The therapeutic benefits of the antidepressant nefazodone have been hampered by several cases of acute hepatotoxicity/liver failure. Although the mechanism of hepatotoxicity remains unknown, it is possible that reactive metabolites of nefazodone play a causative role. Studies were initiated to determine whether nefazodone undergoes bioactivation in human liver microsomes to electrophilic intermediates. Following incubation of nefazodone with microsomes or recombinant P4503A4 in the presence of sulfhydryl nucleophiles, conjugates derived from the addition of thiol to a monohydroxylated nefazodone metabolite were observed. Product ion spectra suggested that hydroxylation and sulfhydryl conjugation occurred on the 3-chlorophenylpiperazine-ring, consistent with a bioactivation pathway involving initial formation of p-hydroxynefazodone, followed by its two-electron oxidation to the reactive quinone-imine intermediate. The formation of novel N-dearylated nefazodone metabolites was also discernible in these incubations, and 2-chloro-1,4-benzoquinone, a by-product of N-dearylation, was trapped with glutathione to afford the corresponding hydroquinone-sulfhydryl adduct. Nefazodone also displayed NADPH-, time-, and concentration-dependent inactivation of P4503A4 activity, suggesting that reactive metabolites derived from nefazodone bioactivation are capable of covalently modifying P4503A4. A causative role for 2-chloro-1,4-benzoquinone and/or the quinone-imine intermediate(s) in nefazodone hepatotoxicity is speculated. Although the antianxiety agent buspirone, which contains a pyrimidine ring in place of the 3-chlorophenyl-ring, also generated p-hydroxybuspirone in liver microsomes, no sulfhydryl conjugates of this metabolite were observed. This finding is consistent with the proposal that two-electron oxidation of p-hydroxybuspirone to the corresponding quinone-imine is less favorable due to differences in the protonation state at physiological pH and due to weaker resonance stabilization of the oxidation products as predicted from ab initio measurements.

2-[3-[4-(3-Chlorophenyl)-1-piperazinyl]propyl-5-ethyl-2,4-dihydro-4-(2-phenoxethyl)-3H-1,2,4-triazol-3-one (nefazodone) (Fig. 1) was approved as an antidepressant in the United States in late 1994. Nefazodone is structurally distinct from selective serotonin reuptake inhibitors, tri- and tetracyclics, and monoamine oxidase inhibitors. Nefazodone derives its clinical efficacy by inhibiting serotonin and norepinephrine reuptake and by antagonizing the postsynaptic 5-hydroxytryptamine 2-receptor and α1-adrenergic receptors (Eison et al., 1990).

However, despite its therapeutic benefits, there are several reported cases of idiosyncratic adverse reactions including hepatobiliary dysfunction and cholestasis that are associated with the use of this drug (Aranda-Michel et al., 1999; Lucena et al., 1999; García-Pando et al., 2002; Stewart, 2002; Andrade and Lucena, 2003; Choi, 2003). The U.S. Food and Drug Administration has received reports of at least 55 cases of liver failure, including 20 deaths, and another 39 cases of less severe liver injury since nefazodone sales commenced in 1994. Although the exact cause of hepatotoxicity by nefazodone is currently unknown, a probable causal link between nefazodone use and hepatic injury has been established based on the temporal relationship between nefazodone administration and the onset of hepatotoxicity in most cases. Furthermore, liver biopsy specimens from a patient who succumbed to the hepatic injury revealed marked centrazonal necrosis, which is consistent with a toxic etiology (García-Pando et al., 2002).

The principal clearance mechanism of nefazodone in humans involves intestinal and hepatic metabolism catalyzed by cytochrome P450 3A4 (Mayol et al., 1994; Greene and Barbhaiya, 1997; von Moltke et al., 1999; Rotzinger and Baker, 2002). Of particular interest...
in the many biotransformation pathways of nefazodone is the aromatic hydroxylation, which occurs para to the piperazinyl nitrogen affording p-hydroxynefazodone (metabolite 1) (Fig. 1), which has been detected as a circulating metabolite in plasma following oral administration to humans and in vitro microsomal incubations (Kaul et al., 1995; von Moltke et al., 1999). In addition, 1-(m-chlorophenyl)piperazine (m-CPP), which results from the N-dealkylation of nefazodone (Mayol et al., 1994; von Moltke et al., 1999; Rotzinger and Baker, 2002), undergoes further P450 2D6-mediated oxidation, yielding p-hydroxy-m-CPP (metabolite 2) (see Fig. 1) (Rotzinger et al., 1998). We postulated that metabolites 1 and 2 are oxidatively bioactivated to the corresponding quinone-imine species 3 and 4, respectively (Fig. 1), and that these reactive species may play a role in nefazodone-induced hepatic necrosis. It is noteworthy to point out that, like nefazodone, the antianxiety drug (8-[4-[4-(2-pyrimidinyl)-piperazinyl]butyl]-8-azaspiro[4,5]-decane-7,9-dione (buspirone) also undergoes a P450 3A4-catalyzed aromatic hydroxylation that occurs para to the piperazinyl nitrogen leading to p-hydroxybuspirone (metabolite 5) (Fig. 1) (Gammans et al., 1986; Jajoo et al., 1989; Kivisto et al., 1997). Furthermore, buspirone-N-dealkylation generates the corresponding 1-(2-pyrimidinyl)piperazine (1-PP) metabolite (Mayol et al., 1985; Caccia et al., 1986), which upon further oxidation furnishes p-hydroxy-1-PP (metabolite 6) (Fig. 1) (Jajoo et al., 1989; von Moltke et al., 1998). These hydroxylated metabolites also can undergo further two-electron oxidation to generate an electrophilic quinone-imine intermediate (e.g., intermediate 7). However, despite the similarity in oxidative biotransformation pathways of nefazodone and buspirone, there are no documented reports on idiosyncratic hepatotoxicity associated with buspirone use in the clinic.

Consequently, we examined the ability of nefazodone and buspirone and their respective metabolites m-CPP and 1-PP to undergo oxidative bioactivation in human liver microsomes and recombinant P450 enzymes. The studies reported here provide evidence that the p-hydroxylated metabolite of nefazodone, but not of buspirone, is indeed metabolically activated in vitro and that this activation is catalyzed by P450 3A4.

**Materials and Methods**

**Chemicals.** Nefazodone hydrochloride, buspirone hydrochloride, 1-PP, 2-chloro-1,4-benzoquinone, NADPH, reduced glutathione (GSH), and reduced glutathione ethyl ester (GSH-EE) were purchased from Sigma-Aldrich (St. Louis, MO). m-CPP hydrochloride was purchased from Avocado Research Chemicals Ltd. (Lancashire, UK). Recombinant human P450 3A4 and 2D6 isozymes, coexpressed with NADPH-P450 oxidoreductase in baculovirus-insect cells, were obtained from BD Gentest (Woburn, MA).

**Human Liver Microsomal Preparations.** Microsomal fractions were prepared from human livers (International Institute for the Advancement of Medicine, Jessup, PA) using standard protocols. Protein concentrations were determined using the bicinchoninic acid assay method (Pierce Chemical, Rockford, IL). Total P450 content was measured according to published protocols (Oamura and Sato, 1964), and human liver microsomes were characterized using P450-specific marker substrate activities. Human liver microsomes were isolated from 56 individual livers, and aliquots from the individual preparations were pooled on the basis of equivalent protein concentrations to yield a representative microsomal pool.

**Microsomal Incubations.** Stock solutions of the test compounds were prepared in methanol. The final concentration of methanol in the incubation media was 0.2% (v/v). Incubations were carried out at 37°C for 60 min in a shaking water bath. The incubation volume was 1 ml and consisted of the following: 0.1 M potassium phosphate buffer (pH 7.4), human liver microsomes (P450 concentration = 0.5 μM) or recombinant enzymes (25 pmol of P450 1A2, P450 2D6, P450 2C9, P450 3A4, or P450 2C19), NADPH (1.2 mM), and substrate (20 μM). The reaction mixture was prewarmed at 37°C for 2 min before adding NADPH. GSH (5 mM) or GSH-EE (5 mM) was added 3 min after initiation of the reaction with NADPH. Incubations that lacked either NADPH or GSH/GSH-EE served as negative controls, and reactions were terminated by the addition of ice-cold acetonitrile (1 ml). The solutions were centrifuged (3000g, 15 min), and the supernatants were dried under a steady nitrogen stream. The residue was reconstituted with mobile phase and analyzed for metabolite formation by liquid chromatography/tandem mass spectrometry (LC/MS/MS).

**Characterization of the GSH-EE Conjugate(s) of 2-Chloro-1,4-benzoquinone.** Human liver microsomes (P450 concentration = 0.3 μM) containing nefazodone (100 μM), GSH-EE (1 mM), and NADPH (1.2 mM) in 100 mM potassium phosphate buffer (pH 7.4) were incubated for 30 min at 37°C. The final incubation volume was 250 μl. Samples without either NADPH or nefazodone were used as negative controls. Incubations of synthetic 2-chloro-
1,4-benzoquinone (100 μM) and GSH-EE (1 mM) in 100 mM potassium phosphate buffer (pH 7.4) were also conducted for 30 min at 37°C in the absence or presence of microsomes containing NADPH. The reactions were quenched by the addition of acetonitrile (375 μL) and after centrifugation (3000g, 15 min), the supernatant was concentrated under a steady nitrogen stream. Sulfhydril conjugates were extracted from each sample using a Waters Oasis HLB 96-well microextraction solid phase extraction plate (Waters, Milford, MA). A 384-channel personal-150 pipettor fitted with a 96-channel head (Apricot Designs Inc., Monrovia, CA) was used during solid phase extraction (SPE) to facilitate solvent transfer. The SPE plate was conditioned by passing methanol (200 μL), followed by water (200 μL), through each of the SPE cartridges. To initiate solvent flow through the absorbent, vacuum was applied to the receiving side of the SPE plate using a 96-well extraction manifold (Tomtec, Orange, CT). Samples were added to the 96-well plate and washed with water (200 μL). Analyte was desorbed using 40:60 (v/v%) acetonitrile/isopropanol (100 μL). The desorption solvent was collected in a 96-well polypropylene plate. Solvent was evaporated using a 96-channel EvaporE VX-192 evaporator (Apricot Designs Inc.) utilizing nitrogen as a drying gas. Samples were reconstituted with 5:95:0.05 (v/v/v%) acetonitrile/water/formic acid, 5 mM ammonium formate (50 μL) before analysis.

**P450 3A4 Inhibition Studies in Human Liver Microsomes.** For non-preincubation (time-independent) P450 3A4 inhibition, a pooled human liver microsomal preparation (P450 concentration = 0.25 μM) was incubated with midazolam (3 μM) and nefazodone at concentrations ranging from 0.5 to 50 μM at 37°C for 5 min in the presence of NADPH (1.2 mM). For preincubation-dependent (time-dependent) inhibition, microsomes (P450 concentration = 0.25 μM) were incubated with nefazodone at concentrations ranging from 0.5 to 50 μM in the presence of NADPH (1.2 mM) for 30 min at 37°C, after which incubation with midazolam (3 μM) was carried out for 5 min. To determine whether the preincubation-dependent inhibition also was NADPH-dependent, a third incubation in which NADPH was absent during the preincubation period was carried out. Incubations were quenched by the addition of acetonitrile containing a proprietary internal standard (0.2 μg/mL) (molecular weight = 580, clofibrate = 5.96). Remaining P450 3A4 activity, as measured by the formation of 1'-hydroxymidazolam, was determined by LC/MS/MS. Inhibition studies were conducted in triplicate.

**Computational Methods.** Ab initio calculations were performed using the Gaussian 03 quantum chemistry package (Gaussian Inc., Wallingford, CT). The geometry of N-methyl-1-(3-chloro-4- hydroxyphenyl)piperazine and N-methyl-1-(4-hydroxy pyrimidyl)piperazine motifs was optimized at the B3LYP/6-31G* level of theory in vacuum. Single-point energy calculations were performed utilizing the polarized continuum model (Cancès et al., 1997; Cossi et al., 1998) to represent aqueous solution. The cavity sizes were described by the UAHF (united atom for Hartree-Fock) atomic radii method (Barone et al., 1997).

**LC/MS/MS Assay for 1'-Hydroxymidazolam Analysis.** 1'-Hydroxymidazolam formation was assessed on a Micromass Quattro Ultima (Waters) triple quadrupole mass spectrometer in line with a Hewlett Packard Series 1100 HPLC system (Hewlett Packard, Palo Alto, CA). Analytes were chromatographed on a Phenomenex Primesphere 5-μm C18 30 × 2.0 mm column (Phenomenex, Torrance, CA) using a 2-min gradient consisting of a mixture of 95% water/5% acetonitrile with 0.1% formic acid (solvent A) and 95% acetonitrile/5% water with 0.1% formic acid (solvent B) and a flow rate of 1.0 to 1.5 mL/min. The LC gradient was programmed as follows. Solvent A to solvent B ratio was held at 95:5 (v/v) until sample injection and then adjusted to 95:5 (v/v) at 0.15 min, and the flow rate was increased to 1.5 mL/min. The mobile phase was held at 95:5 (v/v) for 1 min. The gradient was then returned to a solvent ratio (A/B) of 95:5 (v/v) and a flow rate of 1 mL/min until the end of the run. Postcolumn flow was split such that mobile phase was introduced into the mass spectrometer via an electrospray interface at a rate of 30 to 45 μL/min. The remaining flow was diverted to waste. A CTC PAL autosampler (LEAP Technologies, Carrboro, NC) injected 20 μL of sample onto the HPLC system. Under these conditions, 1'-hydroxymidazolam and the internal standard eluted at 0.9 and 1.0 min, respectively. Ionization was conducted in the positive ion mode at a source temperature of 120°C and a desolvation temperature of 350°C. The capillary voltage was set to 3.50 kV and the cone voltage was optimized at 25 V, and the collision energy was adjusted to −12 eV. 1'-Hydroxymidazolam and proprietary internal standard were analyzed using multiple reaction monitoring (MRM) at the anticipated mass transitions [M]+→202 and [M]+→317, respectively. The assay had a dynamic range of 0.003 to 10.0 μg/mL.

**LC/MS/MS Assay for Identification of Nefazodone Metabolites.** Metabolites were identified by LC/electrospray ionization (ESI)-MS. The LC system consisted of a Phenomenex phenyl-hexyl column (5 μm, 4.6 × 100 mm), a Finnigan Surveyor LC system comprising a high-performance liquid chromatograph with a built-in degasser, autosampler, UV detector, and a Finnigan LCQ-Classic ion trap mass spectrometer (Thermo Finnigan, San Jose, CA). The UV detector was set to scan between 240 and 260 nm, the mass spectrometer was auto-tuned with nefazodone in the positive ion mode, and data-dependent scans were acquired up to MS3 with dynamic exclusion parameters set to 5 scans and an exclusion time limit of 0.5 min. A constant flow rate of 1.0 mL/min was used. Samples were injected on the column equilibrated in 10% acetonitrile/90% 5 mM ammonium formate (pH 3.0) and held for 5 min under these conditions. The acetonitrile concentration was then ramped linearly at 1.33%/min up to 90% and held at this condition for 5 min, and then returned to the original conditions. Nefazodone and its identifiable metabolites eluted in the first 30 min. Metabolites were identified in the full scan mode (from m/z 100 to 850) by comparing t = 0 samples to t = 60-min samples (with or without cofactor), and structural information was generated from the CID spectra of the corresponding molecular ions (MH+) and/or comparison with synthetic standards.

**LC/MS/MS Assay for GSH and GSH-EE Conjugate Formation.** Metabolites were identified by electrospray LC/MS/MS using a Finnigan TSQ Quantum Ultra mass spectrometer (Thermo Finnigan) in conjunction with a Finnigan Surveyor LC system comprising a high-performance liquid chromatograph with a built-in degasser, autosampler, and UV detector. Argon was used as a nebulizing and heating gas. Analytes were introduced into the electrospray source via a Zorbax SB-C8 4.6 × 150 mm column at a flow rate of 0.7 mL/min. Separation of the analytes was achieved using a gradient consisting of 10 mM ammonium formate, 0.1% formic acid (solvent A), and acetonitrile (solvent B). The LC gradient was programmed as follows. Solvent A to solvent B ratio was held at 100:0 (v/v) for 3 min and then adjusted from 100:0 (v/v) to 10:90 (v/v) for 32 min and from 10:90 (v/v) to 100:0 (v/v) from 35 to 40 min. The column was re-equilibrated for 6 min before the next analytical run. Postcolumn flow was split such that mobile phase was introduced into the mass spectrometer via an electrospray interface at a rate of 50 μL/min. The remaining flow was diverted to the PDA detector to provide simultaneous UV detection (λ = 240–260 nm) and total ion chromatogram. The capillary temperature was 250°C, and CID analyses were performed using a collision energy of 30 eV. Sulfhydril conjugates of nefazodone were identified in the full scan mode (from m/z 100 to 850) by comparing t = 0 samples to t = 60-min samples (with or without cofactor or sulfydryl trapping agent), and structural information was generated from the CID spectra of the corresponding protonated molecular ions. To improve sensitivity, conjugates were further covalently modified by MS2 followed by MS3 fragmentation, corresponding to the loss of the pyroglutamate moiety (loss of 12 mass units): p-hydroxynefazodone-GSH conjugate, 791→662; p-hydroxynefazodone-GSH-EE conjugate, 819→690; p-hydroxy-4’-CPP-GSH conjugate, 518→389; p-hydroxy-4’-CPP-GSH-EE conjugate, 546→417; p-hydroxybuspirone-GSH conjugate, 707→578; p-hydroxybuspirone-GSH-EE conjugate, 735→606; para-hydroxy-1-PP-GSH conjugate, m/z 486→357; and para-hydroxy-1-PP-GSH conjugate, m/z 514→385.

**Characterization of the GSH-EE Conjugate of 2-Chloro-1,4-benzoquinone by MicroESI.** A capillary liquid chromatography system (Dionex Corp., Sunnyvale, CA) was used for the analysis. The autosampler module was configured to inject sample from 96-well plates. Chromatography was performed in a Vydac 300 μm i.d. × 5 cm C18 column that contained 5-μm particles with a pore size of 300 Å (Grace Vydac, Hesperia, CA). GSH-EE conjugates were chromatographed using a binary mobile phase consisting of acetonitrile/ammonium formate (5 mM)formic acid (10:90:0.05, v/v/v) (solvent A) and acetonitrile/ammonium formate (5 mM)formic acid (80:20:0.05, v/v/v) (solvent B) at a flow rate of 0.5 μL/min. Following injection of 0.6 μL of sample, a starting mobile phase composition of 90% solvent system A/10% solvent system B was increased linearly to 40% solvent system A/60% solvent system B from 0 to 5 min. From 5 to 10 min, the percentage of solvent system B was held isocratic. At 10 min, the solvent system was returned to 90% solvent
system A/10% solvent system B and the column was allowed to re-equilibrate for 5 min before the next injection. A Thermo Finnigan Quantum triple quadrupole mass spectrometer with an orthogonal electrospray ionization interface was used in the analysis. MicroESI was initiated by applying voltage of 3.8 kV (positive polarity). MicroESI spray stability was enhanced using a sheath gas (nitrogen) setting of 5 psi. The auxiliary gas pressure and source transfer capillary temperature were maintained at 0 and 250°C, respectively, throughout the study. The ESI probe was held at a position that placed it as close to 90° from the entrance of the sweep cone as possible. The GSH-EE conjugate(s) of 2-chloro-1,4-benzoquinone was characterized by MRM detection of anticipated mass transition corresponding to the loss of the pyroglutamate moiety (loss of 129 mass units) from the parent molecular ion of the conjugate (MH⁺ = 478).

Results
Metabolite Identification Studies. Nefazodone. Figure 2 shows chromatograms of the MS total ion current and UV absorption (λ = 240–260 nm) for extracts from NADPH-supplemented human liver microsomal incubations with nefazodone (20 μM). Consistent with previous reports on nefazodone metabolism in human liver microsomes (von Moltke et al., 1999) and in vivo (Mayol et al., 1994), product ion spectra of the monohydroxylated metabolites established the 3-chlorophenylpiperazine motif or the ethyl group on the 5-ethyltriazol-3-one moiety (Rt = 24.92 min; Fig. 2) as the site(s) of oxidation. Additional metabolites derived from nefazodone N-dealkylation, including 5-ethyl-2-(3-hydroxypropyl)-4-(2-phenoxyethyl)-2,4-dihydrotriazol-3-one (Rt = 21.50 min; Fig. 2) and its oxidation product 3-(3-ethyl-5-oxo-4-(2-phenoxyethyl)-4,5-dihydrotriazolyl)propionic acid (Rt = 18.57 min; Fig. 2), were also detected in the incubates as previously reported (Mayol et al., 1994). Of interest to the present studies was the detection of 1 (MH⁺ = 486, Rt = 22.84 min), m-CPP (MH⁺ = 197, Rt = 9.35 min), and 2 (MH⁺ = 213, Rt = 2.85 min). The product ion spectrum obtained by CID of the molecular ion (MH⁺) of 1 is displayed in Fig. 3. The Rt and product ion spectrum of m-CPP was identical to that observed with the synthetic standard, whereas the product ion spectrum of 2 was consistent with that reported in the literature (Mayol et al., 1994).

Of considerable interest were our current observations on the formation of three novel nefazodone metabolites 8, 9, and 10 that eluted at Rt = 8.87 min, 10.63 min, and 4.03 min, respectively (see Fig. 2). The characteristic chlorine isotope pattern observed with the parent compound was missing in the three metabolites. Metabolite 8 displayed a protonated molecular ion (MH⁺) at 360, 110 mass units lower than the MH⁺ for nefazodone. The formation of 8 was not observed in control incubations lacking NADPH, implicating the involvement of P450 in its formation. The product ion spectrum (Fig. 4) obtained by CID of the molecular ion (MH⁺) for 8 indicated fragment ions at m/z 274, 246, and 140 that corresponded with the phenoxethyl-5-ethyltriazolone propyl moiety. Based on the CID data, the metabolite 8 was tentatively identified as the product of O-dearylation of the 3-chlorophenyl-ring in nefazodone (see Fig. 4). Metabolite 9 displayed a protonated molecular ion (MH⁺) at 374, 96 mass units lower than the MH⁺ for nefazodone and 14 mass units higher than the MH⁺ for 8. This observation suggested that 9 was derived from the further oxidation of 8. The product ion spectrum obtained by CID of the molecular ion (MH⁺) for 9 indicated fragment...
ions at m/z 288, 260, 246, 168, and 140 (Fig. 5). The fragment ion at m/z 288 was consistent with the addition of 14 mass units to the fragment ion at m/z 274 observed in the product ion spectra of 8. This fragment ion indicated that the piperazine ring in 9 was unaltered. The fragment ions 246 and 140 corresponded with the phenoxethyl-5-ethyltriazolone-ethyl moiety, implying that this region of the molecule remained unchanged. Based on these observations, metabolite 9 was tentatively identified as the amide metabolite obtained by the further oxidation of 8 (see Fig. 5). Metabolite 10 displayed a protonated molecular ion (MH⁺) at 376, 94 mass units lower than the MH⁺ for nefazodone and 16 mass units higher than the MH⁺ for 8. This observation suggested that 10 was a monohydroxylated derivative of 8. The presence of the fragment ion at m/z 290 in the product ion spectrum of 10 suggested that the piperazine ring was not the site of monohydroxylation (Fig. 6). The detection of fragment ions at m/z 262 and 170 was consistent with monohydroxylation on the 5-ethyltriazolone substituent. Addition of TiCl₃ to the microsomal incubation did not lead to the disappearance of the metabolite signal, suggesting that 10 was not derived from N-oxidation of the triazolone nitrogen. Therefore, we proposed hydroxylation of the ethyl group in 8 as the probable structure for 10 (see Fig. 6).

Separate incubations of nefazodone in recombinant P450 isozymes including P450 1A2, 2C9, 2C19, 2D6, and 3A4 revealed that only P450 3A4 catalyzed the oxidative metabolism of buspirone in humans (Gammans et al., 1986; Jajoo et al., 1989). Individual incubations of buspirone in several recombinant P450 isozymes indicated that only P450 3A4 catalyzed the conversion of buspirone to reactive metabolites. The origins of the characteristic ions are as indicated.

Buspirone. Consistent with previous reports on buspirone metabolism in humans (Gammans et al., 1986; Jajoo et al., 1989), metabolite identification studies in NADPH-supplemented human liver microsomes indicated the presence of N-dealkylated and several mono- and dihydroxylated metabolites of the parent compound. A full scan total ion chromatogram and UV (λ = 240–260 nm) of an NADPH-supplemented human liver microsomal incubation with buspirone (20 μM) is depicted in Fig. 7. The Rₜ and product ion spectrum of 1-PP (MH⁺ = 165, Rₜ = 10.04 min) and 6 (MH⁺ = 181, Rₜ = 8.43 min) were identical to those of their respective synthetic standards. The metabolite at Rₜ = 17.89 min (MH⁺ = 402) was tentatively identified as 5 on the basis of the following observations. First, the diagnostic fragment ions in the mass spectrum at m/z 265 and 222 that corresponded with the butylazaspirodecaneone substituent implied that this region of the molecule was unaltered. Furthermore, the fragment ion at m/z 138, which was indicative of the addition of 16 mass units to the fragment ion at m/z 122 (corresponding with the pyrimidinyl piperazine ring cleavage fragment) observed in the mass spectrum of buspirone and 6, was consistent with hydroxylation on the pyrimidinyl ring system. Finally, the assignment of the para regiochemistry for pyrimidine ring hydroxylation was assumed based on the unambiguous identification of 5 and several of its downstream metabolites in humans (Gammans et al., 1986; Jajoo et al., 1989). Individual incubations of buspirone in several recombinant P450 isozymes indicated that only P450 3A4 catalyzed the oxidative metabolism of buspirone (data not shown). The role of P450 3A4 in buspirone metabolism is
consistent with the in vivo observations on the marked increases in buspirone plasma concentrations in humans pretreated with selective P4503A4 inhibitors including grapefruit juice, erythromycin, and itraconazole (Kivisto et al., 1997; Lilja et al., 1998).

**Formation of GSH and GSH-EE Conjugates.** Reduced GSH and a close analog of GSH, reduced GSH-EE, were used as exogenous nucleophiles in human liver microsomal incubations to trap reactive metabolites of the test compounds. Reduced GSH-EE was also chosen based on the recent report (Soglia et al., 2004) on the improved sensitivity in conjugate detection with the ethyl ester derivative of GSH relative to the free carboxylic acid analog.

**Nefazodone.** LC/MS/MS analysis of NADPH-supplemented human liver microsomal incubations containing nefazodone and GSH led to the detection of a single conjugate, 11 ($R_t = 16.9$ min), with a molecular ion (MH$^+$) at 791 (Fig. 8A). The molecular weight of this conjugate was consistent with the addition of GSH to a monohydroxylated nefazodone metabolite. The product ion spectrum obtained by CID of the MH$^+$ at m/z 791 produced fragment ions at m/z 662, 518,
274, and 140 (Fig. 8B). The presence of the fragment ions at m/z 274 and 140 established that the N-propyl-5-ethyl-2,4-dihydro-4-(2-phenoxethyl)-triazolone substituent in nefazodone was unaltered (see Fig. 8B), indicating that hydroxylation and subsequent GSH conjugation had occurred on the 3-chlorophenylpiperazine-ring system. The fragment ion at m/z 662 corresponded with the loss of the pyroglutamate moiety, which represents a characteristic fragment ion derived from GSH conjugates (Baillie and Davis, 1993). The fragment ion at m/z 518 was assigned as a cleavage adjacent to the cysteinyl thioether moiety with charge retention on the hydroxynefazodone residue. The occurrence of the fragment ion at m/z 518 is consistent with the presence of an aromatic thioether motif in 11 (Baillie and Davis, 1993). A proposed structure for 11 that is consistent with the observed mass spectrum is shown in Fig. 8. The assignment of the para regiochemistry for aromatic hydroxylation in 11 is based upon the report by von Moltke et al. (1999), which demonstrated the exclusive formation of 1 from nefazodone in human liver microsomes. The corresponding ortho- and meta-isomers were not detected.

When GSH was replaced with GSH-EE in the microsomal incubations, conjugate 12 eluting at R<sub>t</sub> = 18.1 min (MH<sup>+</sup> = 819) was observed (Fig. 9A). The molecular weight of 12 was once again consistent with the addition of GSH-EE to a monohydroxylated nefazodone metabolite. The product ion spectrum obtained by CID of the MH<sup>+</sup> for 12 produced fragment ions at m/z 690, 518, 274, and 140 (Fig. 9B). The fragment ions at m/z 274 and 140 established that hydroxylation and subsequent GSH conjugation had occurred on the 3-chlorophenylpiperazine-ring system (Fig. 9B). Based on this information and the characteristic fragment ion at m/z 690 (loss of pyroglutamate) and at m/z 518 (aromatic thioether bond cleavage), the proposed structure for 12, analogous to 11, is depicted in Fig. 9. Furthermore, GSH and GSH-EE conjugates 11 and 12 of 1 were only formed in incubation mixtures containing recombinant P450 3A4. The formation of 11 and 12 was not observed in incubations containing recombinant P450 1A2, 2C9, 2C19, and 2D6.

**Buspirone.** LC/MS/MS analysis of NADPH-supplemented human liver microsomal or recombinant P450 3A4 incubates of buspirone and GSH or GSH-EE in the full scan or in the MRM mode (5-GSH conjugate, m/z 707→578; 5-GSH-EE conjugate, m/z 735→606; loss of the pyroglutamate moiety) did not indicate the formation of GSH and/or GSH-EE conjugates of 5.

**m-CCP and 1-PP.** LC/MS/MS analysis of NADPH-supplemented human liver microsomal incubations of m-CCP or 1-PP and GSH or GSH-EE in the full scan or MRM mode (2-GSH conjugate: m/z 518→389; 2-GSH-EE conjugate, m/z 546→417; 6-GSH conjugate, m/z 486→357; 6-GSH-EE conjugate, m/z 514→385; loss of the pyroglutamate moiety) did not indicate the formation of GSH and/or GSH-EE conjugates of 2 and 6, respectively. Likewise, no conjugates were detected when m-CCP and 1-PP were incubated with recombinant P450 2D6, the enzyme primarily responsible for the para aromatic hydroxylation of m-CCP and 1-PP.

**Evidence for the Formation of 2-Chloro-1,4-benzoquinone in Liver Microsomal Incubations of Nefazodone: Characterization of the Sulfydryl Conjugate(s) of 2-Chloro-1,4-benzoquinone.** The

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**Fig. 8.** Representative LC/MS/MS chromatogram (A) and product ion spectrum (B) obtained by CID of the MH<sup>+</sup> ion (m/z 791) of 11 (R<sub>t</sub> = 16.9 min) in NADPH-supplemented human liver microsomal incubations. The origins of the characteristic ions are as indicated.

**Fig. 9.** Representative LC/MS/MS chromatogram (A) and product ion spectrum (B) obtained by CID of the MH<sup>+</sup> ion (m/z 819) of 12 (R<sub>t</sub> = 18.1 min) in NADPH-supplemented human liver microsomal incubations. The origins of the characteristic ions are as indicated.

**Fig. 10.** Representative LC/MS/MS analysis of a solid phase-extracted sample following incubation of nefazodone (100 μM) in NADPH-supplemented human liver microsomes in the presence of GSH-EE (1 mM) (A), incubation of 2-chloro-1,4-benzoquinone (100 μM) with GSH-EE in phosphate buffer (B), and incubation of 2-chloro-1,4-benzoquinone (100 μM) in NADPH-supplemented human liver microsomes in the presence of GSH-EE (1 mM) (C).
possibility that N-dearylization of nefazodone results in the liberation of the electrophilic 2-chloro-1,4-benzoquinone was also examined in NADPH-supplemented human liver microsomes containing nefazodone (100 μM) and GSH-EE (1 mM). LC/MS/MS analysis using the anticipated mass transition (m/z 478 → m/z 349) that corresponds to the loss of the pyroglutamate moiety from the GSH-EE conjugate of 2-chloro-1,4-benzoquinone (compound 15) led to the detection of a prominent peak at R_t = 7.21 min (Fig. 10A). This peak was also observed upon nonenzymatic reaction of commercially available 2-chloro-1,4-benzoquinone (100 μM) with GSH-EE (1 mM) in phosphate buffer (Fig. 10B) and upon incubating 2-chloro-1,4-benzoquinone (100 μM) and GSH-EE (1 mM) in the presence of NADPH-supplemented human liver microsomes (Fig. 10C). The product ion spectrum obtained by CID of the MH^+ ion (m/z 478) of 15 (R_t = 7.21 min) from NADPH-supplemented human liver microsomal incubations containing nefazodone (100 μM) and GSH-EE (1 mM) (A), chemical reaction of 2-chloro-1,4-benzoquinone (100 mM) and GSH-EE (1 mM) in phosphate buffer (B), and incubation of 2-chloro-1,4-benzoquinone (100 μM) in NADPH-supplemented human liver microsomes in the presence of GSH-EE (1 mM) (C). The origins of the characteristic ions are as indicated.

**Inhibitory Effect of Nefazodone on Human Liver Microsomal Midazolam-1′-Hydroxylase Activity.** Figure 12 shows the effect of varying concentrations of nefazodone on P450 3A4-mediated midazolam-1′-hydroxylation in human liver microsomes both with and without preincubation of microsomes with the antidepressant. The magnitude of enzyme inhibition was higher when the experiment was carried out with preincubation in the presence of NADPH. The IC_{50} value for the time-independent inhibition of P450 3A4 activity by nefazodone was 45.5 ± 12.8 μM, whereas the IC_{50} value for the time-dependent inhibition of P450 3A4 activity by nefazodone was 3.21 ± 0.90 μM. When NADPH was omitted from the preincubation inhibition studies, the IC_{50} value for the time-independent inhibition of P450 3A4 activity by nefazodone was 42.4 ± 19.6 μM. These data suggested that nefazodone is an NADPH- and time-dependent inhibitor of P450 3A4 activity in human liver microsomes.

**Ab Initio Predictions of the Relative Oxidative Stability of N-Methyl-1-(3-chloro-4-hydroxy)phenylpiperazine and N-Methy-1-(4-hydroxy-2-pyrimidinyl)imino.** Ab initio quantum chemical calculations were performed to estimate the relative oxidative stability of the (3-chloro-4-hydroxy)phenylpiperazine and the 1-(4-hydroxy-2-pyrimidinyl)imino piperazine ring system in nefazodone and buspirone, respectively. For the purpose of simplicity, the analysis was performed on the corresponding N-methyl derivatives of p-hydroxy-m-CPP and p-hydroxy-1-PP. Furthermore, considering that the reported pK_a values of trazodone [a nefazodone analog that also contains the 1-(3-chlorophenyl)piperazine ring] and buspirone are 6.13 ± 0.04 (Ruiz et al., 2003) and 7.60 ± 0.01 (Takacs-Novak and Avdeef, 1996), respectively, it was assumed for the calculations that at physiological pH (7.4), N-methyl-1-(3-chloro-4-hydroxy)phenylpiperazine (A) would exist primarily in the deprotonated state, whereas N-methyl-1-(4-hydroxy-2-pyrimidinyl)imino (B) would exist primarily in the protonated state as shown in Table 1. The energetics of the sequential thermodynamic steps involving the two-electron oxidation of A and B to the corresponding quinone-imines was studied (Table 1). Step I depicts the first single-electron transfer step in the oxidation of A and B in aqueous medium, and step II illustrates subsequent hydrogen atom abstraction from the phenolic hydroxyl group to generate the corresponding quinone imines. The relative oxidative stability of A and B was evaluated by calculating the free energy difference for A and B for each thermodynamic step, so that for reaction N, ΔΔG(N) = ΔG(N → B) − ΔG(N → A). Calculation of the relative free energies ΔΔG(N) (Table 1) of the reactions allowed counterbalancing contributions and corrections such as zero-point and thermal corrections to the molecular free energies, which were not considered in the current theoretical study.

Our experimental observation that p-hydroxybuspirone (5) does not undergo further two-electron oxidation to the corresponding quinone-imine 7 in a manner similar to that observed with p-hydroxynefazodone (1) is consistent with the ab initio calculations on the simple N-methyl derivatives, which suggest both oxidation steps to be significantly less favorable for buspirone. A plausible explanation for the oxidative stability differences is that the stronger aromatic nature of the 3-chloro-4-hydroxyphenyl ring in 1, relative to the 4-hydroxy pyrimidine group in 5, leads to oxidation product(s) of greater stability. Another explanation is the pK_a differences between the two compounds; buspirone is protonated at physiological pH, whereas nefazodone is charge-neutral. Therefore, electron transfer in the case of 5 (or molecule B) is less favored relative to 1 (or molecule A). To test this hypothesis, calculations were also performed with the neutral form of molecule B. Although this process dramatically lowers ΔΔG for the initial electron transfer step, the overall calculated free energy difference for both steps together is only reduced by about half (data not shown). These observations suggest that the differences in the protonation states of the p-hydroxylated metabolites of nefazodone
and buspirone at physiological pH and the difference in the resonance stabilization of the subsequent two-electron oxidation products could contribute about equally to the observed experimental difference in reactivity.

**Discussion**

The results from our current investigation clearly demonstrate the bioactivation of the 3-chlorophenylpiperazine motif in nefazodone to the reactive quinone-imine species 3, which can be trapped by GSH or the corresponding GSH-EE derivative. This investigation is the first to report on the bioactivation of nefazodone. Apart from the literature reports on the exclusive involvement of P450 3A4 in the metabolism of nefazodone in humans, our studies also demonstrated a key role for the heme microsomes remains unclear. One possibility is that the aromatic thioether conjugates undergo hydrolysis across the iminium bond, resulting in the formation of the aromatic thiocarbonyl compound. Evidence for the formation of the electrophilic 2-chloro-1,4-benzoquinone was also obtained via characterization of the corresponding GSH-EE conjugate 15 (see Fig. 13). Additional studies designed to probe the mechanism of N-dearylation in greater detail are currently in progress. In the light of literature reports on the cytotoxicity (Moore et al., 1987) and genotoxicity (Westmoreland et al., 1992) observed with structurally diverse 1,4-benzoquinone derivatives, we speculate that 2-chloro-1,4-benzoquinone and quinone-imine 3 may contribute to the etiology of nefazodone hepatotoxicity. The reason(s) for the lack of metabolic activation of the para-hydroxy-m-CPP metabolite 2 of nefazodone in human liver microsomes remains unclear. One possibility is that 2 escapes from the active site of the P450 prior to the bioactivation step.

Although not investigated in this preliminary analysis, it is reasonable to expect that the reactive quinone-imine or p-benzoxoquinone intermediates will form covalent adducts to hepatic proteins, with potentially deleterious consequences. That the potency of P450 3A4 inhibition by nefazodone significantly increases with time certainly provides preliminary evidence for covalent adduct formation with the enzyme that results in its inactivation. On the basis of the time-dependent P450 3A4 inhibition data, it is tempting to speculate that the nonlinear pharmacokinetics of nefazodone in humans after q.i.d. and b.i.d. dose escalation (Barbhaiya et al., 1995a, 1996; Kaul et al., 1995) occur due to autoinactivation of P450 3A4, the primary enzyme responsible for nefazodone metabolism in humans. The P450 3A4 inactivation data in our studies are consistent with the clinical data that suggest that nefazodone may be an inhibitor of P450 3A4 in vivo to a significant extent. A plethora of examples on the pharmacokinetic interactions of nefazodone with diverse P450 3A4 substrates such as triazolam (Barbhaiya et al., 1995b), alprazolam (Greene et al., 1995), carbamazepine (Ashton and Wolin, 1996), cyclosporine (Helms-Smith et al., 1996; Wright et al., 1999), terfenadine (Abernethy et al., 2001), astemizole (Dresser et al., 2000), and tacrolimus (Olyaei et al., 1998) has appeared in the literature.

The lack of bioactivation of buspirone despite heteroaromatic hydroxylation para to the piperazinyl nitrogen is consistent with our ab initio calculations that suggest that a weaker resonance stabilization of the oxidation products and the greater acidity make p-hydroxybuspi- rone less favorable for the two-electron oxidation. Overall, these observations appear to correlate with the lack of idiosyncratic hepatotoxicity with buspirone in the clinic. Finally, the observed differences in the bioactivation of the phenyl- and the pyrimidinylpiperazine ring systems is consistent with the notion that the 2-aminoxypridine or 2-aminoxyprimidinamide derivatives present a “safer” alternative to aniline-based compounds, which are prone to bioactivation. However, additional examples may be required to further validate this hypothesis.

**TABLE 1**

Relative free energies of thermodynamic oxidation steps for N-methyl-1-(3-chloro-4-hydroxyphenyl)piperazine (A) and N-methyl-1-(4-hydroxyphenylmethyl)piperazine (B)

<table>
<thead>
<tr>
<th>Thermodynamic step (N)</th>
<th>ΔΔG(N) (^{a}), kCal/mol</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>13.4</td>
</tr>
<tr>
<td>II</td>
<td>7.1</td>
</tr>
<tr>
<td>I + II</td>
<td>20.5</td>
</tr>
</tbody>
</table>

*ΔΔG(N) = ΔG(N-B) - ΔG(N-A), where ΔG(N-X) is the calculated free energy difference for the reaction N-X.*

![Diagram of reaction steps](image-url)
**Fig. 13.** Proposed mechanisms for the P450-catalyzed dearylation reaction of nefazodone resulting in the liberation of the electrophilic 2-chloro-1,4-benzoquinone.

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**References**


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