct, dG-C8-AP [11]. This adduct is responsible for 1-nitropyrene mutagenicity in *Salmonella typhimurium* [11, 12], Chinese hamster ovary cells [13], and cultured human foreskin fibroblasts [14].

A second route for the metabolism of 1-nitropyrene is through cytochrome P450-mediated C-oxidation to non-K-region phenols (1-nitropyren-3-ol, 1-nitropyren-6-ol, and 1-nitropyren-8-ol), and K-region oxides (1-nitropyrene-4,5-oxide and 1-nitropyrene-9,10-oxide) [15–21]. The K-region oxides are further metabolized to *trans*-dihydrodiols (1-nitropyrene-4,5-diol and 1-nitropyrene-9,10-diol) via epoxide hydrolase, or rearrange to phenols (1-nitropyrene-

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§ Abbreviations: nitro-PAH, nitrated polycyclic aromatic hydrocarbon; HGPRT, hypoxanthine-guanosine phosphoribosyl transferase; TCDD, 2,3,7,8-tetrachlorodibenzo-*p*-dioxin; dG-C8-AP, *N*-(2'-deoxyguanosin-8-yl)-1-aminopyrene; MEM, minimal essential medium; HI-FBS, heat-inactivated fetal bovine serum; HBSS, Hanks' Balanced Salts Solution; SET, 0.25 M sucrose, 0.05 M Tris-HCl, pH 7.4; 3MC, 3-methylcholanthrene; C-OXID/N-REDUC, ratio of 1-nitropyrene C-oxidation to nitroreduction; dG-C8-ANP, *N*-(2'-deoxyguanosin-8-yl)-1-amino-(6 or 8)-nitropyrene; EROD, ethoxyresorufin O-deethylase; AHH, benzo[a]pyrene hydroxylase activity; and CAT, chloramphenicol acetyltransferase.

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ren-4-ol, 1-nitropyren-5-ol, 1-nitropyren-9-ol, or 1-nitropyren-10-ol). Many of these metabolites have been detected *in vitro* and *in vivo*, and several are mutagenic in *S. typhimurium* [19, 22]. A difference exists in the 1-nitropyrene metabolites formed in rodents versus man. All species that have been tested, with the exception of human, preferentially metabolize 1-nitropyrene to 1-nitropyren-6-ol and 1-nitropyren-8-ol [15–21]; however, human liver microsomes preferentially metabolize 1-nitropyrene to 1-nitropyren-3-ol [23, 24]. Therefore, humans may be at a greater mutagenic risk from 1-nitropyrene, since 1-nitropyren-3-ol is considerably more mutagenic than 1-nitropyren-6-ol or 1-nitropyren-8-ol [22].

One limitation of *in vitro* metabolism and mutagenicity experiments is that few cultured cells express the complete complement of enzymes necessary for the activation and/or detoxification of procarcinogens or promutagens. The use of exogenous activation systems often results in the production of reactive intermediates outside the cell, followed by translocation of the reactive intermediate into the cell, and formation of DNA adducts within the cells. Similarly, highly purified reactive intermediates have been added to cells to determine "direct-acting mutagenicity" of chemicals. Both of these approaches are constrained by the generation of the reactive intermediate outside the cell membrane. We have sought to validate the HepG2 human hepatoblastoma cell line as a model for human hepatocellular metabolism of 1-nitropyrene. HepG2 cells retain many characteristics of a well-differentiated hepatocyte, including cholesterol transport [25], albumin and glycogen synthesis [26], low-density lipoprotein synthesis [26, 27], bile canaliculus formation [28], and bile acid synthesis [28]. HepG2 cells have also been shown to bioactivate several types of procarcinogens [29–33], and possess the ability to metabolize 1-nitropyrene through both cytochrome P450-mediated C-oxidation and nitroreduction [34]. In the following studies, we have used the HepG2 cell to examine the relative role of nitroreduction and cytochrome P450-mediated C-oxidation in the metabolic activation of 1-nitropyrene to DNA-reactive species.

MATERIALS AND METHODS

Materials

[³H]1-Nitropyrene (1 Ci/mmol; >98% radiochemical purity) and 1-nitropyrene (99.5%; 0.5% dinitropyrenes) were obtained from Chemsyn, Inc. (Lenexa, KS). The 1-nitropyrene C-oxidized metabolites, 1-nitropyren-3-ol, 1-nitropyren-6-ol, and 1-nitropyren-8-ol, were isolated as previously described [35, 36]. 3MC was purchased from the Aldrich Chemical Co. (Milwaukee, WI), and TCDD from Alltech Associates Inc. (Deerfield, IL). Dexamethasone and triacetyloleandomycin were from the Sigma Chemical Co. (St. Louis, MO). Unless otherwise indicated, all other reagents were the best available grade.

Cell Culture

HepG2 cells (American Type Culture Collection, Rockville, MD) were grown in continuous culture in minimal essential medium containing 10 U/mL penicillin, 10 µg/mL streptomycin, and 2 mM L-glutamine (MEM), and 10% (v/v) heat-inactivated (57°, 30 min) fetal bovine serum (MEM + 10% HI-FBS) [37]. The cells were maintained at 37° under 5% CO₂ and high humidity, and were subcultured at 1:2 splits every 3–4 days. All cell culture reagents were from Gibco (Grand Island, NY).

Metabolic Studies in Cell Culture

Inducers of metabolic enzymes, 3MC or TCDD, were added at the indicated concentrations (see text below) to HepG2 cells seeded at a density of 1×10^6 cells/100 mm² plate. The media containing the inducers was removed at the times indicated in the text, and changed to MEM + 2% HI-FBS. [³H]1-Nitropyrene was added to a final concentration of 10 µM, and the cells were incubated with [³H]1-nitropyrene for up to 24 hr. The medium was collected, the cells were washed with HBSS, and the monolayer was removed with 0.25% trypsin-EDTA. The medium and cells were combined and stored at –20°. A 1-mL aliquot of the cells and medium was incubated overnight at 37° following the addition of sodium acetate to 0.1 M, pH 5.1, 15 U/mL aryl sulfatase (Type V; Sigma), and 1500 U/mL β-glucuronidase (Type IXA; Sigma). Proteinase K (Sigma) was added to a final concentration of 1 mg/mL and incubated for another hour at 37°. Then samples were extracted twice with 1 mL chloroform, and the chloroform extracts were combined and dried under nitrogen. The [³H]1-nitropyrene and its metabolites were dissolved in methanol and subjected to HPLC analysis as described below.

Preparation of HepG2 Cell Post-Mitochondrial Supernatant Fractions (S12)

HepG2 cells were removed from 100 mm² plates with a rubber policeman, combined, centrifuged at 275 g for 5 min, washed once with HBSS, and then resuspended in SET. The suspension was sonicated (Bransonic Cell Disrupter) and centrifuged at 12,000 g for 20 min. Aliquots of the HepG2 S12 were stored at –80°. Protein concentrations were determined by the method of Lowry *et al.* [38].

Metabolic Studies Using HepG2 S12

Samples were incubated under nitrogen at 37° in capped 13 × 100 mm test tubes in a final volume of 1 mL containing 8 U/mL glucose oxidase, 10 mM glucose, 40 U/mL catalase, 10 µM [³H]1-nitropyrene, 0.05 M potassium phosphate, pH 7.4, 3 mM MgCl₂, 4 mM glucose-6-phosphate, and 0.1 U/mL glucose-6-phosphate dehydrogenase. Following addition of HepG2 S12 at 1 mg/mL, the tubes were purged with nitrogen, capped, and preincubated

at 37° for 5 min. Then NADP was added to 1 mM to initiate NADPH-dependent nitroreduction. Reactions were terminated after 60 min by the addition of an equal volume of chloroform:methanol (2:1). Following thorough mixing, the tubes were centrifuged at 180 g for 10 min, and the chloroform was removed. The aqueous component was reextracted with 1 mL chloroform, and the two chloroform fractions were combined and dried under nitrogen. Samples were then subjected to HPLC analysis as described below.

Quantitation of DNA Adducts

HepG2 cells were incubated with or without inducers (3MC, 2.5 μ M; TCDD, 0.05 pM to 5 nM) for 24 hr. The media were changed to MEM + 2% HI-FBS, and 10 μ M [3 H]1-nitropyrene was added for up to 24 hr. The medium was removed, the cells were washed with HBSS, and the monolayer was removed using 0.25% trypsin-EDTA. The cells were washed once with PBS, and resuspended in PBS. The DNA was purified from the cells using an anion-exchange column (Qiagen Corp., LaJolla, CA) following an overnight incubation of the DNA at 50° with 0.5 mg/mL proteinase K in 0.05 M Tris-HCl, pH 7, 1% sodium dodecyl sulfate. The DNA was precipitated with 0.5 M NaCl and 50% ethanol (-20°), washed with 70% ethanol, and resuspended in 5 mM bis-Tris-HCl, pH 7.1, 1 mM EDTA. The purity and concentration of the DNA were determined spectrophotometrically.

DNA adducts were quantified using the 32 P-postlabeling technique [39–41]. Typically, 1 μ g of DNA from each sample was used for 32 P-postlabeling. DNA samples and standards were added to 10 mM sodium succinate buffer (pH 6.0), with 5 mM CaCl₂, and hydrolyzed with 10 μ g spleen phosphodiesterase (Type II, Sigma) and 10 μ g micrococcal nuclease (*Staphylococcus aureus*, Sigma) in a total volume of 10 μ L at 37° for 3 hr. Following the addition of 40 μ L containing 3.3 mM tetrabutylammonium chloride and 33 mM ammonium formate (pH 3.5), the samples were extracted twice with 50 μ L *n*-butanol (water-saturated). The *n*-butanol extracts were combined, and back-extracted twice with 100 μ L of water (*n*-butanol-saturated). To the *n*-butanol extracts were added 3 μ L of 25 mM bicine, pH 9.5, 50 mM dithiothreitol, and the samples were dried *in vacuo* (Savant SpeedVac Concentrator, Farmingdale, NY). The nucleotides were dissolved in 25 μ L of distilled water and stored at -70° overnight. The following day, 5 μ L of a solution containing 180 mM bicine, pH 9.5, 60 mM MgCl₂, 60 mM dithiothreitol, 6 mM spermidine, 0.01 U T4 polynucleotide kinase (US Biochemicals, Cleveland, OH), and 200 μ Ci [γ - 32 P]ATP (>2000 Ci/mmol, ICN Biochemicals, Costa Mesa, CA) was added to each sample, and incubated at 37° for 40 min. The kinase reaction was terminated by the addition of 0.03 U of potato apyrase (20 U/ μ L; Grade I, Sigma) to each tube, and the samples were incubated for another 30 min at 37°.

Each sample was applied to PEI-cellulose thin-layer chromatography sheets (10 \times 10 cm; Scientific Absorbants,

Atlanta, GA) and developed in the first direction in 0.9 M sodium phosphate, pH 6.8 (D1 buffer) onto a Whatman No. 1 paper wick (10 \times 20 cm). The wick was removed, and the plates were washed with water, dried, and developed in 3.6 M lithium formate, 8.5 M urea, pH 3.5 (D2 buffer). After washing in water, the plates were rotated 90°, developed with 1.2 M lithium chloride, 0.5 M Tris-HCl, 8.0 M urea, pH 8.0 (D3 buffer), washed and dried, and then developed with D1 buffer onto a Whatman No. 1 paper wick (3 \times 10 cm). For some experiments, plates were developed in the first direction in D1 buffer onto an 11 \times 35 cm Whatman No. 1 paper wick, rotated 180°, and developed with D2 buffer. These directions are noted in the text. 5'-[32 P]Phospho-3'-phosphodeoxyribonucleotides were visualized by autoradiography, and the *R_f* values were compared with those of authentic dG-C8-AP. The 32 P-containing spots were removed and liquid scintillation counting was used to quantify the 32 P, comparing the samples to the dG-C8-AP standard.

The standard was made using [3 H]1-nitropyrene and *S. typhimurium* TA98. *S. typhimurium* TA98 cultures from overnight plates were harvested by centrifugation, washed with 0.067 M potassium phosphate, pH 7.4, resuspended in the same buffer at 100 mg/mL, and kept on ice. The bacteria were diluted to 10 mg/mL in 0.05 M potassium phosphate, pH 7.4, 0.08 M glucose, and a 9 μ M concentration of the test compound ([3 H]1-nitropyrene, 1-nitropyren-3-ol, 1-nitropyren-6-ol, or 1-nitropyren-8-ol) was added. After shaking for 3 hr at 37°, the bacteria were harvested by centrifugation and washed, and the pellets were frozen at -75°. The DNA was isolated by the standard phenol/chloroform technique. 32 P-Postlabeling was performed as described above. The levels of dG-C8-AP were determined using the specific activity of the [3 H]1-nitropyrene. Calf-thymus DNA reacted with 1-nitropyrene-4,5-epoxide was provided by L. C. King (U.S. Environmental Protection Agency, Research Triangle Park, NC).

HPLC Analysis of [3 H]1-Nitropyrene Metabolism

Analysis of the metabolism of [3 H]1-nitropyrene was accomplished using previously described HPLC techniques [15–21, 23, 24]. Approximately 0.05 μ Ci of [3 H]1-nitropyrene and metabolites was injected onto a 10 μ m μ Bondapak C₁₈ reversed-phase column (0.34 \times 25 cm; Waters Associates, Milford, MA) using a Varian 5500 HPLC (Varian Associates, Walnut Creek, CA) equipped with a Rheodyne 7125 injector. The metabolites were separated using a mobile phase at 1 mL/min of water:ethanol (54:46), increasing to water:ethanol (30:70) in 36 min (linear), followed by a linear increase to ethanol at 5 min. The 3 H was quantified using a flow-through scintillation counter (Flo-One β ; Packard Instruments, Meridian, MA) with Ecolite “+” (ICN) as the scintillant at 2 mL/min. The counting efficiency for 3 H was approximately 34%. Non-radiolabeled 1-nitropyrene and metabolites were routinely co-injected, and retention was determined using UV-VIS absorbance [15–21, 23, 24].

TABLE 1. Comparison of [^3H]1-nitropyrene metabolism in untreated and TCDD-treated HepG2 cells

HepG2 pretreatment	1-Nitropyrene-4,5-diol and -9,10-diol	1-Nitropyren-6-ol and -8-ol	1-Nitropyren-3-ol	1-Aminopyrene	C-OXID/N-REDUC
	(pmol/24 hr/10 ⁶ cells)				
None	37.47 \pm 0.91	76.8 \pm 2.9	50.5 \pm 6.5	516.0 \pm 32.5	0.32
TCDD, 5 nM	13.64 \pm 2.09	449.1 \pm 62.6	40.6 \pm 4.6	6.3 \pm 2.3	79.90

Cells were treated for 24 hr with TCDD or control media, the media was changed to MEM + 2% HI-FBS, and 10 μM [^3H]1-nitropyrene was added for 24 hr. The medium and cells were collected, and [^3H]1-nitropyrene metabolites were determined as described in Materials and Methods, using HPLC techniques. Results are expressed as the means \pm SD for three separate experiments.

RESULTS

Effect of Cytochrome P450 Induction on [^3H]1-Nitropyrene Metabolism in HepG2 Cells

The incubation of HepG2 cells with [^3H]1-nitropyrene resulted in the production of 1-nitropyrene-4,5-diol, 1-nitropyrene-9,10-diol, 1-nitropyren-6-ol, 1-nitropyren-8-ol, 1-nitropyren-3-ol, and 1-aminopyrene (Table 1). This metabolism was linear for 24 hr (data not shown). In nonpretreated HepG2 cells, nitroreduction was responsible for the largest portion of [^3H]1-nitropyrene metabolism, with 1-aminopyrene being formed at three times the level of the C-oxidation metabolites [ratio of oxidative metabolites to 1-aminopyrene (C-OXID/N-REDUC) was 0.32]. In nonpretreated HepG2 cells, C-oxidation of 1-nitropyrene to 1-nitropyren-6-ol and 1-nitropyren-8-ol was preferred over the formation of 1-nitropyren-3-ol, 1-nitropyrene-4,5-diol, and 1-nitropyrene-9,10-diol. Pretreatment of the HepG2 cells with 5 nM TCDD 24 hr prior to the addition of [^3H]1-nitropyrene resulted in an approximately 6-fold increase in 1-nitropyren-6-ol and 1-nitropyren-8-ol formation, and an 82-fold decrease in 1-aminopyrene formation. The C-OXID/N-REDUC ratio increased from 0.32 in the untreated cells to 79.9 in TCDD-induced cells. The pretreatment of HepG2 cells with 2.5 μM 3MC, another cytochrome P450 inducer, resulted in a lower magnitude of

induction of C-oxidation metabolism (3-fold) and a 6.6-fold decrease in aminopyrene formation (data not shown). With 3MC, the C-OXID/N-REDUC ratio increased from 0.6 in untreated HepG2 cells to 9 in 3MC-induced HepG2 cells (data not shown).

The induction of [^3H]1-nitropyrene C-oxidative metabolism in HepG2 cells was dependent on the TCDD concentration, with a maximum increase in 1-nitropyren-6-ol and 1-nitropyren-8-ol formation at 0.5 nM TCDD (Fig. 1). The increase in metabolism occurred solely in the formation of 1-nitropyren-6-ol and 1-nitropyren-8-ol, while the formation of 1-nitropyren-3-ol and 1-nitropyrene-4,5-diol and 1-nitropyrene-9,10-diol was unaffected. Specificity for 1-nitropyrene C-oxidation at the C6 and C8 positions is characteristic of cytochromes P450 1A, which are inducible by TCDD and 3MC [15, 23, 42].

The involvement of cytochrome P450 1A isozymes in the oxidative metabolism of 1-nitropyrene in HepG2 cells is further supported by α -naphthoflavone inhibition of 1-nitropyrene metabolism. α -Naphthoflavone, a specific inhibitor of cytochromes P450 1A [43, 44], inhibited oxidative metabolism of 1-nitropyrene by 70% at 1 μM , 73% at 10 μM , and 93% at 100 μM (Fig. 2). The formation of 1-nitropyren-3-ol was affected only by the inclusion of 100 μM α -naphthoflavone, while the formation of 1-nitropy-

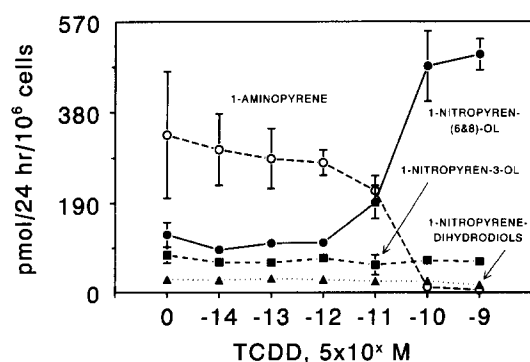


FIG. 1. Effect of TCDD pretreatment on the metabolism of [^3H]1-nitropyrene in HepG2 cells. HepG2 cells were incubated with the indicated concentrations of TCDD for 24 hr, washed, and then 10 μM [^3H]1-nitropyrene was added for another 24 hr. The cells and medium were collected, extracted as described in the text, and analyzed by HPLC techniques. The data are presented as the mean \pm SD of three experiments. Where error bars are not present, the error is smaller than the symbol.

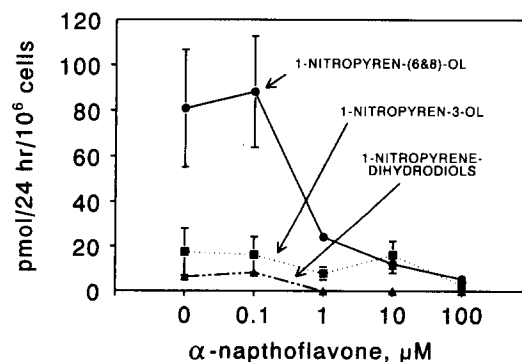


FIG. 2. Effect of α -naphthoflavone on the HepG2 metabolism of [^3H]1-nitropyrene. HepG2 cells were incubated with the indicated concentrations of α -naphthoflavone for 24 hr, washed, and then 10 μM [^3H]1-nitropyrene was added for another 24 hr. The cells and medium were collected, extracted as described in the text, and analyzed by HPLC techniques. The data are presented as the mean \pm SD of three experiments. Where error bars are not present, the error is smaller than the symbol.

ren-6-ol, 1-nitropyren-8-ol, and the *trans*-dihydrodiols was inhibited by 1 μ M α -naphthoflavone.

Previous studies have shown that cytochrome P450 3A isozymes are the predominant cytochromes P450s involved in human microsomal metabolism of 1-nitropyrene [23, 24]. To determine whether cytochrome P450 3A was involved in HepG2 cell metabolism of 1-nitropyrene, inducers and inhibitors of cytochrome P450 3A were incubated with HepG2 cells, and the effect on 1-nitropyrene metabolism was quantified. Dexamethasone is an inducer of several enzymes including cytochromes P450 3A *in vivo* and *in vitro* [45, 46]. Dexamethasone at concentrations from 1 to 10 μ M did not induce C-oxidative metabolism of 1-nitropyrene, with or without charcoal pretreatment of the serum (data not shown). Triacetyloleandomycin is a mechanism-based inhibitor of cytochromes P450 3A [47], and has been shown to inhibit human liver microsomal 1-nitropyrene metabolism [24]. The incubation of HepG2 cells with 50–100 μ M triacetyloleandomycin did not affect 1-nitropyrene metabolism (data not shown). Together, these results suggest that the cytochrome P450 3A subfamily does not participate in HepG2 cell metabolism of 1-nitropyrene.

The increase in 1-nitropyrene C-oxidative metabolism with both 3MC and TCDD treatment of HepG2 cells was accompanied by a concomitant decrease in 1-nitropyrene nitroreduction to 1-aminopyrene (Fig. 1). To determine whether this effect was due to the decreased expression of an enzyme involved in 1-nitropyrene nitroreductive metabolism, the subcellular location of the HepG2 1-nitropyrene nitroreductase was determined and the activity of the fraction in uninduced and TCDD-induced cells was measured. The 1-nitropyrene nitroreductase activity was associated with the cytosolic fraction (90% of total activity), while only 10% of the total 1-nitropyrene nitroreductase activity was present in the microsomal fraction (data not shown). HepG2 cells were then incubated, the cells were isolated and sonicated, and the nitroreductase activity of the subcellular fractions was measured under anaerobic conditions using 10 μ M [3 H]1-nitropyrene as the substrate. Under these conditions, there was no difference in the ability of uninduced or TCDD-induced HepG2 S12 to nitroreduce [3 H]1-nitropyrene to 1-aminopyrene (2.7 ± 1.0 and 3.4 ± 2.3 pmol/min/mg protein, respectively).

These results suggest that the decrease in the ability of HepG2 cells to nitroreduce 1-nitropyrene under TCDD induction was not due to a change in the levels of nitroreductase enzyme(s), but was perhaps due to a competition of enzymes for limiting amounts of 1-nitropyrene when the oxidative pathway is induced. The decrease in nitroreduction of 10 μ M 1-nitropyrene following TCDD treatment of the cells can be minimized by increasing the concentration of 1-nitropyrene (Fig. 3). HepG2 cells were preincubated for 24 hr with 5 nM TCDD, and incubated for another 24 hr with 10, 30, or 55 μ M [3 H]1-nitropyrene. Increasing the [3 H]1-nitropyrene concentration increased the formation of [3 H]1-aminopyrene, indicating that the ability of the TCDD-induced HepG2 cells to nitroreduce

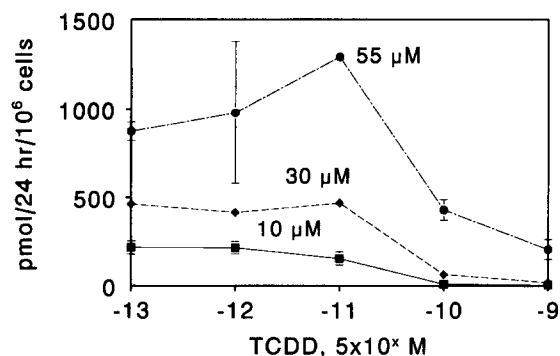


FIG. 3. Effect of [3 H]1-nitropyrene concentration on nitroreductive metabolism. Increasing concentrations of [3 H]1-nitropyrene were added to HepG2 cells to determine if the rate of nitroreduction was dependent on substrate concentration. The data are presented as the mean \pm SD of three experiments. Where error bars are not present, the error is smaller than the symbol.

1-nitropyrene is due to limited levels of 1-nitropyrene in the cells.

Effect of Cytochrome P450 Induction on 1-Nitropyrene DNA Adduct Formation in HepG2 Cells

We sought to determine the identity of the DNA adduct(s) formed by 1-nitropyrene in either uninduced or TCDD-pretreated HepG2 cells. Treatment of HepG2 cells with 1-nitropyrene resulted in the formation of one major DNA adduct, as shown in Fig. 4. The 1-nitropyrene DNA adduct from HepG2 cells co-migrated with the DNA adduct produced following incubation of 1-nitropyrene with *S. typhimurium*, which has been identified as dG-C8-AP [11]. The 1-nitropyrene used to generate the dG-C8-AP adduct in *S. typhimurium* was contaminated with 0.5% 1,6- or 1,8-dinitropyrene. This contamination resulted in the formation of a dinitropyrene DNA adduct(s) in the *S. typhimurium* DNA, which is indicated as dG-C8-ANP in Fig. 4; however, with the same 1-nitropyrene, no dG-C8-ANP adducts were detected in the DNA isolated from HepG2 cells exposed to 1-nitropyrene.

To generate DNA adduct standards for the phenolic metabolites of 1-nitropyrene, *S. typhimurium* TA98 cultures were treated with a 9 μ M concentration of either 1-nitropyren-3-ol, 1-nitropyren-6-ol, or 1-nitropyren-8-ol, and the DNA was isolated. The migration of the corresponding DNA adducts of 1-nitropyren-3-ol, 1-nitropyren-6-ol, 1-nitropyren-8-ol, and 1-nitropyrene-4,5-oxide under our 32 P-postlabeling conditions was determined, and the results are indicated in Fig. 4. None of the phenolic DNA adducts co-migrated with dG-C8-AP. Identical DNA adducts were detected for each phenol when HepG2 cells were incubated separately with purified 1-nitropyren-3-ol, 1-nitropyren-6-ol, and 1-nitropyren-8-ol (data not shown). In neither the uninduced HepG2 cells nor the TCDD-treated HepG2 cells were DNA adducts of the phenols or epoxide detected following incubation with 1-nitropyrene.

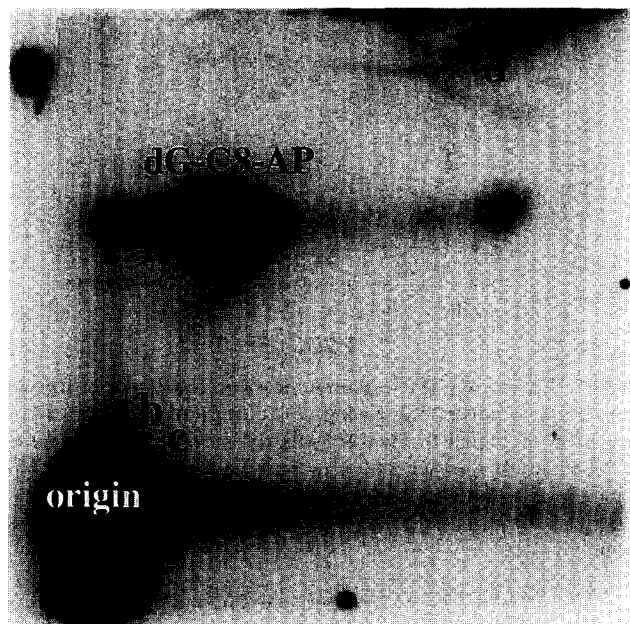


FIG. 4. DNA adduct formation following metabolism of 1-nitropyrene in HepG2 cells. DNA adduct formation was quantified by the ^{32}P -postlabeling technique as described in Materials and Methods. Shown is the chromatogram for HepG2 exposed to 1-nitropyrene, and the origin and location of dG-C8-AP are shown. The migration of the DNA adducts from 1,6-dinitropyrene (a), 1-nitropyren-3-ol (b), 1-nitropyren-6-ol (c), 1-nitropyren-8-ol (c), and 1-nitropyrene-4,5-oxide (d) is indicated in the figure.

Pretreatment of HepG2 cells with TCDD resulted in an increase in the formation of 1-nitropyren-6-ol and 1-nitropyren-8-ol, and a decrease in the formation of 1-aminopyrene (Fig. 1). The DNA was isolated from TCDD-pretreated HepG2 cells incubated with [^3H]1-nitropyrene in order to determine the effect of this change in 1-nitropyrene metabolism on DNA adduct formation. The only DNA adduct detected by the ^{32}P -postlabeling method under these conditions was dG-C8-AP. TCDD treatment alone did not produce ^{32}P -postlabeling detectable DNA adducts (data not shown). TCDD pretreatment of the HepG2 cells resulted in a 99% reduction of the dG-C8-AP adduct in HepG2 cells (Fig. 5), which correlated with the loss of nitroreduction of [^3H]1-nitropyrene.

DISCUSSION

These experiments were initiated to determine the metabolism and DNA adduct formation of 1-nitropyrene in HepG2 cells, and to determine if the HepG2 cells might be a useful *in vitro* model for studying *in vivo* human metabolism and tumorigenicity of 1-nitropyrene.

We previously reported that HepG2 cells metabolize 1-nitropyrene to C-oxidized and nitroreduced metabolites, and that 1-nitropyrene is mutagenic in HepG2 cells [37]. We were unable at that time to determine the DNA adduct responsible for the mutagenicity in HepG2 cells at the HGPRT locus. In the present study, we determined that the

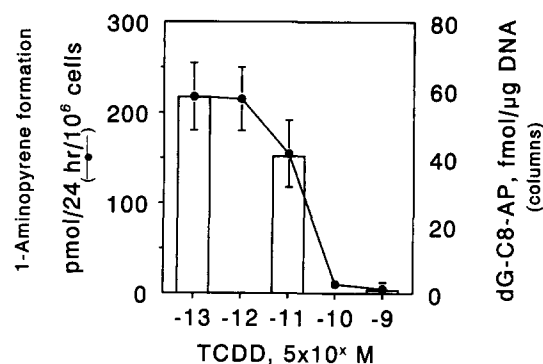


FIG. 5. Comparison of [^3H]1-nitropyrene nitroreduction and dG-C8-AP formation in HepG2 cells following TCDD pretreatment. Data (mean \pm SD) are from three representative experiments measuring [^3H]1-nitropyrene nitroreduction and [^3H]1-nitropyrene DNA adduct formation following 24-hr TCDD induction and 24-hr exposure to $10 \mu\text{M}$ [^3H]1-nitropyrene. Where error bars are not present, the error is smaller than the symbol.

only DNA adduct formed in HepG2 cells following treatment with 1-nitropyrene is dG-C8-AP. This DNA adduct is responsible for 1-nitropyrene mutagenicity in several other prokaryotic and eukaryotic cells [11–14], and evidently is responsible for the 1-nitropyrene mutagenicity reported in HepG2 cells [37]. Therefore, since dG-C8-AP formation is the result of 1-nitropyrene nitroreduction, the presence of a low C-OXID/N-REDUC ratio in cells or tissues would be consistent with an increased likelihood of DNA adduct formation and subsequent mutations.

The metabolism of 1-nitropyrene has been studied extensively using rodent and human microsomes, and in rodents *in vivo*. Most rodent species preferentially metabolize 1-nitropyrene to 1-nitropyren-6-ol and 1-nitropyren-8-ol, positions distal to the nitro group on pyrene. The ratio of 1-nitropyren-6-ol and 1-nitropyren-8-ol to 1-nitropyren-3-ol (proximal to nitro group) formation by rodent liver microsomes has been reported at 1.1 to 5.4 for Sprague-Dawley rats, CF1 mice, B6C3F1 mice, Hartley guinea pigs, Syrian golden hamsters, and New Zealand white rabbits [15–18]. Cytochromes P450 2B and 2C11 are predominantly responsible for untreated rat liver microsomal metabolism of 1-nitropyrene (Howard PC, unpublished observations); however, pretreatment of rats with CYP1A inducers such as 3MC, TCDD, or polychlorinated biphenyl mixtures (e.g. Aroclor-1254) results in increased metabolism of 1-nitropyrene by liver microsomes, and increased generation of 1-nitropyren-6-ol and 1-nitropyren-8-ol [15–18, 35, 42]. The metabolism of 1-nitropyrene by reconstituted rat CYP1A1 or 1A2 has not been reported; however, these data together indicate that although the cytochromes P450 1A are not involved in the C-oxidative metabolism in untreated rat livers, exposure of the rodents to CYP1A inducers results in CYP1A-dependent metabolism of 1-nitropyrene at the C6 and C8 positions forming 1-nitropyren-6-ol and 1-nitropyren-8-ol. These conclusions are consistent with our observations and those of others concerning the

role of CYP1A in 1-nitropyrene metabolism following treatment with CYP1A inducers [15–21, 35, 42, 48–50].

The metabolism of 1-nitropyrene by human cytochromes P450 has been reported with expressed proteins and with liver microsomal samples. Individual human cytochromes P450 were expressed in HepG2 cells using a *Vaccinia* virus expression system [23]. Of the twelve cytochromes P450 tested, cytochromes P450 3A3 and 3A4, and to a lesser extent 2B7, significantly increased the metabolism of 1-nitropyrene with the HepG2 cell lysates, with 1-nitropyren-3-ol being the major metabolite [23]. Cytochrome P450 1A2 did not display any catalytic activity towards 1-nitropyrene with the *Vaccinia* system. In additional studies using sixteen human liver microsomal samples, approximately 85% of the metabolism of 1-nitropyrene occurred through cytochrome P450 3A4, with 1-nitropyren-3-ol being the major metabolite [24]. Therefore, these studies demonstrate that human microsomal metabolism of 1-nitropyrene differs from that of rodents in that the cytochromes P450 3A are involved in the human samples and 1-nitropyren-3-ol is the predominant metabolite.

The levels of cytochrome P450 in untreated HepG2 cells are too low for detection by western or northern blot analysis [51, 52]; however, using reverse-transcription polymerase chain reaction, mRNAs for cytochrome P450 1A1, 1A2, and 3A3 have been detected in HepG2 cells [53]. Specific cytochrome P450 isozymes have also been detected in some studies by using inducers and/or growing the cells on specialized substrates using hormonally supplemented medium [54–56]. Using monoclonal human 3A antibodies and cDNA probes for CYP3A RNA, Schuetz *et al.* [57] showed that the only CYP3A isozyme present in HepG2 cells grown on Matrigel is 3A7, a fetal liver form. This enzyme was measured at levels of 17 pmol/mg microsomal protein, which was 10-fold lower than that detected in human liver. Cytochrome P450 3A7 is glucocorticoid-inducible and shares some substrate specificity with the adult forms of cytochromes P450 3A [58–62]; however, in HepG2 cells grown under our conditions, inducers and inhibitors of cytochrome P450 3A isozymes had little effect on 1-nitropyrene metabolism. This would indicate either that the 3A7 isozyme does not participate in 1-nitropyrene metabolism, as shown for *Vaccinia*-expressed human cytochrome P450 3A5 [23], or that the level of 3A7 expression in our system is too low to contribute significantly to 1-nitropyrene metabolism.

The cytochromes P450 in HepG2 cells are inducible by 3MC and TCDD, and are much less responsive to induction with phenobarbital [62–64]. The prototypical response used to measure CYP1A induction is an increase in either EROD activity or AHH activity. An increase in AHH activity from TCDD in HepG2 cells was initially shown by Cresteil *et al.* [65] who reported that the EC_{50} for TCDD induction was 1 nM. These results were confirmed by Labruzzo *et al.* [66] using similar concentrations of TCDD. Merchant *et al.* [67] demonstrated that a 100-fold increase in HepG2 cell EROD activity with 1 nM TCDD was

accompanied by an increased CYP1A1 mRNA in HepG2 cells. While this study and another by McManus *et al.* [68] suggest that cytochrome P450 1A1 is the only 1A isozyme induced in HepG2 cells, a study by Fukuda *et al.* [53] has shown that CYP1A2 mRNA is detectable upon induction with 3MC. Doodstar *et al.* [62] have also suggested that both isozymes are induced by PAHs in HepG2 cells, since anti-cytochrome P450 1A1 antibodies inhibited 75% of activity in both untreated and benzantracene-induced cells, while anti-cytochrome P450 1A2 antibodies inhibited EROD activity by 50% in HepG2 cell homogenates in untreated groups, and by 25% in benzantracene-induced cells. Furthermore, transfection of the CYP1A2 promoter and CAT gene into HepG2 cells yielded a 2- to 3-fold induction of CAT activity using 2 nM 3MC [69]. These studies suggest that both isozymes are inducible in HepG2 cells, and the role of either in the 3MC- and TCDD-induced HepG2 cell metabolism of 1-nitropyrene cannot be established at this time.

The results from several studies, however, support the conclusion that CYP1A1 and not CYP1A2 is responsible for 1-nitropyrene C-oxidation in HepG2 and human cells. We determined that the rates of rabbit CYP1A1 and CYP1A2 catalyzed C-oxidation of 1-nitropyrene were 2.2 and 0.09 nmol/min/nmol P450, respectively [15]. A similar result was reported with a different nitro-PAH, 3-nitrofluoranthene, where the CYP1A1 and CYP1A2 catalyzed C-oxidation rates were 2.1 and 0.4 nmol/min/nmol P450, respectively [42]. Additionally, HepG2 cell lysates containing *Vaccinia*-expressed CYP1A2 did not catalyze the C-oxidation of 1-nitropyrene [23]. The role of CYP1A2 in human liver microsome C-oxidative metabolism must be minor since approximately 85% of human liver microsome metabolism of 1-nitropyrene is catalyzed by CYP3A4 [24]. Together these results suggest that the liver-specific CYP1A2 does not contribute to the C-oxidative metabolism of 1-nitropyrene; however, the CYP1A1 that is expressed in several extrahepatic tissues [70] could contribute to extrahepatic 1-nitropyrene C-oxidation.

1-Nitropyrene is an environmental contaminant that has shown marginal carcinogenic activity in rodents. Ohgaki *et al.* [71] originally reported 1-nitropyrene induced injection site sarcomas in adult male F344 rats; however, a later report indicated that the carcinogenicity was due to 0.8% contamination of the 1-nitropyrene with dinitropyrene isomers, and that administration of 40 mg of highly purified 1-nitropyrene was not tumorigenic [72]. 1-Nitropyrene was not tumorigenic when painted on 4- to 5-week-old CrI/CD-1(ICR)BR mice [73], and was not tumorigenic when peritoneally injected or skin-painted onto 7-week-old SEN-CAR mice [74]. 1-Nitropyrene did not produce tumors following subcutaneous injection in BALB/c mice [75], nor did it produce tumors when injected into the lungs of F344/DuCrj rats [76]. However, suprascapular injection of 1-nitropyrene in newborn S/D rats produced injection site histiocytomas in 28–32% of the rats, and mammary adenocarcinomas in the females [77, 78]. Both intraperitoneal

and subcutaneous injection of 1-nitropyrene into weanling female CD rats resulted in the development of mammary fibroadenomas [79], while liver carcinomas were detected in newborn B6C3F1 mice treated with 1-nitropyrene [80]. These studies suggest that 1-nitropyrene is tumorigenic when administered to newborn rodents; however, it is not tumorigenic when administered to adult rodents.

The liver cytochrome P450 content of rabbits does not increase until 4 weeks of age, and increases in the rat at day 15 [81–83]. This correlates with an increase in rat liver microsomal 1-nitropyrene C-oxidation at day 12 (Howard PC, unpublished observation). At this time, the ontogenic expression of the rodent nitroreductases has not been reported. Therefore, the reduced cytochrome P450 expression in the newborn (low C-OXID/N-REDUC) and the considerably higher cytochrome P450 expression in adult liver (high C-OXID/N-REDUC) offer one possible explanation for the difference in 1-nitropyrene tumorigenicity. In newborn rodents, low cytochrome P450 expression would allow more 1-nitropyrene to be reduced to the proximate carcinogenic form (hydroxylamine) than in the adult rodent where abundant cytochromes P450 are present. Therefore, as with the HepG2 cells, dG-C8-AP formation would be favored in the newborn and not in the adult rodent. While these studies suggest one explanation for the 1-nitropyrene tumorigenicity differences in newborn and adult rodents, further studies involving cytochrome P450 expression in newborn rats are required to substantiate this observation.

One of the goals of this study was to develop an *in vitro* model for the *in vivo* metabolism and mutagenicity of 1-nitropyrene. The TCDD-pretreated HepG2 may serve as a model for rodent metabolism of 1-nitropyrene, since cytochrome P450-mediated C-oxidation results predominantly in the formation of 1-nitropyren-6-ol and 1-nitropyren-8-ol [15–18]. The TCDD-pretreated HepG2 model may not be a good surrogate for human metabolism of 1-nitropyrene since human liver microsomal metabolism of 1-nitropyrene is through cytochrome P450 3A4, resulting in the formation of predominantly 1-nitropyren-3-ol [24]. In the present studies, 1-nitropyren-6-ol and 1-nitropyren-8-ol are predominantly formed in TCDD-pretreated HepG2. Our results have demonstrated that the formation of phenolic metabolites of 1-nitropyrene in the HepG2 does not result in DNA adduct formation, and only nitroreduction results in DNA adduct formation (Fig. 4). As a result, the TCDD-pretreated HepG2 may serve as a model for *in vivo* metabolism and mutagenicity, since the critical determinant in DNA adduct formation is the ratio of C-oxidation (detoxification) to nitroreduction (activation).

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