Role of CYP2A5 in the Clearance of Nicotine and Cotinine: Insights from Studies on a Cyp2a5-null Mouse Model

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ABSTRACT

CYP2A5, a mouse cytochrome P450 monoxygenase that shows high similarities to human CYP2A6 and CYP2A13 in protein sequence and substrate specificity, is expressed in multiple tissues, including the liver, kidney, lung, and nasal mucosa. Heterologously expressed CYP2A5 is active in the metabolism of both endogenous substrates, such as testosterone, and xenobiotic compounds, such as nicotine and cotinine. To determine the biological and pharmacological functions of CYP2A5 in vivo, we have generated a Cyp2a5-null mouse. Homozygous Cyp2a5-null mice are viable and fertile; they show no evidence of embryonic lethality or developmental deficits; and they have normal circulating levels of testosterone and progesterone. The Cyp2a5-null mouse and wild-type mouse were then used for determination of the roles of CYP2A5 in the metabolism of nicotine and its major circulating metabolite, cotinine. The results indicated that the Cyp2a5-null mouse has lower hepatic nicotine 5′-hydroxylation activity in vitro, and slower systemic clearance of both nicotine and cotinine in vivo. For both compounds, a substantially longer plasma half-life and a greater area under the concentration-time curve were observed for the Cyp2a5-null mice, compared with wild-type mice. Further pharmacokinetics analysis confirmed that the brain levels of nicotine and cotinine are also influenced by the Cyp2a5 deletion. These findings provide direct evidence that CYP2A5 is the major nicotine and cotinine oxidase in mouse liver. The Cyp2a5-null mouse will be valuable for in vivo studies on the role of CYP2A5 in drug metabolism and chemical toxicity, and for future production of CYP2A6- and CYP2A13-humanized mouse models.

The mouse Cyp2a gene subfamily encompasses four genes (Cyp2a4, Cyp2a5, Cyp2a12, and Cyp2a22), whereas the human CYP2A gene subfamily has three genes (CYP2A6, CYP2A7, and CYP2A13) (Wang et al., 2003). Human CYP2A6 and CYP2A13 are known to be functional, and they are most similar to mouse CYP2A5, with respect to tissue distribution and substrate specificity (Su and Ding, 2004). Both CYP2A6 and CYP2A13 are expressed in the olfactory mucosa and other tissues of the respiratory tract, whereas CYP2A6 is also expressed in the liver; mouse CYP2A5 is expressed in many tissues, including tissues of the respiratory tract, liver, and kidney. CYP2A5 shares many substrates with CYP2A6 and/or CYP2A13, such as coumarin, nicotine, cotinine, testosterone, and the tobacco-specific carcinogen 4-(methylnitrosamo-no)-1-(3-pyridyl)-1-butane and other nitrosamines (Su and Ding, 2004; Wong et al., 2005; Raunio et al., 2008a).

Nicotine is the pharmacologically active (and addictive) ingredient in cigarette products. Nicotine is also used as a therapeutic agent for smoking cessation, and it is being tested as a potential preventative agent for neurodegenerative diseases, both in animal models and in clinical trials (Ravina et al., 2003; Quik et al., 2007). Nicotine can be metabolized via several pathways in humans, including 5′-hydroxylation to yield cotinine, catalyzed mainly by CYP2A6 (Nakajima et al., 1996; Messina et al., 1997); N-demethyla-tion (Murphy et al., 2005), also mediated by CYP2A6; N-
oxidation (Cashman et al., 1992; Cashman, 2000), catalyzed by flavin-containing monoxygenase; and N-glucuronidation (Kuehl and Murphy, 2003; Kaivosoari et al., 2007), catalyzed by various UDP-glucuronosyltransferases. In humans, ~75% of administered nicotine is converted to cotinine (Hukkanen et al., 2005), a γ-lactam metabolite formed via 5'-hydroxylation. Indeed, cotinine is used as a chemical marker for human exposure to cigarette smoking (de Leon et al., 2002). In addition, genetic polymorphisms in the human CYP2A6 gene have been linked to interindividual differences in the rates of nicotine clearance (Benowitz et al., 2006).

Mouse CYP2A5 is also believed to play a major role in the clearance of nicotine and cotinine, based on in vitro data and in vivo pharmacological evidence (Siu et al., 2006; Siu and Tyndale, 2007; Raunio et al., 2008b), although direct in vivo evidence, such as the disposition in a Cyp2a5-null mouse, has yet to be reported. However, a remarkable species difference exists between humans and mice in the rates of nicotine clearance, with the metabolism being much more rapid in mice than in humans. This notable species difference makes it difficult to extrapolate pharmacological and toxicological findings obtained in mouse experiments to human contexts. Furthermore, the rapid metabolism of nicotine in mice has hindered efforts to use this species for studies on the mechanisms of nicotine addiction, or for studies on the potential of nicotine as an agent for prevention of diseases such as Parkinson’s disease (Quik et al., 2007). Biochemical studies have suggested that the species difference between mouse and humans in nicotine clearance is largely due to differences in the efficiencies of human CYP2A6 and mouse CYP2A5 in nicotine 5'-hydroxylation, with CYP2A5 being much more efficient than CYP2A6 (Murphy et al., 2005). Indeed, other mouse hepatic P450 enzymes seem to be either similar to, or less efficient than, human CYP2A6, with respect to their enzymatic activities toward nicotine (Murphy et al., 2005; Siu and Tyndale, 2007). Thus, a Cyp2a5-null mouse will not only be valuable for determination of the specific roles of CYP2A5 in drug metabolism and toxicity in a mouse model, but it will also represent a more “humanized” model that is suitable for various studies concerning the pharmacology of nicotine and cotinine. A Cyp2a5-null knockout mouse model has not been described previously.

In the present study, we have generated a Cyp2a5-null mouse through homologous recombination in embryonic stem (ES) cells derived from the C57BL/6 (B6) mouse strain. Homozygous Cyp2a5-null mice were characterized for viability and fertility, growth rates, potential compensatory expression in other enzymes that can influence nicotine clearance, and circulating levels of testosterone and progesterone, endogenous compounds that are among known CYP2A5 substrates. The Cyp2a5-null mice were then compared with the WT B6 mice, for their abilities to clear nicotine and cotinine in vivo, and for the activities of their hepatic microsomes to metabolize nicotine in vitro. Pharmacokinetic analyses were then performed to determine the impact of the Cyp2a5 deletion on levels of nicotine and cotinine in the brain (the pharmacological target organ), the liver (the major site of metabolic clearance), and the blood (the medium for biomonitoring).
saline. Blood samples (20 µl each) were collected from the tail of individual mice, at various time points (5 min to 8 h) after the injection. The samples were centrifuged at 1000g, for 5 min, at 4°C, for preparation of plasma. For studies on tissue nicotine and cotinine levels, tissue samples and blood samples (from the heart) were obtained after animals were killed by CO2 asphyxiation. Pharmacokinetic parameters were calculated by use of the noncompartmental method in the WinNonlin software (Pharsight, Mountain View, CA). Statistical significance of differences between two groups was examined with Student's t test. For total body clearance, the hybrid constant CL/F was used according to Statler et al., (2007), instead of CL (clearance), given that F (bioavailability) is not known.

For plasma samples, 0.1 ng of cotinine-d3 was added as internal standard to 10 µl of plasma, which had been diluted in 1.0 ml of 0.6 M phosphate buffer, pH 6.8, as described previously (Heavner et al., 2005). The resultant mixture was extracted with an Isolute Extraction Cartridge (C18; 1 ml/100 mg) (Biotage, Charlottesville, VA). The samples were eluted with 1 ml of methanol, dried under nitrogen, and then reconstituted with 50% (v/v) methanol in water for LC/MS analysis. The recovery of added nicotine and cotinine standards in blank plasma was analyzed. The recovery of added nicotine and cotinine standards in plasma samples was 70%, at all concentrations tested. For tissue samples, brain and liver (400 mg each) were homogenized in 3 ml of saline (0.9% NaCl), followed by addition of 0.1 ng of cotinine-d3. The mixtures were centrifuged, at 3000g, for 10 min, and the supernatant was then extracted with an Isolute Extraction Cartridge (C18; 3 ml/100 mg), as described above for plasma samples. The recovery of added standards in blank tissues was >70% at all concentrations tested.

The levels of nicotine and cotinine were determined by use of a LC/MS system composed of an Agilent 1200 Series HPLC and an ABI 4000 Q-Trap mass spectrometer (Applied Biosystems, Foster City, CA), fitted with a 5-µm Gemini C18 column (50 × 2.0 mm). The samples were eluted at a flow rate of 0.2 ml/min, with solvent A (10 mM ammonium acetate in water) and solvent B (100% acetonitrile); the column was equilibrated with 100% A for 1 min, and the solvent gradient consisted of linear increases from 0% B to 100% B between 1 and 8 min, followed by a wash at 100% B for 1 min. The MS was operated in the positive ion mode, using electrospray ionization. The parent/product ion pair of m/z 163/130 (for nicotine), m/z 177/80 (for cotinine), and m/z 180/80 (for cotinine-d3) were monitored in the Multiple Reaction Monitoring scan mode. The parameters for the chamber were as follows: curtain gas, 40 psig; heated nebulizer temperature, 350°C; ion spray voltage, 4000 V; nebulizer gas, 50 psig; turbo gas, 50 psig, declustering potential, 40 V; and entrance potential, 10 V. For both compounds, the detection limit was 0.5 pg/µl or 5 pg on column.

**Identification of Hepatic Microsomal Nicotine Metabolites by LC/MS.** Assay mixtures contained 50 mM potassium phosphate buffer, pH 7.4, 10 µM nicotine, 1.0 mg/ml liver microsomal protein, with or without 1 mM KCN, and 1.0 mM NADPH, in a final volume of 0.3 ml. Reactions were carried out at 37°C for 0 or 60 min, and were terminated by the addition of 0.3 ml of acetonitrile, followed by removal of denatured proteins through centrifugation. The supernatant was analyzed by use of an LC/UVMS system consisting of a Waters 2690 separation module (Waters, Milford, MA), a Surveyor photodiode array detector (Thermo Fisher Scientific), and an LCQ Deca XP ion-trap mass spectrometer (Thermo Fisher Scientific). The chromatographic separation of metabolites was achieved on a 5-µm Gemini C18 (150 × 2.0 mm) column (Phenomenex, Torrance, CA). The mobile phase consisted of solvent A (10 mM ammonium acetate in water) and solvent B (100% acetonitrile). The samples were eluted, at a flow rate of 0.5 ml/min, with 100% A for 20 min, followed by a linear increase to 100% B between 1 and 8 min, followed by a wash at 100% B for 1 min. The MS was operated in the positive ion mode, using electrospray ionization. The parent/product ion pair of m/z 163/130 (for nicotine), m/z 177/80 (for cotinine), and m/z 180/80 (for cotinine-d3) were monitored in the Multiple Reaction Monitoring scan mode. The parameters for the chamber were as follows: curtain gas, 40 psig; heated nebulizer temperature, 350°C; ion spray voltage, 4000 V; nebulizer gas, 50 psig; turbo gas, 50 psig, declustering potential, 40 V; and entrance potential, 10 V. For both compounds, the detection limit was 0.5 pg/µl or 5 pg on column.

**Fig. 1.** Targeted disruption of the mouse Cyp2a5 gene. Structures of the WT Cyp2a5 allele and the Cyp2a4/Cyp2a12 allele (A), the targeting vector (B), and the targeted allele (C) are depicted. Both external (probe E) and internal (probe I) probes were used for Southern blot analysis. The restriction site PvuII (P) was used to distinguish between Cyp2a4/Cyp2a12 and Cyp2a5 WT alleles. D, detection of the targeted Cyp2a5 allele by Southern blot analysis of mouse tail genomic DNA. The 7.0-, 4.0-, and 2.0-kb bands (detected with probe E) represent the WT Cyp2a5 allele (+), targeted Cyp2a5 allele (−), and WT Cyp2a4/Cyp2a12 alleles, respectively. E, absence of full-length or truncated CYP2A5 mRNA in tissues of the Cyp2a5-null mice. RNA-PCR was performed as described in Materials and Methods. E2_E3 and E8_E9 represent primer sets flanking exons 2 and 3 and sets flanking exons 8 and 9, respectively. OM, olfactory mucosa.
by linear increases from 0% B to 100% B between 21 and 25 min, and then 100% B for a further 10 min. The mass spectrometer was set for a data-dependent scan mode, and was operated in a positive ion mode with an atmospheric pressure chemical ionization source. The parameters for the chamber were: m/z range, 50 to 500; capillary temperature, 350°C; nitrogen sheath gas flow rate, 30 (arbitrary units); auxiliary gas, 10 (arbitrary units); spray voltage, 4 kV; capillary voltage, 10 V; and tube lens offset, 30 V.

**In Vitro Metabolism of Testosterone and Nicotine.** Microsomal preparation was carried out essentially as described previously (Ding and Coon, 1990); the postmicrosomal supernatant fraction was used as cytosol. Metabolism of testosterone was assayed essentially as described previously (Zhou et al., 2009). Reaction mixtures contained 5.0 or 10 μM testosterone and 0.1 mg/ml liver microsomal protein, and the reaction was carried out for 10 min. Testosterone metabolites were identified by use of an LC/MS system consisting of an Agilent 1200 Series HPLC and an ABI 4000 Q-Trap mass spectrometer, essentially as described elsewhere (Zhou et al., 2009), with minor modifications, as detailed in the Supplemental Materials. For assay of nicotine C-5′-oxidation, the reaction mixture contained 1.0 or 10 μM nicotine, 0.5 mg/ml liver microsomal protein, and 1.0 mg/ml cytosolic protein. The reactions were carried out under conditions that support constant rates of product formation, according to a protocol described previously (Su et al., 2006). The reaction was stopped by the addition of 1 ml of methanol (containing 1 ng of cotinine-d₈), and the mixture was centrifuged, to precipitate protein. The supernatant was dried under nitrogen, and then reconstituted with 50% (v/v) methanol in water, for the measurement of cotinine by LC/MS analysis (as described above for the pharmacokinetics of plasma cotinine). Metabolite standard was added to reaction mixtures containing boiled microsomes, with recoveries being >85% at all concentrations tested.

**Quantitative Analysis of Serum Testosterone and Progesterone by LC/MS.** Two-month-old male and female mice, respectively, were used for testosterone and progesterone determination. For serum testosterone, samples were prepared and analyzed essentially as described previously (Zhou et al., 2009). For serum progesterone, the sample preparation method was modified from the protocol of Tai et al. (2006). The internal standard, [3,4-13C] progesterone, was added to serum samples at 1.0 ng/ml. Samples were extracted twice, each time with 10 volumes of hexane; the extracts were dried with nitrogen, and then reconstituted in 50% methanol for LC/MS analysis. To construct calibration curves, we added progesterone and stable isotope-labeled progesterone to charcoal-stripped bovine serum (Hyclone, Logan, UT). The recovery of added progesterone was >90%, at all concentrations tested. Details of LC/MS analysis for progesterone are included in the Supplemental Materials.

**Results**

**Generation and Characterization of the Cyp2a5-Null Mouse.** The structures of the WT Cyp2a5 allele, the targeting construct, and the targeted Cyp2a5-null allele are shown in Fig. 1, A to C. A Cyp2a5 bacterial artificial chromosome genomic clone, isolated from the B6 strain, was used for construction of the targeting vector. The strategy used for targeted disruption of the mouse Cyp2a5 gene by homologous recombination in ES cells was to replace the last exon (exon 9), which encodes the active-site Cys residue, with a neomycin-resistance gene. ES cells from a homologous recombinant clone (clone 221) were used for subsequent injection into the blastocyst cavity of albino B6(Cg)-Tyrc-2J/J embryos from which a chimeric male was generated. When bred with WT B6 females, the chimera exhibited germline transmission. The absence of random integration of the targeting construct was confirmed by use of both internal (probe I) and external (probe E) probes for Southern blot analysis (data not shown). Homozygous Cyp2a5-null mice (Cyp2a5−/−) were produced by cross-breeding between heterozygous littermates (Cyp2a5+/−). Homozygotes, heterozygotes, and WT littermates were identified by the presence of the characteristic bands for the WT (7-kb) and the Cyp2a5-null (4-kb) alleles, on Southern blots (Fig. 1D). As a control, the integrity of the Cyp2a4/12 genes, which are highly similar to Cyp2a5 in genomic structure, is confirmed by the detection of the unique 2-kb genomic fragment in mice of all three genotypes.

The absence of Cyp2a5 expression in various tissues of the Cyp2a5-null mice was confirmed by RNA-PCR, with use of two sets of gene-specific primers, which are complementary to sequences near either the 5′ end (E2–E3) or the 3′ end (E8–E9) of the CYP2A5 transcript. The results (Fig. 1E) indicated that neither the full-length CYP2A5 mRNA, nor a truncated CYP2A5 mRNA containing the first eight exons (which are intact), was present at detectable levels in any of the tissues examined of either male or female Cyp2a5-null mice.

Mice homozygous for the disrupted allele were indistinguishable from their WT littermates, or from WT B6 mice, in growth rate and reproductive ability. No deviation from Mendelian distribution of genotypes was observed in pups derived from F1 heterozygous breeding pairs (Supplemental Table 1), a result suggesting that CYP2A5 is not critical for embryonic development. Adult body and organ weights (liver, kidney, lung, and testis for males, and liver, kidney, and lung for females) were identical between Cyp2a5-null and WT B6 mice (Supplemental Table 2), indicating that CYP2A5 is not essential for normal growth. Homozygous breeding pairs were established to produce Cyp2a5-null mice for subsequent studies.

Given our previous finding of a neighboring effect of Cyp2g1 gene disruption on the expression of the (downstream) Cyp2a5 gene (Zhuo et al., 2004), we examined the potential effects of the disruption to Cyp2a5, on the expression of the neighboring Cyp2g1. We found that there was no significant difference between Cyp2a5-null and WT B6 mice, in CYP2G1 mRNA levels in the olfactory mucosa, a site where CYP2G1 is uniquely expressed (Supplemental Fig. 1). Thus, the genomic disruption at Cyp2a5 exon 9 did not lead to noticeable changes in the expression of the upstream Cyp2g1 gene.

The expression of various Cyp2b genes, which are located further upstream of the Cyp2g1 gene, also seemed to be unaffected by the neo insertion, as exemplified by the results from immunoblot analysis of CYP2B protein expression (Supplemental Fig. 2). It is noteworthy that immediately downstream of Cyp2a5 is a cluster of Cyp2a genes and pseudogenes, including (in order of increasing distance from Cyp2a5) Cyp2a23-ps, Cyp2a22, Cyp2a21-ps, Cyp2a12, and Cyp2a20-ps, with Cyp2a23-ps, a pseudogene, located at a distance of >100 kb from Cyp2a5 (Wang et al., 2003). The expression of Cyp2a22, a gene immediately downstream of Cyp2a23-ps, was not detected in the liver of either WT or Cyp2a5-null mice (data not shown); there has been no previous report of studies on Cyp2a22 expression or function. Thus, the first functional gene downstream of Cyp2a5 is Cyp2a12 (Su and Ding, 2004). Hepatic expression of Cyp2a12 was also not different between WT and Cyp2a5-null mice.
(data not shown), thus further confirming the absence of any neighboring effects of the neo insertion.

To examine whether the loss of Cyp2a5 expression in the liver led to compensatory increases in the expression of other biotransformation genes, we compared hepatic microsomal levels of several P450 proteins, namely, CYP2B, 2C, and 3A, as well as cytochrome P450 reductase, UGT1A, and UGT2B proteins, between Cyp2a5-null and WT mice. We found that the expression levels were similar between WT and Cyp2a5-null mice for each of these enzymes in liver microsomes (Supplemental Fig. 2). Furthermore, we examined the metabolism of testosterone, a common substrate for multiple P450 enzymes, in liver microsomal reactions (Table 1). We found that, whereas the rates of formation of 15β-OH-testosterone, a testosterone metabolite known to be produced by CYP2A5, were lower (by ~50%), the rates of formation of two major testosterone metabolites, 16α-OH-testosterone and 6β-OH-testosterone, the preferred products formed by CYP2D9 (Wong et al., 1987) and CYP3A, respectively (Yanagimoto et al., 1992), were not changed in the Cyp2a5-null mice, compared with WT mice. In other studies not shown, we also observed lower rates of formation of 15α-OH-testosterone (also a CYP2A5 product), but not 16β-, 6α-, or 11α-OH-testosterone. Consistent with the lack of a substantial difference in the overall rate of hepatic microsomal testosterone metabolism in vitro, there was no significant difference in circulating testosterone levels between WT males and Cyp2a5-null males (Supplemental Fig. 3A). Likewise, there was also no significant difference in circulating progesterone levels between WT females and Cyp2a5-null females (Supplemental Fig. 3B). These in vivo results indicate that, although CYP2A5 is active toward testosterone and progesterone (Gu et al., 1999), it does not play a major role in the systemic clearance of testosterone or progesterone in the WT mice.

Role of CYP2A5 in the Metabolic Clearance of Nicotine and Cotinine. Systemic clearance of nicotine was compared between Cyp2a5-null and WT mice, with nicotine administered at either 1 mg/kg (Fig. 2A) or 5 mg/kg (Fig. 2B). As expected, clearance of nicotine in the WT mouse was very rapid, with an elimination half-life (t1/2) value of ~13 min after an injection at a dose of 1 mg/kg i.p., and a t1/2 value of ~70 min after an injection at the higher dose, 5 mg/kg i.p. (Table 2). Nicotine clearance was significantly slower (by >70% in CL/F values) in the Cyp2a5-null mice, with concomitant 3.2-fold and 6.1-fold increases in the values for maximal concentration (Cmax) and AUC, respectively, at a dose of 1 mg/kg, and 3.4-fold and 2.7-fold increases in the values for Cmax and AUC, respectively, at a dose of 5 mg/kg. Increases in the t1/2 value were also observed: 2.8-fold and 1.4-fold, for nicotine doses of 1 mg/kg and 5 mg/kg, respectively. Consistent with the notion that CYP2A5 is the low-Km enzyme in metabolizing nicotine, the impact of Cyp2a5 deletion on nicotine clearance was more pronounced at the 1 mg/kg dose, as indicated by the greater magnitude (low-dose group versus high-dose group) of differences between null and WT mice, in both AUC (6.1-fold versus 2.7-fold, respectively) and t1/2 (2.8-fold versus 1.4-fold, respectively). A further examination of the AUC values obtained at the two nicotine doses indicated a greater difference in the WT mice (>8-fold, high-dose/low-dose) than in the Cyp2a5-null mice (<4-fold); this result is consistent with a more efficient clearance in the WT mice than in the Cyp2a5-null mice at the low dose.

The formation and clearance of cotinine, the main circulating metabolite of nicotine, were also monitored in nicotine-treated mice. The AUC and Cmax values for cotinine were much higher (>24-fold and >6-fold, respectively) than the corresponding values for nicotine in WT mice treated at either nicotine dose (Table 2). In nicotine-treated Cyp2a5-null mice, the rates of formation of cotinine seemed to be substantially lower, as indicated by lower Cmax values, and higher time at maximal concentration (Tmax) values, compared with the values for the corresponding WT groups. However, rates of cotinine clearance also seemed to be lower, as reflected by significantly higher t1/2 values.

The lower rate of cotinine clearance, as a result of the Cyp2a5 deletion, was confirmed by additional studies in which circulating levels of cotinine were determined for cotinine-treated WT and Cyp2a5-null mice (Fig. 2C). As shown in Table 3, the rate of cotinine clearance was significantly lower (by 74% in CL/F value), whereas the AUC (by 3.7-fold) and t1/2 (by 2- to 4-fold) values were higher, in the Cyp2a5-null mice than in the WT mice, at a cotinine dose of 1 mg/kg. It is noteworthy that, in cotinine-treated mice, the lower rates of cotinine clearance in the Cyp2a5-null mice were accompanied by only marginally higher (1.3-fold; P > 0.05) cotinine Cmax values, compared with values for WT mice. This result can be explained by the much slower rate of first-pass metabolism of cotinine, compared with metabolism of nicotine, in the liver.

For determination of the role of CYP2A5 in the regulation of tissue levels of nicotine and cotinine, a pharmacokinetic study was also performed for liver, the main metabolic organ, and for brain, the target organ, with nicotine administered at 1 mg/kg. As shown in Fig. 2, D and E, the concentration-time curves for tissue nicotine and cotinine levels were similar between the two organs, and also similar to the curves determined for circulating nicotine and cotinine levels, respectively. Much higher levels of nicotine, and much lower levels of cotinine, were seen in both liver and brain of the Cyp2a5-null mice than in liver and brain of the WT mice, at multiple time points after dosing. A further examination of the pharmacokinetic parameters for tissue nicotine and cotinine (Table 4) confirmed that CYP2A5 has a major impact on the bioavailability of nicotine and cotinine in the brain and the liver. In the Cyp2a5-null mice, the tissue levels of nicotine were higher in both liver (2.3-fold higher AUC, 1.2-fold higher Cmax) and brain (2.7-fold higher AUC, 2.0-fold higher Cmax), whereas tissue levels of cotinine were lower in both organs (>75%
lower $C_{\text{max}}$, and 20–30% lower AUC), compared with the levels for WT mice (Table 4).

Overall, the CYP2A5-associated pharmacokinetic changes for tissue nicotine and cotinine (Table 4) are similar to the changes seen in plasma (Table 2), and they are also comparable between brain and liver. This pattern is consistent with the notion that the impact of CYP2A5 is on systemic clearance, rather than on tissue distribution. In that context, the cotinine/nicotine abundance ratios were much higher for plasma than for liver and brain, in either WT or Cyp2a5-null mice; however, the abundance ratios were uniformly decreased in the Cyp2a5-null mice (Supplemental Table 3). It is noteworthy that tissue nicotine and cotinine levels were found to differ somewhat between brains and livers: AUC and $C_{\text{max}}$ values for both nicotine and cotinine were higher in the liver than in the brain, for either mouse strain (Table 4). This tissue difference can be explained, in part, by the fact that the liver is the portal-of-entry organ for intraperitoneally injected nicotine, and by the fact that the bulk of the cotinine was produced in the liver.
It is noteworthy that, at a nicotine dose of 1 mg/kg, the tissue/plasma abundance ratios for nicotine were higher in the WT mice than in the Cyp2a5-null mice, whereas the ratios for cotinine were similar between the WT and Cyp2a5-null mice (Supplemental Table 4). The lower tissue/plasma abundance ratios for nicotine, but not for cotinine, in the Cyp2a5-null mice can probably be explained by a saturation of nicotine metabolism in the WT mice. The in vivo role of CYP2A5 in nicotine and cotinine metabolism in the WT mice was greater at the lower substrate concentration (1 μM), a result further supporting the proposal that CYP2A5 is the low-K_m enzyme in metabolizing nicotine.

We detected two other nicotine metabolites in mouse hepatic microsomal reaction mixtures (Fig. 3). One, which was detected only when KCN was included in the reaction mixture, was identified as a cyanide adduct (m/z 188), given the characteristic neutral loss of an HCN motif (m/z 27), and the features of other fragment ions in the product ion spectrum of the metabolite (not shown). The formation of the cyanide adduct indicated the presence of an iminium ion intermediate, which we propose to be the dihydroyridinium ion that is formed via the initial CYP2A5-mediated 5′-hydroxylation of nicotine (Fig. 3). The other metabolite (m/z = 149) had a mass fragmentation pattern consistent with that of nornicotine, which is formed from nicotine N-demethylation. Note that this metabolite does not represent a contaminant, because it was not detected in zero-minute incubations. The roles of CYP2A5 in the formation of these apparently less abundant metabolites were not determined.

**Discussion**

The in vivo role of CYP2A5 in nicotine and cotinine clearance has recently been studied by others, who made use of either CYP2A5 chemical inhibitors (Raunio et al., 2008b), or mouse strains (B6 and DBA/2) that have allelic differences in the structure and function of the CYP2A5 protein (Siu and Tyndale, 2007). Pharmacokinetic parameters for plasma nicotine and cotinine were determined both in the study by Siu and Tyndale (2007) and in the present study; therefore, it is tempting to compare the results from these two studies. However, although B6 WT mice were treated with nicotine were 85% and 73% lower for hepatic microsomes from the Cyp2a5-null mice than for hepatic microsomes from WT mice at nicotine concentrations of 1 and 10 μM, respectively. It is noteworthy that the CYP2A5 contribution to micromolar nicotine metabolism in the WT mice was greater at the lower substrate concentration (1 μM), a result further supporting the proposal that CYP2A5 is the low-K_m enzyme in metabolizing nicotine.

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Fig. 3. Identification of nicotine metabolites produced in mouse liver microsomal reactions. The reaction mixtures contained 50 mM potassium phosphate buffer, pH 7.4, 10 μM nicotine, 1.0 mg/ml liver microsomal protein from 2-month-old male WT mice, and 1.0 mM NADPH with or without 10 mM KCN. Metabolite analysis was performed with a LCQ Deca-XP LC/MS instrument, as described under Materials and Methods. Three metabolites (cotinine, nornicotine, and a cyanide adduct of nicotine) were identified; their structures and fragmentation patterns and the metabolic pathways that led to their formation are shown.

and cotinine (both at 1 mg/kg) in both studies, the experiments that correspond between the two studies in terms of compound and dose did not yield fully comparable results, given that the compounds were administered subcutaneously in the earlier study, but intraperitoneally in ours. An examination of the pharmacokinetic data from the two studies indicates a difference in clearance rate, e.g., the CL/F, AUC, and Cmax values for nicotine were 5.2 ± 0.2 ml/min, 80.8 ± 3.2 ng/h/ml, and 160 ± 15 ng/ml, respectively, after subcutaneous injection (their study), and 31.9 ± 2.5 ml/min, 12.7 ± 0.5 ng/h/ml, and 43.2 ± 7.9 ng/ml, respectively, after intraperitoneal injection (our study). This difference in clearance rates can be explained by the essential role of hepatic P450 enzymes in nicotine clearance and the differing proportions of the injected dose that are subjected to hepatic first-pass metabolism. Although essentially all of the intraperitoneally injected dose of nicotine would be subjected to first-pass metabolism in the liver, before appearing in the systemic circulation, only a proportion of the subcutaneously injected dose of nicotine would be distributed to the liver in each pass.

The study design of Siu and Tyndale (2007) also differed from that of the present study, in that total (conjugated and unconjugated) nicotine and cotinine were determined there, but only unconjugated compounds were determined here. The extent of glucuronidation of nicotine or cotinine in mice is not known (Siu and Tyndale, 2007). In earlier work, UGT activities toward nicotine and cotinine had not been detected in mouse liver microsomes in vitro (Ghosheh and Hawes 2002). Therefore, it is unlikely that the use or nonuse of a deconjugation step, between these two pharmacokinetics studies, would have affected the experimental outcome to any large extent.

It is noteworthy that, despite the difference in the route of injection (subcutaneous versus intraperitoneal) between the two studies, and the large differences in pharmacokinetic parameters seen for nicotine clearance, essentially identical pharmacokinetic parameters were seen for cotinine clearance (after comparable cotinine injections at 1 mg/kg to WT B6 mice) in the two studies. This apparent independence on the injection route for cotinine clearance is consistent with a rate of hepatic cotinine metabolism that is much lower than the rate of hepatic nicotine metabolism (as was shown by Siu and Tyndale, 2007). Although the high-affinity Km values for B6 hepatic microsomal metabolism of nicotine and cotinine were similar (11.4 and 9.5 μM, respectively), the Vmax values differed by >10-fold (0.50 and 0.04 nmol/min/mg). Thus, a much smaller proportion of the dose will be removed through first-pass clearance for intraperitoneally injected cotinine than for intraperitoneally injected nicotine; conversely, given the overall differences in clearance rate (slower for cotinine than for nicotine), the majority of subcutaneously injected cotinine will eventually have a chance to pass through the liver and be metabolized by hepatic CYP2A5.

The lower rate of nicotine clearance in the Cyp2a5-null mice was accompanied by a lower level of cotinine formation, compared with the values for WT mice. It is noteworthy that the impact of the Cyp2a5 deletion on nicotine AUC values (2.7-fold to 6.1-fold increases, null versus WT) and the impact of the Cyp2a5 deletion on cotinine Cmax values (56–67% reductions), an impact that mainly reflects the lower rate of nicotine metabolism, were more robust than the impact on cotinine AUC values (18–35% reductions). The latter can be influenced by both rates of cotinine formation and rates of cotinine metabolism in nicotine-treated mice. These findings relating to the effects of the Cyp2a5 gene deletion on pharmacokinetics of circulating nicotine and cotinine may aid in the interpretation of smoke-exposure-biomonitoring results for individuals with genetic polymorphisms in the orthol-
gous CYP2A6 gene. In that regard, the dependence of serum cotinine levels on rates of both formation and elimination has been found previously in human smokers (Pérez-Stable et al., 1998).

Human CYP2A6 is less efficient than CYP2A5 in the metabolism of nicotine; heterologously expressed CYP2A6 was found to have a \( K_m \) value of 144 \( \mu M \) and a \( V_{max}/K_m \) value of 0.01 in nicotine C-5'-oxidation, whereas heterologously expressed CYP2A5 had a \( K_m \) value of 7.7 \( \mu M \) and a \( V_{max}/K_m \) value of 0.20 (Murphy et al., 2005). In liver microsomes from WT B6 mice, a high-affinity component (\( K_m \), 11.4 \( \mu M \)) and a low-affinity component (\( K_m \), 306 \( \mu M \)) were identified, with CYP2A5 being apparently responsible for the high-affinity site (Siu and Tyndale, 2007). Thus, in terms of the pharmacokinetics of nicotine clearance, the Cyp2a5-null mouse more closely resembles humans than the WT B6 mouse does. The residual activities toward nicotine in the Cyp2a5-null mice are likely contributed by other P450 enzymes that have either low affinity or low efficiency for this reaction, in particular, members of the mouse Cyp2b subfamily (Siu and Tyndale, 2007). In this context, human CYP2B6 and rat CYP2B1/2 have been found to be active in nicotine 5'-oxidation (Nakayama et al., 1993; Yamazaki et al., 1999; Schoedel et al., 2001). Efforts are underway to prepare a CYP2A6-humanized mouse model to enable direct study of CYP2A6-mediated nicotine metabolism in vivo.

It is important that we understand the impact of systemic metabolism on tissue levels of nicotine and cotinine in the brain, the pharmacological target organ for nicotine. Although cotinine does not have the same drug action as nicotine does, it does have the potential to modulate nicotine action through its binding to epibatidine-sensitive nicotinic receptors (Vainio and Tuominen, 2001). Our observation of much higher (assuming that 1 g of tissue is equivalent to 1 ml of plasma) levels of nicotine in brain tissue than in plasma most likely reflects the higher tissue binding of nicotine in brain, compared with plasma. In contrast, cotinine levels in the brain were actually slightly lower than levels in the plasma, of nicotine-treated mice. This finding may be explained by the slow rate of cotinine metabolism (relative to the rate of nicotine metabolism) in the liver; it may also reflect rate limitations for penetration of the blood-brain barrier by cotinine (Riahi et al., 1998). Our findings concerning the effects of the Cyp2a5 gene deletion on nicotine and cotinine levels, and on the cotinine/nicotine abundance ratios, in the brains and plasma of nicotine-treated mice should be taken into account when predictions are made on the basis of the measurable plasma levels, for levels of nicotine and cotinine in the brain in nicotine-exposed individuals.

The neuroprotective effects of nicotine against chemically induced neurotoxicity have been consistently demonstrated in experimental rat and monkey models, but conflicting results have been found in mice (Quik et al., 2007). Nicotine clearance is much faster in mice than in humans, monkeys, and rats; it is conceivable that we are not able to maintain adequate levels of nicotine in the mouse brain for a sufficiently long period to enable effective neuroprotection, in particular, for chronic effects involving nicotine-induced alterations in gene expression. Our finding that plasma nicotine \( t_{1/2} \) values, as well as brain nicotine levels, are significantly higher in nicotine-treated Cyp2a5-null mice than in the similarly dosed WT mice suggests that the Cyp2a5-null mouse model is valuable for efforts to establish whether effective neuroprotection by nicotine can be achieved in mouse models through suppression of systemic clearance.

In summary, several features of our Cyp2a5-null mouse make it a suitable model for applications in drug metabolism and toxicology research. These features include the B6 genetic background; the specific deletion of the single mouse Cyp2a5 gene (sparing Cyp2a4 and Cyp2a12); the absence of a negative effect of the Cyp2a5 disruption on the expression of neighboring Cyp2a12, Cyp2g1, and Cyp2b genes; the absence of compensatory changes in the expression of other biotransformation enzymes examined; and the lack of any concomitant reproductive or developmental defects. In a first application of the Cyp2a5-null model to in vivo drug metabolism studies, we have examined the role of CYP2A5 in systemic clearance of nicotine and cotinine. Our findings provided direct evidence that CYP2A5 plays an essential role in the in vivo metabolism of both nicotine and cotinine. Our pharmacokinetic analysis of plasma and tissue nicotine and cotinine levels in the Cyp2a5-null mice should have important implications for an understanding of the impact of genetic polymorphisms in the CYP2A6 gene on pharmacokinetics of nicotine and cotinine in human brain and plasma. In addition, future studies on the efficacy of nicotine as a neuroprotective agent in the Cyp2a5-null mouse model are warranted.

Acknowledgments

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References


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Supplemental Materials

Additional Materials and Methods

**Determination of CYP2G1 and CYP2A12 mRNA levels.** Real-time RNA-PCR analysis was performed for olfactory mucosal CYP2G1 and hepatic CYP2A12, according to the general protocol described previously (Zhang et al., 2005), with use of an ABI 7500 Fast Real-Time PCR System and SYBR Green core reagents (Applied Biosystems, Foster City, CA). The primers used for real-time PCR for CYP2G1 and GAPDH were described previously (Gu et al., 1999). The primers for CYP2A12 quantification were 5’-ttgatcaagatgttgcaggg-3’ and 5’-ttgcatgtggatgagaaagg-3’ (according to Mouse Genome Informatics, the Jackson Lab, Bar Harbor, ME); the PCR was performed at an annealing temperature of 62°C. Based on sequence alignments, the primers for CYP2A12 can amplify both CYP2A12 and CYP2A22 cDNAs; however, sequence analysis of PCR products obtained from the liver indicated that CYP2A22 mRNA was absent (data not shown). PCR products were validated by sequence analysis, and PCR specificity was confirmed by analysis of reaction products on agarose gels. One of the samples was serially diluted for construction of a standard curve. The results were corrected on the basis of the levels of GAPDH mRNA present in the same RNA preparation.

**Immunoblot analysis.** The levels of P450 and UGTs were determined by immunoblot, using the following antibodies: goat anti-rat CYP2B1, goat anti-rat CYP3A2, rabbit anti-rat CPR, and rabbit anti-human CYP2C9/2C10 (BD Gentest, Woburn, MA); rabbit anti-human UGT1A1 and rabbit anti-human UGT2B4 (Santa Cruz, Santa Cruz, CA). Immunoblot analysis was carried out essentially as described previously (Ding and Coon, 1990). The intensity of the detected bands was quantified with a densitometer, as described previously (Zhuo et al., 2004).
Identification and quantitative analysis of testosterone metabolites. A 4-µm Nova-Pak C18 column (3.9 x 150 mm, Waters, Milford, MA) was used. The column was equilibrated with 85%A:15%B, and the samples were eluted using one of two solvent gradient systems, at a flow rate of 1 ml/min. In system one, the solvent gradient consisted linear increases from 15%B to 30%B between 3 and 25 min, and then from 30%B to 40%B between 25 and 26 min, followed by a 4-min wash with 100%B; the parent/product ion pairs of $m/z$ 305/97 (for 16α-OH-T) and 305/269 (for 6β-OH-T) were measured in the Multiple Reaction Monitoring (MRM) scan mode. In system two, the solvent gradient consisted linear increases from 15%B to 30%B between 2 and 60 min, and then from 30%B to 100%B between 60 and 61 min, followed by a 3-min wash with 100%B; the parent/product ion pairs of $m/z$ 305/97 (for 15β-OH-T) was measured in the MRM scan mode.

Quantitative analysis of testosterone and progesterone. A LC/MS system consisting of an Agilent 1200 Series HPLC and an ABI 4000 Q-Trap mass spectrometer (Applied Biosystem), with a 4-µm Nova-Pak C18 column (3.9 x 150 mm, Waters, Milford, MA), was used. The mobile phase consisted of solvent A (0.1% formic acid in water/acetonitrile (95:5)) and solvent B (0.1% formic acid in water/acetonitrile (5:95)). The column was equilibrated with 60%A:40%B; the samples were eluted, at a flow rate of 0.5 ml/min, with 40% B for 2 min; followed by linear increases from 40%B to 100%B, between 2 and 8 min, and then by 100%B for 4 min. The retention time for progesterone (and the internal standard) was 11.2 min. The MS was operated in the positive ion mode, using atmospheric pressure chemical ionization. The parent/product ion pairs of $m/z$ 315/97 and 315/109 (for progesterone), and $m/z$ 317/99 and 317/111 (for 3,4-13C-progesterone), were measured in the MRM scan mode. The parameters for
Role of CYP2A5 in the Clearance of Nicotine and Cotinine: Insights from Studies on a Cyp2a5-null Mouse Model

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the chamber were: curtain gas, 30 psig; needle current, 5 μA; heated nebulizer temperature, 350°C; nebulizing gas, 50 psig; declustering potential, 80 V; and entrance potential, 5.0 V.
Supplemental References


### Supplemental Table S1

**Genotype distribution in pups derived from intercrosses between Cyp2a5<sup>+</sup><sup>-</sup> mice**

<table>
<thead>
<tr>
<th></th>
<th>Number of pups in each genotype</th>
</tr>
</thead>
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<tr>
<td></td>
<td>Homozygous</td>
</tr>
<tr>
<td>Male</td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>11</td>
</tr>
<tr>
<td>Female</td>
<td>10</td>
</tr>
<tr>
<td>Combined</td>
<td>21</td>
</tr>
<tr>
<td>Expected&lt;sup&gt;a&lt;/sup&gt;</td>
<td>24</td>
</tr>
</tbody>
</table>

<sup>a</sup>The number of pups expected in each genotype was calculated by assuming Mendelian distribution for the WT littermates. No significant difference was found (P = 0.865, chi-square test)
Supplemental Table S2

Body and tissue weights of WT and Cyp2a5-null mice

The body weight and organ weights of male and female mice were determined at 2 months of age. Values reported are means ± S.D. (n = 8). There was no significant difference between WT and Cyp2a5-null (Null) mice (P > 0.05).

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Body weight (g)</th>
<th>Tissue weight (g)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Male</td>
<td>Female</td>
</tr>
<tr>
<td></td>
<td>Body weight</td>
<td>Liver</td>
</tr>
<tr>
<td>WT</td>
<td>24.6 ± 0.7</td>
<td>1.42 ± 0.08</td>
</tr>
<tr>
<td>Null</td>
<td>23.8 ± 0.9</td>
<td>1.36 ± 0.09</td>
</tr>
</tbody>
</table>
Supplemental Table S3

Cotinine/nicotine abundance ratios for plasma, liver, and brain of WT and \textit{Cyp2a5}-null mice

The values were calculated from data in Tables 2 and 4, for mice treated at a nicotine dose of 1 mg/kg.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Cotinine/nicotine abundance ratios</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Plasma</td>
</tr>
<tr>
<td></td>
<td>AUC</td>
</tr>
<tr>
<td>WT</td>
<td>31</td>
</tr>
<tr>
<td>(Cyp2a5)-null</td>
<td>3.3</td>
</tr>
</tbody>
</table>
Supplemental Table S4

Tissue/plasma abundance ratios for nicotine and cotinine in WT and Cyp2a5-null mice

The values were calculated from data in Tables 2 and 4, for mice treated at a nicotine dose of 1 mg/kg.

<table>
<thead>
<tr>
<th>Analyte</th>
<th>Strain</th>
<th>Brain/plasma abundance ratios</th>
<th>Liver/plasma abundance ratios</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>AUC</td>
<td>C&lt;sub&gt;max&lt;/sub&gt;</td>
</tr>
<tr>
<td>Nicotine</td>
<td>WT</td>
<td>7.8</td>
<td>5.4</td>
</tr>
<tr>
<td></td>
<td>Cyp2a5-null</td>
<td>3.4</td>
<td>3.4</td>
</tr>
<tr>
<td>Cotinine</td>
<td>WT</td>
<td>0.6</td>
<td>0.8</td>
</tr>
<tr>
<td></td>
<td>Cyp2a5-null</td>
<td>0.6</td>
<td>0.6</td>
</tr>
</tbody>
</table>
Supplemental Figure Legends

Figure S1. Quantitative analysis of CYP2G1 mRNA level in the olfactory mucosa of WT and Cyp2a5-null mice. Total RNA from the olfactory mucosa (OM) of 2-month-old mice was used for real-time RNA-PCR analysis. The values shown represent means ± S.D. (n = 4). There was no significant difference between WT and Cyp2a5-null mice in CYP2G1 expression (P >0.3, for either male or female mice).

Figure S2. Absence of compensatory increases in the expression of selected P450 and UGT enzymes in the livers of the Cyp2a5-null mice. Liver microsomes (5 µg) were analyzed in duplicate on immunoblots. The antibodies used are described above in Additional Materials and Methods. Microsomes were prepared from pooled livers from three male mice (2-month-old). Densitometric analysis indicated that, in each panel, the maximal difference in band intensity between samples from different animal groups was less than 20%.

Figure S3. Serum and testosterone and progesterone levels in WT and Cyp2a5-null mice. (A). Serum testosterone levels in male mice. (B). Serum progesterone levels in female mice. Testosterone and progesterone levels were determined for 2-month-old male and female mice (n=8), respectively. The values shown are the medians, together with the 25% (lower bar) and 75% (upper bar) percentile marks. No significant difference was found, for testosterone or progesterone levels, between WT and Cyp2a5-null groups (Mann-Whitney Rank Sum Test).
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