

Induction of CYP2B1/2 and nicotine metabolism by ethanol in rat liver but not rat brain

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Abstract

A higher proportion of alcoholics than non-alcoholics smoke (>80 vs 30%). In animals, chronic administration of alcohol induces tolerance to some effects of nicotine. To investigate if chronic ethanol (EtOH) induces alterations in CYP2B1/2 and nicotine C-oxidation activity, male rats (N = 4–6/group) were treated once daily with saline or EtOH (0.3, 1.0, and 3.0 g/kg, p.o./by gavage) for 7 days. A quantitative immunoblotting assay was developed to detect CYP2B1/2 in the brain, where constitutive expression is low, and in the liver. Using this method, it was determined that EtOH did not alter CYP2B1/2 protein expression significantly in six brain regions (olfactory bulbs, olfactory tubercles, frontal cortex, hippocampus, cerebellum, and brainstem). However, a dose-dependent induction of CYP2B1/2 protein expression was detected in the liver. Significant induction of 2-, 3-, and 2.7-fold were observed for the 0.3, 1.0, and 3.0 g/kg doses, respectively. Increases were also observed in CYP2B1 mRNA, which was induced by 14, 38, and 43% at the same doses. Liver microsomal nicotine C-oxidation also was increased (1.3 to 4.5-fold). CYP2B selective inactivators demonstrated that approximately 70% of nicotine C-oxidation was mediated by CYP2B1/2 in both EtOH-induced and uninduced hepatic microsomes. In summary, chronic, behaviorally relevant doses of EtOH induce CYP2B1/2 protein, mRNA, and nicotine C-oxidation activity in rat liver but not in rat brain, and these increases could contribute to cross-tolerance and co-abuse of ethanol and nicotine. © 2001 Elsevier Science Inc. All rights reserved.

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1. Introduction

CYPs are a family of heme-containing drug-metabolizing enzymes that are involved in the biotransformation of xenobiotics, environmental contaminants, dietary components, and procarcinogens [1–3]. Rat *CYP2B1/2*, mouse *Cyp2b9/10*, and human *CYP2B6* share approximately 80% nucleotide sequence identity [4]. CYP2B enzymes metabolize a diverse group of compounds including pesticides [5], chemotherapeutics such as cyclophosphamide [6], tobacco-specific nitrosamines (NNK, NMA, NDMA) [7,8], tricyclic antidepressants [4], drugs of abuse such as cocaine [9], and

nicotine [10]. In humans, nicotine is metabolized primarily by hepatic CYP2A6 [11], due to low and variable expression of CYP2B6, which has higher nicotine-metabolizing activity [12]. In rats, nicotine is metabolized primarily by CYP2B1/2, which also has a low level of constitutive expression; rat CYP2A enzymes do not metabolize nicotine [13].

Hepatic CYP2B enzymes are inducible by a variety of structurally diverse compounds such as barbiturates [14], pesticides [15], acetone, isosafrole, and pregnenolone-16 α -carbonitrile [16]. Induction of CYP2B enzymes has been correlated with tumor promotion and increased hepatocarcinogenesis [17,18], perhaps due to their role in the activation of a number of procarcinogens such as aminoanthracene, benzo[a]pyrene [16], and tobacco-specific nitrosamines such as NDMA, NNK, and NMA [7,8].

CYP2B enzymes are also expressed in the brain [19]. CYP2B1/2 enzymes are functional in this organ [20], and are expressed in a region- and cell-specific manner at levels approximately 100-fold lower than in the liver [21]. The

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Abbreviations: CYP, cytochrome P450; C8 xanthate, potassium octylxanthate; NCO, nicotine C-oxidation; NDMA, *N*-nitrosodimethylamine; NMA, *N*-nitroso-*N*-methylamine; NNK, 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone; and SSC, saline–sodium citrate buffer.

expression of CYP2B1/2 can be modulated by centrally acting agents, and may alter the local metabolism of these drugs at their site of action [22]. For example, chronic nicotine can increase CYP2B1/2 protein and activity in several brain regions but not in the liver [23,24]. This could lead to increased nicotine clearance in close proximity to central nicotinic receptors.

A much higher proportion of alcoholics smoke (80–95%) relative to non-alcoholics (25–30%), and 70% of those are heavy smokers [for a review, see Ref. 25]. Alcoholics, as well as social drinkers, consume more cigarettes per day than non-alcohol-consuming smokers [26–28]. Recently, nicotine and alcohol dependence were shown to have substantial common genetic susceptibility, suggesting common underlying causes for the two [29]. Alcoholics report marked tolerance to nicotine and more severe symptoms of nicotine withdrawal when compared with non-alcohol-dependent smokers [30]. Cross-tolerance between ethanol and nicotine has also been observed in animal models [31]. Because smokers titrate their smoking behavior to maintain plasma and central nicotine levels [32], tolerance can lead to increased consumption [25].

Mechanisms by which cross-tolerance occur include changes in target receptors or altered drug metabolism. While acute ethanol appears to stabilize nicotinic receptors in the desensitized state, changes in [³H] nicotine and [¹²⁵I] α -bungarotoxin binding to central nicotinic receptors appear to be modest or non-existent, even after prolonged ethanol administration [31,33,34]. CYP2B1/2 protein and/or mRNA increase after prolonged dietary consumption of high-dose ethanol [35]; however, it is not known whether this occurs at behaviorally relevant doses, whether this result is dose-dependent, or if the increase in CYP2B1/2 protein specifically translates into increased metabolism of nicotine.

The aim of this study was to determine whether short-term, behaviorally relevant doses of ethanol increase CYP2B1/2 protein and mRNA in rat brain and/or liver. A second aim was to determine if the ethanol-induced increases in CYP2B1/2 expression resulted in changes in nicotine metabolism; peripheral or central increases in nicotine metabolism could contribute to the increased smoking observed in alcoholics and social drinkers.

2. Materials and methods

2.1. Materials

Protease inhibitor tablets and Chemiluminescence Blotting Substrate were purchased from Roche Diagnostics. Recombinant baculovirus-expressed CYP2B1 Supersomes and phenobarbital-induced rat liver microsomes were purchased from the Gentest Corp. ProtranTM nitrocellulose membranes were purchased from Schleicher & Schuell Inc. Rat tissue adsorbed biotinylated anti-mouse IgG secondary antibody was purchased from Vector Laboratories Inc., and

NeutravidinTM-conjugated horseradish peroxidase was purchased from the Pierce Chemical Co. The protein assay kit, pre-stained molecular markers, and Zeta-Probe nylon membrane were purchased from Bio-Rad Laboratories. A Strata-prep Total RNA Mini-prep kit was purchased from Stratagene. Yeast tRNA was purchased from GibcoBRL. C8 xanthate was custom synthesized by Toronto Research Chemicals. 5-Methylnicotine was provided by Peyton Jacob III (University of California). Nicotine bitartrate and 8-methoxypsoralen were purchased from Sigma-Aldrich Canada Ltd.

2.2. Animals

Saline, and ethanol (in saline) at doses of 0.3, 1.0, and 3.0 g/kg body weight (N = 4–6 per group), was administered by gavage to adult male Wistar rats (250–300 g; Charles River) once daily for 7 days. Animals were decapitated 4 hr following administration of the last drug dose. Livers were removed, frozen immediately in liquid nitrogen, and stored at –80° until processed for RNA, protein, and activity studies. Brains were dissected on ice into regions (olfactory bulbs, olfactory tubercles, frontal cortex, hippocampus, cerebellum, and brainstem, according to Paxinos and Watson's stereotaxic atlas of the brain [36]), immediately frozen in liquid nitrogen, and stored at –80°. These brain regions were studied because they express nicotinic receptors, and are involved in mediating the central effects of ethanol and nicotine [37,38]. All experimental procedures used in this study were carried out in accordance with guidelines for the care and use of laboratory animals and approved by the Animal Care Committee of the University of Toronto.

2.3. Membrane preparation

For immunoblotting, whole membrane preparations were used because CYPs in the brain, including CYP2B1/2 are located in both the microsomal and mitochondrial fractions [23,39]. Membranes of liver tissue and brain regions were prepared as described previously [23], aliquoted into small volumes, and stored at –80°.

For nicotine metabolism studies, hepatic microsomal preparations were prepared according to established techniques [40]. Protein concentrations were determined according to the instructions of the manufacturer. The cytosolic fractions were pooled and used as a source of aldehyde oxidase [11].

2.4. Immunoblotting

To determine the linear range of detection for the assay, untreated brainstem and liver membranes were diluted serially and used to construct standard curves. Membrane proteins from brain regions and livers (40 μ g) were separated by SDS–PAGE (4% stacking and 8% separating gels), and transferred overnight onto nitrocellulose membranes.

Insect-cell expressed CYP2B1 and phenobarbital-induced rat liver microsomes were used as standards. Membranes were preincubated for 1 hr in a blocking solution containing 3% skim milk powder (w/v), 1% BSA (w/v), and 2% normal rat serum (v/v) in TBST [50 mM Tris (pH 7.4), 150 mM NaCl, 0.1% (v/v) Triton X-100]. Membranes were probed with a monoclonal antibody to rat CYP2B1 (1:3000 dilution), which has been characterized previously [41] (provided by Harry V. Gelboin, NCI, NIH). Membranes were incubated with a secondary (rat tissue adsorbed) biotinylated anti-mouse antibody (1:2000 dilution), followed by incubation with a tertiary Neutravidin™-conjugated horseradish peroxidase (1:30,000 dilution). All antibodies were suspended in a solution of 1% BSA (w/v) in TBST. Membranes were washed in TBST following each antibody incubation step. Control blots were incubated without primary antibody. Protein bands were detected by enhanced chemiluminescence. Membranes were exposed to Kodak X-OMAT-AR film for 0.5 to 2 min. Immunoblots were analyzed using an imaging system (Imaging Research Inc.).

2.5. RNA analysis

RNA was isolated using guanidinium thiocyanate [42] as described by the supplier (Stratagene). RNA quantity and quality were analyzed by the ratio of optical density (260/280 UV wavelength), and agarose gel electrophoresis. For slot blot analysis, a standard curve (0.03 to 0.25 μ g) was generated using total RNA isolated from a phenobarbital-treated rat liver expressing high levels of CYP2B mRNA [43]. Signals detected from all samples were within the linear range of the system. Initial experiments indicated that addition of yeast tRNA to total RNA reduced background and improved the linearity of the system. Therefore, yeast tRNA was added to all samples such that the final amount of RNA in each well was equal to 10 μ g (5.0 to 7.5 μ g of tRNA was added to 2.5 to 5.0 μ g of total RNA). RNA pooled from four animals (by amount of total RNA) was applied directly to nylon membranes under vacuum and denaturing conditions using a Bio-Dot microfiltration apparatus according to the instructions of the manufacturer. Membranes were preincubated (>60 min) at 43° in pre-hybridization buffer [50% formamide, 120 mM Na_2HPO_4 (pH 7.2), 7% SDS, and 250 mM NaCl], and hybridized (1×10^7 cpm in 5 mL of pre-hybridization buffer) with a random-primed (^{32}P)dCTP full-length rat CYP2B1 cDNA generously (provided by Curtis J. Omiecinski, University of Seattle) for 16 hr at 43°. Blots were washed at room temperature for 15 min, each sequentially in $2 \times \text{SSC}$ with 0.1% SDS, $0.5 \times \text{SSC}$ with 0.1% SDS, and $0.1 \times \text{SSC}$ with 0.1% SDS, and then exposed to Kodak X-OMAT-AR film for 24–48 hr at -80° . Blots were then stripped of probe by washing twice for 5 min each at 95° in $0.1 \times \text{SSC}$ with 0.5% SDS. Re-hybridization proceeded as described above, using a randomly-labeled rat β -actin probe. All films were analyzed using an imaging system from Imaging Research Inc.

2.6. NCO activity and chemical inhibition assays

NCO activity was assayed according to the method of Messina *et al.* [11] for human liver microsomes with the following modifications. Incubation mixtures contained 1 mM NADPH and 20 μ L of rat liver cytosol (a source of aldehyde oxidase) in Tris–HCl buffer (pH 7.4). Incubations were carried out at 37°. The reaction was stopped, 5-methyl nicotine (50 μ L of 2 μ g/mL) was added as the internal standard, samples were extracted with 3 mL dichloromethane, and the organic phase was dried under nitrogen. Samples were reconstituted with 200 μ L of 0.01 M HCl, and 50 μ L of each sample was subjected to HPLC analysis with a UV detector (set at 260 nm). Separation of nicotine and metabolites was achieved using a Supercosil LC-8DB column (5 μ m, 150×4.6 mm, Supelco) and a mobile phase consisting of acetonitrile:potassium phosphate buffer [10:90 (v/v), pH 4.6] containing 1 mM octanesulfonic acid and 0.5% (v/v) triethylamine. The separation was performed with isocratic elution at a flow rate of 1 mL/min. The retention times for nicotine, cotinine, and 5-methyl nicotine were 4.1, 5.1, and 7.4 min, respectively. CYP2B1 nicotine-to-cotinine kinetics were performed by incubating 0.55, 1, 1.7, 3, 5.5, 10, 1.7, 30, 55, and 100 μ M (*S*)-nicotine with 5 pmol of expressed CYP2B1 for 20 min. Standard curves were created for cotinine (0.13 to 4.2 μ M). Chemical inhibition studies were conducted in conjunction with nicotine assays. Samples of 1.0 mg of hepatic microsomal protein (pooled from four animals by protein concentration) or 5 pmol expressed CYP2B1 were preincubated with either 24 μ M C8 xanthate or 29 μ M 8-methoxypsoralen, or vehicle controls (HCl buffer or methanol, respectively) for 15 min at 30°. Incubations also contained 20 μ L rat cytosol, 1 mM NADPH, and Tris–HCl buffer. Nicotine metabolism was then initiated with 25 μ M (*S*)-nicotine, and proceeded as described above. Nicotine and inhibitor concentrations were chosen based on K_m and K_i values for the compounds (approximately $3.5 \times K_m$, and $10 \times K_i$ for nicotine and inhibitors, respectively [44,45]). Negative controls consisted of incubations without NADPH or with heat-denatured microsomal protein.

2.7. Statistics

Treatment groups were considered to be significantly different from control if $P < 0.05$, using unpaired Student's *t*-tests. Correlation analysis was performed using a Pearson correlation co-efficient (R value) followed by a Fisher *z*-test.

3. Results

3.1. CYP2B1 in rat brain

An immunoblotting assay was developed in order to detect CYP2B1/2 in brain tissue where constitutive expres-

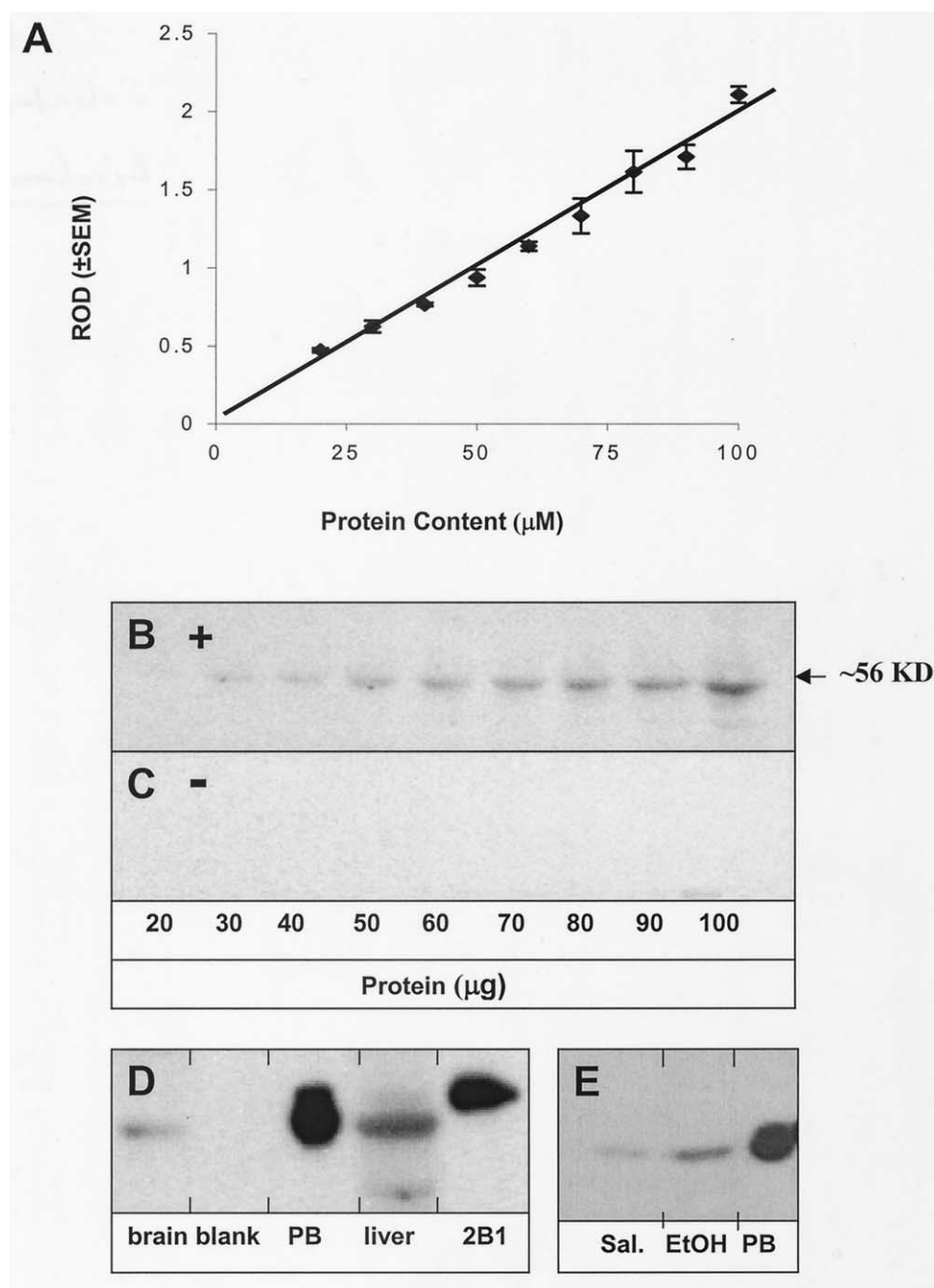


Fig. 1. Immunoblotting assay for CYP2B in rat brain. (A) A dilution curve of untreated rat brainstem CYP2B1/2 protein detected by western blotting (\pm SEM, 4 experiments). (B and C) Representative immunoblots incubated with (B) and without (C) primary antibody. (D) Immunodetectable CYP2B1 protein from brain co-migrated with a band from untreated and phenobarbital-treated (PB) rat liver microsomes. The migration of insect-cell expressed CYP2B1 (2B1) was slightly slower. The blank contained only loading buffer. (E) Relative induction of CYP2B1 by ethanol (2.5-fold), and PB (approximately 150-fold). ROD = relative optical density, as determined by image analysis.

sion is low. The CYP2B1 reactive signal detected in these tissues was linear with the amount of protein loaded up to 100 μ g of protein (Fig. 1, A and B), and selectivity was confirmed by incubating immunoblots without primary antibody (Fig. 1C). A CYP2B1 reactive signal could not be detected below 20 μ g of brain membranes loaded. The immunoreactive band from brain tissues co-migrated with a band from untreated and phenobarbital-treated rat liver mi-

croosomes, while insect-cell expressed CYP2B1 migrated slightly more slowly (Fig. 1D). A second immunoreactive band of lower mobility was detected in phenobarbital-treated liver microsomes, and is probably CYP2B2 which is slightly larger than CYP2B1, with lower expression (approximately 10-fold lower, undetectable in brain tissue) [21,24]. Ethanol at the highest dose administered (3 g/kg) did not alter CYP2B1 levels significantly in six brain re-

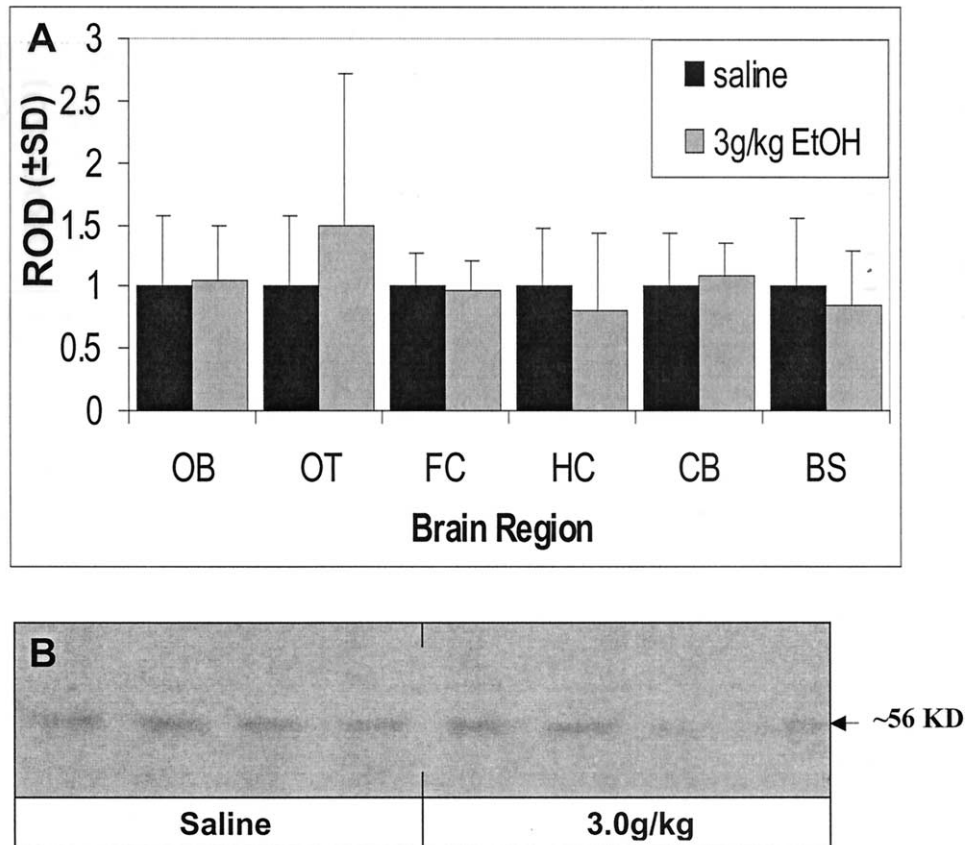


Fig. 2. CYP2B1/2 expression in six brain regions following chronic ethanol treatment. (A) Means (\pm SD) of six animals/group; saline means from each brain region were adjusted to equal 1 ROD unit, and standard deviations were adjusted by the same proportion. (B) Representative immunoblot from rat hippocampus, showing data from four saline and four ethanol-treated rats (3 g/kg), indicating the lack of induction by ethanol. Abbreviations: OB, olfactory bulbs; OT, olfactory tubercles; FC, frontal cortex; HC, hippocampus; CB, cerebellum; BS, brainstem.

gions (frontal cortex, olfactory bulbs, olfactory tubercles, hippocampus, cerebellum, and brainstem), when compared with saline controls (Fig. 2, A and B). A slight increase was observed for the olfactory tubercles, but this effect did not reach significance, most likely due to high interindividual variation (Fig. 2A).

3.2. Dose-dependent induction of CYP2B1 protein in rat liver by ethanol

A serial dilution also was performed with untreated rat liver membranes (data not shown). Ethanol dose-dependently induced CYP2B1 protein in rat liver whole membranes (Fig. 3). CYP2B1 protein was increased by 2.0-fold ($P < 0.05$), 3.0-fold ($P < 0.001$), and 2.7-fold ($P < 0.001$) compared with saline controls for 0.3, 1.0, and 3.0 g/kg doses, respectively. The magnitudes of induction were similar to those observed for the ethanol-inducible CYP2E1 (1.6-, 1.9-, and 2.4-fold for the three doses, respectively) in the same animals.¹ By comparison, liver microsomes from phenobarbital-treated rats (commercial preparation, see Ma-

terials) showed approximately a 150-fold induction in CYP2B1 protein (Fig. 1E); although the assay was not optimized for this level of expression, this value is in agreement with reported values [43].

3.3. Dose-dependent induction of CYP2B1 mRNA in rat liver by ethanol

Linear detection of CYP2B1 mRNA signal measured by slot blotting was established using serial dilution of phenobarbital-treated rat liver containing high levels of CYP2B mRNA [43]; all subsequent measurements were within the linear range of the assay (Fig. 4A). No detectable signal was observed with tRNA alone. CYP2B1 mRNA was induced significantly by chronic ethanol at all three doses (Fig. 4, B and D). Significant increases of 1.14-, 1.38-, and 1.43-fold (relative to saline) were observed for 0.3 ($P < 0.05$), 1.0 ($P < 0.001$), and 3.0 ($P < 0.001$) g/kg of ethanol, respectively (Fig. 4, B and D). Phenobarbital-treated rat liver RNA (used to construct the serial dilution curve and to serve as a positive control) showed a 25-fold induction of CYP2B1 mRNA (Fig. 4A). Blots were stripped and re-probed for β -actin mRNA (Fig. 4C), and no significant differences in

¹ Howard L and Tyndale R, unpublished results.

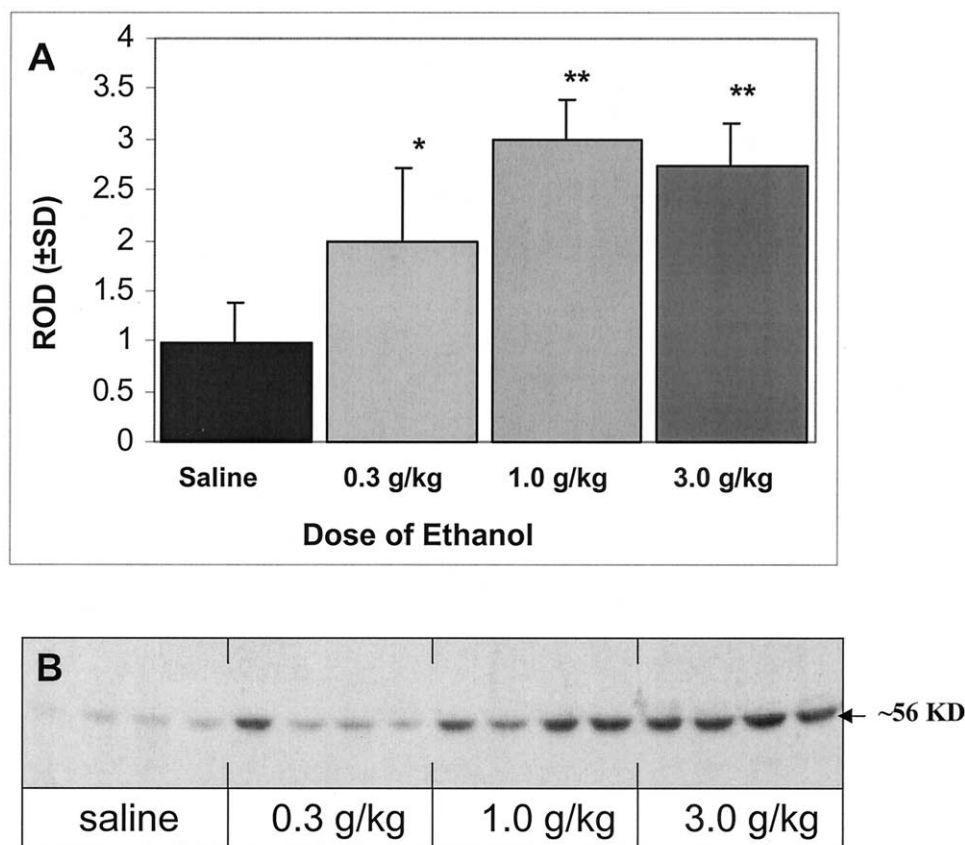


Fig. 3. Dose-dependent induction of CYP2B1 protein by ethanol in rat liver. (A) Dose-response for saline and three doses of ethanol; means (\pm SD) of four animals/group, and (B) representative immunoblot. The saline group was adjusted to equal 1 ROD unit; other groups (\pm SD) were adjusted by the same proportion. Significant differences from saline are indicated by: (*) $P < 0.05$, and (**) $P < 0.001$.

loading were detected between the saline and the ethanol treatment groups (ANOVA, $P = 0.34$). CYP2B mRNA levels correlated significantly with protein expression across the four treatment groups ($R = 0.96$, $P = 0.05$).

3.4. Induction of nicotine metabolism by ethanol in rat liver microsomes

Microsomes from the same livers used in the preceding experiments were analyzed for NCO to the major metabolite cotinine. Initial experiments determined protein concentrations and incubation times that resulted in linear production of cotinine with less than 15% nicotine disappearance. Microsomes incubated without NADPH or heat-denatured microsomes produced no detectable cotinine. Expressed CYP2B1 had a K_m of 7 μ M and a V_{max} of 0.074 μ mol cotinine/pmol CYP2B1/min (Fig. 5).

Ethanol dose-dependently induced NCO activity in rat liver microsomes (Fig. 6A). At 25 μ M nicotine (approximately 3.5 times the K_m), NCO was increased by 2.4-fold ($P < 0.005$), 1.3-fold ($P < 0.05$), and 4.5-fold ($P < 0.05$) compared with saline in the 0.3, 1.0, and 3.0 g/kg ethanol-treated microsomes, respectively (Fig. 6A). Nicotine metabolism was only weakly correlated to CYP2B1/2 protein for

saline and the three ethanol doses ($R = 0.43$, $P = 0.65$). This was due primarily to the relatively low induction of nicotine metabolism (1.3-fold) for the 1.0 g/kg dose (Fig. 6A); the cause of this is unknown. The correlation between nicotine metabolism and CYP2B1 protein increased considerably when this dose was not included in the analysis ($R = 0.98$, $P < 0.05$). A similar relationship was observed for CYP2B1/2 mRNA and NCO ($R = 0.59$, $P = 0.5$, and $R = 0.99$, $P < 0.005$ with and without the 1.0 g/kg dose, respectively).

3.5. Inhibition of nicotine metabolism by CYP2B1-selective inhibitors

At 25 μ M nicotine expressed CYP2B1 metabolized nicotine to cotinine with a velocity of 16.2 ± 8.1 nmol cotinine formed per pmol CYP2B1 per min. At 1 mg protein, control rat liver microsomes metabolized nicotine to cotinine with a velocity of 19.5 ± 8.7 nmol cotinine formed per mg protein per min. Using the same incubation conditions with 5 pmol of CYP2B1 (resulting in approximately 5 times the production of cotinine), expressed CYP2B1-mediated NCO was abolished completely by the CYP2B1/2 selective mechanism-based inactivator C8 xanthate [44] and significantly

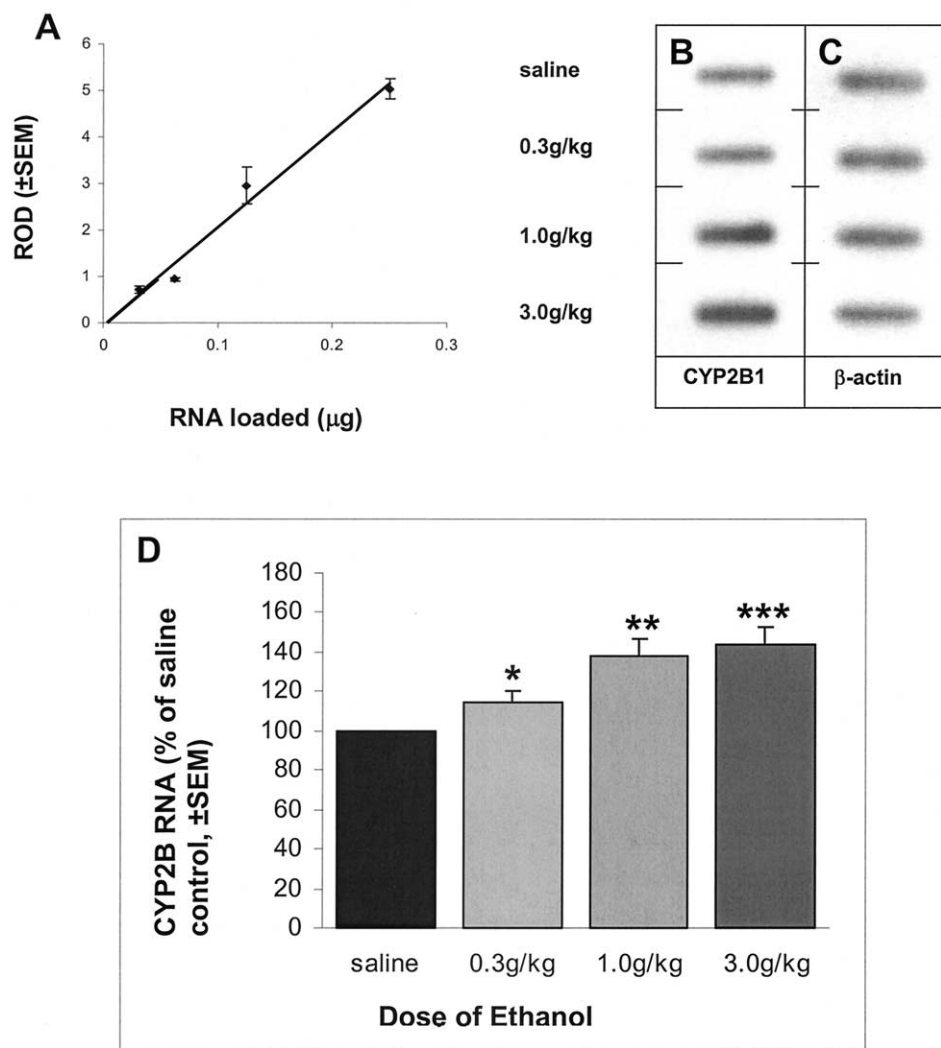


Fig. 4. Induction of CYP2B1 mRNA by ethanol in rat liver. (A) Dilution curve of phenobarbital-induced rat liver demonstrating linear detection of CYP2B RNA (means \pm SEM, of 3 experiments). (B) Representative image of CYP2B mRNA detected by slot blotting. (C) Corresponding image of B re-probed for β -actin mRNA demonstrating equal loading of total RNA. (D) Dose-response for saline and three doses of ethanol. Increases in total CYP2B1/2 mRNA are expressed as a percentage of the saline control (means \pm SEM, of 9 experiments). Significant differences from saline are indicated by: (*) $P < 0.05$, (**) $P < 0.01$, and (***) $P < 0.001$.

inhibited by 8-methoxypsoralen, a CYP2B and CYP2A-selective inhibitor [45] (Fig. 6B, $P < 0.05$). Inhibitor concentrations chosen were approximately 10 times the K_i values (K_i of 2.4 and 2.9 μM for C8 xanthate and 8-methoxypsoralen, respectively [44,45]) to ensure complete inactivation of CYP2B1 in liver microsomes. C8 xanthate significantly inhibited ($P < 0.05$) NCO by 77, 67, 67, and 75% for saline, 0.3, 1.0, and 3.0 g/kg ethanol, respectively (mean $71.4 \pm 5.1\%$), suggesting that this portion of NCO is mediated by CYP2B1 (Fig. 6A). The inhibition was more variable for 8-methoxypsoralen, with values of 58, 73, 67, and 75% (all $P < 0.05$) inhibition for saline and the three ethanol doses (mean of $68.4 \pm 6.9\%$). The relatively constant proportion of NCO inhibited by CYP2B1-selective inactivators across treatment groups suggests that chronic ethanol induces a non-CYP2B component of NCO, which is also present in saline-treated controls.

4. Discussion

In this study, behaviorally relevant doses of chronic ethanol were chosen to model light social drinking to heavy binge drinking by alcoholics [46] over a relatively short time course of 7 days. Previous studies [35] examining the effects of ethanol on cytochromes P450 employed periods of 20–30 days using the Lieber–DeCarli liquid ethanol diet [47], which provides approximately 12–13 g/kg per day of ethanol [48]. In rats, the dose of 0.3 g/kg of ethanol represents approximately 1–2 drinks per day (12–25 g of ethanol; 0.2–0.4 g/kg for a 70 kg individual) equivalent to light social drinking in humans. The dose of 1.0 g/kg represents slightly more, approximately 3–6 drinks per day (40–80 g of ethanol; 0.6–1.1 g/kg). The dose of 3.0 g/kg is approximately equivalent to 12–14 drinks per day (150–190 g;

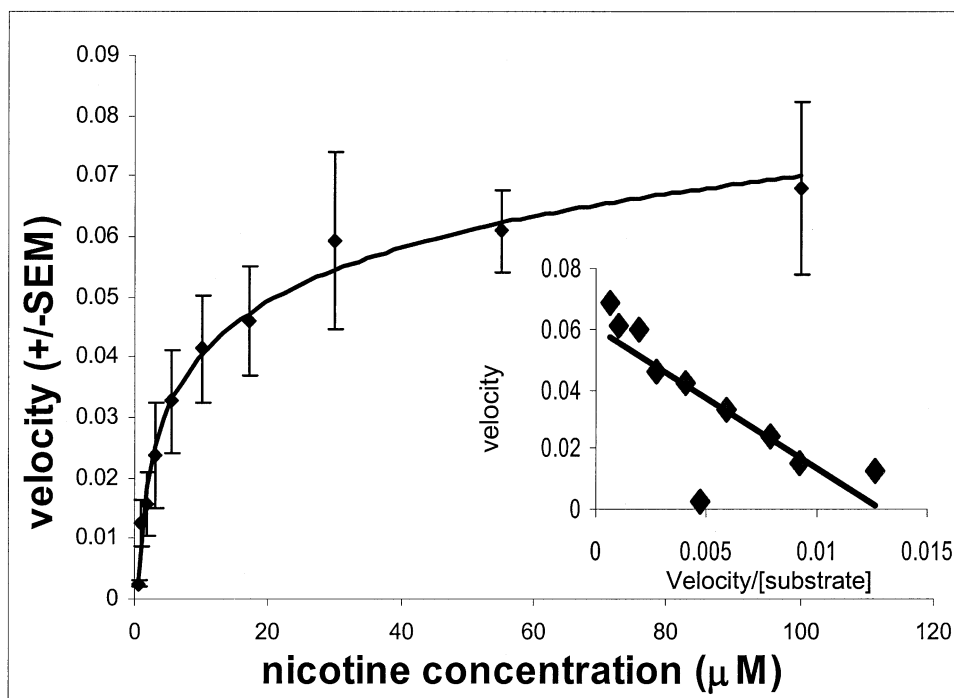


Fig. 5. Nicotine metabolism to the inactive metabolite cotinine by expressed CYP2B1. Expressed CYP2B1 metabolizes nicotine to cotinine with a K_m of 7 μM and a V_{max} of 0.074 μmol cotinine/pmol CYP2B1/min. An Eadie-Hofstee plot is shown in the inset. Velocity is expressed as μmol cotinine/pmol CYP2B1/min.

2.1–2.7 g/kg), which models the heavy drinking often seen with chronic alcoholics.

Chronic nicotine induces CYP2B1/2 in several brain regions, including olfactory bulbs, olfactory tubercles, frontal cortex, and brainstem [23]. We were therefore interested in determining if chronic ethanol also affects CYP2B1/2 in rat brain, possibly accounting for a component of the cross-tolerance observed between ethanol and nicotine [31]. This could occur by inducing changes in local nicotine metabolism at the site of central nicotinic receptors. Therefore, brain regions known to contain nicotinic receptors and/or are sites of ethanol-induced neuronal changes were selected [37,38]. No effect of chronic ethanol on the selected regions (olfactory bulbs/tubercles, frontal cortex, hippocampus, cerebellum, and brainstem) was observed at the doses and duration used in this study. The dose of 3 g/kg of ethanol was sufficient to produce observable central effects, including sedation and ataxia. Even at 0.3 g/kg, significant increases in hepatic CYP2B were observed. Therefore, it is unlikely that the lack of effect was due to insufficient dosing or hepatic first-pass effects (oral route of administration).

In another study, while chronic nicotine increased CYP2B1 in rat brain, it had no effect on rat liver CYP2B1/2 [23]. Conversely, we found a dose-dependent increase in CYP2B1/2 protein by ethanol in rat liver but not rat brain. Although peripheral or central alterations in nicotine-metabolizing CYP2B1/2 by nicotine or ethanol could contribute to nicotine tolerance and cross-tolerance between these two drugs, our data suggest that regulatory control of

CYP2B1 by these drugs differs. There is evidence that CYP2B1 can be regulated differently in different tissues. For example, acetone and phenytoin, which induce CYP2B enzymes in the liver, decrease CYP2B1 in rat nasal mucosa, and primary astrocytes, respectively [49,50]. The reasons for differential regulation of CYP2B1 by ethanol in different tissues are unknown, but it is possible that there are tissue-specific regulatory factors present in the liver but not in the brain.

Previous work on ethanol induction of hepatic CYP2B1 mRNA has been conflicting. One study demonstrated an increase in both CYP2B1 mRNA and protein [35], while another study did not detect a change in mRNA [51]. Our data, demonstrating a dose-dependent increase in CYP2B1 mRNA in response to chronic ethanol, confirm that the induction is occurring, at least in part, at the level of mRNA regulation.

This is the first report of an increase in hepatic nicotine metabolism following chronic ethanol treatment specifically related to induction of CYP2B1/2. Adir *et al.* [52] reported a decrease in plasma nicotine in rats after chronic treatment with a high dose of ethanol (8 g/kg). Although this effect was attributed to an increase in volume of distribution, this does not explain the observed increase in plasma cotinine in parallel with the decrease in plasma nicotine. Another group observed a slight decrease in nicotine metabolism in liver microsomes from ethanol-treated rats [53]. In humans, one study showed only a slight effect of ethanol on urinary nicotine clearance, and no effect on overall plasma clear-

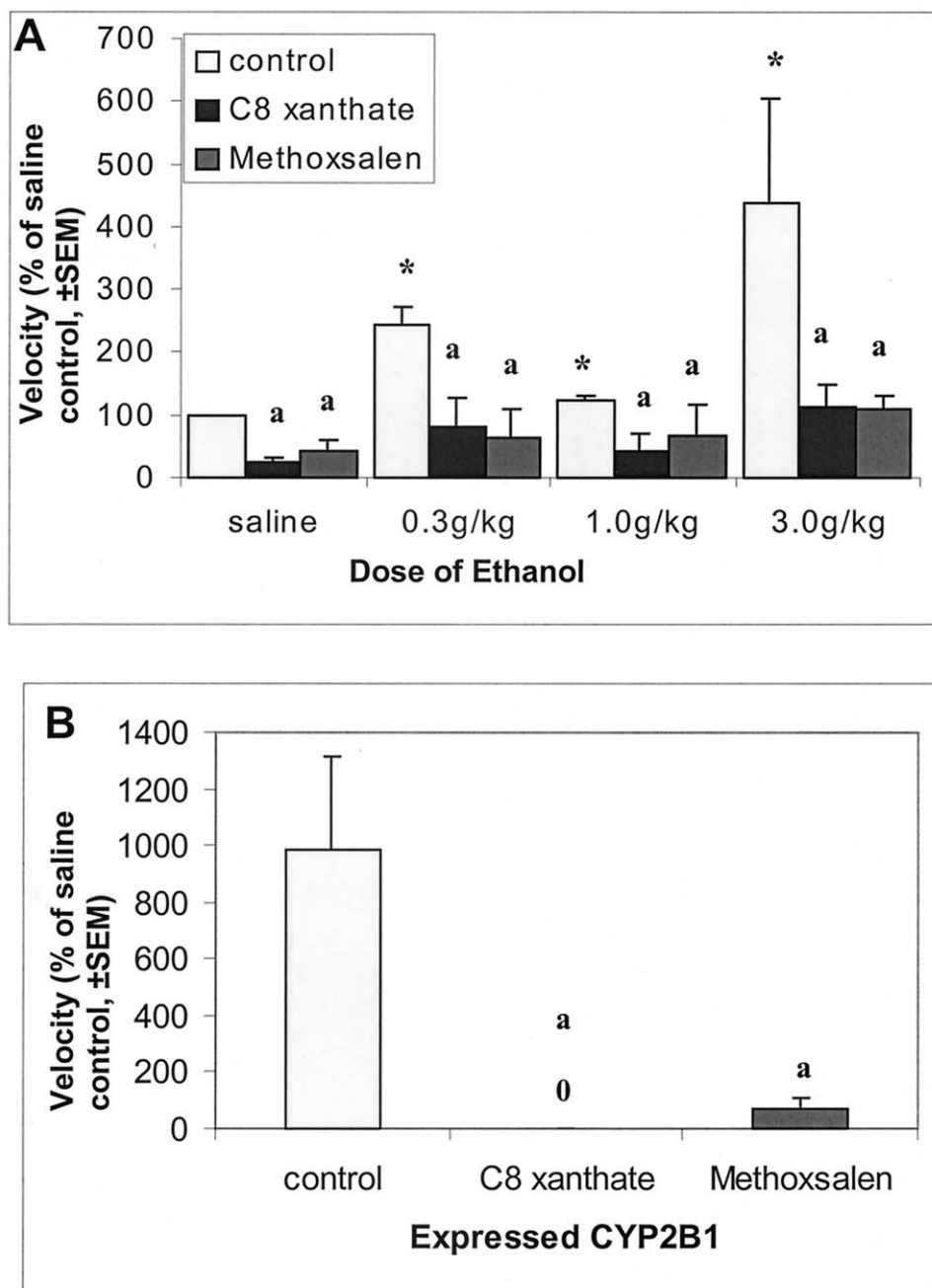


Fig. 6. Induction of NCO to cotinine by ethanol in rat liver. (A) NCO by liver microsomes from rats treated with saline and three doses of ethanol, expressed as a percentage of the saline control (\pm SEM). Values for percent inhibition by the CYP2B selective inactivator C8 xanthate were 77, 67, 67, and 75% for saline and the three doses of ethanol, respectively, and 58, 73, 67, and 75% for 8-methoxypsoralen. (B) NCO expressed CYP2B1 (5 pmol of CYP2B1), and inhibition by C8 xanthate and 8-methoxypsoralen. Key: (*) significant difference from saline, $P < 0.05$; and (a) significant inactivation by C8 xanthate and 8-methoxypsoralen (compared with control), $P < 0.05$.

ance; however, acute not chronic doses of ethanol were used [54]. Our study did show significant increases in nicotine metabolism at all three doses used. We used CYP2B-selective mechanism-based inactivators to show that approximately 70% of hepatic nicotine metabolism in rats was mediated by CYP2B1/2 in both uninduced and ethanol-induced livers. C8 xanthate is a very selective inactivator of CYP2B1 with a K_i of 2.4 μ M [44]. At higher concentra-

tions, there is some inactivation of CYP2E1 ($K_i = 60 \mu$ M), an enzyme with no detectable NCO activity [13]. In our study, C8 xanthate (24 μ M, 10 times the K_i) completely abolished NCO activity (25 μ M nicotine, approximately 3.5 times the K_m) by expressed CYP2B1, at conditions that produced 5 times more cotinine than in the liver microsomal assays. While CYP2B2 is not inactivated by some compounds that inactivate CYP2B1 [55], it is not known

whether C8 xanthate also inactivates CYP2B2. However, CYP2B2 was not detected by immunoblotting, suggesting that 70% of NCO is mediated by CYP2B1 in rat liver. 8-Methoxypsoralen is slightly less selective, inactivating enzymes in the CYP2A as well as the CYP2B family [45]. This should not affect nicotine metabolism as CYP2A enzymes do not appreciably metabolize nicotine in rats [13]; however, this decreased selectivity may account for the increased variability in inhibition seen with this compound as compared with C8 xanthate. The finding that the fraction metabolized by CYP2B1 remained relatively constant in the induced and uninduced states suggests that the other enzymes involved in NCO are also being induced proportionately by ethanol. These could be CYP2C11, CYP2D1, and/or CYP1A2, which have low levels of NCO [13].

CYP2B1/2 metabolize a number of procarcinogens including the tobacco-specific nitrosamines NMA, NNK, and NDMA [7,8]. Induction of CYP2B enzymes has been correlated with increased tumor promotion and hepatocarcinogenesis [17,18]. Ethanol by itself is a weak carcinogen, but has a synergistic effect on tobacco-related cancers [56]. In fact, alcohol consumption stimulates CYP-mediated activation of tobacco-associated and dietary carcinogens in the liver, lungs, esophagus, and intestines [57]. Therefore, this could be another important consequence of ethanol induction of CYP2B enzymes.

CYP2B enzymes metabolize a number of clinically important drugs, including diazepam [4], bupropion [4], and chemotherapeutic pro-drugs such as cyclophosphamide [6]. Induction of hepatic CYP2B1/2 by ethanol could alter plasma drug levels. Therefore, in alcoholics this could lead to reductions in efficacy of drugs metabolized to inactive compounds. Conversely, pro-drugs could be metabolized to their active metabolite more quickly, leading to toxicity. This is particularly relevant for agents like cyclophosphamide, which have a very low therapeutic index [58]. CYP2B1/2 also metabolize cocaine to a toxic metabolite [9], suggesting additive or synergistic increases in liver damage when ethanol and cocaine are used concurrently. In fact, inhibition of CYP2B enzymes protects against cocaine-mediated hepatotoxicity in rats [9].

The mechanism(s) by which CYP2B enzymes are induced by ethanol is not known. Our observation that CYP2B1 mRNA is induced, as well as protein, suggests that the regulation is, in part, at the level of mRNA. CYP2B1 induction by a wide range of compounds occurs primarily at the transcriptional level [59]. This could occur by a number of mechanisms including increased transcription or mRNA stabilization. This mechanism has been described in detail for barbiturate induction [60–62]. It is not known whether this mechanism is involved in the ethanol induction of CYP2B1/2 observed here. The relatively low level of ethanol induction (3-fold) compared with the increases (10- to 100-fold) seen with barbiturates [43] suggests that the mechanisms may be different. In addition, we observed changes in mRNA that were quantitatively lower than the

changes seen in protein. This could indicate a different mechanism such as increased translation or protein stabilization, or a combination of mechanisms at both the protein and mRNA level. The magnitudes of induction are similar to those observed for CYP2E1 in the same animals. Ethanol is thought to regulate CYP2E1 by protein stabilization [63]. In addition, the regulatory mechanism may not be a direct action of ethanol on CYP2B1/2 regulation. For example, chronic ethanol consumption alters hormonal secretion [64–66], and CYP2B expression is known to be modulated by a number of these different hormones including corticosteroids [60,67], insulin [68–71], and growth hormone [72–74]. Therefore, the specific mechanism(s) of induction of CYP2B enzymes by ethanol remains to be determined, but could include direct or indirect effects.

In summary, we showed that low, behaviorally relevant doses of chronically administered ethanol induced CYP2B1/2 protein, mRNA, and nicotine metabolism in a dose-dependent manner in the liver but not the brain of rats. Chronic ethanol could contribute to the cross-tolerance seen between ethanol and nicotine by increasing the clearance of nicotine. This may be an important factor leading to increased smoking by alcoholics. Due to procarcinogen activation by CYP2B enzymes, this could also be a contributing factor of the synergistic effect of alcohol on smoking-related cancers. In addition, differences in the metabolism of clinically important CYP2B substrates may be observed in alcoholics versus non-alcoholics.

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